

Biodiversity assessment of the
PNG LNG Upstream Project Area,
Southern Highlands and Hela Provinces,
Papua New Guinea



Edited by Stephen Richards

ISBN: 978-0-646-98050-8 (PDF version)

Suggested citation: Richards, S.J. (Editor) 2017. Biodiversity Assessment of the PNG LNG Upstream Project Area, Southern Highlands and Hela Provinces, Papua New Guinea. ExxonMobil PNG Limited. Port Moresby.

© 2017 ExxonMobil PNG

Cover image: Formerly considered a bird-of-paradise, the Crested Satinbird (*Cnemophilus macgregorii*) is now known to belong to a small family of birds that occurs only in New Guinea's central cordillera. Not previously reported from the PNG LNG Project Area, an isolated population of this restricted range species was found in the higher elevation forests at the western end of Hides Ridge. This bird was banded and released as part of the bird survey.



PNG LNG is operated by a subsidiary of ExxonMobil in co-venture with:



**Biodiversity Assessment of the PNG LNG Upstream Project Area,
Southern Highlands and Hela Provinces,
Papua New Guinea**

Stephen Richards (Editor)

TABLE OF CONTENTS

Participants.....	i
Acknowledgements.....	i
Acronyms and Abbreviations.....	ii
Glossary of Technical Terms.....	iii
Report Summary.....	v
Background and aims.....	vi
Major results.....	viii
References.....	xii
Appendices.....	xx
Ripot Sameri.....	xxii
Bekgraun na as bilong sevei.....	xxii
Ol bikpela risal.....	xxiv
Chapter 1 – Vegetation. <i>Fanie Venter and Amos Ona</i>	1
Summary.....	2
Introduction.....	2
Methods.....	3
Results and Discussion.....	9
Conclusions.....	14
References.....	14
Appendices.....	18
Chapter 2 – Frogs. <i>Stephen Richards and Kyle Armstrong</i>	53
Summary.....	54
Introduction.....	55
Methods.....	55
Results and Discussion.....	60
Conclusions.....	77
References.....	78
Appendices.....	81
Chapter 3 – Birds. <i>Iain Woxvold and Leo Legra</i>	91
Summary.....	92
Introduction.....	93
Methods.....	93
Results and Discussion.....	96
Conclusions.....	106
References.....	106
Appendices.....	111
Chapter 4 – Camera trap monitoring of terrestrial birds and mammals: A pilot study. <i>Iain Woxvold and Ken Aplin</i>	121
Summary.....	122
Introduction.....	123
Methods.....	124
Results and Discussion.....	125
Conclusions.....	132
References.....	132

Chapter 5 – Non-volant mammals (Rodents and Marsupials). <i>Ken Aplin and Muse Opiang</i>	141
Summary.....	142
Introduction.....	144
Methods	145
Results and Discussion.....	151
Conclusions.....	168
References	169
Appendices	171
Chapter 6 – Bats. <i>Kyle Armstrong</i>	209
Summary.....	210
Introduction.....	211
Methods	213
Results.....	217
Discussion.....	231
Conclusions.....	234
References	235
Appendices	239
Chapter 7 – Enhancing biological monitoring with genetic information. <i>Kyle Armstrong and Ken Aplin</i>	255
Summary.....	256
Introduction.....	257
Genetic methods used for PMA3 Phase 1	260
Selected results from the genetic analysis	264
A vision for the future of genetic analysis in PMA3	266
Conclusions	268
References	268

PARTICIPANTS

Ken P. Aplin (Mammals)

Division of Mammals
National Museum of Natural History
Smithsonian Institution
P.O. Box 37012, MRC 108
Washington, D.C. 20013-7012
USA
Email: aplin.ken@gmail.com

Kyle N. Armstrong (Bats)

Australian Centre for Evolutionary
Biology and Biodiversity
The University of Adelaide
South Australia; and
Specialised Zoological
Email: kyle.n.armstrong@gmail.com

Leo Legra (Birds)

Coffey-PNG
Level 1, Wokples Building,
Section 531, Lot 12, Stratos Avenue
Hohola, National Capital District
Papua New Guinea
Email: llegra09@gmail.com

Amos Ona (Vegetation)

Coffey-PNG
Level 1, Wokples Building,
Section 531, Lot 12, Stratos Avenue
Hohola, National Capital District
Papua New Guinea
Email: amos.ona@gmail.com

Muse Opiang (Mammals)

PNG Institute of Biological Research
P.O. Box 1550, Goroka,
Eastern Highlands Province,
Papua New Guinea
Email: mopiang@pngibr.org

Stephen Richards (Team leader, Frogs)

Research Associate, Department of Herpetology
South Australian Museum
North Terrace, Adelaide, SA 5000
Australia
Email: richards.steve0@gmail.com

Fanie Venter (Plants)

Research Associate
Australian Tropical Herbarium
James Cook University Cairns Campus
Smithfield, QLD 4878
Australia
Email: fanie.venter@viewnaturalhistory.com

Iain Woxvold (Birds)

Museum Victoria Sciences Department
GPO Box 666, Melbourne,
VIC 3001 Australia
Email: iainwoxvold@gmail.com

ACKNOWLEDGEMENTS

Successful completion of the Phase 1 PMA3 Biodiversity Monitoring Survey relied on the considerable efforts of an excellent support team from ExxonMobil. We are extremely grateful to Jane Mogina, Anita Mosby and Rebekah Ilave for their organisational skills and ongoing support during the survey and to our drivers Dopo Uriye, Richard Tiki and Henry Helo who transported the team to and from site at all hours of the day and night carrying passengers ranging from muddy biologists to angry rodents. We are also grateful to the PGA support crew Simon Gawa, Simon Maka and Luem Narawec at HGCP and Heni Ekari and Samu (Village Liaison Officer) at Moro. Hides Security Services at HGCP and James March at Moro provided security arrangements that ensured the team's safety at all times. Many other people behind the scenes contributed to the success of the project including Ken Rhyason, PIC at HGCP, Mark Monica, PIC at Moro, Tom Tomala, Simon Mawa and Pipi Mea from logistics and Kenny Stevens the Hides Security Contact. We also thank Mathilda Haguai and Luana Koniel, and Simah Epi and Margaret Pehara who provided wonderful admin support at HGCP and Moro respectively and Kelli McCreery who contributed to external review of the report. The Papua New Guinea Conservation and Environment Protection Authority provided the approvals and permits required for this study and we are particularly grateful to Barnabas Wilmott of CEPA for his assistance in this regard.

ACRONYMS AND ABBREVIATIONS

asl	Above sea level
BAA	Biodiversity Assessment Area
CEPA	Conservation and Environment Protection Authority
CITES	Convention on International Trade in Endangered Species of Wild Fauna and Flora
DBH	Diameter at breast height
DD	Data Deficient (IUCN threat category)
EIS	Environmental Impact Statement
EN	Endangered (IUCN threat category)
FIMS	PNG Forest Inventory Mapping System
GLMM	Generalised Linear Mixed Model – a statistical test
GPS	Global Positioning System
IFC	International Finance Corporation
IUCN	International Union for the Conservation of Nature
km	Kilometers
LAE	Acronym for the Papua New Guinea National Herbarium
LC	Least Concern (IUCN threat category)
LNG	Liquefied Natural Gas
m	meters
mm	millimeters
NT	Near Threatened (IUCN threat category)
pers. obs.	Abbrev. 'personal observation'
PFT	Plant Functional Type
PNG	Papua New Guinea
Project	PNG LNG Project
RAI	Relative abundance index
ROW	The pipeline right of way including associated access roads
sp.	Abbrev. 'species' (singular)
spp.	Abbrev. 'species' (plural)
WMA	Wildlife Management Area

GLOSSARY OF TECHNICAL TERMS

Central cordillera	Refers to the central mountainous spine of New Guinea that runs from the eastern edge of the Vogelkop Peninsula in Indonesian New Guinea to the eastern tip of mainland PNG.
Community structure	The taxonomic composition of a community; species assemblage.
Conservation listed species	Includes: (1) species listed under the IUCN Red List as threatened (Critically Endangered, Endangered or Vulnerable), Near Threatened or Data Deficient; (2) species listed as Protected under the PNG <i>Fauna (Protection and Control) Act 1966</i> ; (3) species listed under CITES Appendix I or II.
Diversity	In its broadest sense the concept of biological diversity can refer to multiple organizational levels including (but not limited to) genes, variants and subspecies, species, and ecosystems. In this report the term 'diversity' is restricted to the meaning 'numbers of species' (the most common definition) except where other forms of diversity are also being discussed, when the specific term 'Species Richness' is used.
Endemic	Belonging exclusively or confined to a particular place.
New species	A species new to science, discovered for the first time during the 2015 PMA3 survey.
Protected	Species listed as Protected under the Papua New Guinea <i>Fauna (Protection and Control) Act 1966</i> .
Restricted range	Species which have a total historical breeding range of less than 50,000 km ² .
Taxa	Plural of taxon; a systematic division (e.g. more than one species, genera, etc.).
Taxonomic	Taxonomy is the science of identifying, naming and classifying living organisms.
Undescribed species	A species that has not yet been formally named. It may be a new species or it may be known previously from other locations.

A photograph of a dense, moss-covered forest interior. The scene is dominated by thick, vertical tree trunks and horizontal branches, all heavily encrusted with a thick layer of brownish-green moss. The moss appears to be dripping with moisture, creating a glistening effect. The background is filled with more trees, their trunks also covered in moss, creating a sense of depth and a thick, humid atmosphere. The lighting is soft and diffused, highlighting the textures of the moss and the surrounding vegetation.

REPORT SUMMARY

Dripping mossy interior of lower montane forest near the top of Hides Ridge

BACKGROUND AND AIMS

The island of New Guinea has an exceptionally high biodiversity, and a large proportion of its fauna and flora is found nowhere else on Earth. Charismatic species such as birds-of-paradise, echidnas and tree kangaroos are widely known and often have great cultural significance for local communities in Papua New Guinea (PNG). Less well known is that the flora and smaller fauna of PNG are not only incredibly diverse but remain poorly documented, and numerous plants and animals that are new to science are being discovered every year.

Studies conducted prior to Project development documented substantial biodiversity values in the Upstream Project Area of the Papua New Guinea Liquefied Natural Gas (PNG LNG) Project. These were summarised in ExxonMobil PNG Limited's (EMPNG) Biodiversity Strategy as (i) extensive intact forest, (ii) high floristic diversity, (iii) high faunal diversity, (iv) endemic species, (v) unique assemblages of species, (vi) species of conservation concern, and (vii) biodiversity of importance to local communities for resource use and cultural and spiritual purposes.

As part of its commitment to safeguarding these biodiversity values in the Upstream Project Area EMPNG's Biodiversity Strategy outlines how biodiversity has been, and will continue to be, assessed and managed. To evaluate the success of this long-term strategy, EMPNG has developed a series of four Programmed Monitoring Activities (PMAs). These PMAs will provide data to compare against a series of Key Performance Indicators (KPIs) that align directly with the major objectives of EMPNG's Biodiversity Strategy.

Trends in species diversity are an important KPI, and documenting any changes in diversity will contribute to ongoing evaluation of whether the Project is successfully meeting the four major objectives of the Biodiversity Strategy: *Maintain the intactness of the Upstream area as a whole; Conserve the priority ecosystems; Protect focal habitats; and Identify, measure and offset significant residual impacts* (EMPNG PNG LNG Biodiversity Strategy; available online).

To provide high-quality information on trends in species diversity in the Upstream area of the PNG LNG Project, the Programmed Monitoring Activity PMA3 was developed. The specific objectives of PMA3 are to conduct biodiversity surveys in order to collect quantitative, repeatable data on the diversity of species in Biodiversity Assessment Areas (BAAs) established in and around the areas affected by the PNG LNG Project, and in protected areas established or enhanced as part of EMPNG's biodiversity offset program. Diversity is expressed as the number of species, the composition of species assemblages, and the abundance of target species, as compared with a defined baseline.

The first PMA3 biodiversity surveys were conducted during 2015 in two BAAs, one established at Hides Ridge (BAA 1) and the other on the Agogo Range near Moro (BAA 2). This report presents the results of these surveys; it provides baseline data on biodiversity in the two BAAs against which future monitoring surveys can be compared, assesses the current biodiversity values of the survey areas and the potential impacts of linear infrastructure corridors on these values, and supports EMPNG's goal to safeguard biodiversity values in the Upstream Project Area.

Survey dates

10th June–8th July 2015

Brief description of the survey area

Detailed descriptions of environments in the Upstream Project Area are presented in the Project EIS, and the region's biodiversity values are summarised further in the EMPNG Biodiversity Strategy. Extensive forest cover remains throughout the Upstream Project Area and there are marked variations in vegetation composition and structure in accordance with elevational gradients and substrate type (Figures 9–13). Long-term rainfall data are not available for either BAA but the Upstream Project Area lies within the high-rainfall belt that extends across the southern slopes of PNG's central cordillera and annual rainfall totals in excess of 4,000 mm with limited seasonality are typical. The rainfall regime in this area is classified as 'Continuously heavy' (McAlpine et al. 1983).

The locations of both BAAs are shown in Figure 1 and brief descriptions of the environments encountered in each BAA are presented below.

BAA 1: 10–25 June 2015.

BAA 1 was established on Hides Ridge in Hela Province. It covers elevations between 2,100 and 2,750 m above sea level (asl), and was divided into two elevational bands, with three survey transects located at 2,100–2,400 m asl in the area between Wellpad C and Wellpad D, and three transects at 2,660–2,780 m asl located between Wellpads E and G (Figures 2–4).

The entire length of Hides Ridge, spanning both elevational bands, is covered with lower montane rainforest dominated by *Trisyngyne* (formerly *Nothofagus*). It includes the FIMS vegetation types LN/LsN 'small crowned and very small crowned lower montane forest with *Nothofagus*' (Figures 9–10). At these elevations the forests are cool, moist and mossy, and epiphytes, particularly ferns, orchids and rhododendrons are abundant.

BAA 2: 27 June–8 July 2015.

BAA 2 is located on the Agogo Range near Moro in Southern Highlands Province (Figure 1). Two survey transects were established at elevations of 1,000–1,080 m asl in the area west of Arakubi Quarry and east of the pipeline right of way (ROW), and three survey transects at elevations of 1,340–1,410 m asl in the vicinity of KP107 (Figures 5–7).

The forests in BAA 2 tend to have a wider variety of dominant tree species, and epiphytes are rare or absent. At KP107 the forest is FIMS vegetation type LsN 'very small crowned lower montane forest with *Nothofagus*'. The forest is more varied in composition than in BAA 1 and includes mixed *Trisyngyne* forest and *Papuacedrus papuana-Elaeocarpus-Cryptocarya* forest (Figure 11). Two FIMS vegetation types are present at Arakubi Quarry. The first is HsN/Hm 'Small crowned hill forest with *Nothofagus*/Medium crowned hill forest' which is restricted to an area of secondary forest below 1,000 m asl on the eastern side of Arakubi (Figure 12). Further to the west, adjacent to the ROW, the forest cover is primary and mapped as FIMS vegetation type LsN/L 'Very small crowned lower montane forest with *Nothofagus*/Small crowned lower montane forest' (Figure 13). In this area lower montane forest dominated by *Trisyngyne* is generally restricted to the ridges and upper slopes.

Survey approach

Surveys for frogs, non-volant mammals (rodents, small marsupials), bats, and mist-netting activities for birds were conducted on six permanent transects established in BAA 1 along the Hides Ridge access road and Pipeline ROW (Figure 2), and on the five permanent transects in BAA 2 established along the pipeline ROW at KP107 (Figures 6, 8) and adjacent to the Arakubi Quarry (Figure 5). Each of these 11 transects extended for 220–250 m into the forest and were perpendicular to the ROW or forest edge. Coordinates for all transects are presented in Appendix 1. In addition, plant plot and camera trapping surveys were undertaken in the same elevational bands in each of BAA 1 and BAA 2 but the activities were carried out at some distance from the transects. In the case of plant plots this was to limit disturbance to transect habitats. For camera trapping, the arrays were positioned away from transects to avoid regular disturbance of camera trapped areas. Locations of plant plots and camera trap arrays are illustrated in Figures 3–4 (BAA 1) and 5–7 (BAA 2) and their locations are provided in Chapters 1 and 4 respectively.

The permanent transect method was designed to detect potential impacts of Project activities at various spatial scales and over various time frames. Perpendicular alignment of transects with respect to linear infrastructure (a road, Pipeline ROW or quarry edge) samples a gradient of potential disturbance—heaviest at the forest edge and progressively less so with increasing distance into the forest. Physical changes at the edge ('edge effects') include greater light and wind penetration, potential dust and noise pollution, and edges are also susceptible to invasion by exotic weeds and pests. For most groups of organisms 'edge effects' are likely to attenuate rapidly and the 220–250 m transects should extend beyond any major impacts.

It should be noted that construction of the Hides Wellpad access road began in 2011 and of the Hides spinline ROW in mid-2013; reinstatement was completed in the first quarter of 2014. Reinstatement of the ROW at KP107 was signed off a year earlier in February 2013 but the access road to KP107, and Arakubi Quarry, have been established for many years. Therefore, the plants and animals in forest adjacent to these linear infrastructure corridors have been exposed to edge effects for at least 1–2 years before the 2015 survey.

Patterns in species distributions along the transects should be evident from the 2015 survey results for at least some groups of plants and animals, and these should inform on their variable sensitivity to 'edge effect' impacts. In coming years, as data are collected at the same sites and using the same methods, it will also be possible to determine whether any broader changes are occurring, potentially affecting even the more sheltered areas of forest.

MAJOR RESULTS

At least 579 animal and plant species were documented during the surveys. This includes at least 35 species that were previously unknown to science (new species) or that were known but have yet to be scientifically named (undescribed), and 14 species listed in a category higher than Least Concern by the IUCN. In the following text new and undescribed species are indicated by the term “sp.” followed by a unique identifier (e.g. *Genus* sp. 1). A summary of the major results is presented below and total numbers of species documented are presented in Table 1.

Taxon accounts

Vegetation

A total of 318 plant species was recorded from 12 standardised survey plots, including 234 at BAA 1 and 140 at BAA 2. Only 56 species (17.6%) are shared between the two areas, confirming that they support quite different plant communities. Six undescribed plant species were collected, all but one of these completely new to science. Two plant species listed as ‘Near Threatened’ and one as ‘Endangered’ by the IUCN were also recorded. Three plants were recorded from the island of New Guinea for the first time, and three others represent significant new populations of poorly known species. Examination of vegetation structure and community composition in plots at different distances from the ROW found little evidence for an impact of the ROW on adjacent plant communities. However two groups, epiphytes and bryophytes, were significantly more diverse and abundant respectively closer to the forest edge than further into the forest; both of these groups contain species that thrive in the drier, lighter conditions typical of forest edge habitats. The survey identified two plant families, the filmy ferns (Hymenophyllaceae) and nettles (Urticaceae) as particularly useful subjects for monitoring during the PMA3 program.

Frogs

A total of 37 frog species was documented during this survey using two quantitative and replicable field methodologies: Visual and Audio Encounter Surveys (VAES) and acoustics recorders. Species diversity and composition differed significantly between the two BAAs, with 10 frog species found on Hides Ridge in BAA 1, 29 species on the Agogo Range near Moro in BAA 2, and only two species (5.4%) shared between them.

More than half of the frog species encountered are undescribed (n= 23; 62%) but many of these were previously known to occur in the Upstream Project Area. One of the newly discovered species is currently known only from BAA 2 and genetic analysis suggests that it represents an entirely new genus. Two of the recorded frog species, *Choerophryne burtoni* and *Oreophryne notata*, are classified as Data Deficient by the IUCN due to the lack of information on their extent of occurrence, status and ecological requirements; both are relatively abundant in the survey sites.

Analyses of data from the VAES searches and bioacoustic recorders found no evidence for shifts in species diversity or composition with increasing distance from the ROW in either BAA. To date, establishment of the ROW clearings in BAA 1 on the Hides spine-line and in BAA 2 on the Agogo Range near Moro thus had no detectable impacts on local frog populations. Analyses of the relative abundance of each species highlighted some potential ‘Indicator Species’ that might be useful for detecting future changes in species abundance.

Future monitoring surveys will improve the robustness of the current analysis of ‘edge effects’ and also provide for analyses of changes in frog diversity and community composition over time. However, on current evidence the biodiversity values of frog assemblages in both BAAs appear to remain intact.

Birds

A total of 175 bird species was recorded during the 2015 surveys (Hides Ridge—81 species; Agogo Range—110 species), including nine species not previously reported for any site surveyed within the Kikori Basin or adjacent areas. The limestone forests along Hides Ridge and on the Agogo Range near Moro support numerous rare, conservation-listed, hunting-sensitive and restricted range species. Seventeen conservation listed bird species were recorded, including three species listed by the IUCN as Vulnerable (Papuan Eagle *Harpyopsis novaeguineae*, Pesquet’s Parrot *Psittirichas fulgidus*, Black Sicklebill *Epimachus fastosus*) and one as Near Threatened (Ribbon-tailed *Astrapia Astrapia mayeri*). All conservation-listed species documented during the 2015 surveys are also Protected under PNG law.

Of the various methods trialled in 2015, mist netting proved to be an unviable method for repeated, standardised monitoring of birds in both BAAs due to logistic constraints and the rugged karst terrain. By contrast, trials of the use of camera traps proved successful in detecting normally wary birds and mammals (see below). In addition, a trial of automated sound recordings demonstrated that three iconic birds-of-paradise resident on Hides Ridge (King of Saxony Bird-of-paradise *Pteridophora albertisi*, Black Sicklebill *Epimachus fastosus*, Brown Sicklebill *E. mayeri*) were all significantly less likely to vocalise at positions next to the ROW than in forest 170 m from linear clearings. The causes of this apparent partial avoidance of the forest edges are presently unknown.

Camera traps

A pilot study was conducted to test the effectiveness of camera traps for monitoring wildlife populations in both BAAs. The method proved highly successful. Forty-nine species (21 mammals, 28 birds) were photographed in 366 camera trap events, with most species photographed on multiple occasions. Species of conservation significance recorded on camera traps include Western Montane Tree Kangaroo (*Dendrolagus notatus*; IUCN Endangered), Papuan Eagle (*Harpyopsis novaeguineae*; IUCN Vulnerable), Small Forest Wallaby *Dorcopsulus* cf. *vanheurni* (IUCN Near Threatened), New Guinea Quoll (*Dasyurus albopunctatus*; IUCN Near Threatened), Woolley's Three-striped Dasyure (*Myoictis leucura*; IUCN Data Deficient) and Greater Melampitta (*Melampitta gigantea*; restricted-range). An additional three mammal species and three bird species were recorded for the first time in the Kikori Basin during the pilot study. The results clearly demonstrate the utility of camera trapping for species inventory as well as quantitatively documenting some of the regions rarest and most elusive mammals and birds. With an expanded sampling protocol, camera trapping is expected to provide quantitative datasets that will inform on some of the region's most sensitive animal species.

Non-volant (non-flying) mammals

A total of 11 species of rodents and two species of marsupials was trapped during the survey. Three other species were recorded by other means, one from a capture in a mist net and a daytime sighting, one from a road casualty, and one from bones and teeth contained in dog scats. Only one species was recorded in both BAAs—the IUCN Near Threatened New Guinea Quoll (*Dasyurus albopunctatus*). Camera traps provided records of one monotreme (Short-beaked Echidna, *Tachyglossus aculeatus*), six additional species of marsupials including the IUCN Endangered Western Montane Tree Kangaroo, *Dendrolagus notatus*, and four additional species of rodents. One introduced rodent species (Pacific Rat, *Rattus exulans*) was trapped in BAA 2, while a second (Black Rat, *Rattus rattus*) was recorded at the Hides Gas Conditioning Plant.

One of the native rodent species (*Rattus* sp. 'spiny') recorded at BAA 2 is definitely undescribed although it has been detected on two other recent surveys in Hela and Western Provinces. Several other rodent species within each of the genera *Rattus* and *Paramelomys* are morphologically cryptic (i.e. very similar in appearance) and were distinguished from each other using genetic methods. Although these species are also difficult to assign with confidence to named forms, for all but two of the species, genetic analyses demonstrated connections with other regional populations. The two exceptions—*Paramelomys*, *P. cf. mollis* C and *P. cf. rubex* B—are currently known only from BAA 1 and BAA 2, respectively.

Statistical analysis of the mammal trapping results indicate that species of *Paramelomys* are less common within 100-150 m of the ROWs in both BAAs, whereas the abundance of native *Rattus* species appears to be unaffected by the ROW. The trapping results from transects at the lower elevation in BAA 1 from 2015 were compared with a collection of recently accumulated bones recovered from a nearby cave during pre-construction surveys. While this comparison revealed several differences in composition, it is unclear whether these are due to sampling biases or reflect genuine ecological changes, and if the latter, whether any changes are due to project impacts.

Bats

Acoustic recordings of echolocation calls as well as trapping methods were used to document the diversity of bat communities on all transects in BAA 1 and BAA 2. A total of 66 full nights of acoustic recordings was obtained using bat detectors which were placed at increasing distances (50 metre intervals) starting at the forest edge. A total of 19 bat species was recognised based on their signature echolocation call types. One unique call type recorded at Arakubi Quarry differs from that of all known bats and probably represents a species new to science. Capturing a representative of this species to obtain morphological and genetic information is a high priority for future surveys. The identification of several other bat species also needs to be confirmed from captures followed by genetic and acoustic analysis work.

Bat diversity as calculated by various measures including Species Richness and Phylogenetic Diversity was significantly greater at lower elevations, especially at ~1000 m asl adjacent to Arakubi Quarry in BAA 2 where it is likely that rocky outcrops provide important habitat for cave-roosting species. However, there was no statistically significant contrasts in bat diversity or species composition of bat communities at increasing distances from the forest edge. The 2015 survey results do not identify any negative impacts on the bat communities associated with the ROW linear infrastructure.

By contrast, some species appear to be more abundant along the edges than inside the forest and these may have benefited from the creation of new habitat types. The analyses highlighted some potential Indicator Species that might be useful for detecting subtle changes in community composition that might be related to Project influences.

Table 1. Number of species documented during the 2015 PMA3 Surveys, number estimated to be new to science and/or undescribed, and the number of species holding an IUCN threat classification above Least Concern.

	Plants	Frogs	Birds	Non-volant Mammals*	Bats	TOTALS
Total Species	318	37	175	28	21	579
New Species	6	23	0	5+	1+	35+
IUCN Species	3	2	5	4	0	14+
*Not including bones in an owl roost which added 21 species						

Significant habitats

Both of the BAAs clearly retain high biodiversity values, with forest that remains largely intact and supports a large number of new and conservation-significant plants, frogs, birds and mammals including tree kangaroos and birds-of-paradise. Both BAAs represent special areas for birds as they support numerous rare, conservation listed, hunting-sensitive and restricted range species. The high elevation and rugged karst terrain of Hides Ridge have long protected its resident bird community from hunting and agricultural practices that threaten montane faunal communities in many other parts of PNG. The rugged limestone forests around KP107 support similar biodiversity values, though with a different species complement, notably including one of few known populations of the restricted range Greater Melampitta *Melampitta gigantea*.

Mammal diversity is also high in both BAAs, which support populations of conservation-listed mammals as well as new and undescribed species. Among the non-volant mammals, special note should be made of the high abundance in both BAAs (but especially so in BAA 2) of an undescribed Small Forest Wallaby that is related to the IUCN Near Threatened *Dorcopsulus vanheurni*. Elsewhere this undescribed species has declined dramatically and the Upstream Project Area could be an important future stronghold for this species. Among the bats, diversity was particularly high at the Arakubi transects and this may be due to the nearby occurrence of cave-bearing limestone outcrops. Populations of cave-roosting bats rely on the survival of and access to both roost and foraging habitats, and the Upstream Project Area, with its extensive areas of limestone karst, poses an excellent context for conservation of many bat species. Effective management of the complex landscapes occupied by bats is challenging but important because bats are widely acknowledged to be a keystone group in tropical forest ecology.

Of significance for the long-term maintenance of biodiversity values in the Upstream Project Area is that there was minimal overlap in the fauna and flora encountered in the two BAAs. This is probably due in large part to the different altitudes accessed at these sites, and suggests that establishment of at least one more additional BAA at lower altitudes in the Upstream Project Area may be warranted.

Threats

Apart from the direct impacts of establishing linear infrastructure in forest habitats, including physical disturbance during construction and ongoing risks of mortality to dispersing animals, two additional processes associated with construction of the pipeline ROW in the Upstream Project Area have the potential to effect biodiversity values there in the long term. These are 1) decreasing habitat quality adjacent to the ROW due to edge effects (e.g. Andrews et al. 2015) and 2) improved access to the forest by humans (for hunting and gardening) and by invasive species, both native and exotic.

The 2015 survey found some evidence for 'edge effects' in several of the plant and animal groups studied, including rodents, bats (including some that seem to have benefitted) and birds (three bird-of-paradise species that were less likely to be heard calling next to the ROW than in forest away from these linear clearings). However, in each case the effects seem to be confined to habitats close to the forest edge; this includes the spread of invasive weeds and pests that were only detected along the immediate forest edges.

Longer-term data, collected from the same sites over multiple surveys, are required to determine whether these impacts are stable or changing (potentially increasing or decreasing) and to determine whether there are changes affecting biodiversity values on a broader scale within the Upstream Project Area.

The team identified a number of potentially broad-ranging threats to components of local biodiversity. The construction of the linear ROW infrastructure and associated roads has improved accessibility into formerly remote areas of forest and this may have led to an increase in direct hunting pressure by both local people and by feral dogs. Predation by wild dogs on the IUCN Near Threatened Small Forest Wallaby was documented at the high elevation transects in BAA 1 and it is likely that they also prey on other conservation-listed species of mammals and birds. The impacts of increased predation on large herbivores in particular might have broader ecological consequences that might be felt at considerable distances from the ROW.

Exotic rodent species were detected only at KP107 in BAA 2 where they were confined to the forest edge, and at Hides Gas Conditioning Plant. While the risk of short-term expansion of these species beyond the most disturbed contexts may be quite low, their presence in the BAAs carries with it an additional risk of the transfer of novel pathogens into the native wildlife. This can happen through interspecific contact including predation (e.g. quoll eating exotic rat) and attempted interbreeding (e.g. native and exotic *Rattus* spp.) or through environmental contamination (water, soil etc). The spread of new pathogens into naive wildlife populations is acknowledged globally as a threat to biodiversity.

Overall conclusions

1. The results of the 2015 PMA3 survey indicate that both BAAs retain high biodiversity values for all surveyed taxa.
2. The plant and animal communities found in each of the BAAs are quite distinct, with only a small proportion of species in common. This is consistent with the contrasting elevations of the two BAAs.
3. Both BAAs produced records of numerous undescribed species of plants, frogs, marsupials, rodents and bats. Entirely new species of plants and frogs were discovered, and a potentially new and unknown species of bat was recorded acoustically.
4. Both BAAs continue to support many rare, conservation listed, restricted range and hunting-sensitive species. Hides Ridge in particular supports populations of iconic species of tree kangaroos and birds-of-paradise. The lower elevations of BAA 2 also support high diversities of frogs and mammals including a number of species with known ranges restricted to the Upstream Project Area.
5. Several conservation significant species, and species not previously recorded from the Kikori basin, were detected using camera traps. These results clearly demonstrate the utility of camera trapping in documenting the true diversity of rare and elusive vertebrate fauna within sampling areas. Moreover, given the brevity of this pilot study, it is predicted that statistically useful datasets will be collected for a variety of priority monitoring taxa under an expanded sampling protocol.

6. Analysis of acoustic data on Hides Ridge revealed that three birds-of-paradise were significantly less likely to vocalise next to linear infrastructure clearings than in forest 170 m away. The reasons for this apparent partial avoidance of Project infrastructure are still unclear.
7. Several undescribed rodent species were detected by genetic analysis and this method also demonstrated connections with other regional populations for all but two of the mammal species.
8. Statistical analysis of data from the permanent transects found small but significant differences in diversity or community composition at different distances from the ROW, with some significant contrasts in rodents. In all cases, these changes appear to be confined to a relatively narrow zone within 50–100 m of the ROW clearing. For frogs and bats, some contrasts were noted but with insufficient data to establish statistical significance.
9. The fact that subtle influences were detected from a single year of survey data demonstrates the potential future power of the transect method to detect any changes across all groups of plants and animals. The transect data from 2015 also represent a baseline for future monitoring of broader-scale changes in species diversity and community composition.
10. Overall, the preliminary results indicate that the biodiversity values of the Upstream Project Area remain intact, with only minor impacts detected in close proximity to the Project infrastructure. Significant changes, including criteria exceedance requiring a response, were not detected for any taxa. However, some potential threats warranting further investigation were identified and a more robust assessment will be possible following completion of the 2017 PMA3 survey.

REFERENCES

- Andrews, K.M., Nanjappa, P. & Riley, S.P.D. 2015. *Roads and ecological infrastructure: concepts and applications for small animals*. Baltimore: Johns Hopkins University press.
- McAlpine, J. R., Keig, G. & Falls, R. 1983. *Climate of Papua New Guinea*. Canberra: CSIRO.

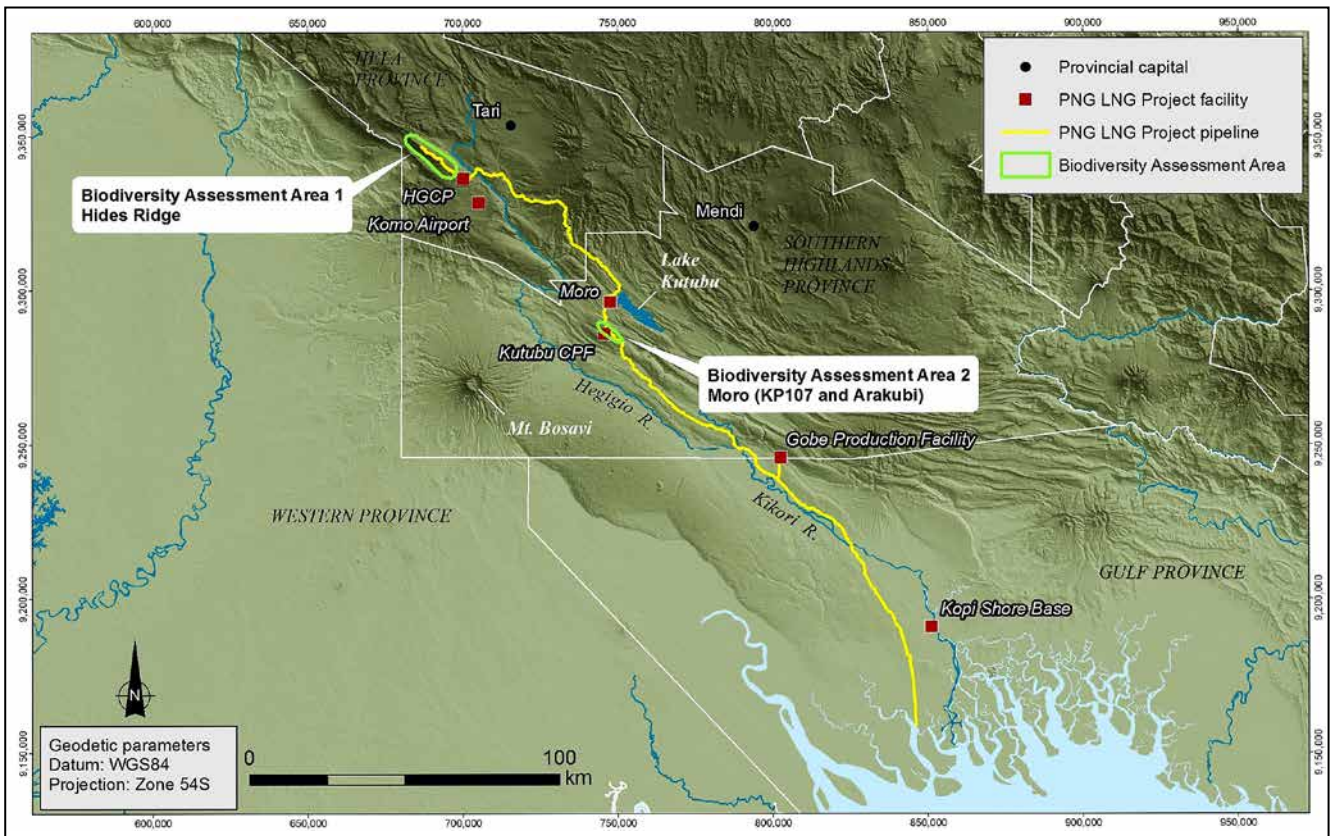


Figure 1. Regional map showing location of the two BAAs surveyed during the PMA3 2015 survey.

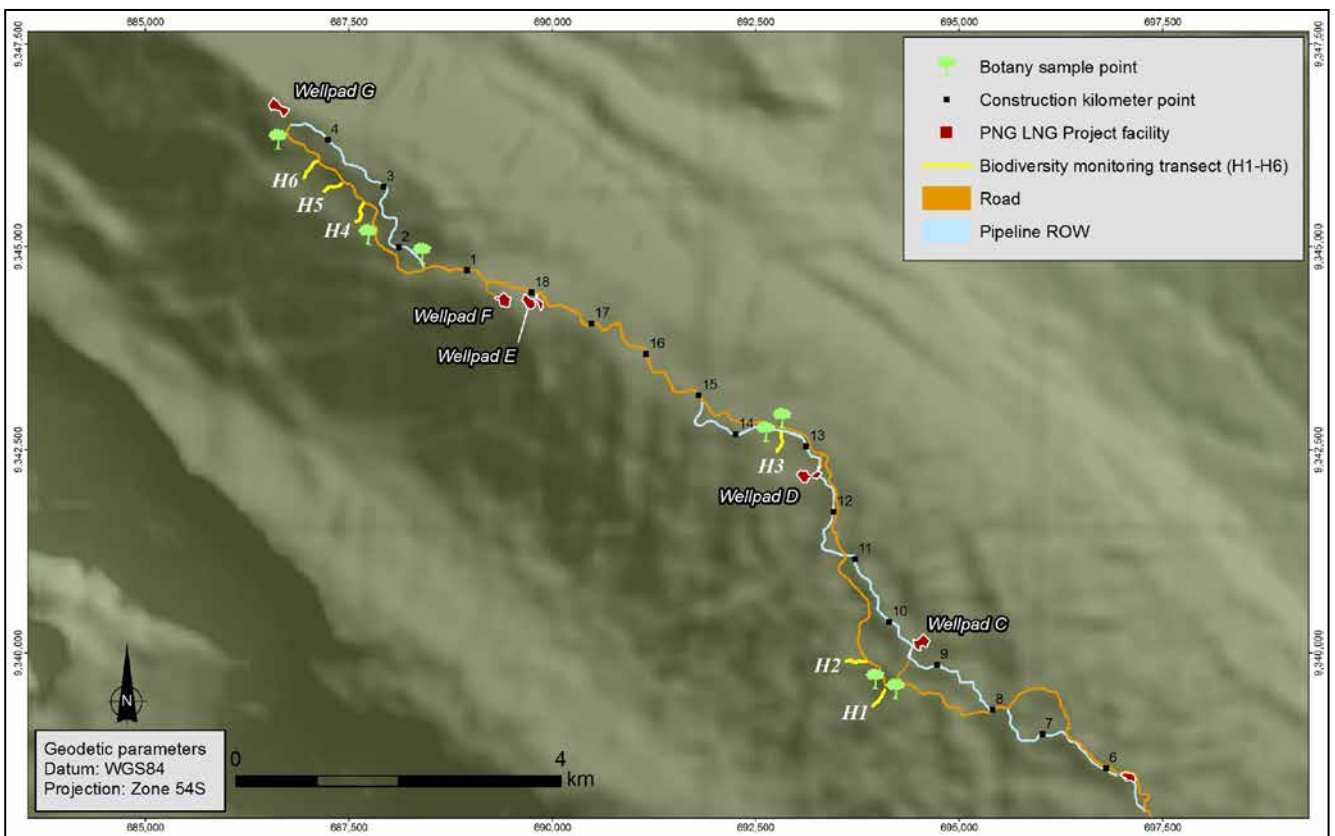


Figure 2. Map showing locations of the six major transects and seven plant plots in BAA 1.

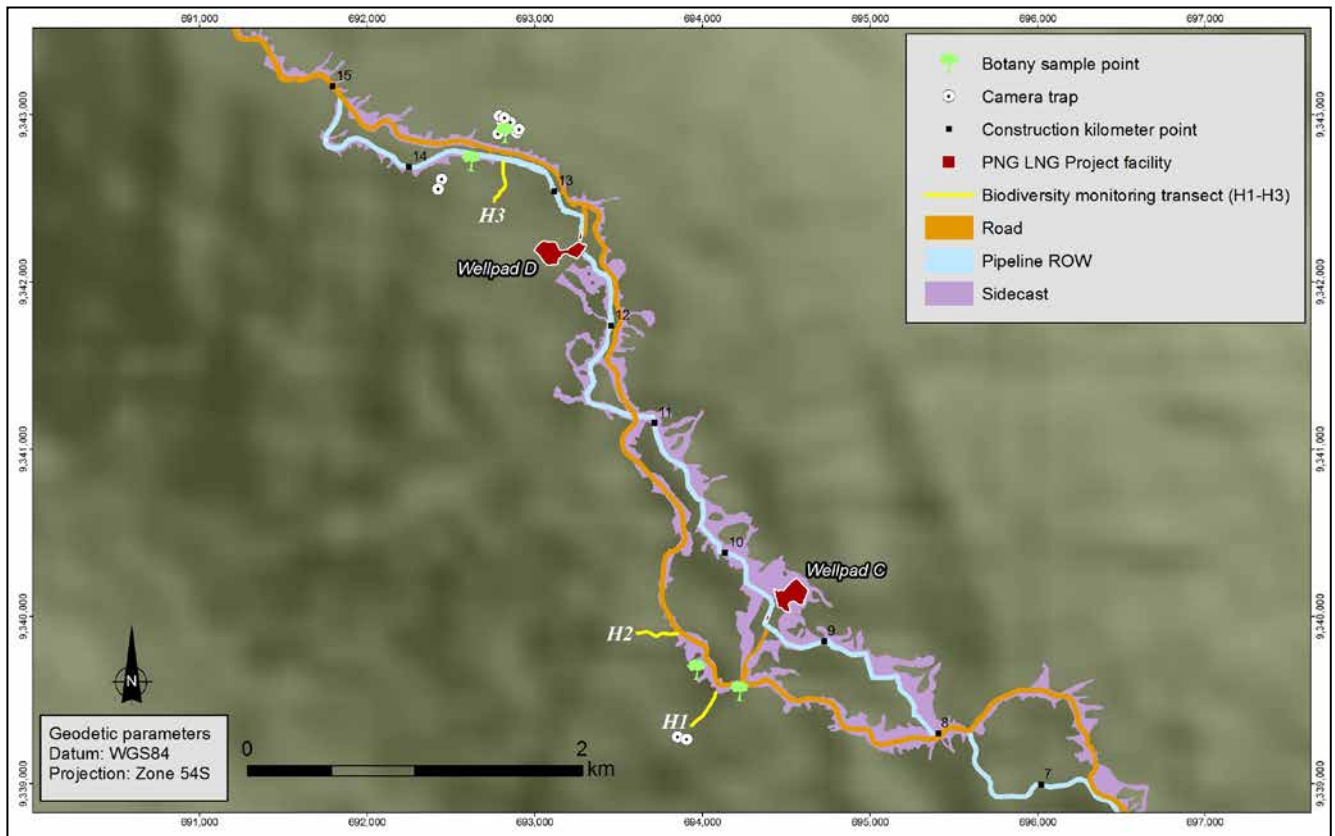


Figure 3. Map of lower elevations in BAA 1 showing details of Transects 1–3, plant plots and camera trap arrays.

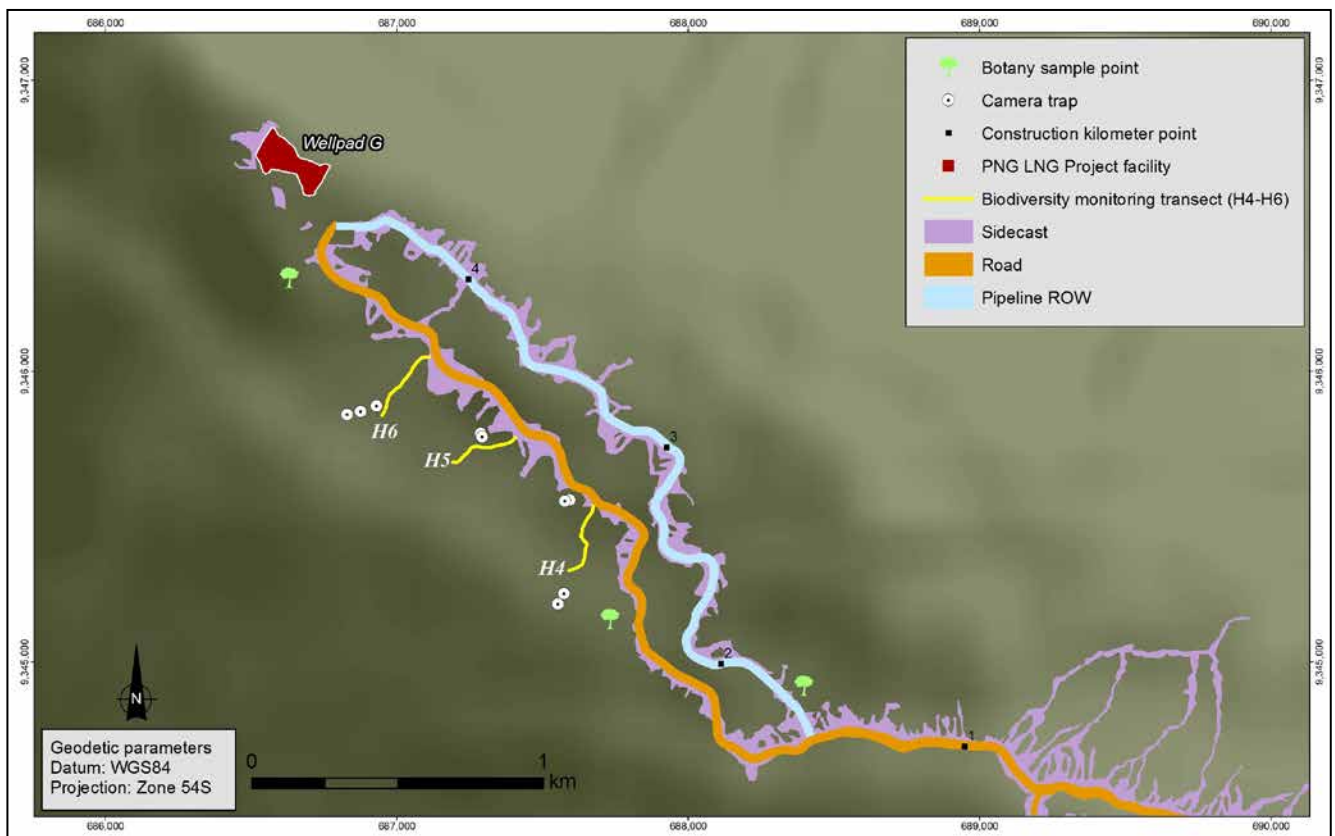


Figure 4. Map of upper elevations in BAA 1 showing details of Transects 4–6, plant plots and camera trap arrays.

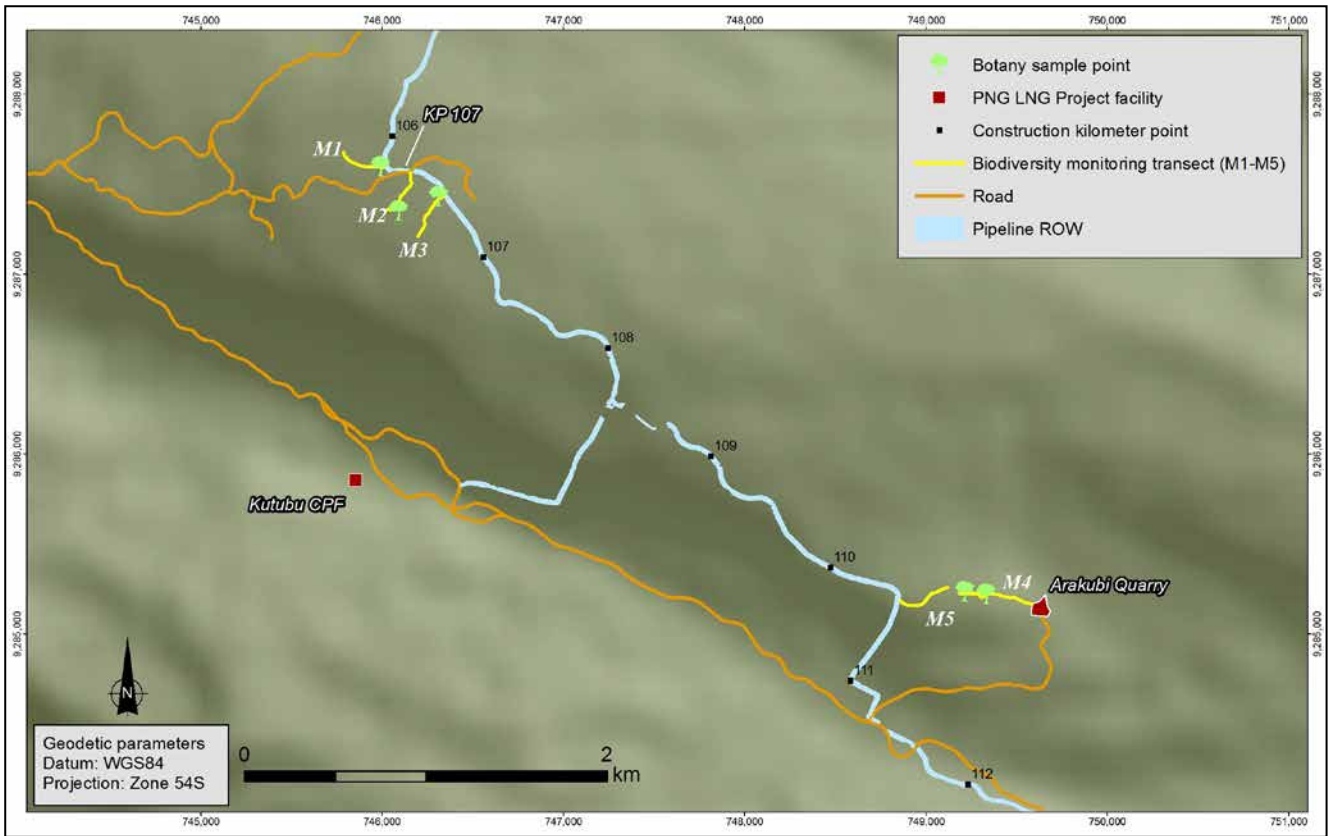


Figure 5. Map showing locations of the five major transects and five plant plots in BAA 2.

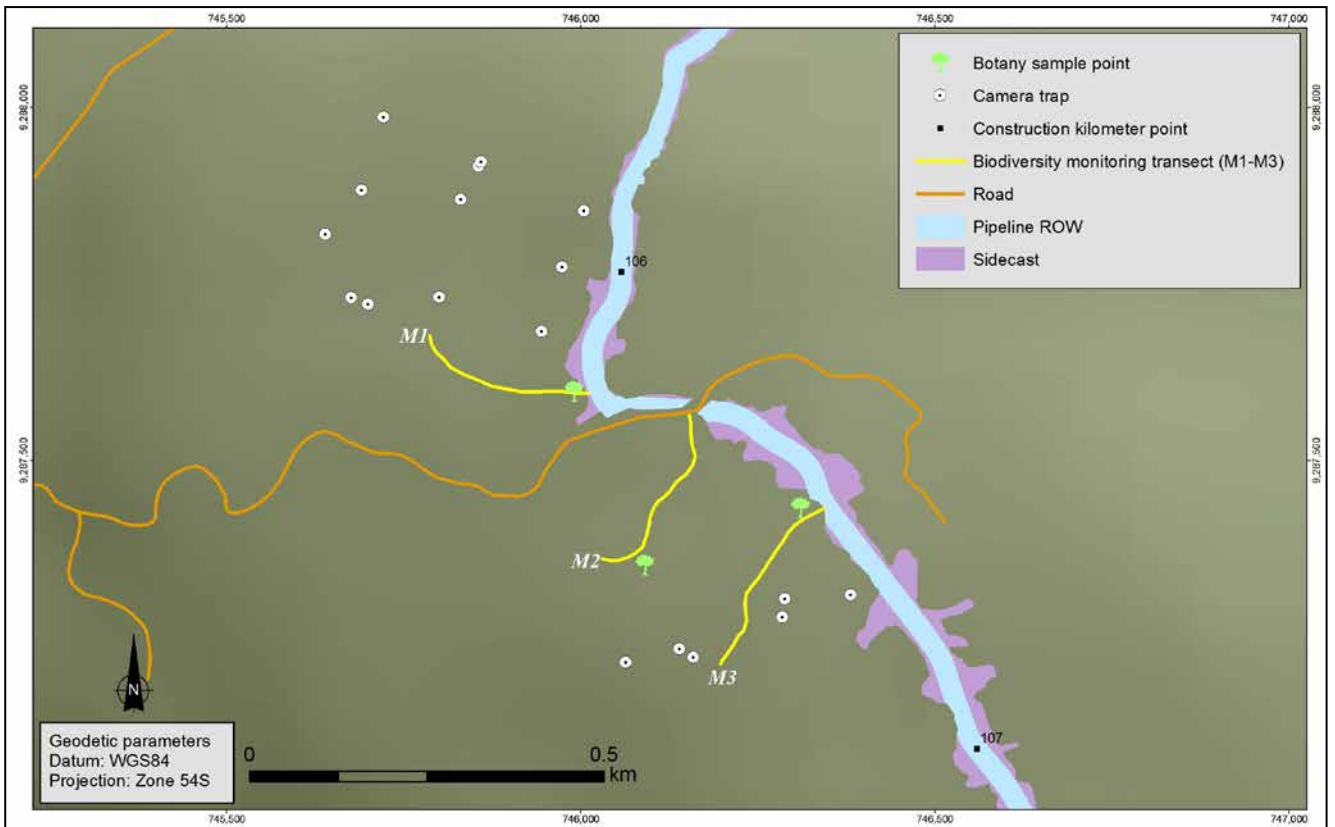


Figure 6. Map showing locations of the three major transects, plant plots and camera trap arrays at KP107 in BAA 2.

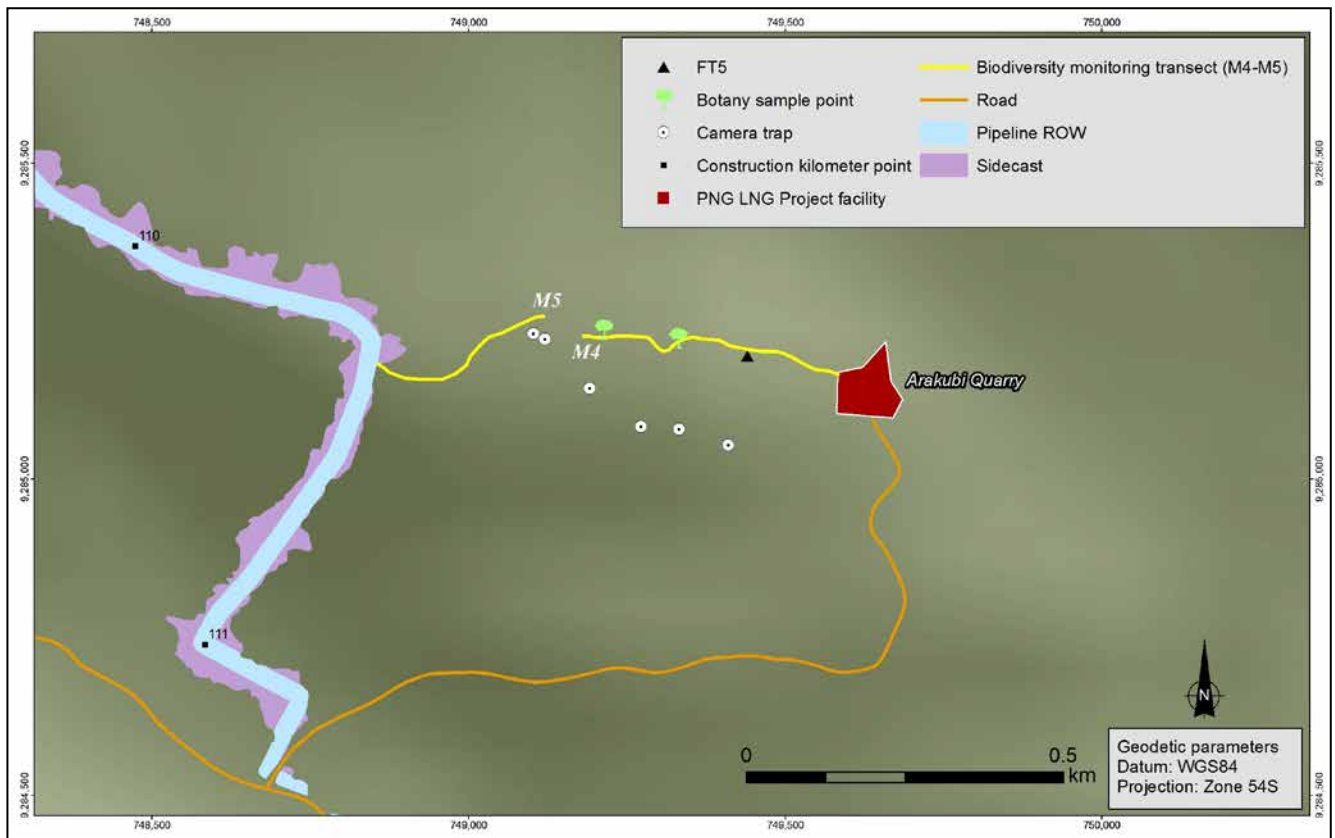


Figure 7. Map showing locations of the two major transects, plant plots and camera trap arrays at Arakubi Quarry in BAA 2.



Figure 8. Linear infrastructure at KP107 in BAA 2. Note the sharp boundary between the ROW clearing and adjacent forest on the left.



Figure 9. Lower montane forest on Hides Ridge in BAA 1



Figure 10. Interior of lower montane forest at the highest elevations on Hides Ridge in BAA 1.



Figure 11. Transect marked with blue tape through lower montane forest at KP107 in BAA 2. Note the minimal disturbance to vegetation when establishing transects. A small temporary shelter from the rain constructed off the transect can be seen in the background.



Figure 12. Secondary hill forest on transect M4 at Arakubi Quarry in BAA 2.



Figure 13. Lower montane forest near transect M5 at Arakubi Quarry



Figure 14. Most of the 2015 PMA3 survey team, from left to right: Dopo Uriye, Kyle Armstrong, Muse Opiang, Amos Ona, Stephen Richards, Fanie Venter, Iain Woxvold, Ken Aplin and Leo Legra

APPENDICES

Appendix I. Coordinates and elevations (at start) for each of the 11 standard survey transects established in BAA 1 and BAA 2.

BAA	Transect	Position	Coordinates	Elevation
1	H1	Start	S5.97229° E142.75333°	2140
1	H1	End	S5.97416° E142.75198°	
1	H2	Start	S5.96915° E142.75127°	2150
1	H2	End	S5.96913° E142.74908°	
1	H3	Start	S5.94369° E142.74177°	2285
1	H3	End	S5.94579° E142.74132°	
1	H4	Start	S5.91835° E142.69531°	2685
1	H4	End	S5.92036° E142.69456°	
1	H5	Start	S5.91621° E142.69289°	2745
1	H5	End	S5.91699° E142.69095°	
1	H6	Start	S5.91372° E142.69021°	2730
1	H6	End	S5.91553° E142.68877°	
2	M1	Start	S6.44023° E143.22424°	1390
2	M1	End	S6.43950° E143.22221°	
2	M2	Start	S6.44051° E143.22552°	1380
2	M2	End	S6.44236° E143.22442°	
2	M3	Start	S6.44169° E143.22724°	1365
2	M3	End	S6.44368° E143.22594°	
2	M4	Start	S6.46206° E143.25662°	995
2	M4	End	S6.46152° E143.25299°	
2	M5	Start	S6.46124° E143.25242°	1050
2	M5	End	S6.46192° E143.25004°	

Appendix 2. IUCN Red list categories used in this report

The conservation status of each species encountered was determined using the internationally recognized IUCN Red List of Threatened Species and the PNG Fauna (Protection and Control) Act 1966.

The Red List provides taxonomic, conservation status and distribution information on plants and animals. The IUCN Red List criteria identify three categories of threatened species which are considered to be facing a heightened risk of extinction: Critically Endangered (CR), Endangered (EN) and Vulnerable (VU). Five additional categories are Extinct, Extinct in the Wild, Near Threatened (NT), Least Concern (LC) and, for those species for which data are insufficient to reach a conclusion, Data Deficient (DD). Species that have not been assessed by the IUCN are listed as Not Evaluated (NE).

In this report the term 'conservation listed' is applied to all species listed by the IUCN as threatened, Near Threatened or Data Deficient and to those species listed as Protected under PNG law.

RIPOT SAMERI

BEKGRAUN NA AS BILONG SEVEI

Niugini em i wanpela ailan we i gat planti kain kain tru ol enimal na pisin na diwai i stap long en. Planti bilong ol dispela enimal na ol pisin na diwai na plent i no stap long ol arapela hap long Graun. Ol kain naispela samting olsem kumul, ekidna na ol sikau bilong diwai em planti lain i save long ol, na ol i bikpela samting tu long kalsa bilong ol pipel bilong Papua Niugini (PNG). Tasol planti lain i no save olsem i gat tu planti ol kain kain diwai na plent na ol liklik enimal long PNG em ol saintis i no kisim gut infomesen bilong ol yet, na olgeta yia, ol saintis i wok long painim moa ol nupela plent na enimal.

Ol stadi i bin kamap bipo long Projek developmen i bin rekodim planti kain kain plent na enimal long Apstrim Projek Eria bilong Papua Niugini Likwifait Nuturel Ges (PNG LNG) Projek. Sotpela ripot bilong ol i stap long ExxonMobil Limited (EMPNG) Biodiversity Strategy i soim olsem (i) bikpela hap bikbus i no gat man i bagarapim yet, (ii) planti kain kain diwai na plent, (iii) planti kain kain enimal na pisin, (iv) ol plent na enimal i save kamap long dispela hap tasol, (v) i gat ol narakain tru ol spises i stap wantaim, (vi) ol diwai, plent, enimal na pisin i stap long konsevesen lista, (vii) ol plent, enimal na pisin ol lokal komyuniti i save yusim long kalsa na ol pasin tumbuna.

Long komitmen bilong en long lukautim na lukim olsem olgeta plent, enimal, pisin, bus, na graun long Apstrim Projek Eria i stap gut, Baiodaivesiti Strateji bilong EMPNG bai i gohet long mekim wok bilong glasim na bosim gut ol wok. Long skelim sapos dispela long-tem strateji i wok gut, EMPNG i kamapim ol wok aninit long foapela Program Monitoring Ektiviti (PMAs) Ol dispela PMAs bai i givim infomesen o data long skelim wantaim ol Ki Pefomens Indiketa (KPIs) i bihainim stret ol bikpela astingting bilong Baiodaivesiti Strateji bilong EMPNG.

We i gat planti kain kain plent na enimal, em i bikpela samting long KPI, na wok bilong rekodim ol senis i kamap, bai i soim sapos Projek i winim ol foapela bikpela astingting bilong Baiodaivesiti Strateji: Holim strong ol samting i stap long ol hap bilong Apstrim eria, Lukautim ol praioriti ekosistem; Stopim ol bagarap inap kamap long ol fokal habitat; na Painimaut, mesa na ofset ol bikpela bagarap inap kamap (EMPNG PNG LNG Biodiversity Strategy: i stap online).

Ol i kamapim Program Monitoring Activity PMA3 long kisim ol hai-kwaliti infomesen long wanem samting i kamap long spises daivesiti long Apstrim Eria bilong PNG LNG Pojek. Astingting bilong PMA3 em long mekim baiodaivesiti sevei, we bai bungim kwantitiv, riptabel data long ol kain kain spises i stap long ol Baiodaivesiti Asesmen Eria (BAA) ol i bin kamapim long ol hap insait na klostu long eria we PNG LNG Projek i bin kamap, na long ol protektet eria ol i bin kirapim insait long dispela baiodaivesiti ofset program bilong EMPNG. Dispela hap tok 'Daivesiti' i karamapim namba bilong ol spises, komposisen bilong ol, na planti moa taget spises sapos yu skelim egensim wanpela difain beslain.

Namba wan PMA3 baiodaivesiti sevei i bin kamap long 2015 long tupela BAA, wanpela long Hides Ridge (BAA 1) na narapela long Agogo Range klostu long Moro (BAA 2). Dispela ripot i soim risal bilong ol dispela sevei; i givim beslain data long baiodaivesiti long dispela tupela BAA we ol monitoring sevei bilong bihain taim i ken skelim, glasim ol baiodaivesiti i stap nau, na wanem kain hevi ol linia infrastraksa korido i ken kamapim, na sapotim astingting bilong EMPNG long was gut long baiodaivesiti i stap long Apstrim Projek Eria.

Ol de bilong sevei

10 Jun–18 Julai 2015

Sotpela toktok long sevei eria

Ful ripot bilong ol envairomen long Apstrim Projek Eria i stap long Projek EIS, na ol toktok bilong baiodaivesiti bilong dispela hap i stap insait long EMPNG Biodiversity Strategy. Bikpela hap tru bilong Apstrim Projek Eria em bikbus i karamapim na i gat ol narakain diwai i gro long ol hap i go antap long maunten (Figures 9–13). I no gat data bilong soim stori bilong ren long dispela tupela BAA, tasol Apstrim Projek Eria i stap long ples we i save gat planti ren tru na i karamapim sauten sait bilong ol maunten bilong sentral PNG we long wan wan yia, mak bilong ren i save winim 4,000mm na i no gat senis. Mak bilong ren long dispela eria em i save pundaun strong oltaim, 'Continuously heavy' (McAlpine et al. 1983).

Hap we tupela BAA i bin kamap i stap long Figure (1) na sotpela stori bilong ol envairomen bilong wan wan BAA i stap daunbilo.

BAA 1: 10–25 Jun 2015.

BAA 1 em i stap long Hides Ridge long Hela Provins. Em i karamapim eria i stap namel long mak bilong 2,100 na 2,750 m antap long mak bilong solwara (asl) na ol i brukim long tupela elevesenel ben, wantaim tripela sevei lain i stap long mak bilong 2,100–2,400 m asl long eria namel long Wellpad C na Wellpad D, na tripela lain long mak bilong 2,660–2,780 m asl namel long Wellpad E na G (Figures 2–4).

Insait long dispela tupela elevesen ben bilong Hides Range, i gat lowa monten renfores na diwai ol i kolim *Trisyngyne* (pastaim *Nothofagus*). Long dispela mak bilong maunten, i gat FIMS vejtesen taip LN/LsN 'liklik kraun na liklik kraun tru lowa monten fores wantaim *Nothofagus*' (Figures 9–10). Long dispela mak tu, ples i kol, i wet oltaim na i gat ol mos na i pulap tu long ol liklik plent olsem ol fen, okid na rododendron.

BAA 2: 27 Jun–8 Julai 2015.

BAA 2 i stap long Agogo Range klostu long Moro long Sauten Hailans Provins (Figure 1). Tupela sevei lain i bin stap antap long mak bilong 1,000–1,080 m asl long eria i stap long west hap bilong Arakubi Quarry na is long paipplain rait ov wei (ROW) na tripela sevei lain i stap antap long mak bilong 1,340–1,410 m asl long hap bilong KP107 (Figures 5–7).

Ol bus long BAA 2 i gat planti kain kain diwai na i no gat ol fen na okid i gro long ol. Bus i stap long KP107 em i FIMS taip LsN 'liklik kraun lowa monten wantaim *Nothofagus*'. I gat kain kain diwai na i narakain long BAA 1 na i gat miks *Trisyngyne* bus na *Papuacedrus papuana-Elaeocarpus-Cryptocarya* bus (Figure 11). Tupela FIMS vejtesen taip i stap long Arakubi Quarry. Namba wan em HsN/Hm 'liklik kraun hil fores' wantaim '*Nothofagus*/Medium kraun hil fores' tasol em i stap long eria bilong sekenderi fores daunbilo long 1,000 m asl long isten sait bilong Arakubi (Figure 12). I go moa long west, klostu long ROW, bus long dispela hap em i praimer i o olupela bus, na ol i makim olsem FIMS vejtesen taip LsN/L 'liklik kraun tru lowa monten fores wantaim *Nothofagus*/liklik kraun lowa monten fores' (Figure 13). Long dispela eria, lowa monten fores we *Trisyngyne* i gro bihainim maunten i go antap na kamap long het bilong maunten.

Sevei i kamap olsem

Sevei bilong ol rokrok, ol non - volan mamel, ol dispela mamel i no save flai (rat na mumut), ol blakbokis na taitim net bilong kisim ol pisin, i bin kamap long sikispela pemanen transek, o lain i katim mak, long hap bilong BBA 1 we i bihainim Hides Ridge akses rot na paipplain ROW (Figure 2), na long faivpela pemanen transek i bihainim paipplain ROW long KP 107 (Figure 6, 8) na i stap klostu long Arakubi Quarry (Figure 5). Wan wan bilong ol dispela 11-pela transek i go inap long mak bilong 220–250 m insait long bikbus na i bihainim ROW o arere bilong bus. Mak bilong ol dispela transek i stap long Apendiks 1. Na tu, sevei bilong plent plot na kamera treping i kamap long wankain elevesen ben long BAA 1 na BAA 2 tasol ol wok i bin kamap longwe liklik long ol dispela transek. Long sevei bilong ol plent plot, ol i no laik distebim ples we ol dispela samting i gro. Na long kamera treping, ol i haitim kamera longwe long transek long stopim planti distebens i kamap long kamera trep eria. Ol ples we plant plot na kamera trep i bin stap, em (Figures 3–4 (BAA 1) na 5–7 (BAA 2) na lokesen bilong ol i stap long Sapta 1 na 4.

Pemanen transek metod i kamap long painim aut wanem kain impek ol ektiviti bilong Projek i kamapim long ol dispela eria. Ol transek i stap long ol hap we i bihainim lain (ol kain samting olsem rot, Paipplain, ROW o arere bilong quarry) bai inap long lukim sampela distebens – bikpela distebens bai kamap long arere bilong bus tasol bai no gat bikpela tumas long ol hap we i go insait moa long bikbus. Ol senis bai kamap long arere 'edge effects' we bai gat moa lait bilong san, na win na bai das i kirap na moa nois i kamap. Na arere bilong bus bai lukim tu ol gras nogut na binatang i kamap. Planti bilong ol dispela samting i kamap (edge effect) bai i no inap stap longtaim olsem na dispela 220–250 m transek mak i mas surik i go moa abrusim mak we ol bikpela impek i kamap.

Yumi mas save olsem konstraksen bilong Hides Wellpas akses rot i bin stat long 2011 na ol wok bilong Hides spinline ROW i kamap namel long yia 2013; ol wok bilong stretim bek graun long dispela hap i bin pinis long 2014. Wok bilong stretim bek graun long ROW long KP107 i bin pinis long begin bilong Februari 2013 tasol akses rot i go long KP107, na Arakubi Quarry i bin stap planti yia pinis. Olsem na, ol plent na enimal long bikbus klostu long ol rot na longpela eria we ol i kliaim bus (linia infrastraksa korido), i bin pilim pinis ol senis long samting olsem 1 o 2 yia bipo long dispela 2015 sevei i bin kamap.

Dispela 2015 sevei risal bai soim we sampela ol plent na enimal i stap, na bai soim klia wanem kain senis 'edge effect' i kamapim long laip bilong ol. Long ol yia i kam bihain, data ol i kisim long dispela hap, we ol i yusim wankain metod, bai inap long tok klia sapos sampela bikpela senis i wok long kamap long arere bilong bus na insait tu long bikbus.

OL BIKPELA RISAL

Ol i kisim ripot bilong 579 enimal na plent spises insait long dispela sevei. I gat 35 spises em ol saintis i no save long en (nupela spises) o ol i bin save tasol i no givim yet saintifik nem (i no gat nem yet), na 14 spises i stap long mak i antap liklik long Least Concern lista bilong IUCN. Long ol toktok i stap daubilo, ol nupela spises na ol dispela spises we i no gat nem yet, em ol i makim wantaim dispela mak "sp." na bihain long en em mak bilong unik aidentifaia, (eksampel *Genus sp.* 1). Sotpela ripot bilong ol bikpela risal i stap daunbilo na total namba bilong ol spises i stap long Table 1.

Ripot bilong ol spises

Ol plent

Ol i painim 318 plent spises long 12-pela stended sevei plot we ol i painim 234 long BAA 1 na 140 long BAA 2. I gat 56 spises tasol (17.6 %) i stap long dispela tupela eria wantaim, na i soim olsem tupela i saptim ol narakain plent komyuniti. Ol i kisim sikispela plent spises em i no gat nem yet, namel long ol dispela plent, wanpela tasol em i nupela long saiens. Ol i painim tu tupela plent spises em IUCN i putim long lista bilong 'Near Threatened' na wanpela long lista bilong 'Endangered'. Ol i painim tu tripela plent we i namba wan taim tru i gat ripot bilong ol long ailan bilong Niugini, na tripela arapela i makim bikpela lain spises ol saintis i no save gut long en. Long taim ol i glasim ol vejjetesen straksa na komyuniti komposisen long ol plot i stap longwe long narapela, long ROW, ol i painim olsem ROW i no bagarapim ol plent i stap klostu long en. Tasol tupela grup, ol fern, okid (epiphytes) na mos (bryophytes), i planti tru na ol kain kain i gro arere long bus na i no gro insait long bikbus. Dispela tupela grup i gat ol spises i save gro gut long ples we i drai na i gat lait, kain olsem long ples arere long bikbus. Sevei i painim tupela plent famili, ol filmi fern (Hymenophyllaceae) na ol salat (Urticaceae) em ol gutpela mak bilong sekap long taim bilong PMA3 program.

Ol rokrok

Ol i painim 37 spises bilong ol rokrok long dispela sevei long taim ol i yusim tupela kwantetiv na replikabel fil metodoloji: Visual and Audio Encounter (VAES) na acoustics recorder. I gat planti kain kain spises i stap long dispela tupela BAA, we ol i painim 10-pela rokrok spises long BAA 1 long Hides Ridge na 29 long Agogo Range klostu long Moro, long BAA 2. Tupela spises tasol (5.4%) em ol i painim long tupela BAA wantaim.

Moa long hap namba bilong ol rokrok spises ol i bin painim em ol saintis i no givim nem yet long en (n=23;62%) tasol ol i save olsem planti bilong ol dispela rokrok i stap tu long Apstrim Projek Eria. Wanpela bilong ol dispela nupela spises ol i bin painim, i save stap tasol long BAA 2 na jenetik analisis i soim olsem em i makim wanpela nupela jenis gen. Tupela bilong ol rokrok spises ol i bin painim, *Choerophryne burtoni* na *Oreophryne notata*, em IUCN i putim long lista bilong Data Deficient bikos i no gat inap infomesen long we ol dispela rokrok i save stap, na wanem kain hap ol i save laik stap long en; tasol i bin gat planti tru long hap we sevei i bin kamap.

Ol data bilong ples we i bin gat VAES sets na baioakustik rekoda i soim olsem i no gat evidens long soim watpo i gat senis long spises daivesiti o komposisen long taim yu go longwe long ROW long dispela tupela BAA. I kam inap nau, long taim ol i klaim bus long ROW long BAA 1 na long Hides spine-line na long BAA 2 long Agogo Range klostu long Moro, i no bin gat bagarap i kamap long populesen long dispela eria. Ol i skelim olsem i gat planti bilong wan wan spises na dispela i soim olsem i gat sampela "Indiketa Spises" em ol i ken yusim long painim aut long bihain taim sapos i gat senis i kamap long namba bilong spises o nogat.

Ol wok painim aut long bihain taim bai strongim dispela wok bilong painim aut ol senis bilong "edge effect" na wanem kain senis i kamap long ol rokrok na komyuniti komposisen bilong ol. Tasol, ol risal bilong wok i kamap nau i soim olsem ol i no gat senis i kamap long ol rokrok long tupela BAA wantaim.

Ol pisin

Sevei bilong 2015 i bin rekodim 175 spises bilong ol pisin (Hides Ridge – 81 spises; Agogo Range 110 spises), we nainpela spises em ol i no bin lukim long ol sait we sevei i bin kamap long hap bilong Kikori Basin o ol eria i stap klostu. Ol ston o laimston bikbus long Hides Ridge na Agogo Range klostu long Moro em ples bilong planti spesel pisin, sampela bilong

ol i stap long konsevesen lista, ol man I wok long kilim na ol i sot nau, na ol dispela i save stap long wanpela hap tasol. Ol i rekodim sikistin pisin i stap long konsevesen lista, we tripela spises em IUCN i putim long lista bilong Vulnerable (Papuan Eagle *Harpyopsis novaeguineae*, Pesquet's Parrot *Psittichas fulgidus*, Black Sicklebill *Epimachus fastosus*) na wanpela i stap long lista bilong Near Threatened (Robin-tailed *Astrapia Astrapia mayeri*). Lo bilong Papua Niugini i tambu long kilim ol dispela spises i stap long konsevesen lista dispela 2015 sevei i bin painim.

Long olgeta metod ol i testim long 2015, mist netting i no gutpela tumas long yusim long holim na stadi ol pisin long tupela BAA bikos i no isi long putim net long kain maunten ples we i gat planti hul bilong ston. Tasol ol test bilong yusim kamera trep i soim olsem em i gutpela long painim ol pisin na blakbokis na ol rat na mumut (lukim daunbilu). Na tu, test bilong automated sound recording i painim tripela kumul i stap long Hides Ridge (King of Saxony Bird-of-paradise *Pteridophora albertisi*, Black Sicklebill *Epimachus fastosus*, Brown Sicklebill *E. mayeri*). Ol i no inap harim krai bilong ol dispela kumul long bus i stap klostu long ROW tasol long bikbus samting olsem 170 m longwe long rot o ples we ol i kliaim bus. Ol i no klia yet bilong wanem ol dispela pisin i no stap klostu long arere bilong bus.

Ol kamera trep

Wanpela paillet stadi i bin kamap long testim kamera trep na lukim sapos em inap monitarim gut ol wel enimal long tupela BAA. Dispela metod i bin gutpela tru. Kamera i kisim piksa bilong foti nain spises (21 mamel na 28 pisin) long 366 kamera trep na planti ol spises i bin kamap planti taim long piksa. Sampela bilong ol spises i stap long lista bilong konsevesen em kamera i bin kisim piksa bilong ol em Western Montane Tree Kangaroo (*Dendrolagus notatus*; IUCN Endangered). Papuan Eagle (*Harpyopsis novaeguineae*; IUCN Vulnerable, Small Forest Wallaby *Dorcopsulus cf. vanheurni* (IUCN Near Threatened), New Guinea Quoll (*Dasyurus albopunctatus*; IUCN Near Threatened); Woolley's Three-striped Dasyure (*Myoictis leucura*; IUCN Data Deficient) na Greater Melampitta (*Melampitta gigantean*; restricted range). Ol i bin rekodim tu tripela mamel spises na tripela pisin spises, namba wan taim tru long hap bilong Kikori Basin long dispela paillet stadi. Ol risal i soim olsem kamera treping i gutpela wei bilong painim aut moa long ol spises na hamas ol spesel pisin na mamel i stap long ol dispela hap. Long taim ol i mekim wok bilong testim, kamera treping bai i wanpela rot bilong painim aut hamas ol kain enimal na pisin i save hait long dispela hap.

Ol non-volan (i no save flai) mamel

Ol i bin trepim 11-pela spises bilong ol rat na tupela masupiel (mumut) long dispela sevei. Ol tripela narapela spises em ol i rekodim long narapela wei, wanpela em ol i trepim long mist net na lukim long san, narapela em i dai long rot na narapela em long ol bun na tit ol i painim long pekpek bilong dok. Wanpela spises tasol i stap long tupela BAA wantaim em – IUCN Near Threatened New Guinea Quoll (*Dasyurus albopunctatus*). Dispela enimal, kwol, i luk olsem mumut tasol nus bilong em i longpela moa. Ol kamera trep i rekodim tu wanpela monotreme (Short-beaked Echidna, *Tachyglossus aeleatus*), siskispela moa spises bilong ol masupiel em wanpela bilong ol i dispela IUCN Endangered Western Montane Tree Kangaroo, *Dendrolagus notatus*, na foapela moa spises bilong ol rat. Wanpela rat spises bilong narapela hap (Pacific Rat, *Rattus exulans*) em ol i bin trepim long BAA 2 na narapela (Black Rat, *Rattus rattus*) em ol i kisim long Hides Gas Condition Plant.

Wanpela rat spises bilong dispela hap, (*Rattus sp. 'spiny'*) ol i painim long BAA 2 em i no gat nem yet long en, tasol ol i bin painim dispela rat tu long tupela sevei long Hela na Westen Provins. Sampela bilong ol dispela rat spises bilong *Rattus* na *Paramelomys* jenera, i luk wankain tru, na jenetik metod tasol i ken soim klia olsem ol i no wankain. Em i no isi long givim nem long ol dispela spises, tasol jenetik analisis i soim olsem klostu olgeta i gat koneksen wantaim ol rat bilong rijon, tupela tasol i narakain. Ol tupela i narakain em – *Paramelomys*, *P. cf. molis* C ol i painim long BAA 1 na *P. cf. rubex* B – em ol i painim long BAA 2.

Stetistiks bilong ol mamel ol i bin trepim i soim olsem spises bilong *Paramelomys* i no planti tumas insait long mak bilong 100–150 m bilong ROW long tupela BAA wantaim, tasol planti ol rat bilong dispela ples, *Rattus* spises i no wari long ROW. Ol i bin skelim risal bilong enimal ol i kisim long trep long trensek i stap long lowa elevesen long BAA 1 long 2015, wantaim ol bun ol i bin kisim i no longtaim i go pinis, long wanpela hul bilong ston long maunten, long wanpela sevei bipo long konstraksen i bin stat. Long taim ol i skelim, ol i lukim sampela samting i narakain, tasol i no klia yet long wanem as tru, o sapos i soim senis i kamap bikos long senis long ikoloji, na sapos ol senis i kamap bikos long impek bilong Projek.

Ol blakbokis

Ol rekoding bilong krai bilong blakbokis na treping metod em tupela rot ol i bihainim long rekodim ol kain kain blakbokis komyuniti long olgeta transek long BAA 1 na BAA 2. Ol i bin rekodim krai bilong blakbokis long 66 ful nait we ol i yusim ditekta bilong ol blakbokis em ol i putim long mak bilong 50 mita longwe long narapela, stat long arere bilong bus. Ol i luksave long krai bilong 19 spises bilong ol blakbokis. Wanpela narakain krai tru em ol i rekodim long Arakubi Quarry i no olsem krai bilong ol blakbokis ol i save long en, olsem na ol i ting em i wanpela nupela spises ol saintis i no save yet long en. Ol sevei long bihainim taim i mas traim long holim wanpela bilong dispela blakbokis na ol i ken kisim mofolojikel na jenetik infomesen. Wok bilong aidentifaim na konfemim sampela arapela blakbokis spises tu i mas kamap, wantaim wok bilong jenetik na bilong painim aut moa long krai bilong ol blakbokis.

Ol i yusim kain kain wei bilong mesarim ol blakbokis we ol i painim olsem Species Richness na Phylogenetic Diversity i bikpela moa long ples i daunbilo olsem long mak bilong – 1000 m asl klostu long Arakubi Quarry long BAA 2 we ol i ting ol bikpela ston i kam aut long maunten em ples we ol blakbokis bilong hul bilong ston i save stap. Tasol, i no gat gutpela statistik yet long ol blakbokis daivesiti na komyuniti bilong ol long ples i lusim arere bilong bikbus. Dispela 2015 sevei i no soim sapos sampela bagarap i bin kamap long laip bilong ol blakbokis long taim bilong kliaim bus long wokim ROW.

Table 1. Namba bilong ol spises ol i rekodim long 2015 PMA3 Sevei, namba ol i ting i nupela long saiens o i no gat nem yet long en, na namba bilong ol spises i stap long lista bilong IUCN long mak i stap antap long Least Concern.

	Ol Plent	Rokrok	Pisin	Ol Mamel i no save flai*	Blakbokis	TOTAL
Total Spises	318	37	175	28	21	579
Nupela Spises	6	23	0	5+	1+	35+
IUCN Spises	3	2	5	4	0	14+
*I no kaunim tu ol bun long ples slip bilong wanpela aul we i mekim 21 spises						

Ol ples bilong ol

Ol tupela BAA wantaim i gat planti kain kain laip o baiodaivesiti, we bikbus i stap stret yet na i sapotim planti tru ol nupela na ol konsevesen lista plent, rokrok, pisin na mamel wantaim ol sikau bilong diwai na ol kumul. Tupela BAA wantaim i gat ol spesel eria bilong ol pisin bikos i gat planti ol pisin i stap long konsevesen lista, ol pisin we ol man i save kilim na i no gat planti i stap nau (hunting sensitive), na ol pisin i save stap tasol long wanpela hap (restricted range). Ol bikpela ston maunten bilong Hides Ridge i save haitim gut ol pisin i stap long en long ol pipel i go painim pisin na long taim ol i katim diwai na kukim bus long wokim gaden. Dispela kain pasin bilong wokim gaden i bagarapim planti ol monten bikbus long ol arapela hap bilong PNG. Ol karanas bikbus long hap bilong KP107 tu i sapotim wankain ol enimal, tasol i gat ol narakain spises, wanpela bilong ol dispela em populesen bilong ol Greater Melampitta *melampitta gigantean*, dispela pisin i save stap tasol long wanpela hap.

I gat kain kain ol mamel tu long dispela tupela BAA, na i gat tu ol dispela kain i stap long konsevesen lista, na i gat tu ol nupela spises na ol dispela spises em ol saintis i no givim nem yet long en. Namel long ol non-volant mamel (ol dispela mamel i no save flai), spesel tok save i mas kamap long planti tru ol Small Forest Wallaby, ol saintis i no givim nem yet, i stap long tupela BAA wantaim (tasol i gat moa moa yet long BAA 2). Dispela liklik sikau i famili bilong *Dorcopsulus vanheurni* em IUCN i putim long Near Threatened lista. Long ol narapela hap, dispela liklik sikau i no planti tumas olsem na Apstrim Projek Eria i ken kamap wanpela ples we ol bai stap gut long bihain taim. Na long ol blakbokis, i gat planti kain kain long Arakubi transek we ol bikpela ston i kam aut long ol hul bilong maunten. Populesen bilong ol blakbokis i save stap insait long hul bilong ston, i mas gat ples bilong slip na bilong painim kaikai, olsem na long Apstrim Projek eria we i gat planti ol hul bilong maunten, em i gutpela ples we ol kain spises bilong blakbokis i ken stap gut. Wok bilong was gut long dispela kain ples we ol blakbokis i stap, bai i kamapim bikpela salens, tasol ol blakbokis em wanpela grup i save mekim bikpela wok long kamapim ol diwai samting long ol tropikal bikbus.

Ol wok bilong lukautim ol enimal na pisin long dispela Apstrim Projek Eria long ol yia i kam bihain, i mas save olsem namba bilong ol wankain enimal na diwai long dispela BAA em i daunbilo. As bilong dispela em ating mak bilong maunten we wok i kamap i bin narakain long dispela tupela sait.

Ol birua

Long taim ol wok i bin kamap long kliam bus long wokim rot na ROW, i bin gat distebens i kamap long ples we ol pisin na ol enimal na ol plent i save stap, sampela i dai na sampela i ranawe. Tasol i gat tupela arapela birua i kamap long taim bilong konstraksen bilong paipain ROW long Apstrim Projek Eria we inap long kamapim bikpela bagarap long ol pisin na enimal. Ol dispela tupela em (1) i no gat gutpela ples bilong ol enimal na plent moa klostu long ROW bikos long ol senis i kamap (e.g. Andrews et al. 2015) na (2) mekim isi long ol pipel i go insait long bikbus (long painim abus na wok gaden) na ol plent bilong narapela hap i kam insait.

Dispela 2015 sevei i bin painim 'edge effect' long sampela plent na enimal grup ol i stadi long en, dispela i karamapim tu ol rat, blakbokis (wantaim sampela dispela senis i bin helpim) na ol pisin (tripela kumul spises, em ol i no harim krai bilong ol klostu long ROW tasol i ken harim insait long bikbus longwe long ol rot na ples we ol i klaim bus). Tasol i luk olsem dispela distebens i kamap long ol ples i stap klostu long arere bilong bus; sampela bilong ol em ol gras nogut na ol binatang i kamap long arere bilong bus.

Ol data bilong planti yia i kam bihain, em ol i kisim long dispela hap long planti ol sevei i kamap bihain, bai soim ples klia sapos ol dispela senis i pinis o i wok long kamap yet (i kamap bikpela o i go daun liklik). Em bai soim tu sapos ol senis i wok long bagarapim ol arapela enimal na plent long ol hap i stap long Apstrim Projek Eria.

Sevei tim i bin luksave tu long planti ol birua inap kamap long bus na laip bilong ol enimal. Konstraksen bilong ROW na ol rot long ol hap we i bin gat bikbus tru, i mekim isi nau long moa lokal pipel na ol weldok tu, i go insait long painim abus. Antap long maunten long BAA 1, ol i bin lukim ol weldok i kilim ol liklik sikau, Small Forest Wallaby em IUCN i putim long lista bilong Near Threatened. Ol i ting ol weldok i kilim tu ol narapela mamel na pisin i stap long konsevesen lista. Sapos moa birua i kamap long ol bikpela enimal, bai em inap long kamapim tu moa hevi long ol hap i stap longwe long ROW.

Ol i bin painim ol nupela rat long KP107 tasol long BAA 2 we ol i stap tasol arere long bus, na tu long Hides Gas Conditioning Plant. I luk olsem ol dispela rat i stap tasol long hap we ol distebens i bin kamap, tasol ol i stap nau long ol tupela BAA na ol inap long givim sik nogut long ol wel enimal long dispela eria. Dispela i ken kamap long taim ol i bung o wanpela i kilim na kaikai narapela, (eksampel long taim wanpela kwol i kaikaim nupela rat) na long taim wanpela rat i maritim narapela (netiv rat na nupela rat *Rattus spp.*) o long taim jerm nogut i go insait long wara o graun. Long olgeta hap long wol, ol i luksave olsem sapos ol jerm bilong wanpela nupela enimal i kalap long ol netiv enimal, bai em inap long kilim indai ol dispela netiv enimal.

Ol konklusen

1. Ol risal bilong 2015 PMA3 i soim olsem tupela BAA wantaim i gat kain kain ol enimal na plent long ol hap we sevei i kamap.
2. Ol plent na enimal komyuniti long wan wan BAA i narakain, wan wan bilong ol spises tasol i wankain. Dispela i bihainim mak bilong maunten we ol wok bilong tupela BAA i bin kamap.
3. Tupela BAA wantaim i gat planti spises bilong ol plent, rokrok, marsupial, rat na blakbokis em ol saintisi no givim nem yet long en. Ol i painim nupela spises bilong ol plent na rokrok, na wanpela nupela spises bilong blakbokis em ol i bin rekodim krai bilong en.
4. Tupela BAA wantaim i gat ol enimal i stap long konsevesen lista, ol enimal na pisin i save stap long wanpela hap tasol na ol dispela klostu i pinis nau bikos long ol man i wok long kilim ol. Long Hides Ridge i gat planti ol kain enimal olsem sikau bilong diwai, na ol kumul. Ol ples i stap daunbilo long BAA 2 i gat planti ol rokrok na mamel na sampela spises we i save stap tasol long Apstrim Projek Eria.

5. Sampela ol spises long konsevsen lista, na ol spises em i no bin gat rekod bipo long Kikori Basin, em ol i bin painim long taim ol i yusim ol kamera trep. Dispela i soim tru olsem kamera treping em i gutpela wei bilong rekodim ol kain kain enimal husat i save hait gut tru, insait long dispela sevei eria. Dispela em i sotpela paillet stadi, olsem na ol i ting bai ol i kolektim ol yusful dataset bilong mekim stadi long ol spises long taim ol i skruim wok i go moa.
6. Glasim ol rekoding bilong krai bilong pisin long Hides Ridge, i soim olsem yu no inap harim krai bilong ol tripela kumul klostu long ol kain hap olsem ol rot, tasol inap harim krai bilong ol samting olsem 170 m i go insait long bikbus. I no klia tumas watpo ol i save stap longwe long ol Projek infrastraksa.
7. Sampela bilong ol rat we i no gat nem yet, em ol i luksave long ol taim i bin gat jenetik analisis. Dispela metod i soim koneksen wantaim ol arapela populesen long dispela hap. Tupela rat tasol i narakain.
8. Statistikal analisis i kam long pemanen transek i painim liklik senis long daivesiti o komyunti komposisen long wan wan hap longwe long ROW, na i gat sampela bikpela senis long ol rat. Long olgeta yet, ol dispela senis i stap long liklik eria tasol olsem 50 – 100 m long ples ol i kliaim long ROW. Long ol rokrok na blakbokis, i bin gat sampela samting i narakain, tasol i no gat inap data long tok klia.
9. I bin gat sampela samting i kamapim ol senis long wanpela yia bilong mekim dispela sevei, i soim pawa bilong transek metod long painim ol senis i kamap long olgeta grup bilong ol plent na enimal. Transek data bilong 2015 i makim wanpela beslain bilong ol stadi long bihain taim bilong moa senis long spises daivesiti na komyuniti komposisen.
10. Long olgeta yet, ol prelimeneri risal i soim olsem daivesiti velu bilong Apstrim Projek Eria i stap gut, liklik bagarap tasol i kamap long ol hap i stap klostu long ol infrastraksa bilong Projek. Ol bikpela senis, kain olsem long kraiteria we i mas gat rispons, i no bin stap long ol dispela spises. Tasol, ol i luksave olsem sampela birua inap kamap olsem na bai i mas gat moa wok i kamap long was gut long dispela bihain long ol sevei wok bilong 2017 PMA3 i pinis.

CHAPTER 1 – VEGETATION

Fanie Venter and Amos Ona



Dendrobium cuthbertsonii is a miniature orchid species that is commonly hybridised with other orchids to obtain the beautiful red colour of its flowers. It was common in the Hides Ridge area

SUMMARY

Background and aims

Plant communities are useful indicators of environmental change because they can be sampled using standardized and replicated plot designs, and because plants are not mobile. These characteristics make plants particularly useful for documenting and monitoring edge effects, the diverse physical and biotic changes that are associated with verges of roads and other linear clearings.

Species composition and vegetation structure was surveyed in seven plots in BAA 1 on Hides Ridge, and in five plots in BAA 2 on the Agogo Range near Moro. These plots were established at different distances from the ROW to 1) document the overall diversity of plants and plant communities in both BAAs and to identify species of conservation significance, and 2) to assess the diversity and structure of vegetation communities at different distances from the forest edge to detect any changes that may be attributable to construction of the ROW.

Major results

A total of 318 plant species was recorded, including 234 in BAA 1 and 140 in BAA 2. Only 56 species are shared between the two areas, confirming that they have substantially different floras. Six undescribed plant species were documented, all but one completely new to science; and two species listed as 'Near Threatened' and one as 'Endangered' by the IUCN were also encountered. Three plant species were recorded from the island of New Guinea for the first time, and three others represent important new populations for poorly known species.

Preliminary analyses of plant diversity in plots established at different distances from the ROW revealed a significant negative correlation between bryophyte (mosses and liverworts) and epiphyte diversity and increasing distance from the forest edge, with both groups being more diverse in plots closer to the ROW. This suggests that the ROW is providing conditions beneficial to some plant groups. No other significant differences in floral diversity or structure were documented in plots located close to and further away from the ROW.

Conclusions

These preliminary results indicate that the impacts of ROW establishment on local plant communities in both BAA 1 and BAA 2 have, to date, been minimal. Both of the BAAs retain significant biodiversity values, with forests that remain largely intact and support a large number of new and conservation-significant plant species.

INTRODUCTION

Plant communities are useful indicators of environmental change because they can be sampled using standardized and replicated plot designs and because, unlike animals, individual plants are not mobile organisms. These characteristics make plants particularly useful for documenting and monitoring edge effects (Pohlman et al. 2009), the diverse physical and biotic changes that are associated with verges of roads and other linear clearings.

Edge effects are particularly important in tropical rainforests (Laurance et. al. 2009; Pohlman et al. 2009), a habitat that covers most of PNG. Altered physical conditions along habitat edges can alter the distribution and abundance of interior-dwelling species, allow exotic species to invade the area, and result in secondary effects from changes in ecological processes such as pollination, seed dispersal, nutrient cycling and carbon storage (Harris 1984; Janzen 1986; Lovejoy et al. 1986; Wilcove et al. 1986; Kremen et al. 1994; Laurance 2000).

In order to document the diversity and vegetation structure of plant communities adjacent to the ROW at Hides Ridge in BAA 1 and on the Agogo Range near Moro in BAA 2, we conducted rapid vegetation assessments in 12 standard plant plots. We used the plant functional approach recommended by Gillison (2013) because it is highly sensitive to disturbance and modification of vegetation, with shifts in Plant Functional Types (PFTs) rapidly apparent in disturbed areas.

METHODS

Sampling protocols are outlined below, and additional information on the methodology used is contained in the VegClass User Manual (Gillison 2006).

Permanent monitoring plots

Twelve permanent monitoring plots were established during the survey, seven on Hides Ridge in BAA 1 and five on the Agogo Range near Moro in BAA 2. Plots were all situated on the top of limestone ridges with 0–5° slopes and placed so that each covered only a single vegetation type and avoided ecotones. They were aligned along relatively flat areas or along contours to avoid major changes in slope altering the total area being sampled. Plots were established at distances of between 10–200 m from the ROW in order to sample vegetation exposed to different disturbance regimes (Table 1.1).

Plots were gradient-directed transects (“gradsects” sensu Gillison and Brewer 1985; Wessels et al. 1998; Cognan et al. 2006; Gillison et al. 2009) measuring 40 m long and 10 m wide (400 m²). Each plot was divided into eight quadrats measuring 10 m x 5 m (50 m²). Seven plots were established in BAA 1, three in the high-elevation band (2,660–2,730 m asl) between Wellpads E and G and four in the lower elevation band (2,156–2,330 m asl) between Wellpads C and D; and five plots were established in BAA 2, three at KP107 (1,384–1,400 m asl) and two at Arakubi Quarry (1,069–1,080 m asl). The coordinates, altitudes and sampling date for each plot are presented in Table 1.1 and their locations are illustrated in Figures 1.1–1.2.

Table 1.1. Locations, altitudes and sample dates for each plant plot.

Survey plot	Location	Survey date	Plot start coordinates		Plot end coordinates		Distance from ROW	Distance from regrowth forest	Elevation (m)
			Latitude(S)	Longitude(E)	Latitude(S)	Longitude(E)			
PLANT A	BAA 1 Hides Ridge (Lower)	17/06/2015	5.97225	142.754583	5.97261	142.75433	10 m		2188
PLANT B	BAA 1 Hides Ridge (Lower)	19/06/2015	5.971111	142.752278	5.9714	142.75189	106 m		2156
PLANT C	BAA 1 Hides Ridge (Lower)	14/06/2015	5.9435	142.740333	5.94413	142.73979	12 m		2282
PLANT D	BAA 1 Hides Ridge (Lower)	18/06/2015	5.942139	142.741889	5.94192	142.74188	100 m		2330
PLANT E	BAA 1 Hides Ridge (Upper)	15/06/2015	5.921861	142.695833	5.92178	142.69557	60 m		2701
PLANT F	BAA 1 Hides Ridge (Upper)	16/06/2015	5.923917	142.701861	5.92369	142.70207	18 m		2664
PLANT G	BAA 1 Hides Ridge (Upper)	21/06/2015	5.911278	142.685861	5.91163	142.68739	25 m		2728
PLANT H	BAA 2 KP107	28/06/2015	6.44022	143.22406	6.44023	143.22366	62 m		1400
PLANT I	BAA 2 KP107	30/06/2015	6.442417	143.224972	6.44268	143.22527	140 m		1388
PLANT J	BAA 2 KP107	1/7/2015	6.441694	143.226944	6.44192	143.22659	130 m		1384
PLANT K	BAA 2 Arakubi	1/7/2015	6.461417	143.253278	6.46138	143.25293		200 m	1069
PLANT L	BAA 2 Arakubi	2/7/2015	6.461556	143.254361	6.46134	143.25395		110 m	1080

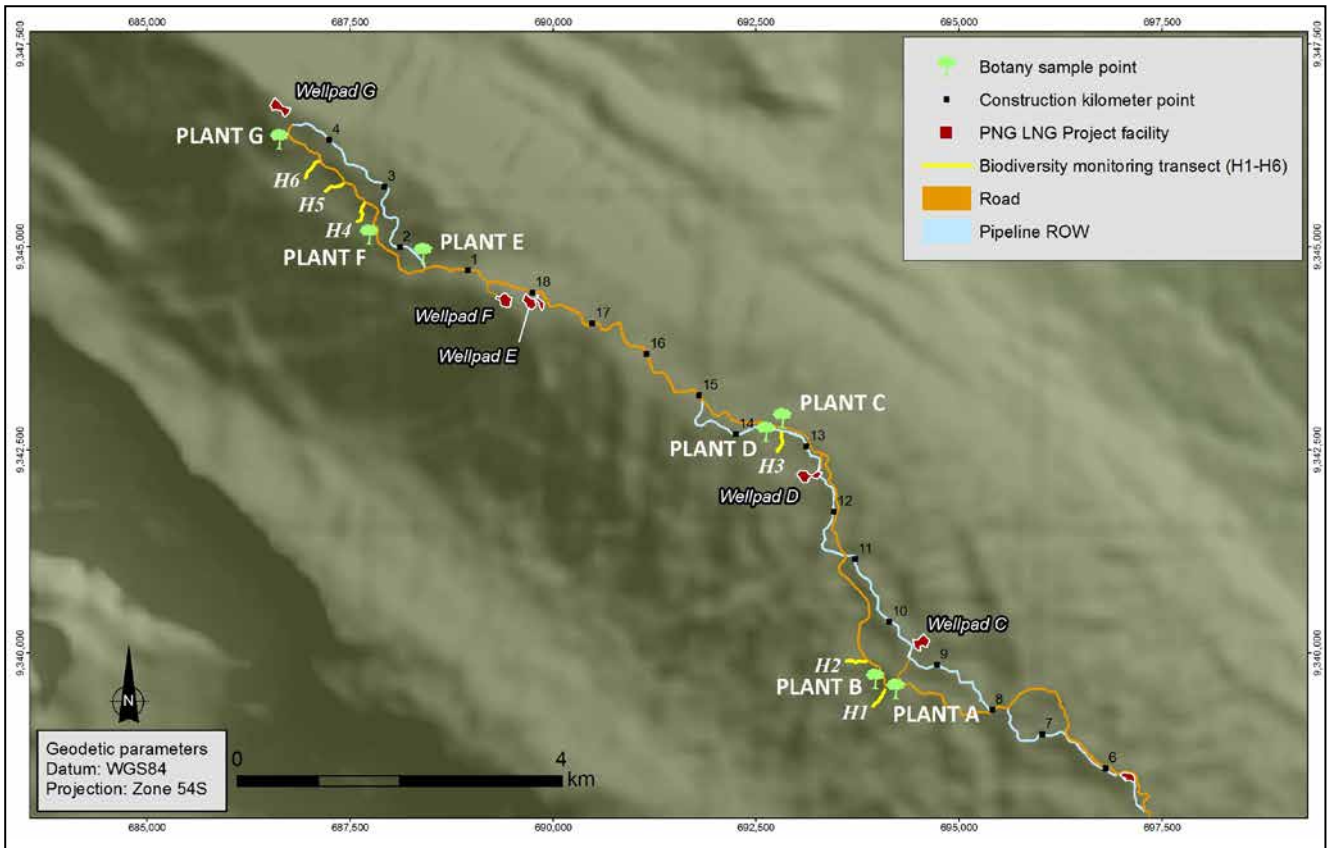


Figure 1.1. Map showing the locations of plots in BAA 1.

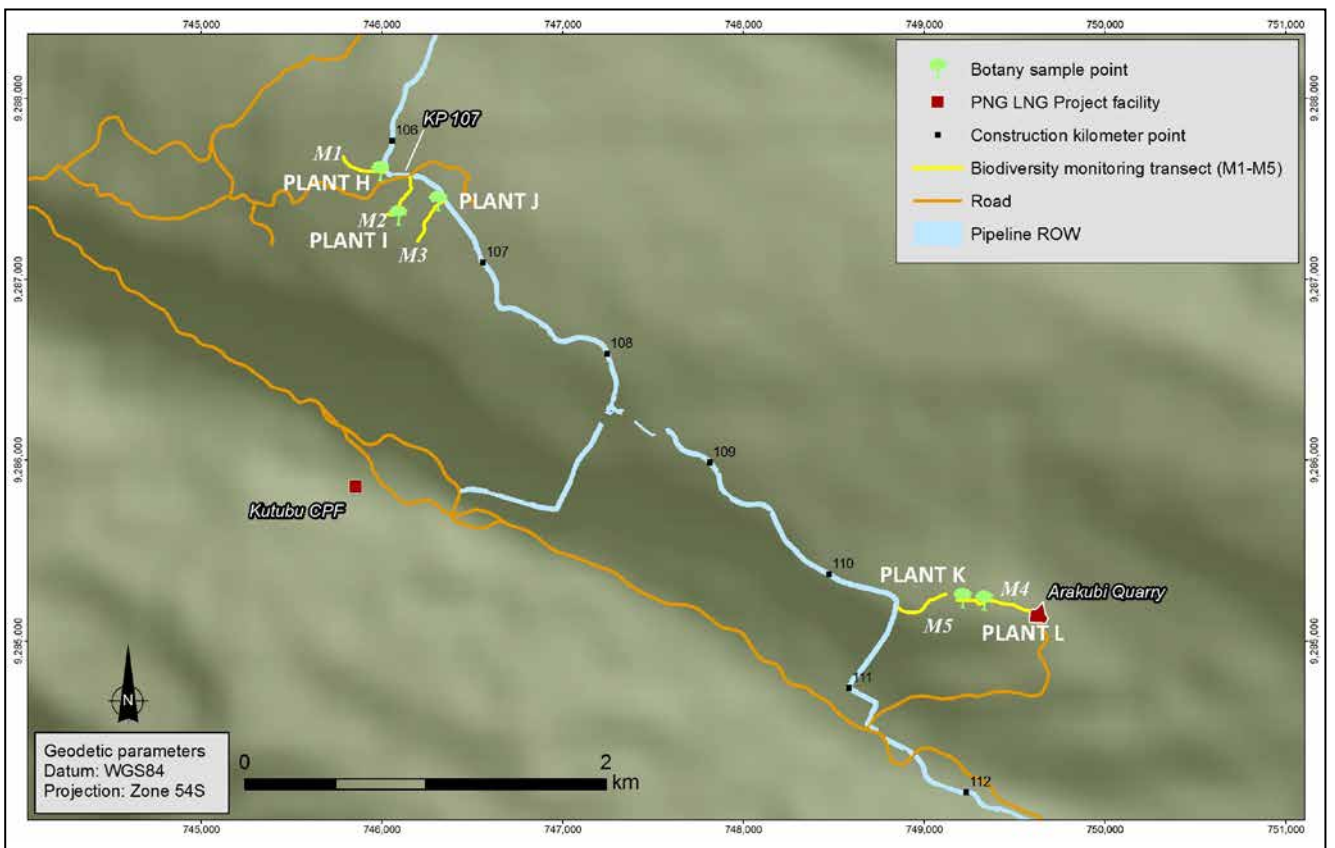


Figure 1.2. Map showing the locations of plots in BAA 2.

Plot layout and demarcation

The start and end points of each plot were marked with a star picket; each was placed at the mid-point of the plot's 10-metre width. A permanent aluminium tag with the name of the plot (ie 'Plant A') was attached to each star picket. To delineate eight quadrats within each plot, a white rope marked at 5 m intervals was first placed between the two star pickets. The rope was placed at least 1 metre above the ground to maximise visibility. To mark out the eight quadrat boundaries, 5 metres was measured in both directions perpendicular to the central rope every five metres, and the outside boundary was marked with a 5 m length of rope.

Data collection

To ensure consistency of data collection pro-forma data sheets were used to collect plot data. For each plot a one-off description of the terrain, soil type, presence of rocks and leaf litter, and other relevant features (slope, aspect, drainage) was recorded. All vascular plant species were then recorded in each plot. Collection methods consisted of systematically recording every species in each successive quadrat, until all eight quadrats in each plot had been completed. Each plant species was recorded only once, in the first quadrat where it was encountered. All plant species in the plots were recorded, including all woody species taller than 1 metre, and non-woody plant forms (shrubs, herbs and epiphytes). Exceptions were sexually immature woody plants more than 2 metres tall, which were included only if there were no sexually mature representatives present. Seedlings were not included. The abundance of bryophytes was calculated using a 'Bryophyte dominance scale'; an explanation of abundance categories is provided in Appendix 1.3.

This study also quantified and classified structural features of woody plants in the plots, such as furcation and basal area measures using the Plant Functional Type (PFT) approach. These structural classifications, incorporating features of lifeform, canopy cover and the height classes of dominant species, are described in Appendix 1.4.

Vouchering plant specimens

If a species could not be identified in the field, samples from fruiting and flowering specimens were vouchered. Photographs that illustrated structural features of the flower and the fruit were also taken. A jewellers tag with a unique number was attached to each specimen and this was cross-referenced to the field datasheet and the photographs.

Plant specimens were then placed between several sheets of newspaper, and the collection number was also written on the newspaper. Newspaper-wrapped specimens were placed into a plant press, which was closed tightly and placed in a dry position for three to five days. The specimens were then removed from the press, still in the newspaper, and each bundle was tied together with string. These bundles were then placed in a plastic bag with sufficient 70% ethanol to saturate the specimens, tied securely and stored in a cool place before being delivered to the Lae Herbarium (Papua New Guinea National Herbarium) where final identifications took place.



Figure 1.3. The Hides Ridge access road in BAA 1. Plot PLANT A is situated on the ridge in the background.



Figure 1.4. The pipeline ROW in BAA 1. The plot PLANT D is situated in the background.

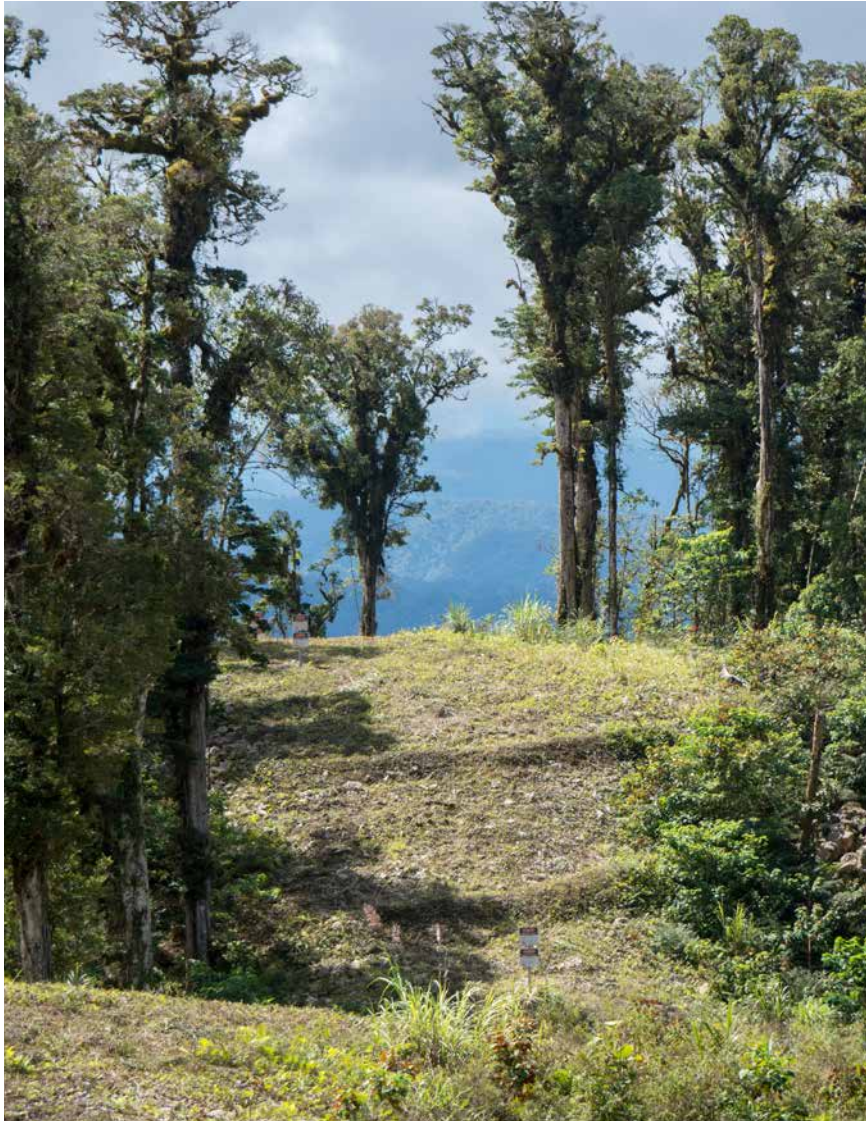


Figure 1.5. The pipeline ROW at KP107 in BAA 2. Note the natural regeneration of ferns, shrubs and young trees on the edge of the ROW.

Analysis

Data from the plots were collated and analysed using the VegClass© Version 2.00 computer software (Gillison 2002), which is a data-entry and analytical tool for general vegetation classification and analysis. It is built around a system of classifying vegetation according to species, their morphological adaptations, and vegetation structure and site physical features. Plant Functional Types are not species-based; individual species can and do exhibit multiple PFTs, and the species to PFT ratio is a powerful indicator of vegetation response along a disturbance gradient. If there is a change in the number of PFT's per species with subsequent monitoring, it indicates changes in long-term light, temperature and moisture levels. The Species: PFT ratio is higher in undisturbed forest than in disturbed forest because in disturbed forest the vegetation is responding to more variable light, water, and nutrient regimes. These provide more, though temporary, environmental niches than climax forest. To avoid biases our final analyses used only 'unique' species records that are not replicated across PFTs and 'unique' PFTs that are not influenced by species weighting (i.e. the number of species per individual PFT)" to examine structural differences across plots (Gillison 2002).

VegClass also automatically calculated a range of diversity indices that will be useful in future for comparing diversity in plots over time.

Because they represent a significant proportion of species in montane New Guinea rainforests we conducted Pearson correlation analyses to determine whether there was an association between the diversity of bryophytes (mosses and liverworts) and epiphytes at different distances from the ROW.

RESULTS AND DISCUSSION

Overview of vegetation in the BAAs

BAA 1 - Hides Ridge is covered by the FIMS vegetation type LN/LsN 'small crowned and very small crowned lower montane forest with *Nothofagus*'. The forest at these elevations is dominated by *Trisyngyne* (formerly *Nothofagus*) species and is generally referred to as *Nothofagus* forest. It has a high percentage of epiphytes, particularly ferns, orchids and Ericaceae.

BAA 2 – Forests in BAA 2 tend to have a wider variety of dominant tree species with a noticeable decrease in *Trisyngyne* species, and epiphytes are rare or absent. At KP107 the forest is FIMS vegetation type LsN 'Very small crowned lower montane forest with *Nothofagus*'. The forest communities are, however, less dominated by *Trisyngyne* and include mixed *Trisyngyne* forest and *Papuacedrus papuana-Elaeocarpus-Cryptocarya* forest. Two FIMS vegetation types are present at Arakubi Quarry. The first is HsN/Hm 'Small crowned hill forest with *Nothofagus*/Medium crowned hill forest'; these hill forest types were restricted to the eastern-most edge of the forest at Arakubi, the only part of BAA 2 below 1,000 m asl. This area was also entirely secondary forest. Further to the west, adjacent to the ROW, the forest is FIMS vegetation type LsN/L 'Very small crowned lower montane forest with *Nothofagus*/Small crowned lower montane forest'. Components of the lower montane forest dominated by *Trisyngyne* are generally restricted to the ridges and upper slopes in this area.

A total of 318 plant species was recorded from plots in the two BAAs, with 234 species recorded in BAA 1 and 140 species in BAA2. Only 56 species were shared between the two study areas. A list of all vascular plant species recorded in plots is presented in Appendix 1.1 and a breakdown of species by plot and quadrat is presented in Appendix 1.2.

New and undescribed species

Six undescribed plant species were documented in the Upstream Project Area, all but one completely new to science. These are described briefly below. Numbers following the species name are unique voucher numbers.

Begonia sp. 1. (Venter 15443) (Figure 1.6)

A fleshy vine with purplish climbing stems that grows to 3 m long. The leaves are light green with prominent purple venation on the undersides. Young leaves have white markings, but these soon disappear. The large (to 40 mm diameter) pink flowers have darker pink parallel veins. The fruit is deep pink turning light brown at maturity. This new species is only known from two small populations in BAA 1 at Hides Ridge.

Cyrtandra sp. 1. (Venter 15429) (Figure 1.7)

This plant is a low-level epiphyte growing to 45 cm tall. It is fleshy and the whole plant is covered in long dense brownish hairs. The soft leaves are prominently quilted. The flowers are very fleshy, white, with the corolla lobes forming a small opening. The flower bracts are dark brown. This new species is only known from three populations in BAA 1 at Hides Ridge.

Psychotria sp.1 (Venter s. n.) (Figure 1.8)

A woody, sparsely branched shrub growing up to 2 m tall. The dark green leaves have a hard leathery texture, are prominently quilted on the upper leaf surface, and the leaf apices are recurved. The drooping inflorescences consist of 4–12 flowers. The fragrant white waxy flowers are some of the largest known for the genus (Sohmer 1988). This new species is only known from a single population at Hides Ridge.

Rhododendron sp. 1 (Venter 15428) (Figure 1.11)

A high-level epiphytic shrublet growing to 50 cm tall and having hard leathery leaves with red petioles. The pendulous flowers are tubular, up to 50 mm long and have an intense purplish red color. One plant was found at Hides Ridge. This undescribed species was previously known from Kawarobip near the Hindenburg Wall in Western Province.

Saurauia sp. 1 (Venter 15433) (Figure 1.10)

A small, sparsely branched tree growing up to 4 m tall. The branches are spreading and the leaves are dark glossy green above and light green below with a prominent sunken midrib. There are long spines scattered along the midrib on the

underside of the leaf. The drooping flowers are white and fragrant with 10 mm long corolla lobes. This species is known only from 19 scattered individuals at Hides Ridge.

Vaccinium sp. 1 (Venter 15449) (Figure 1.9)

A high-level epiphytic shrub with erect stems that grows up to 1 m tall. The leaves are erect and have a hard leathery texture. They are glossy and dark green above, paler below, and have short red petioles. The pink flowers are a depressed globular shape, a character that is unique for the genus (Sleumer 1967), and are densely hairy with a very small opening formed by the fused fleshy corolla lobes. It is known only from a single plant at Hides Ridge.

Species of conservation significance (IUCN-Listed)

One species listed as 'Endangered' and two species listed as 'Near Threatened' by the IUCN were encountered. Each is described briefly below.

Calymmodon cucullatus (Polypodiaceae) (IUCN Endangered) (Figure 1.13)

A small, low-level epiphytic fern with a rosette of spreading leaves that grows up to 20 cm long. According to material in the Lae Herbarium it occurs in Eastern Highlands Province (Mt. Piora) and Central Province (Murray Pass) on mainland Papua New Guinea and on New Ireland (Weitin River and Mt. Tumbumpo). It also occurs at Lake Habbema in Indonesian Papua Province, and in China, Malaysia, and New Caledonia (China Plant Specialist Group 2004). A small population of 23 individuals was found on Hides Ridge in BAA 1. It is threatened by habitat degradation elsewhere in its range.

Helicia latifolia (Proteaceae) – Garramuta, Ohesali - (IUCN Near Threatened)

A tree growing up to 20 m tall (but normally not exceeding 10 m) in open forest. The leaves are hard and leathery, and glossy on the upper surface. The midrib is very prominent on both surfaces and the petiole is stout and short. The drooping inflorescences are up to 16 cm long with paired light yellow flowers that are sparsely hairy. The fruit is glabrous and 30–40 mm long (White 1923). This species is endemic to Papua New Guinea where it occurs in Gulf, Central, Milne Bay, Northern and East New Britain Provinces. It was recorded in BAA 1 on Hides Ridge. It is threatened by habitat degradation elsewhere in its range.

Myristica globosa (Myristicaceae) – Round-fruited Nutmeg (IUCN Near Threatened)

This species is normally a sub-canopy tree growing up to 30 m tall with the branches growing at right angles to the main stem. The bark is smooth to shallowly fissured. The young shoots and buds are clothed in rusty brown hairs and the leaves are much lighter ventrally than dorsally with the petiole deeply channeled on the upper surface. Male and female flowers occur on different plants. The male flowers are in fascicles on woody tubercles and the female flowers in fascicles on the branches. The fruit is ellipsoidal and 25–30 mm long and 20 mm in diameter, covered in brownish hairs when immature but soon glabrous. It occurs over most of Mainland PNG, New Britain and Bougainville (De Wilde 2000) and was found in BAA 2. This species is targeted by logging companies elsewhere in PNG, leading to its Near Threatened status.

Other significant records

Several plant species found during this survey are important new populations of poorly known species within mainland New Guinea, and three others were recorded from the island of New Guinea for the first time.

Aquilaria filaria (Thymelaeaceae)

A sub-canopy tree that reaches a maximum height of 20 m. Young twigs are covered in long hairs but soon become glabrous and the leaves are arranged spirally. The inflorescences are axillary and the flowers are 5–7 mm long. The fruit is yellow, 1.2–1.5 cm long, and each contains two bluish seeds. It is sparsely distributed throughout the Philippines, Maluku Islands and PNG where most records for this species are in West Sepik Province. There are now two records for Southern Highlands Province, the first on the southern slopes of Mt. Bosavi and the second is the newly discovered population near Moro in BAA 2.

Calanthe wernerii (Orchidaceae) (Figure 1.14)

A rare terrestrial orchid with dark green leaves up to 30 cm long and 10 cm wide with prominent light yellow spots. The inflorescence is 45–50 cm tall with 8–15 moderately large flowers with light yellow sepals and deep yellow lips

(Schlechter 1912; Clayton and Cribb 2013). It occurs as scattered individuals on the forest floor growing in deep leaf litter. This species is endemic to PNG where it was previously known only from a single collection in Southern Highland Province and a single collection in Eastern Highlands Province. The records from BAA 2 on the Agogo Range are important new populations of a poorly known species.

Ficus cereicarpa (Moraceae) (Figure 1.15)

A small tree with hairy branchlets that grows up to 9 m tall. The leaves are relatively large, 13–30 x 6–13 cm, slightly hairy above and extremely hairy below. The petioles are 5–18 cm long and densely hairy. The figs are cauliflorous, with the oblong to round fruit sometimes occurring on the main roots. This species was previously known only from northern Borneo, and the populations at Hides Ridge in BAA 1 are the first records of this species for the island of New Guinea (Berg et al. 2005).

Gaultheria nummularioides (Ericaceae) (Figure 1.16)

A small, low-growing plant with prostrate stems that are up to 20 cm long and produce roots at the nodes. The glossy leaves are 6–13 x 5–9 mm with serrated leaf margins. The solitary flower is fleshy, ovoid and white turning pinkish with age. This species is distributed from China, Sumatra, and Java to Bali (Sleumer 1967) and this is the first record for the island of New Guinea where it is known from a single specimen on Hides Ridge.

Macadamia ternifolia (Proteaceae) (Figure 1.17)

A small tree that grows up to 8 m tall. The leathery leaves occur mostly in threes and have coarse serrations or 'teeth' along the edges. The inflorescences are axillary, up to 18 cm long and consist of many pinkish flowers. The fruit is 1.5–2 cm long, globular and slightly compressed, greyish in color but turning brown at maturity. The narrow leaves with coarse uneven teeth-shaped serrations easily identify the young plants. The genus is distributed from New Caledonia in the east to Australia and to Celebes in Indonesia (Sleumer 1955, Wrigley & Fagg 1989, Gross 1995) but this is the first record of the genus *Macadamia* for the island of New Guinea.

Rhododendron rubineiflorum (Ericaceae)

Regarded as the smallest *Rhododendron* in the world, this tiny epiphyte is a mere 10 mm tall and forms spreading branches up to 20 mm long. The leaves are just 5–7 mm long and glossy green. The flower is ruby-red, trumpet-shaped and up to 20 mm in diameter. For many years it was known only from the type locality but it is now known from additional localities on Mt. Giluwe and Hides Ridge in BAA 1.

Influence of the ROW on plant diversity and vegetation structure

Table 1.2 summarises the major structural features of the vegetation in each plot. Structural elements that were examined are summarized and described in Appendix 1.4. Correlation analyses of all structural vegetation features examined failed to detect any significant association between vegetation structure (including PFT's) and distance of plots from the ROW. Although there was no significant trend detected by current data, the addition of data from future surveys will permit more robust analyses. The Species:PFT ratio is a particularly useful baseline measure from which to monitor any future changes, because it is widely accepted as an indicator of increasing disturbance.

Influence of the ROW on bryophyte abundance

There was a significant negative correlation between increasing distance of the plots from the ROW and bryophyte abundance (Pearson's Correlation $P < 0.05$; Figure 1.18). The bryophytes were dominated by moss species. Although liverworts were included in counts they were not differentiated from mosses because this is an extremely time consuming process in the field. High bryophyte diversity near the ROW is not unexpected because many moss genera and species favour lighter and more windy conditions.

Influence of the ROW on plant diversity

There was no significant association between plant diversity and distance of plots from the ROW. However when treated separately there was a significant negative correlation between epiphyte diversity and increasing distance of plots from the ROW (Pearson's Correlation $P < 0.05$; Figure 1.19) when all plots in both BAAs were combined. Data for the numbers of epiphytic plants in each plot are presented in Table 1.2. Plots PLANT A, C, D and G in BAA 1 were the

most diverse while plots PLANT I and K in BAA 2 each contained only four epiphyte species. Epiphytes in both BAAs were dominated by species in the families Araliaceae, Ericaceae, Hymenophyllaceae, Orchidaceae, Pandanaceae, Piperaceae and Rubiaceae. The higher diversity of epiphytes closer to the ROW at plots PLANT A, C, D and G is at least partially explained by their colonisation by a number of additional species having a greater tolerance of higher light and wind, and lower moisture levels. Unfortunately, due to terrain constraints most plots in BAA 1 were closer to the ROW than plots in BAA 2 so these results may also be influenced by elevation. With an additional plot established in BAA 2 (see below) and additional data collected after the second survey, a more robust analysis will be possible that considers the effects of both distance of plots from the ROW and elevation.

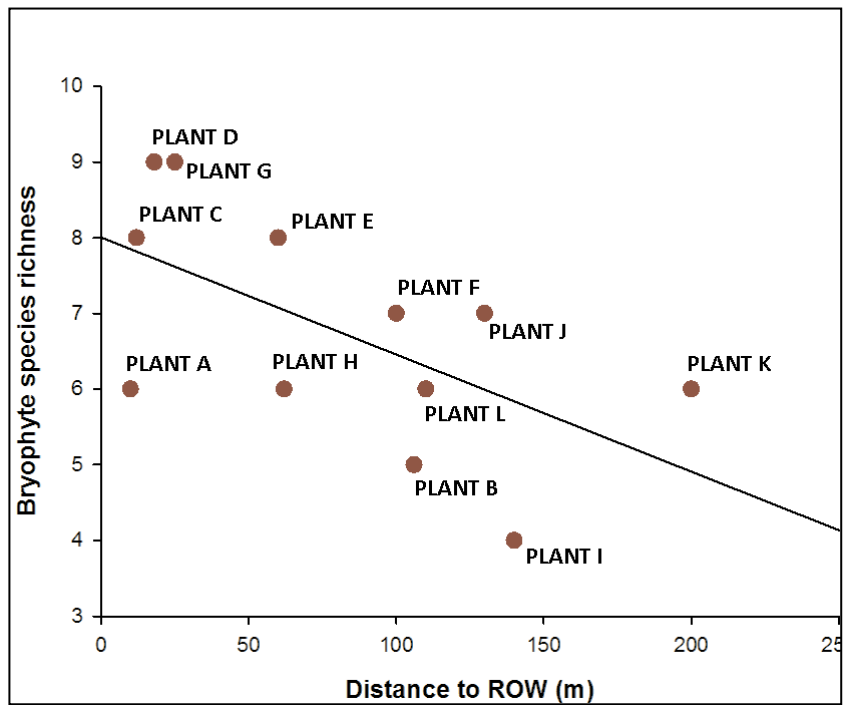


Figure 1.18. Correlation between bryophyte abundance and distance of plots from ROW.

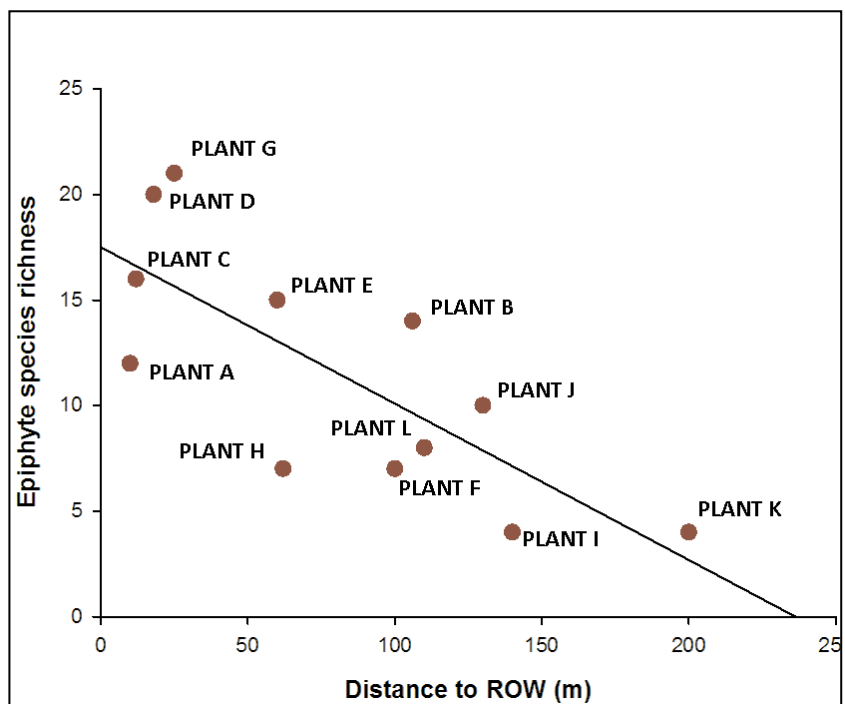


Figure 1.19. Correlation between epiphyte diversity and distance of plots from ROW.

Table 1.2. Plot location, distance from ROW, and major structural features of plants in both BAAs

Plot	Location	Distance from ROW (m)	Total Species Records	Unique Species	Unique PFTs	Unique Species /PFT ratio	Unique PFTs /Rec	Plant Functional Complexity	Mean Canopy Height (m)	Canopy Cover (%)	Canopy Woody (%)	Woody Plants (0-10)	Bryophytes (0-10)	Epiphyte species	Litter Depth (cm)	Mean Basal Area	Mean Furcation Index	Furcation Index CV%	Plant Functional Complexity
PLANT A	BAA 1	10	63	63	39	1.62	0.62	50	40	80	99	5	6	12	10	23.33	37.5	23.89	50
PLANT B	BAA 1	106	79	75	46	1.63	0.58	216	25	60	98	8	5	14	1	23.67	33.25	40.9	216
PLANT C	BAA 1	12	79	76	40	1.9	0.51	256	30	60	98	5	8	16	15	23	27.75	51.79	256
PLANT D	BAA 1	18	57	56	46	1.22	0.81	258	30	70	99	8	9	20	5	36	38.75	39.47	258
PLANT E	BAA 1	60	61	53	42	1.26	0.69	220	40	60	98	5	8	15	16	30.33	31.25	27.41	220
PLANT F	BAA 1	100	74	73	52	1.4	0.7	256	40	80	99	5	7	7	5	26	37.4	25.13	256
PLANT G	BAA 1	25	56	53	39	1.36	0.7	72	20	60	95	8	9	21	10	20.33	38.5	35.78	72
PLANT H	BAA 2	62	66	66	36	1.83	0.55	232	30	60	99	9	6	7	5	22.33	40	24.33	232
PLANT I	BAA 2	140	38	37	27	1.37	0.71	182	30	70	99	7	4	4	5	29.67	39.5	17.38	182
PLANT J	BAA 2	110	68	66	37	1.78	0.54	184	40	70	98	8	6	8	5	30	30.25	26.53	184
PLANT K	BAA 2	200	55	51	34	1.5	0.62	212	30	80	98	6	6	4	5	29.67	32	25.55	212
PLANT L	BAA 2	130	70	67	39	1.72	0.56	204	40	70	99	7	7	10	5	22	38	25.04	204

Other observations on plant assemblages

Although not significantly different from other plots based on total PFTs or other structural traits, Plot PLANT I had a distinct vegetation type consisting of tall *Papuacedrus papuana* - *Elaeocarpus* spp. – *Cryptocarya* rainforest. It was also the plot with the lowest number of species, and had a particularly depauperate bryophyte flora and only 27 unique PFTs (Table 1.2). This plot is located at KP107 on the Agogo Range in close proximity to two other plots, and the factors generating this unusual vegetation assemblage are unclear.

Although we failed to detect any significant differences between plant diversity and vegetation structure in plots at different distances from the ROW, we observed at BAA 1 that in areas where cleared vegetation was pushed against the edge of the forest during construction, the effects of higher light intensity, higher temperatures and drier conditions are less visible than in areas where the edge of the ROW was cleared of trees and debris. The leaf litter and soil in areas with decaying vegetation adjacent to the forest were moist and the dead vegetation appeared to be trapping, and providing shelter for, seeds that had washed or blown in. Growth of shrubs and young trees appeared to be enhanced in these areas compared to the regrowth in areas devoid of dead vegetation and debris at the forest edge. These more exposed forest edges are exposed to increased light levels and temperatures, and to lower moisture levels and are more likely to harbor native pioneer plants such as Bleeding Heart Tree (*Homalanthus novoguineensis*) and Native Mulberry (*Pipturus argenteus*) which were observed growing well into the forest where the edge was more exposed.

CONCLUSIONS

Our results indicate that the impacts of ROW establishment on local plant communities in both BAA 1 and BAA 2 have, to date, been minimal. Both of the BAAs retain significant biodiversity values, with forests that remain largely intact and support a large number of new and conservation-significant plant species.

1. There was no overall correlation between plant diversity and distance of plots from the ROW
2. However when treated separately two plant groups, epiphytes and bryophytes, show significant correlations of diversity and abundance respectively with distance of plots from the ROW. The relative contributions of elevation and disturbance to these observed patterns are unclear and will be examined in more detail following the second survey.

REFERENCES

- Berg, C.C., Corner, E.J.H. & Nootboom, H.P. 2005. Moraceae - *Ficus*. *Flora Malesiana* 17: 410–411.
- China Plant Specialist Group. 2004. *Calymmodon cucullatus*. The IUCN Red List of Threatened Species 2004. <http://www.iucnredlist.org/details/46614/0>
- Clayton, D. & Cribb, P. 2013. The genus *Calanthe*. Natural History Publications, Borneo.
- De Wilde, W.J.J. 2000. Myristicaceae. *Flora Malesiana* 14: 480–483.
- Gillison, A.N. 2002. A generic, computer-assisted method for rapid vegetation classification and survey: tropical and temperate case studies. *Conservation Ecology* 6: 3.
- Gillison, A.N. 2006. A Field Manual for Rapid Vegetation Classification and Survey for general purposes [Including instructions for the use of a rapid survey proforma and 'VegClass© 2.00 computer software]. Centre for International Forestry Research, Jakarta.
- Gillison, A.N. 2013. Plant functional types and traits at the community, ecosystem and world level. Pp. 347–386 in (Van der Maarel E & Franklin, J (eds) *Vegetation ecology*, 2nd edn. Wiley, Chichester.
- Gillison, A.N. & Brewer, K.R.W. 1985. The use of gradient directed transects or gradsects in natural resource surveys. *Journal of Environmental Management* 20: 103–127.
- Gillison, A.N., Asner, G.P., Fernandes, E.C.M., Mafalacusser, J., Banze, A., Izidine, S., De Fonseca, A.R. & Pacate, H. 2009. Biodiversity and agriculture in dynamic landscapes: Integrating ground and remotely sensed baseline surveys. *Journal of Environmental Management* 177: 9–19.
- Gross, C.L. 1995. *Macadamia*. Pp. 419–425 in (Orchard, A.E. & P.M. McCarthy eds) *Flora of Australia*. 16. Canberra: ABRS and Melbourne: CSIRO.
- Harris, L. D. 1984. *The fragmented forest: Island biogeography theory and the preservation of biotic diversity*. University of Chicago Press, Chicago, Illinois.
- Janzen, D. H. 1986. The external threat. Pp. 286–303 in (Soule, M.E. ed.) *Conservation biology: The science of scarcity and diversity*. Sinauer Associates, Sunderland, Massachusetts.
- Kremen, C., Merenlender, A.M. & Murphy, D.D. 1994. Ecological Monitoring: A Vital Need for Integrated Conservation and Development Programs in the Tropics. *Conservation Biology* 8: 388–397.
- Laurance, W.F. 2000. Do edge effects occur over large spatial scales? *Trends in Ecology and Evolution*. 15: 134–135.
- Laurance, W.F., Goosem, M. & Laurance, S.G.W. 2009. Impacts of roads and linear clearings on tropical forests. *Trends in Ecology and Evolution* 24: 659–669.

- Lovejoy, T. E., Bierregaard, R.O., Rylands, A. B., Malcolm, J.R., Quintela, C.E., Harper, L.H., Brown, K.S., Powell, A.H., Powell, G.V.N., Schubart, H.O.R. & Hays, M.B. 1986. Edge and other effects of isolation on Amazon Forest fragments. Pp. 257–285 in (Soule, E.M. Ed) *Conservation biology*. Sinauer Associates, Sunderland, Massachusetts.
- Pohlman, C.L., Turton, S.M. & Goosem, M. 2009. Temporal variation in microclimatic edge effects near powerlines, highways and streams in Australian tropical rainforest. *Agricultural and Forest Meteorology* 149: 84–95.
- Schlechter, F.R.R. 1912. *Calanthe weneri*. *Repertorium Specierum Novarum Regni Vegetabilis. Centralblatt für Sammlung und Veröffentlichung von Einzeldiagnosen neuer Pflanzen*. 1: 382.
- Sohmer, S.H. 1988. The Nonclimbing Species of the Genus *Psychotria* (Rubiaceae) in New Guinea and the Bismarck Archipelago. *Bishop Museum Bulletin in Botany* 1. Bishop Museum Press, Honolulu.
- Wessels, K. J., van Jaarsveld, A.S., Grimbeek, J.D. & van der Linde, M.J. 1998. An evaluation of the gradsect biological survey method. *Biodiversity and Conservation* 7: 1093–1121.
- White, C.T. 1923. A Contribution to our Knowledge of the Flora of Papua (British New Guinea). *Proceedings of the Royal Society of Queensland* 34: 26–27.
- Wilcove, D. S., McLellan, C.H. & Dobson, A.P. 1986. Habitat fragmentation in the temperate zone. Pp. 237–256 in M. E. Soule (Editor) *Conservation Biology: The science of scarcity and diversity*. Sinauer Associates, Sunderland, Massachusetts.
- Wrigley, J.W. & Fagg, M. 1989. Genus *Macadamia*. *Banksias, Waratahs & Grevilleas*. Collins Publishers, Australia.

New and undescribed plant species



Figure 1.6. *Begonia* sp. 1.



Figure 1.7. *Cyrtandra* sp. 1.



Figure 1.8. *Psychotria* sp. 1.



Figure 1.9. *Vaccinium* sp. 1.



Figure 1.10. *Saurauia* sp. 1.



Figure 1.11. *Rhododendron* sp. 1.

Other significant plant records



Figure 1.12. Fanie Venter and Anita Mosby examine a rare plant at KP107



Figure 1.13. *Calymmodon cucullatus*



Figure 1.14. *Calanthe wernerii*



Figure 1.15. *Ficus cereicarpa*



Figure 1.16. *Gaultheria nummularioides*



Figure 1.17. *Macadamia ternifolia*

APPENDICES

Appendix I.I. Plant species recorded in survey plots at Hides Ridge (BAA 1) and on the Agogo Range near Moro (BAA 2).

Family	Scientific Name	BAA 1	BAA 2
FERNS AND LYCOPHYTES			
Adiantaceae	<i>Adiantum aculeolatum</i>	X	
Aspleniaceae	<i>Asplenium bipinnatifidum</i>	X	
Aspleniaceae	<i>Asplenium marattioides</i>	X	X
Blechnaceae	<i>Blechnum revolutum</i>	X	
Blechnaceae	<i>Diploblechnum fraseri</i>	X	
Cyatheaceae	<i>Cyathea brackinridgei</i>	X	
Cyatheaceae	<i>Cyathea contaminans</i>	X	X
Cyatheaceae	<i>Cyathea cucullifera</i>	X	
Cyatheaceae	<i>Gymnosphaera hornei</i>	X	X
Dryopteridaceae	<i>Dryopteris papuana</i>	X	
Dryopteridaceae	<i>Dryopteris wallichiana</i>	X	
Dryopteridaceae	<i>Polystichum daymanense</i>	X	
Gleicheniaceae	<i>Dicranopteris linearis</i>	X	
Grammitidaceae	<i>Grammitis dolichosora</i>	X	
Hymenophyllaceae	<i>Cephalomanes obscurum</i>	X	X
Hymenophyllaceae	<i>Crepidomanes aphlebioides</i>	X	
Hymenophyllaceae	<i>Hymenophyllum melanosorum</i>	X	
Hymenophyllaceae	<i>Hymenophyllum ooides</i>	X	
Lindsaeaceae	<i>Lindsaea pulchella</i>	X	
Marattiaceae	<i>Marattia tafaensis</i>	X	
Oleandraceae	<i>Oleandra pilosa</i>		X
Osmundaceae	<i>Leptopteris alpina</i>	X	
Polypodiaceae	<i>Calymmodon cucullatus</i>	X	
Polypodiaceae	<i>Ctenopterella blechnoides</i>	X	
Polypodiaceae	<i>Lepisorus novoguineensis</i>	X	
Polypodiaceae	<i>Selliguea albidosquamata</i>	X	
Polypodiaceae	<i>Selliguea plantaginea</i>	X	
Polypodiaceae	<i>Themelium yoderi</i>	X	
Pteridaceae	<i>Antrophyum alatum</i>	X	
Pteridaceae	<i>Syngamma schlechteri</i>	X	

Family	Scientific Name	BAA 1	BAA 2
Thelypteridaceae	<i>Metathelypteris</i> sp.nov.		X
Thelypteridaceae	<i>Sphaerostephanos adenostegius</i>	X	X
Vittariaceae	<i>Vittaria elongata</i>	X	
GYMNOSPERMS			
Cupressaceae	<i>Papuacedrus papuana</i>	X	
Podocarpaceae	<i>Dacrydium nidulum</i>	X	
Podocarpaceae	<i>Podocarpus neriifolius</i>	X	
MONOCOTS			
Araceae	<i>Alocasia hollrungii</i>	X	X
Araceae	<i>Alocasia lancifolia</i>		X
Araceae	<i>Alocasia nicholsonii</i>	X	
Araceae	<i>Epipremnum papuana</i>		X
Araceae	<i>Holochlamys beccarii</i>		X
Araceae	<i>Rhaphidophora neoguineensis</i>		X
Araceae	<i>Schismatoglottis calyptrata</i>		X
Arecaceae	<i>Areca multifida</i>		X
Arecaceae	<i>Calamus fertilis</i>	X	
Arecaceae	<i>Calamus heteracanthus</i>		X
Arecaceae	<i>Caryota rumphii</i>		X
Arecaceae	<i>Gronophyllum chaunostachys</i>		X
Arecaceae	<i>Heterospathe elegans</i>	X	X
Arecaceae	<i>Hydriastele cariosa</i>		X
Arecaceae	<i>Hydriastele pinagnoides</i>		X
Arecaceae	<i>Linospadix albertisianus</i>		X
Asparagaceae	<i>Cordyline fruticosa</i>		X
Cyperaceae	<i>Scleria</i> sp.	X	
Marantaceae	<i>Phrynium pedunculatum</i>	X	
Orchidaceae	<i>Aglossorrhyncha biflora</i>	X	
Orchidaceae	<i>Agrostophyllum brachiatum</i>	X	
Orchidaceae	<i>Agrostophyllum superpositum</i>	X	
Orchidaceae	<i>Anoectochilus papuanus</i>		X
Orchidaceae	<i>Appendicula polystachya</i>		X
Orchidaceae	<i>Bulbophyllum fractiflexum</i>		X
Orchidaceae	<i>Bulbophyllum leucothyrsus</i>		X
Orchidaceae	<i>Calanthe rhodochila</i>	X	X

Family	Scientific Name	BAA 1	BAA 2
Orchidaceae	<i>Calanthe weneri</i>		X
Orchidaceae	<i>Ceratostylis acutifolia</i>	X	
Orchidaceae	<i>Ceratostylis subulata</i>	X	
Orchidaceae	<i>Dendrobium cuthbertsonii</i>	X	
Orchidaceae	<i>Dendrobium subclausum</i>	X	
Orchidaceae	<i>Dendrochilum longifolium</i>	X	X
Orchidaceae	<i>Epiblastis basilis</i>	X	
Orchidaceae	<i>Glomera aurea</i>		X
Orchidaceae	<i>Glomera hamadryas</i>	X	
Orchidaceae	<i>Glossorhyncha tubisepala</i>	X	
Orchidaceae	<i>Mediocalcar bifolium</i>	X	
Pandanaceae	<i>Freycinetia angustissima</i>	X	X
Pandanaceae	<i>Freycinetia archboldtiana</i>	X	X
Pandanaceae	<i>Pandanus brosimos</i>	X	X
Pandanaceae	<i>Pandanus kaernbachii</i>		X
Poaceae	<i>Nastus longispicula</i>	X	X
Smilacaceae	<i>Smilax calophylla</i>		X
Zingiberaceae	<i>Alpinia stenobracteolata</i>	X	X
Zingiberaceae	<i>Hornstaedtia scottiana</i>		X
Zingiberaceae	<i>Pleuranthodium tephrochlamys</i>		X
Zingiberaceae	<i>Riedelia corallina</i>		X
Zingiberaceae	<i>Riedelia microbotrya</i>	X	X
Zingiberaceae	<i>Riedelia montana</i>	X	X
DICOTS			
Actinidiaceae	<i>Saurauia calyprata</i>	X	
Actinidiaceae	<i>Saurauia conferta</i>		X
Actinidiaceae	<i>Saurauia holotricha</i>		X
Actinidiaceae	<i>Saurauia naumannii</i>	X	
Actinidiaceae	<i>Saurauia pleurilocularis</i>	X	
Actinidiaceae	<i>Saurauia purgand</i>		X
Actinidiaceae	<i>Saurauia sp.nov.</i>	X	
Actinidiaceae	<i>Saurauia stichophylla</i>	X	
Anacardiaceae	<i>Camptosperma brevipetiolatum</i>	X	
Anacardiaceae	<i>Rhus taitensis</i>		X
Apiaceae	<i>Mackinlaya schlechteri</i>		X

Family	Scientific Name	BAA 1	BAA 2
Apocynaceae	<i>Alyxia lamii</i>	X	X
Apocynaceae	<i>Cerbera floribunda</i>		X
Apocynaceae	<i>Marsdenia</i> sp.	X	
Apocynaceae	<i>Melodinus forbesii</i>	X	
Araliaceae	<i>Harmsiopanax ingens</i>	X	
Araliaceae	<i>Polyscias ledermannii</i>	X	X
Araliaceae	<i>Schefflera actinophylla</i>	X	
Araliaceae	<i>Schefflera dentata</i>	X	X
Araliaceae	<i>Schefflera setulosa</i>	X	
Begoniaceae	<i>Begonia randiana</i>	X	
Calophyllaceae	<i>Calophyllum collinum</i>	X	
Calophyllaceae	<i>Calophyllum soulattri</i>		X
Clusiaceae	<i>Garcinia archboldtiana</i>	X	
Clusiaceae	<i>Garcinia hollrungii</i>	X	
Clusiaceae	<i>Garcinia hunsteinii</i>	X	
Clusiaceae	<i>Garcinia latissima</i>	X	X
Clusiaceae	<i>Garcinia ledermannii</i>	X	X
Clusiaceae	<i>Garcinia schraderi</i>		X
Clusiaceae	<i>Sphenostemon arfakensis</i>	X	
Clusiaceae	<i>Sphenostemon papuanum</i>	X	X
Cunoniaceae	<i>Caldcluvia celebica</i>	X	
Cunoniaceae	<i>Caldcluvia nymanii</i>	X	
Cunoniaceae	<i>Pullea glabra</i>	X	
Cunoniaceae	<i>Schizomeria serrata</i>	X	
Cunoniaceae	<i>Weinmannia pullei</i>	X	
Daphniphyllaceae	<i>Daphniphyllum gracile</i>	X	
Ebenaceae	<i>Diospyros buxifolia</i>	X	
Elaeocarpaceae	<i>Dubouzetia</i> sp.		X
Elaeocarpaceae	<i>Elaeocarpus sarcanthus</i>	X	
Elaeocarpaceae	<i>Elaeocarpus sayeri</i>	X	
Elaeocarpaceae	<i>Elaeocarpus</i> sp. A		X
Elaeocarpaceae	<i>Sericolea arfakensis</i>	X	
Elaeocarpaceae	<i>Sericolea pullei</i>	X	
Elaeocarpaceae	<i>Sloanea pulchra</i>		X
Elaeocarpaceae	<i>Sloanea sogerensis</i>	X	X

Family	Scientific Name	BAA 1	BAA 2
Ericaceae	<i>Dimorphanthera brevipes</i>	X	
Ericaceae	<i>Dimorphanthera ingens</i>	X	
Ericaceae	<i>Dimorphanthera inopinata</i>		X
Ericaceae	<i>Diplycosia rupicola</i>	X	
Ericaceae	<i>Pahia</i> sp.	X	
Ericaceae	<i>Rhododendron beyerinckianum</i>		X
Ericaceae	<i>Rhododendron cristii</i>	X	
Ericaceae	<i>Rhododendron macgregorii</i>	X	
Escalloniaceae	<i>Polyosma integrifolia</i>		
Escalloniaceae	<i>Polyosma subfoliosa</i>		X
Euphorbiaceae	<i>Claoxylon paucinerve</i>	X	X
Euphorbiaceae	<i>Codiaeum variegatum</i>	X	X
Euphorbiaceae	<i>Euphorbia plumerioides</i>		X
Euphorbiaceae	<i>Homalanthus novoguineensis</i>	X	
Euphorbiaceae	<i>Macaranga inermis</i>	X	
Euphorbiaceae	<i>Macaranga strigosa</i>	X	
Fabaceae	<i>Mucuna</i> sp.		X
Gentianaceae	<i>Fagraea ceilanica</i>	X	
Geraniaceae	<i>Aeschynanthus kermesinus</i>	X	
Gesneriaceae	<i>Cyrtandra decurrens</i>		X
Gesneriaceae	<i>Cyrtandra fuscovellea</i>		X
Gesneriaceae	<i>Cyrtandra hellwigii</i>	X	X
Gesneriaceae	<i>Cyrtandra hispidissima</i>	X	X
Gesneriaceae	<i>Cyrtandra</i> sp. A	X	
Gesneriaceae	<i>Cyrtandra terra-guilelmi</i>	X	
Gesneriaceae	<i>Cyrtandra waryana</i>	X	
Gunneraceae	<i>Gunnera macrophylla</i>	X	
Himantandraceae	<i>Galbulimima belgraveana</i>	X	
Lamiaceae	<i>Oxera splendida</i>	X	X
Lauraceae	<i>Cinnamomum ledermannii</i>		
Lauraceae	<i>Cryptocarya apimifolia</i>	X	
Lauraceae	<i>Cryptocarya densiflora</i>	X	
Lauraceae	<i>Cryptocarya depressa</i>		X
Lauraceae	<i>Cryptocarya multipaniculata</i>		X
Lauraceae	<i>Cryptocarya schoddei</i>	X	X

Family	Scientific Name	BAA 1	BAA 2
Lauraceae	<i>Cryptocarya xylophylla</i>	X	
Lauraceae	<i>Endiandra glauca</i>	X	
Lauraceae	<i>Litsea guppyi</i>	X	X
Lauraceae	<i>Litsea nitida</i>	X	
Lauraceae	<i>Neolitsea</i> sp.	X	
Lecythidaceae	<i>Barringtonia</i> sp.		X
Loganiaceae	<i>Neuburgia corynocarpa</i>	X	
Lythraceae	<i>Duabanga moluccana</i>		X
Malvaceae	<i>Sterculia conwentzii</i>		X
Malvaceae	<i>Talipariti albertisii</i>		X
Melastomataceae	<i>Astronia ferruginea</i>		X
Melastomataceae	<i>Astronia ledermannii</i>	X	
Melastomataceae	<i>Astronia papuana</i>	X	X
Melastomataceae	<i>Medinilla maluensis</i>		X
Melastomataceae	<i>Medinilla rubiginosa</i>	X	X
Melastomataceae	<i>Medinilla rubrifructus</i>	X	
Melastomataceae	<i>Medinilla sogerensis</i>	X	
Melastomataceae	<i>Medinilla versteegii</i>		X
Meliaceae	<i>Aglaiia sapindina</i>		X
Meliaceae	<i>Chisocheton lasiocarpus</i>	X	
Meliaceae	<i>Dysoxylum papuanum</i>		X
Meliaceae	<i>Dysoxylum pettigrewianum</i>		X
Menispermaceae	<i>Stephania japonica</i>	X	X
Monimiaceae	<i>Kibara carrii</i>		X
Monimiaceae	<i>Kibara laurifolia</i>	X	
Monimiaceae	<i>Levieria acuminata</i>		X
Monimiaceae	<i>Levieria squarrosa</i>	X	
Monimiaceae	<i>Steganthera hentyi</i>	X	X
Monimiaceae	<i>Steganthera hirta</i>	X	
Monimiaceae	<i>Steganthera ilicifolia</i>	X	
Monimiaceae	<i>Steganthera stevensii</i>	X	X
Moraceae	<i>Ficus armitii</i>	X	
Moraceae	<i>Ficus cereicarpa</i>	X	
Moraceae	<i>Ficus subulata</i>	X	X
Moraceae	<i>Ficus wassa</i>	X	X

Family	Scientific Name	BAA 1	BAA 2
Moraceae	<i>Streblus glaber</i>	X	
Moraceae	<i>Syzygium benamina</i>	X	
Myristicaceae	<i>Gymnacranthera farquariana</i>	X	
Myristicaceae	<i>Horsfieldia hellwigii</i>		X
Myristicaceae	<i>Myristica globosa</i>		X
Myristicaceae	<i>Myristica schleinitzii</i>	X	
Myristicaceae	<i>Myristica sabululata</i>	X	X
Myrtaceae	<i>Decaspermum urvillei</i>		X
Myrtaceae	<i>Metrosideros ramiflora</i>		X
Myrtaceae	<i>Syzygium anomalum</i>	X	X
Myrtaceae	<i>Syzygium buettnerianum</i>		X
Myrtaceae	<i>Syzygium nemorale</i>	X	X
Myrtaceae	<i>Syzygium nutans</i>	X	
Myrtaceae	<i>Syzygium pachycladum</i>	X	
Myrtaceae	<i>Syzygium pallens</i>		X
Myrtaceae	<i>Syzygium plumeum</i>	X	
Myrtaceae	<i>Syzygium pyrocarpum</i>	X	
Myrtaceae	<i>Syzygium stipularis</i>	X	X
Myrtaceae	<i>Xanthomyrtus scolopacina</i>	X	X
Nothofagaceae	<i>Trisyngyne grandis</i>	X	X
Nothofagaceae	<i>Trisyngyne pullei</i>	X	
Nothofagaceae	<i>Trisyngyne rubra</i>	X	
Oleaceae	<i>Chionanthus novoguineensis</i>	X	
Paracryphiaceae	<i>Quintinia ledermannii</i>	X	
Pentaphyllaceae	<i>Eurya acuminata</i>	X	
Pentaphyllaceae	<i>Eurya tigang</i>	X	
Pentaphyllaceae	<i>Ternstroemia britteniana</i>	X	
Pentaphyllaceae	<i>Ternstroemia cherrei</i>		X
Phyllanthaceae	<i>Antidesma excavatum</i> var. <i>indutum</i>	X	
Phyllanthaceae	<i>Breynia cernua</i>	X	
Phyllanthaceae	<i>Phyllanthus clamboideus</i>	X	
Piperaceae	<i>Piper fragile</i>	X	
Piperaceae	<i>Peperomia tenuipila</i>	X	
Piperaceae	<i>Piper caninum</i>	X	X
Piperaceae	<i>Piper macropiper</i>	X	X

Family	Scientific Name	BAA 1	BAA 2
Piperaceae	<i>Piper pubipes</i>	X	
Piperaceae	<i>Piper subcaniramum</i>		X
Pittosporaceae	<i>Pittosporum cravenei</i>	X	
Pittosporaceae	<i>Pittosporum ramiflorum</i>	X	
Primulaceae	<i>Fittingia tubiflora</i>	X	
Primulaceae	<i>Maesa bismarckiana</i>	X	
Primulaceae	<i>Myrsine leucantha</i>	X	
Proteaceae	<i>Helicia hypoglauca</i>		X
Proteaceae	<i>Helicia latifolia</i>		X
Proteaceae	<i>Helicia sleumeri</i>	X	
Proteaceae	<i>Helicia ternifolia</i>	X	X
Proteaceae	<i>Macadamia ternifolia</i>	X	
Putranjivaceae	<i>Drypetes longifolia</i>	X	
Ranunculaceae	<i>Clematis cruttwellii</i>	X	
Rhamnaceae	<i>Alphitonia macrocarpa</i>		X
Rhamnaceae	<i>Gouania microcarpa</i>		X
Rosaceae	<i>Prunus arborea</i>	X	
Rosaceae	<i>Prunus dolichobotrys</i>	X	
Rosaceae	<i>Prunus oligantha</i>	X	
Rosaceae	<i>Rubus archboldtianus</i>	X	
Rosaceae	<i>Rubus ferdinandii-muelleri</i>	X	
Rosaceae	<i>Rubus moluccanus</i>	X	X
Rubiaceae	<i>Amaracarpus grandifolius var. humilis</i>	X	X
Rubiaceae	<i>Argostemma bryophyllum</i>		X
Rubiaceae	<i>Cyclophyllum longiflorum</i>		X
Rubiaceae	<i>Dolianthus epiphyticus</i>	X	
Rubiaceae	<i>Gardenia lamingtonii</i>	X	
Rubiaceae	<i>Gardenia pallens</i>	X	
Rubiaceae	<i>Hydnophytum microphylla</i>	X	
Rubiaceae	<i>Hydnophytum parvifolium</i>	X	
Rubiaceae	<i>Ixora minor</i>		X
Rubiaceae	<i>Ixora sp.</i>		X
Rubiaceae	<i>Lasianthus strigosus</i>		X
Rubiaceae	<i>Mussaenda scratchleyi</i>	X	X
Rubiaceae	<i>Psychotria amplithyrsa</i>	X	

Family	Scientific Name	BAA 1	BAA 2
Rubiaceae	<i>Psychotria asekiensis</i>	X	
Rubiaceae	<i>Psychotria chonantha</i>	X	
Rubiaceae	<i>Psychotria crassipedunculata</i>		X
Rubiaceae	<i>Psychotria dienensis</i>	X	
Rubiaceae	<i>Psychotria leiophloea</i>	X	
Rubiaceae	<i>Psychotria leucococca</i>	X	
Rubiaceae	<i>Psychotria montisgiluwensis</i>	X	
Rubiaceae	<i>Psychotria murmurensis</i>	X	
Rubiaceae	<i>Psychotria tephrosantha</i>	X	
Rubiaceae	<i>Timonius belensis</i>	X	
Rubiaceae	<i>Uncaria lanosa</i>	X	
Rutaceae	<i>Acronychia foveata</i>	X	X
Rutaceae	<i>Acronychia pedunculata</i>	X	
Rutaceae	<i>Melicope conjugata</i>	X	X
Rutaceae	<i>Melicope rubra</i>	X	X
Salicaceae	<i>Casearia clutiifolia</i>	X	
Salicaceae	<i>Casearia papuana</i>	X	
Santalaceae	<i>Santalum macgregorii</i>		X
Sapindaceae	<i>Guioa comosperma</i>		X
Sapindaceae	<i>Pometia pinnata</i>		X
Sapotaceae	<i>Planchonella firma</i>	X	X
Sapotaceae	<i>Pouteria densinervia</i>	X	
Stemonuraceae	<i>Gomphandra papuana</i>	X	
Stemonuraceae	<i>Medusanthera laxiflora</i>		X
Symplocaceae	<i>Symplocos conchinchinensis</i>	X	X
Thymelaeaceae	<i>Aquilaria filaria</i>		X
Thymelaeaceae	<i>Wikstroemia androsae</i>	X	
Trimeniaceae	<i>Trimenia papuana</i>	X	
Urticaceae	<i>Cypholophus kerewensis</i>	X	
Urticaceae	<i>Cypholophus ledermannii</i>	X	
Urticaceae	<i>Cypholophus nummularis</i>	X	
Urticaceae	<i>Elatostema filicinum</i>	X	
Urticaceae	<i>Elatostema mongiensis</i>	X	X
Urticaceae	<i>Elatostema morobensis</i>	X	
Urticaceae	<i>Elatostema tridens</i>	X	

Family	Scientific Name	BAA 1	BAA 2
Urticaceae	<i>Nothocnide melastomatifolia</i>	X	
Urticaceae	<i>Pilea cuneata</i>	X	
Urticaceae	<i>Pilea melastomoides</i>	X	X
Urticaceae	<i>Pilea papuana</i>	X	
Urticaceae	<i>Procris grueningii</i>		X
Vitaceae	<i>Cayratia geniculata</i>	X	
Vitaceae	<i>Leea indica</i>	X	X
Vitaceae	<i>Tetrastigma petrophilum</i>	X	
Winteraceae	<i>Tasmannia piperita</i>	X	
Winteraceae	<i>Zygogynum argenteum</i>	X	
Winteraceae	<i>Zygogynum sylvestre</i>	X	X

Appendix 1.2. Total PFTs per plot and quadrat for all plant species recorded in survey plots in BAA 1 and BAA 2.

PFTs are described in Appendix 1.4.

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT A	me-co-do-ph	Stemonuraceae	<i>Gomphandra</i>	<i>papuana</i>	1
PLANT A	mg-co-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT A	me-co-is-pv-ph-li-ep	Pandanaceae	<i>Freycinetia</i>	<i>angustissima</i>	1
PLANT A	mi-la-do-pv-hc-ep	Orchidaceae	<i>Ceratostylis</i>	<i>acutifolia</i>	1
PLANT A	me-co-is-ro-fi-cr	Hymenophyllaceae	<i>Cephalomanes</i>	<i>obscurum</i>	1
PLANT A	me-co-do-ch-li	Putranjivaceae	<i>Drypetes</i>	<i>longifolia</i>	1
PLANT A	no-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>hunsteinii</i>	1
PLANT A	pl-la-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	1
PLANT A	me-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>grandis</i>	1
PLANT A	no-la-do-ph	Monimiaceae	<i>Levieria</i>	<i>beccariana</i>	1
PLANT A	me-la-do-ph	Rutaceae	<i>Melicope</i>	<i>rubra</i>	1
PLANT A	me-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>pyrocarpum</i>	1
PLANT A	me-la-do-ph	Rutaceae	<i>Acronychia</i>	<i>foveata</i>	1
PLANT A	me-co-do-ph	Myrtaceae	<i>Syzygium</i>	<i>nemorale</i>	1
PLANT A	me-la-do-ch	Urticaceae	<i>Cypholophus</i>	<i>kerewensis</i>	1
PLANT A	me-la-do-ch-li	Vitaceae	<i>Tetrastigma</i>	<i>petrophilum</i>	1
PLANT A	me-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>hollrungii</i>	1
PLANT A	mi-la-do-ph	Symplocaceae	<i>Symplocos</i>	<i>cochinchinensis</i>	1
PLANT A	me-co-is-pv-ch-li	Poaceae	<i>Nastus</i>	<i>longispicula</i>	1
PLANT A	no-co-do-ph	Rubiaceae	<i>Psychotria</i>	sp.	1
PLANT A	no-co-do-ph	Thymelaeaceae	<i>Wikstroemia</i>	<i>androsaemifolia</i>	1
PLANT A	me-la-do-ph	Rubiaceae	<i>Psychotria</i>	<i>leiophloea</i>	1
PLANT A	ma-co-do-ph	Actinidia	<i>Saurauia</i>	<i>naumannii</i>	1
PLANT A	me-co-do-ch-li	Vitaceae	<i>Cayratia</i>	<i>geniculata</i>	1
PLANT A	me-co-do-ph	Rubiaceae	<i>Timonius</i>	<i>belensis</i>	2
PLANT A	me-la-do-ch-li-ep	Ericaceae	<i>Dimorphanthera</i>	<i>brevipes</i>	2
PLANT A	no-co-do-ph	Moraceae	<i>Ficus</i>	<i>wassa</i>	2
PLANT A	me-co-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	2
PLANT A	na-la-do-ch	Rubiaceae	<i>Amaracarpus</i>	<i>grandifolius</i> var. <i>humilis</i>	2
PLANT A	no-pe-do-ch-li-ep	Piperaceae	<i>Piper</i>	<i>caninum</i>	2
PLANT A	pl-la-do-ph	Loganiaceae	<i>Neuburgia</i>	<i>corynocarpa</i>	2
PLANT A	pl-co-do-ph	Myrtaceae	<i>Syzygium</i>	<i>pachycladum</i>	2

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT A	no-la-do-ro-ph	Gesneriaceae	<i>Cyrtandra</i>	<i>hellwigii</i>	2
PLANT A	me-co-do-ro-ch-li	Apocynaceae	<i>Alyxia</i>	<i>lamii</i>	2
PLANT A	na-la-do-ch	Cupressaceae	<i>Papuacedrus</i>	<i>papuana</i>	2
PLANT A	me-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>rubra</i>	2
PLANT A	mg-co-is-ro-pv-ph-ad	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	2
PLANT A	no-co-do-ch-li-ep	Gesneriaceae	<i>Cyrtandra</i>	<i>hispidissima</i>	3
PLANT A	no-co-do-ph	Lauraceae	<i>Endiandra</i>	sp.	3
PLANT A	mg-co-do-ro-pv-ch	Arecaceae	<i>Heterospathe</i>	<i>elegans</i>	3
PLANT A	ma-co-do-ro-fi-ch	Thelypteridaceae	<i>Sphaerostephanos</i>	<i>adenostegius</i>	3
PLANT A	no-co-do-ph	Pentaphyllaceae	<i>Ternstroemia</i>	<i>britteniana</i>	3
PLANT A	mg-co-do-fi-cr	Fern	<i>Cyathea</i>	sp.	3
PLANT A	me-pe-do-ph-li-ep	Ericaceae	<i>Paphia</i>	sp.	3
PLANT A	me-la-do-ch	Rutaceae	<i>Melicope</i>	<i>conjugata</i>	4
PLANT A	me-co-do-ph	Rubiaceae	<i>Psychotria</i>	<i>leucococca</i>	4
PLANT A	no-la-do-ph	Monimiaceae	<i>Steganthera</i>	<i>hirsuta</i>	4
PLANT A	me-ve-is-ro-fi-cr	Hymenophyllaceae	<i>Hymenophyllum</i>	<i>melanosorum</i>	4
PLANT A	me-co-do-ch-li	Lamiaceae	<i>Oxera</i>	<i>splendida</i>	4
PLANT A	mi-co-do-ch-ep	Ericaceae	<i>Vaccinium</i>	sp.	4
PLANT A	no-co-do-ch	Melastomataceae	<i>Medinilla</i>	<i>rubrifructus</i>	5
PLANT A	ma-co-do-ph	Araliaceae	<i>Polyscias</i>	<i>ledermannii</i>	5
PLANT A	me-co-do-ph	Primulaceae	<i>Maesa</i>	<i>bismarckiana</i>	5
PLANT A	me-co-do-pv-hc-ep	Orchidaceae	<i>Agrostophyllum</i>	<i>brachiatum</i>	5
PLANT A	me-co-do-ph	Proteaceae	<i>Helicia</i>	<i>ternifolia</i>	5
PLANT A	ma-la-do-ph	Araliaceae	<i>Schefflera</i>	<i>actinophylla</i>	5
PLANT A	mg-co-do-pv-ch-li	Arecaceae	<i>Calamus</i>	<i>fertilis</i>	5
PLANT A	me-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>xylophylla</i>	5
PLANT A	pl-co-do-ph	Lauraceae	<i>Neolitsea</i>	sp.	5
PLANT A	na-la-do-pv-ch-ep	Orchidaceae	<i>Glossorhyncha</i>	<i>tubisepala</i>	6
PLANT A	me-co-do-fi-cr-ep	Polypodiaceae	<i>Lepisorus</i>	<i>novoguineensis</i>	6
PLANT A	mi-co-do-pv-ch-ep	Orchidaceae	<i>Glomera</i>	<i>hamadryas</i>	6
PLANT A	ma-co-do-ro-ch-ep	Araliaceae	<i>Schefflera</i>	<i>setulosa</i>	6
PLANT B	ma-la-do-ph	Araliaceae	<i>Schefflera</i>	<i>setulosa</i>	1
PLANT B	no-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>hunsteinii</i>	1
PLANT B	no-co-do-ch-li	Rubiaceae	<i>Psychotria</i>	<i>asekiensis</i>	1
PLANT B	me-co-is-pv-ph-li	Poaceae	<i>Nastus</i>	<i>longispicula</i>	1

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT B	me-la-do-ph	Cunoniaceae	<i>Weinmannia</i>	<i>pullei</i>	1
PLANT B	me-co-do-ch	Salicaceae	<i>Casearia</i>	<i>clutiifolia</i>	1
PLANT B	no-co-do-ch	Myrtaceae	<i>Syzygium</i>	sp.	1
PLANT B	me-la-do-ch-li-ep	Ericaceae	<i>Dimorphanthera</i>	<i>brevipes</i>	1
PLANT B	pl-co-do-ro-fi-cr	Thelypteridaceae	<i>Sphaerostephanos</i>	<i>adenostegius</i>	1
PLANT B	no-la-do-ph	Rubiaceae	<i>Timonius</i>	<i>belensis</i>	1
PLANT B	no-la-do-ch	Urticaceae	<i>Pilea</i>	<i>melastomoides</i>	1
PLANT B	me-co-do-pv-cr	Pentaphragmaceae	<i>Ternstroemia</i>	<i>britteniana</i>	1
PLANT B	no-la-do-pv-cr-ep	Orchidaceae	<i>Agrostophyllum</i>	<i>superpositum</i>	1
PLANT B	me-la-do-ph	Putranjivaceae	<i>Drypetes</i>	<i>longifolia</i>	1
PLANT B	me-co-do-ch-li-ad	Moraceae	<i>Ficus</i>	<i>subulata</i>	1
PLANT B	no-la-do-pv-hc-ep	Orchidaceae	<i>Glossorhyncha</i>	<i>tubisepala</i>	1
PLANT B	me-la-do-ch	Rubiaceae	<i>Psychotria</i>	<i>leiophloea</i>	1
PLANT B	no-co-do-ch	Trimeniaceae	<i>Trimenia</i>	<i>papuana</i>	1
PLANT B	me-co-do-ch	Lauraceae	<i>Litsea</i>	<i>guppyi</i>	1
PLANT B	ma-co-do-ph	Araliaceae	<i>Polyscias</i>	<i>ledermannii</i>	1
PLANT B	no-la-do-ph	Rosaceae	<i>Prunus</i>	<i>oligantha</i>	1
PLANT B	mi-co-do-ch	Myrtaceae	<i>Syzygium</i>	<i>benjaminum</i>	1
PLANT B	me-co-do-ph	Sapotaceae	<i>Planchonella</i>	<i>firma</i> var. <i>microcarpa</i>	1
PLANT B	me-co-do-fi-cr-ep	Hymenophyllaceae	<i>Hymenophyllum</i>	<i>melanosorum</i>	1
PLANT B	me-la-do-ph	Monimiaceae	<i>Steganthera</i>	<i>stevensii</i>	1
PLANT B	mi-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>pullei</i>	1
PLANT B	mi-co-do-ro-ch-li	Apocynaceae	<i>Alyxia</i>	<i>lamii</i>	1
PLANT B	me-co-do-fi-cr	Polypodiaceae	<i>Selliguea</i>	<i>albidosquamata</i>	1
PLANT B	me-co-do-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	<i>sayeri</i>	1
PLANT B	me-la-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	2
PLANT B	le-co-is-ph	Cupressaceae	<i>Dacrydium</i>	<i>nidulum</i>	2
PLANT B	me-la-do-ch	Euphorbiaceae	<i>Codiaeum</i>	<i>variegatum</i>	2
PLANT B	no-co-do-ph	Calophyllaceae	<i>Calophyllum</i>	<i>collinum</i>	2
PLANT B	me-co-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>montana</i>	2
PLANT B	me-co-do-ph-li	Rubiaceae	<i>Uncaria</i>	<i>lanosa</i>	2
PLANT B	me-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>latissima</i>	2
PLANT B	ma-co-do-fi-cr	Polypodiaceae	<i>Grammitis</i>	<i>dolichosora</i>	2
PLANT B	me-co-is-pv-ch-li-ep	Pandanaceae	<i>Freycinetia</i>	<i>angustissima</i>	2
PLANT B	me-la-do-ph	Cunoniaceae	<i>Caldcluvia</i>	<i>celebica</i>	3

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT B	no-co-do-ch-li	Vitaceae	<i>Tetrastigma</i>	<i>petrophilum</i>	3
PLANT B	na-la-do-ph	Cupressaceae	<i>Papuacedrus</i>	<i>papuana</i>	3
PLANT B	me-co-do-ph	Proteaceae	<i>Macadamia</i>	<i>ternifolia</i>	3
PLANT B	me-co-do-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	sp.	3
PLANT B	na-la-do-ch	Rubiaceae	<i>Amaracarpus</i>	<i>grandifolius</i> var. <i>humilis</i>	3
PLANT B	me-co-do-ch	Oleaceae	<i>Chionanthus</i>	<i>rupicolus</i>	3
PLANT B	me-co-do-ph	Moraceae	<i>Ficus</i>	<i>wassa</i>	3
PLANT B	me-co-do-ch	Primulaceae	<i>Fittingia</i>	<i>tubiflora</i>	3
PLANT B	me-la-do-ph	Rosaceae	<i>Prunus</i>	<i>arborea</i>	3
PLANT B	no-co-do-pv-cr-ep	Orchidaceae	<i>Bulbophyllum</i>	sp.	3
PLANT B	pl-la-do-ph	Myristicaceae	<i>Myristica</i>	<i>schleinitzii</i>	3
PLANT B	me-co-do-ch-li-ep	Melastomataceae	<i>Medinilla</i>	<i>rubiginosa</i>	3
PLANT B	na-la-do-pv-ch-ep	Orchidaceae	<i>Glossorhyncha</i>	<i>tubisepala</i>	3
PLANT B	no-la-do-ch-li	Rosaceae	<i>Rubus</i>	<i>archbodianus</i>	4
PLANT B	no-co-do-ph	Podocarpaceae	<i>Podocarpus</i>	<i>neriifolius</i>	4
PLANT B	no-co-do-ch	Pittosporaceae	<i>Pittosporum</i>	<i>ramiflorum</i>	4
PLANT B	me-co-do-ph	Melastomataceae	<i>Astronia</i>	<i>papuana</i>	4
PLANT B	mg-co-is-ro-pv-ph	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	4
PLANT B	no-co-do-ph	Monimiaceae	<i>Kibara</i>	<i>laurifolia</i>	5
PLANT B	me-co-is-ro-fi-cr	Polypodiaceae	<i>Themelium</i>	<i>yoderi</i>	5
PLANT B	me-co-do-ch	Rubiaceae	<i>Psychotria</i>	<i>leucococca</i>	5
PLANT B	me-co-do-fi-cr-ep	Polypodiaceae	<i>Selliguea</i>	<i>albidosquamata</i>	5
PLANT B	me-co-do-ph-li	Rubiaceae	<i>Psychotria</i>	<i>amplithyrsa</i>	5
PLANT B	no-co-do-su-ph-li-ep	Gesneriaceae	<i>Cyrtandra</i>	sp.	5
PLANT B	mi-co-do-ch	Elaeocarpaceae	<i>Sericolea</i>	<i>pullei</i>	6
PLANT B	no-co-do-ph	Myrtaceae	<i>Syzygium</i>	<i>nutans</i>	6
PLANT B	me-la-do-ph	Rubiaceae	<i>Gardenia</i>	<i>lamingtonii</i>	6
PLANT B	me-pe-is-fi-cr-ep	Hymenophyllaceae	<i>Hymenophyllum</i>	<i>ooides</i>	6
PLANT B	ma-pe-do-fi-cr	Fern	<i>Loxogramme</i>	sp.	7
PLANT B	ma-la-do-fi-cr	Gleicheniaceae	<i>Dicranopteris</i>	<i>linearis</i>	7
PLANT B	no-co-do-ph	Moraceae	<i>Ficus</i>	<i>wassa</i>	7
PLANT B	ma-co-do-ro-fi-cr	Blechnaceae	<i>Blechnum</i>	<i>revolutum</i>	7
PLANT B	no-co-do-hc-ep	Rubiaceae	<i>Hydnophytum</i>	<i>microphyllum</i>	7
PLANT B	no-co-do-ph-li-ep	Ericaceae	<i>Dimorphanthera</i>	sp.	7
PLANT B	me-la-do-ph	Pentaphyllaceae	<i>Eurya</i>	<i>acuminata</i>	7

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT B	na-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>benjaminum</i>	7
PLANT B	no-la-do-hc-ep	Ericaceae	<i>Rhododendron</i>	<i>macgregoriae</i>	8
PLANT B	mi-la-do-ch	Myrtaceae	<i>Syzygium</i>	sp.	8
PLANT B	mi-co-do-ph	Lauraceae	<i>Cinnamomum</i>	<i>ledermannii</i>	8
PLANT B	no-co-do-ph	Pittosporaceae	<i>Pittosporum</i>	<i>cravenianum</i>	8
PLANT C	no-la-do-ph	Cunoniaceae	<i>Schizomeria</i>	<i>serrata</i>	1
PLANT C	me-la-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	1
PLANT C	mi-la-do-ch-li-ep	Urticaceae	<i>Pilea</i>	<i>papuana</i>	1
PLANT C	no-la-do-ch	Cunoniaceae	<i>Weinmannia</i>	<i>pullei</i>	1
PLANT C	no-la-do-ph	Myristicaceae	<i>Gymnacranthera</i>	<i>farquhariana</i>	1
PLANT C	no-co-do-ro-pv-ph-ad	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	1
PLANT C	no-la-do-ph	Monimiaceae	<i>Steghanthera</i>	<i>stevensii</i>	1
PLANT C	no-la-do-ph	Lauraceae	<i>Litsea</i>	<i>guppyi</i>	1
PLANT C	pl-co-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT C	no-co-do-ch-li-ep	Ericaceae	<i>Dimorphanthera</i>	<i>ingens</i>	1
PLANT C	no-la-do-ch	Rubiaceae	<i>Psychotria</i>	<i>murmurensis</i>	1
PLANT C	no-la-do-ph	Monimiaceae	<i>Laviera</i>	<i>squarrosa</i>	1
PLANT C	no-la-do-ph	Proteaceae	<i>Helicia</i>	sp.	1
PLANT C	me-la-do-ro-cr-ad	Araceae	<i>Alocasia</i>	<i>nicolsonii</i>	1
PLANT C	me-la-do-ph	Actinidiaceae	<i>Saurauia</i>	<i>plurilocularis</i>	1
PLANT C	no-la-do-ph	Melastomataceae	<i>Astronia</i>	<i>ledermannii</i>	1
PLANT C	no-co-do-ch-li	Rosaceae	<i>Rubus</i>	<i>archboldiana</i>	1
PLANT C	me-la-do-ph	Dilleniaceae	<i>Dillenia</i>	<i>montana</i>	1
PLANT C	me-la-do-ph	Myristicaceae	<i>Myristica</i>	<i>subalulata</i>	1
PLANT C	me-co-do-ch	Urticaceae	<i>Nothocnide</i>	<i>melastomatifolia</i>	1
PLANT C	no-co-do-pv-ch-ad	Poaceae	<i>Nastus</i>	<i>longispicula</i>	1
PLANT C	no-la-do-ch-li	Vitaceae	<i>Cayratia</i>	<i>geniculata</i>	1
PLANT C	me-co-do-ph	Rutaceae	<i>Melicope</i>	<i>rubra</i>	1
PLANT C	mg-co-do-ro-fi-cr-ep	Marattiaceae	<i>Marattia</i>	<i>tafaensis</i>	1
PLANT C	no-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>stipulare</i>	1
PLANT C	no-la-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT C	no-co-do-ph-li	Rubiaceae	<i>Mussaenda</i>	<i>scratchlyi</i>	2
PLANT C	no-co-do-ch	Urticaceae	<i>Cypholophus</i>	<i>ledermannii</i>	2
PLANT C	no-co-do-ph	Myrtaceae	<i>Syzygium</i>	<i>anomalum</i>	2
PLANT C	no-la-do-ch	Paracryphiaceae	<i>Sphenostemon</i>	<i>papuanum</i>	2

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT C	no-co-do-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	<i>culminicola</i>	2
PLANT C	me-co-do-ph	Symplocaceae	<i>Symplocos</i>	<i>cochinchinensis</i>	2
PLANT C	pl-pe-do-fi-cr-ep	Vittariaceae	<i>Vittaria</i>	<i>elongata</i>	2
PLANT C	mi-co-do-ch-li	Gesneriaceae	<i>Cyrtandra</i>	sp.	2
PLANT C	no-co-do-pv-cr-ep	Orchidaceae	<i>Bulbophyllum</i>	sp.	3
PLANT C	no-co-do-ph	Sapotaceae	<i>Planchonella</i>	<i>firma</i> var. <i>microcarpa</i>	3
PLANT C	no-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>ledermannii</i>	3
PLANT C	mi-la-do-ph	Myrtaceae	<i>Xanthomyrtus</i>	<i>scolopacina</i>	3
PLANT C	no-co-do-ph	Rutaceae	<i>Acronychia</i>	<i>pedunculata</i>	3
PLANT C	no-la-do-ph	Paracryphiaceae	<i>Quintinia</i>	<i>ledermannii</i>	3
PLANT C	me-co-do-ph	Lauraceae	<i>Endiandra</i>	sp.	3
PLANT C	me-co-do-fi-ch-ad	Nephrolepidaceae	<i>Lindsaea</i>	<i>pulchella</i>	3
PLANT C	no-co-do-fi-cr-ad	Aspleniaceae	<i>Asplenium</i>	<i>marattioides</i>	3
PLANT C	me-co-do-ph	Primulaceae	<i>Fittingia</i>	<i>tubiflora</i>	3
PLANT C	mi-co-do-ph-ad	Elaeocarpaceae	<i>Elaeocarpus</i>	sp.	3
PLANT C	no-co-do-pv-cr-ep	Zingiberaceae	<i>Riedelia</i>	<i>montana</i>	4
PLANT C	me-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>grandis</i>	4
PLANT C	me-la-do-ro-cr-ad	Araceae	<i>Alocasia</i>	<i>nicolsonii</i>	4
PLANT C	no-la-do-ch	Chloranthaceae	<i>Chloranthus</i>	<i>elatior</i>	4
PLANT C	no-co-do-ch	Rubiaceae	<i>Psychotria</i>	sp.	4
PLANT C	pl-co-do-ph	Meliaceae	<i>Chisocheton</i>	<i>lasiocarpus</i>	4
PLANT C	no-la-do-ph-li	Apocynaceae	<i>Marsdenia</i>	sp.	4
PLANT C	me-co-do-ph	Winteraceae	<i>Zygogynum</i>	<i>sylvestre</i>	4
PLANT C	no-la-do-ch	Rosaceae	<i>Rubus</i>	<i>ferdinandimuelleri</i>	4
PLANT C	me-pe-do-fi-cr-ep	Pteridaceae	<i>Atrophyum</i>	<i>alatum</i>	4
PLANT C	me-pe-do-fi-cr-ep	Hymenophyllaceae	<i>Hymenophyllum</i>	<i>melanosorum</i>	5
PLANT C	me-la-do-cr-ep	Gesneriaceae	<i>Cyrtandra</i>	sp. 1	5
PLANT C	na-co-do-ch	Rubiaceae	<i>Amaracarpus</i>	<i>grandifolia</i> var. <i>humilis</i>	5
PLANT C	me-co-do-ch	Rosaceae	<i>Rubus</i>	<i>archboldianus</i>	5
PLANT C	me-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>plumeum</i>	5
PLANT C	me-la-do-ph	Rutaceae	<i>Melicope</i>	<i>conjugata</i>	5
PLANT C	me-co-do-ch	Vitaceae	<i>Leea</i>	<i>indica</i>	5
PLANT C	me-co-do-ch	Primulaceae	<i>Myrsine</i>	<i>leucantha</i>	5
PLANT C	no-co-do-ph-li	Rubiaceae	<i>Uncaria</i>	<i>lanosa</i>	6
PLANT C	no-co-do-ph-li	Anacardiaceae	<i>Camposperma</i>	<i>brevipetiolatum</i>	6

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT C	me-co-do-pv-cr-ep	Rubiaceae	<i>Timonius</i>	<i>xanthocarpus</i>	6
PLANT C	me-co-do-pv-cr-ep	Ericaceae	<i>Vaccinium</i>	<i>fissiflorum</i>	6
PLANT C	na-co-do-pv-cr-ep	Orchidaceae	<i>Dendrobium</i>	<i>cuthbertsonii</i>	6
PLANT C	mi-co-do-ph-li	Moraceae	<i>Ficus</i>	<i>cereicarpa</i>	6
PLANT C	pl-co-do-ph	Moraceae	<i>Ficus</i>	<i>wassa</i>	6
PLANT C	me-pe-is-pv-ch-li-ep	Pandanaceae	<i>Freycinetia</i>	<i>angustissima</i>	6
PLANT C	no-co-do-ch-li-ep	Piperaceae	<i>Piper</i>	<i>caninum</i>	6
PLANT C	me-co-do-ph	Melastomataceae	<i>Medinilla</i>	<i>rubiginosa</i>	7
PLANT C	no-co-do-hc	Begoniaceae	<i>Begonia</i>	<i>randiana</i>	7
PLANT C	me-co-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>hispidissima</i>	7
PLANT C	no-co-do-fi-cr-ep	Polypodiaceae	<i>Lepisorus</i>	<i>novoguineensis</i>	7
PLANT C	mg-co-do-ro-fi-cr-ad	Thelypteridaceae	<i>Sphaerostephanos</i>	<i>edenostegius</i>	7
PLANT C	pl-co-do-ro-hc-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	7
PLANT C	ma-pe-do-fi-ph-li-ad	Saccolomataceae	<i>Saccoloma</i>	<i>sorbifolium</i>	7
PLANT D	mg-co-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT D	no-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>pullei</i>	1
PLANT D	me-la-do-ct-ch	Rubiaceae	<i>Psychotria</i>	<i>leiophloea</i>	1
PLANT D	pl-co-do-ro-fi-cr-ep	Dryopteridaceae	<i>Dryopteris</i>	<i>papuana</i>	1
PLANT D	no-la-do-ch	Rubiaceae	<i>Psychotria</i>	sp.	1
PLANT D	no-co-do-fi-cr-ep	Polypodiaceae	<i>Lepisorus</i>	<i>novoguineensis</i>	1
PLANT D	me-co-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>montana</i>	1
PLANT D	no-la-do-ph-li	Piperaceae	<i>Piper</i>	<i>macropiper</i>	1
PLANT D	me-co-is-fi-cr-ep	Hymenophyllaceae	<i>Hymenophyllum</i>	<i>melanosorum</i>	1
PLANT D	pl-co-is-cr-ep	Polypodiaceae	<i>Selliguea</i>	<i>albidosquamata</i>	1
PLANT D	me-co-do-fi-cr-ep	Polypodiaceae	<i>Ctenopterella</i>	<i>blechnoides</i>	1
PLANT D	me-co-is-ro-pv-cr	Cyperaceae	<i>Scleria</i>	sp.	1
PLANT D	me-pe-do-su-ch-ep	Ericaceae	<i>Dimorphanthera</i>	sp.	1
PLANT D	mi-la-do-hc	Rosaceae	<i>Rubus</i>	<i>ferdinandimuelleri</i>	1
PLANT D	me-co-do-ct-ph	Moraceae	<i>Ficus</i>	<i>cereicarpa</i>	1
PLANT D	no-co-do-ct-ph	Lauraceae	<i>Cryptocarya</i>	sp.	1
PLANT D	me-la-do-ct-ch	Winteraceae	<i>Zygogynum</i>	<i>sylvestre</i>	1
PLANT D	me-co-do-ch-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	1
PLANT D	no-co-do-ch-li	Rosaceae	<i>Rubus</i>	<i>archboldianus</i>	1
PLANT D	me-co-do-ct-ph	Rutaceae	<i>Melicope</i>	<i>conjugata</i>	1
PLANT D	no-la-do-ph-li-ep	Gesneriaceae	<i>Cyrtandra</i>	sp.	1

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT D	mi-la-do-ch-ep	Ericaceae	<i>Rhododendron</i>	<i>christi</i>	1
PLANT D	me-la-do-ct-ph	Lauraceae	<i>Litsea</i>	<i>nitida</i>	1
PLANT D	no-la-do-ct-ch	Rubiaceae	<i>Timonius</i>	<i>belensis</i>	1
PLANT D	me-la-do-ph-li	Rubiaceae	<i>Mussaenda</i>	<i>scratchleyi</i>	2
PLANT D	ma-la-do-ro-hc	Araceae	<i>Alocasia</i>	<i>nicolsonii</i>	2
PLANT D	no-co-do-ct-ph	Monimiaceae	<i>Steganthera</i>	<i>stevensii</i>	2
PLANT D	me-co-do-ph	Rubiaceae	<i>Psychotria</i>	sp.	2
PLANT D	le-la-do-hc-ep	Urticaceae	<i>Elatostema</i>	<i>mongiensis</i>	2
PLANT D	me-pe-do-pv-cr-ep	Marantaceae	<i>Phrynium</i>	<i>pedunculatum</i>	2
PLANT D	me-pe-is-pv-ph-li-ep	Pandanaceae	<i>Freycinetia</i>	<i>archboldiana</i>	2
PLANT D	mi-la-do-su-hc	Urticaceae	<i>Procris</i>	<i>grueningii</i>	2
PLANT D	me-co-do-ph	Melastomataceae	<i>Astronia</i>	<i>papuana</i>	2
PLANT D	me-la-do-su-ph-li-ep	Urticaceae	<i>Procris</i>	sp.	2
PLANT D	pl-co-do-ct-ch	Winteraceae	<i>Drimys</i>	<i>piperita</i>	2
PLANT D	ma-co-do-ro-fi-cr	Fern			3
PLANT D	ma-co-do-fi-cr	Polypodiaceae	<i>Themelium</i>	<i>yoderi</i>	3
PLANT D	me-co-do-hc	Melastomataceae	<i>Medinilla</i>	<i>sogerensis</i>	3
PLANT D	me-co-do-ph	Primulaceae	<i>Fittingia</i>	<i>tubiflora</i>	3
PLANT D	no-la-do-ct-ch-li-ep	Ericaceae	<i>Vaccinium</i>	sp.	3
PLANT D	me-co-do-ct-ph	Gentianaceae	<i>Fagraea</i>	<i>ceilanica</i>	3
PLANT D	me-la-do-ch	Actinidiaceae	<i>Saurauia</i>	sp. 1	3
PLANT D	na-co-is-pv-hc-ep	Orchidaceae	<i>Glossorhyncha</i>	<i>tubisepala</i>	3
PLANT D	pl-pe-do-fi-cr	Adiantaceae	<i>Adiantum</i>	<i>aculeolatum</i>	3
PLANT D	mi-la-do-ch-li	Vitaceae	<i>Tetrastigma</i>	<i>petrophilum</i>	3
PLANT D	mi-co-do-ph	Paracryphiaceae	<i>Quintinia</i>	<i>altigena</i>	3
PLANT D	mi-co-do-ch	Urticaceae	<i>Pilea</i>	<i>brassii</i>	3
PLANT D	na-co-do-ch-ep	Ericaceae	<i>Diplycosia</i>	<i>rupicola</i>	4
PLANT D	mi-co-do-pv-cr-ep	Orchidaceae	<i>Ceratostylis</i>	<i>acutifolia</i>	4
PLANT D	no-co-do-pv-cr-ep	Orchidaceae	<i>Epiblastus</i>	<i>basilis</i>	4
PLANT D	no-co-do-ph	Elaeocarpaceae	<i>Sericolea</i>	<i>arfakensis</i>	4
PLANT D	pl-co-do-pv-cr-ep	Orchidaceae	<i>Calanthe</i>	<i>rhodochila</i>	5
PLANT D	no-la-do-ch	Phyllanthaceae	<i>Phyllanthus</i>	<i>archboldianus</i>	5
PLANT D	mi-co-do-ch	Myrtaceae	<i>Syzygium</i>	sp.	6
PLANT D	pl-co-do-ph	Euphorbiaceae	<i>Macaranga</i>	<i>inermis</i>	6
PLANT D	pl-la-do-ph	Loganiaceae	<i>Neuburgia</i>	<i>corynocarpa</i>	7

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT D	na-la-do-pv-cr-ep	Orchidaceae	<i>Dendrobium</i>	<i>cuthbertsonii</i>	7
PLANT E	me-la-do-ch-li	Urticaceae	<i>Elatostema</i>	<i>tridens</i>	1
PLANT E	me-co-is-ch	Urticaceae	<i>Cypholophus</i>	<i>ledermannii</i>	1
PLANT E	me-co-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	1
PLANT E	mg-co-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT E	no-co-do-ph	Rubiaceae	<i>Timonius</i>	<i>belensis</i>	1
PLANT E	me-la-do-ph	Lauraceae	<i>Endiandra</i>	<i>glauca</i>	1
PLANT E	mg-co-do-ro-ch	Araceae	<i>Alocasia</i>	<i>nicolsonii</i>	1
PLANT E	no-co-do-ph	Monimiaceae	<i>Steghanthera</i>	<i>hentyi</i>	1
PLANT E	me-co-do-ph	Rubiaceae	<i>Psychotria</i>	<i>leiophloea</i>	1
PLANT E	pl-co-do-ro-fi-cr	Aspleniaceae	<i>Asplenium</i>	<i>bipinnatifidum</i>	1
PLANT E	me-co-do-ch-li	Rosaceae	<i>Rubus</i>	<i>archboldianus</i>	1
PLANT E	na-co-do-ch	Ericaceae	<i>Diplycosia</i>	<i>rupicola</i>	1
PLANT E	me-la-do-ph	Rubiaceae	<i>Timonius</i>	<i>belensis</i>	1
PLANT E	mg-co-do-ro-fi-cr	Cyatheaceae	<i>Cyathea</i>	sp.	1
PLANT E	na-co-do-ph	Phyllanthaceae	<i>Phyllanthus</i>	<i>clamboides</i>	1
PLANT E	no-co-do-ch-li-ep	Piperaceae	<i>Piper</i>	<i>caninum</i>	1
PLANT E	no-co-do-ph	Rubiaceae	<i>Psychotria</i>	sp.	1
PLANT E	na-la-do-ch	Urticaceae	<i>Elatostema</i>	<i>morobense</i>	1
PLANT E	na-la-do-su-ch-ep	Piperaceae	<i>Peperomia</i>	<i>tenuipila</i>	1
PLANT E	na-la-do-ph	Urticaceae	<i>Elatostema</i>	<i>mongiensis</i>	1
PLANT E	na-co-do-pv-ch-ep	Orchidaceae	<i>Glossorhyncha</i>	<i>tubisepala</i>	1
PLANT E	me-la-do-ph	Monimiaceae	<i>Steghanthera</i>	<i>ilicifolia</i>	1
PLANT E	mg-la-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT E	me-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>rubra</i>	1
PLANT E	me-co-do-ch-ep	Melastomataceae	<i>Medinilla</i>	sp.	1
PLANT E	pl-co-is-pv-ph	Orchidaceae	<i>Epiblastus</i>	<i>basilis</i>	1
PLANT E	me-co-do-fi-cr-ep	Urticaceae	<i>Cephalomanes</i>	<i>obscurum</i>	2
PLANT E	me-co-do-ph-li	Moraceae	<i>Ficus</i>	<i>armitii</i>	2
PLANT E	me-la-do-ph	Actinidiaceae	<i>Saurauia</i>	<i>stichophylla</i>	2
PLANT E	me-co-do-ph	Moraceae	<i>Ficus</i>	<i>cereicarpa</i>	2
PLANT E	na-co-do-pv-cr-ep	Orchidaceae	<i>Ceratostylis</i>	<i>subulata</i>	2
PLANT E	me-co-do-pv-ch-ep	Pandanaceae	<i>Freycinetia</i>	<i>archboldiana</i>	2
PLANT E	pl-co-do-ro-cr	Orchidaceae	<i>Glossorhyncha</i>	<i>tubisepala</i>	2
PLANT E	me-co-do-fi-cr	Pandanaceae	<i>Freycinetia</i>	<i>archboldiana</i>	2

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT E	me-la-do-ch	Rosaceae	<i>Rubus</i>	<i>moluccanus</i>	2
PLANT E	me-pe-do-fi-cr-ep	Polypodiaceae	<i>Selliguea</i>	<i>albidosquamata</i>	3
PLANT E	pl-co-do-fi-cr	Dryopteridaceae	<i>Dryopteris</i>	<i>wallichiana</i>	3
PLANT E	na-la-do-ph	Myrtaceae	<i>Xanthomyrtus</i>	<i>scolopacina</i>	3
PLANT E	no-la-do-ch-ep	Ericaceae	<i>Rhododendron</i>	<i>christi</i>	3
PLANT E	me-co-do-ph-li	Rubiaceae	<i>Mussaenda</i>	<i>scratchleyi</i>	3
PLANT E	me-co-do-ph	Melastomataceae	<i>Astronia</i>	<i>papuana</i>	3
PLANT E	me-co-do-ph	Primulaceae	<i>Fittingia</i>	<i>tubiflora</i>	3
PLANT E	me-la-do-ch-li-ep	Ericaceae	<i>Paphia</i>	sp.	3
PLANT E	no-co-do-ch-ep	Ericaceae	<i>Dimorphanthera</i>	sp.	4
PLANT E	no-co-do-ch-ep	Blechnaceae	<i>Blechnum</i>	sp.	4
PLANT E	no-co-do-ch	Rosaceae	<i>Rubus</i>	<i>ferdinandimuellerii</i>	5
PLANT E	no-la-do-ch-ep	Gesneriaceae	<i>Cyrtandra</i>	sp.	5
PLANT E	me-co-do-ph	Lauraceae	<i>Cryptocarya</i>	sp.	5
PLANT E	mi-co-do-ch-li	Rubiaceae	<i>Psychotria</i>	sp.	5
PLANT E	mi-co-is-pv-hc-ep	Orchidaceae	<i>Mediocalcar</i>	<i>bifolium</i>	5
PLANT E	ma-la-do-ro-hc	Gunneraceae	<i>Gunnera</i>	<i>macrophylla</i>	5
PLANT E	me-co-do-ph	Monimiaceae	<i>Steganthera</i>	<i>stevensii</i>	6
PLANT E	no-co-do-ch-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	6
PLANT E	no-co-do-ch-li	Menispermaceae	<i>Stephania</i>	<i>japonica</i>	6
PLANT E	no-co-do-ch-li	Rosaceae	<i>Rubus</i>	<i>archboldianus</i>	6
PLANT E	mg-co-is-ro-pv-ch-ad	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	6
PLANT E	pl-la-do-ph	Winteraceae	<i>Zygogynum</i>	<i>sylvestre</i>	7
PLANT E	mi-la-do-ch-li	Vitaceae	<i>Tetrastigma</i>	<i>petrophilum</i>	7
PLANT E	no-la-do-ph	Euphorbiaceae	<i>Homalanthus</i>	<i>novoguineensis</i>	8
PLANT F	pl-co-do-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>brackenridgei</i>	1
PLANT F	me-la-do-ct-ph	Primulaceae	<i>Fittingia</i>	<i>tubiflora</i>	1
PLANT F	mi-la-do-ct-ch	Rubiaceae	<i>Amaracarpus</i>	<i>grandifolius</i> var. <i>humilis</i>	1
PLANT F	no-co-do-ct-ph-li-ep	Piperaceae	<i>Piper</i>	<i>caninum</i>	1
PLANT F	pl-la-do-ct-ph	Monimiaceae	<i>Steganthera</i>	<i>stevensii</i>	1
PLANT F	me-co-is-ro-fi-cr	Hymenophyllaceae	<i>Crepidomanes</i>	<i>aphlebioides</i>	1
PLANT F	me-la-do-ct-ph	Monimiaceae	<i>Steganthera</i>	<i>hentyi</i>	1
PLANT F	no-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>terrae-guilelmi</i>	1
PLANT F	me-la-do-ph	Salicaceae	<i>Casearia</i>	<i>clutiifolia</i>	1
PLANT F	me-la-do-ct-ch	Lauraceae	<i>Cryptocarya</i>	<i>densiflora</i>	1

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT F	me-co-do-ph	Cunoniaceae	<i>Caldcluvia</i>	<i>nymannii</i>	1
PLANT F	mi-la-do-ch	Urticaceae	<i>Elatostema</i>	<i>filicinum</i>	1
PLANT F	me-la-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>montanum</i>	1
PLANT F	me-co-do-ph	Phyllanthaceae	<i>Antidesma</i>	<i>excavatum</i> var. <i>indutum</i>	1
PLANT F	ma-la-do-ro-fi-cr	Aspleniaceae	<i>Asplenium</i>	<i>marattioides</i>	1
PLANT F	no-la-do-ct-ph-li	Rubiaceae	<i>Psychotria</i>	<i>tephrosantha</i>	1
PLANT F	ma-la-is-ro-fi-cr	Dryopteridaceae	<i>Polystichum</i>	<i>daymanense</i>	1
PLANT F	no-co-is-fi-cr	Hymenophyllaceae	<i>Hymenophyllum</i>	<i>melanosorum</i>	1
PLANT F	ma-la-do-ph	Actinidiaceae	<i>Saurauia</i>	<i>naumannii</i>	1
PLANT F	me-co-is-pv-ch-li	Pandanaceae	<i>Freycinetia</i>	<i>angustissima</i>	1
PLANT F	me-co-is-ro-fi-cr	Hymenophyllaceae	<i>Cephalomanes</i>	<i>obscurum</i>	1
PLANT F	pl-la-do-ch	Proteaceae	<i>Helicia</i>	sp.	1
PLANT F	me-la-do-ct-ph	Rubiaceae	<i>Psychotria</i>	<i>dieniensis</i>	1
PLANT F	pl-co-do-ct-ph	Sapotaceae	<i>Planchonella</i>	<i>densinervia</i>	1
PLANT F	no-co-do-ct-ph	Lauraceae	<i>Cryptocarya</i>	<i>densiflora</i>	1
PLANT F	me-la-do-ch	Urticaceae	<i>Pilea</i>	<i>cuneata</i>	1
PLANT F	mg-co-do-ro-pv-ph	Arecaceae	<i>Heterospathe</i>	<i>elegans</i>	1
PLANT F	no-co-do-ct-pv-ph-li	Poaceae	<i>Nastus</i>	<i>longispicula</i>	1
PLANT F	no-co-do-ch	Proteaceae	<i>Helicia</i>	<i>ternifolia</i>	1
PLANT F	ma-co-is-ro-pv-ch-li-ep	Pandanaceae	<i>Freycinetia</i>	<i>archboldiana</i>	1
PLANT F	me-la-do-ct-ph	Myrtaceae	<i>Syzygium</i>	<i>pyrocarpum</i>	1
PLANT F	no-la-do-ct-ph	Rutaceae	<i>Melicope</i>	<i>conjugata</i>	1
PLANT F	mg-co-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	2
PLANT F	no-co-do-hc	Symplocaceae	<i>Symplocos</i>	<i>cochinchinensis</i>	2
PLANT F	me-co-do-ct-ph	Winteraceae	<i>Zygogynum</i>	<i>sylvestre</i>	2
PLANT F	mg-co-do-ro-fi-ch	Polypodiaceae	<i>Grammitis</i>	<i>dolichosora</i>	2
PLANT F	me-co-do-ph	Cunoniaceae	<i>Schizomeria</i>	<i>serrata</i>	2
PLANT F	me-co-do-ch-li	Apocynaceae	<i>Melodinus</i>	<i>forbesii</i>	2
PLANT F	pl-pe-do-ch-li	Piperaceae	<i>Piper</i>	<i>pubipes</i>	2
PLANT F	no-co-do-pv-cr-ep	Orchidaceae	<i>Bulbophyllum</i>	sp.	2
PLANT F	no-co-do-fi-cr	Polypodiaceae	<i>Lepisorus</i>	<i>novoguineensis</i>	2
PLANT F	no-co-do-ct-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	sp.	2
PLANT F	pl-co-do-ch	Vitaceae	<i>Leea</i>	<i>indica</i>	2
PLANT F	me-co-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	2
PLANT F	me-la-do-ph	Himantandraceae	<i>Galbulimima</i>	<i>belgraveana</i>	3

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT F	me-co-do-ph	Podocarpaceae	<i>Podocarpus</i>	<i>neriifolius</i>	3
PLANT F	me-co-do-ph	Rubiaceae	<i>Psychotria</i>	sp.	3
PLANT F	me-co-do-ct-ph	Moraceae	<i>Ficus</i>	<i>cereicarpa</i>	3
PLANT F	me-co-do-ro-fi-cr	Osmundaceae	<i>Leptopteris</i>	<i>alpina</i>	3
PLANT F	mi-co-do-ct-ph	Clusiaceae	<i>Garcinia</i>	<i>maluensis</i>	4
PLANT F	no-co-do-ct-ph	Rutaceae	<i>Acronychia</i>	<i>foveata</i>	4
PLANT F	pl-co-do-ph	Winteraceae	<i>Zygygynum</i>	<i>sylvestre</i>	4
PLANT F	me-co-do-ch	Melastomataceae	<i>Astronia</i>	<i>ledermannii</i>	4
PLANT F	mg-co-is-ro-pv-ph	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	4
PLANT F	ma-la-do-ch-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	4
PLANT F	ma-co-do-ro-fi-cr	Polypodiaceae	<i>Ctenopterella</i>	<i>blechnoides</i>	4
PLANT F	me-pe-do-fi-cr	Cyatheaceae	<i>Cyathea</i>	sp.	4
PLANT F	me-co-do-ph	Myristicaceae	<i>Horsfieldia</i>	<i>hellwigii</i>	4
PLANT F	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>wariana</i>	4
PLANT F	me-co-do-ph-li	Ranunculaceae	<i>Clematis</i>	<i>cruttwellii</i>	4
PLANT F	mi-la-do-ct-ch	Rubiaceae	<i>Amaracarpus</i>	<i>montisgiluwensis</i>	5
PLANT F	ma-co-do-ct-ro-ph	Araliaceae	<i>Polyscias</i>	<i>ledermannii</i>	5
PLANT F	no-la-do-ct-ch-li	Rubiaceae	<i>Mussaenda</i>	<i>scratchleyi</i>	5
PLANT F	no-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>pullei</i>	5
PLANT F	mi-la-do-ch-li-ep	Bignoniaceae	<i>Aeschynanthus</i>	<i>kermesinus</i>	5
PLANT F	me-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>grandis</i>	5
PLANT F	me-co-do-ph	Rutaceae	<i>Melicope</i>	<i>rubra</i>	5
PLANT F	me-co-do-ch	Winteraceae	<i>Drimys</i>	<i>piperita</i>	5
PLANT F	na-la-do-ch-ep	Rubiaceae	<i>Hydnophytum</i>	<i>parvifolium</i>	6
PLANT F	me-co-do-pv-cr	Moraceae	<i>Ficus</i>	<i>wassa</i>	6
PLANT F	me-la-do-ct-ph	Rosaceae	<i>Prunus</i>	<i>dolichobotrys</i>	6
PLANT F	no-la-do-ph	Piperaceae	<i>Piper</i>	<i>fragile</i>	6
PLANT F	no-la-do-ct-ph-li-ep	Myrtaceae	<i>Syzygium</i>	<i>anomalum</i>	6
PLANT G	mg-co-is-ro-pv-ph-ad	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	1
PLANT G	no-la-do-ch	Rubiaceae	<i>Psychotria</i>	<i>chonantha</i>	1
PLANT G	me-co-do-ch	Urticaceae	<i>Cypholophus</i>	<i>nummularis</i>	1
PLANT G	me-la-do-ch-li	Rosaceae	<i>Rubus</i>	<i>archboldianus</i>	1
PLANT G	pl-co-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	1
PLANT G	no-la-do-ph	Rosaceae	<i>Prunus</i>	<i>arborea</i>	1
PLANT G	na-la-do-ch	Rubiaceae	<i>Dolianthus</i>	<i>epiphyticus</i>	1

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT G	ma-la-do-ph	Araliaceae	<i>Harmsiopanax</i>	<i>ingens</i>	1
PLANT G	no-co-do-ph	Actinidiaceae	<i>Saurauia</i>	<i>calyptrata</i>	1
PLANT G	mi-la-do-ph	Monimiaceae	<i>Levieria</i>	<i>beccariana</i>	1
PLANT G	no-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	sp.	1
PLANT G	na-co-do-pv-ch-ep	Orchidaceae	<i>Glossorhyncha</i>	<i>tubisepala</i>	1
PLANT G	pl-co-do-ph	Salicaceae	<i>Casearia</i>	<i>papuana</i>	1
PLANT G	mg-la-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT G	me-la-do-fi-cr-ep	Hymenophyllaceae	<i>Hymenophyllum</i>	<i>melanosorum</i>	1
PLANT G	me-pe-do-fi-cr-ep	Polypodiaceae	<i>Selliguea</i>	<i>albidosquamata</i>	1
PLANT G	me-co-do-fi-cr-ep	Polypodiaceae	<i>Calymmodon</i>	<i>cucullatus</i>	1
PLANT G	ma-pe-do-fi-cr-ep	Vittariaceae	<i>Vittaria</i>	<i>ledermannii</i>	1
PLANT G	me-pe-do-pv-hc-ep	Orchidaceae	<i>Bulbophyllum</i>	sp.	1
PLANT G	mi-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>pullei</i>	1
PLANT G	ma-pe-do-fi-cr-ep	Adiantaceae	<i>Adiantum</i>	<i>aculeolatum</i>	1
PLANT G	me-co-do-ph	Loganiaceae	<i>Neuburgia</i>	<i>corynocarpa</i>	1
PLANT G	me-ve-do-ph	Euphorbiaceae	<i>Claoxylon</i>	<i>paucinerve</i>	2
PLANT G	no-pe-do-pv-hc-ep	Orchidaceae	<i>Dendrobium</i>	<i>subclausum</i>	2
PLANT G	no-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>apamifolia</i>	2
PLANT G	no-co-do-ph	Symplocaceae	<i>Symplocos</i>	<i>cochinchinensis</i>	2
PLANT G	no-co-do-pv-hc-ep	Orchidaceae	<i>Bulbophyllum</i>	sp.	2
PLANT G	no-co-do-ph	Elaeocarpaceae	<i>Sericolea</i>	<i>arfakensis</i>	2
PLANT G	no-co-do-ph	Monimiaceae	<i>Sphenostemon</i>	<i>arfakense</i>	2
PLANT G	mi-co-do-ph	Phyllanthaceae	<i>Phyllanthus</i>	<i>clamboides</i>	2
PLANT G	no-co-do-ch-li	Vitaceae	<i>Tetrastigma</i>	<i>petrophilum</i>	2
PLANT G	me-la-do-fi-cr-ep	Osmundaceae	<i>Leptopteris</i>	<i>alpina</i>	2
PLANT G	na-co-do-pv-cr-ep	Orchidaceae	<i>Ceratostylis</i>	<i>subulata</i>	2
PLANT G	no-la-do-hc-ep	Piperaceae	<i>Piper</i>	<i>caninum</i>	2
PLANT G	no-co-do-ch-ep	Ericaceae	<i>Rhododendron</i>	<i>christi</i>	2
PLANT G	mi-co-do-ch-ep	Ericaceae	<i>Vaccinium</i>	sp.	2
PLANT G	me-la-do-pv-cr-ep	Zingiberaceae	<i>Riedelia</i>	<i>microbotrya</i>	2
PLANT G	me-la-do-ph	Daphniphyllaceae	<i>Daphniphyllum</i>	<i>gracile</i>	2
PLANT G	me-co-do-ph	Euphorbiaceae	<i>Homalanthus</i>	<i>novoguineensis</i>	2
PLANT G	me-la-do-ph	Rubiaceae	<i>Timonius</i>	<i>belensis</i>	3
PLANT G	na-co-do-ph	Phyllanthaceae	<i>Breynia</i>	<i>cernua</i>	3
PLANT G	me-co-do-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	<i>sayeri</i>	3

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT G	na-co-do-pv-hc-ep	Orchidaceae	<i>Mediocalcar</i>	<i>bifolium</i>	4
PLANT G	na-la-do-ch	Urticaceae	<i>Elatostema</i>	<i>mongiensis</i>	4
PLANT G	mi-pe-do-ch-ep	Gesneriaceae	<i>Cyrtandra</i>	sp.	4
PLANT G	na-co-do-ch	Ericaceae	<i>Diplycosia</i>	<i>rupicola</i>	4
PLANT G	me-co-do-ch-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	4
PLANT G	nc-pe-do-fi-cr-ep	Polypodiaceae	<i>Lepisorus</i>	<i>novoguineensis</i>	4
PLANT G	no-co-do-ch-li	Rubiaceae	<i>Mussaenda</i>	<i>scratchleyi</i>	4
PLANT G	pl-co-do-fi-cr-ep	Blechnaceae	<i>Diploblechnum</i>	<i>fraseri</i>	4
PLANT G	me-la-do-ch-li	Rosaceae	<i>Rubus</i>	<i>moluccanus</i>	4
PLANT G	me-pe-do-fi-cr-ep	Polypodiaceae	<i>Selliguea</i>	<i>albidosquamata</i>	5
PLANT G	no-la-do-ph	Pentaphyllaceae	<i>Eurya</i>	<i>tigang</i>	5
PLANT G	me-co-do-ph	Proteaceae	<i>Helicia</i>	<i>sleumeri</i>	5
PLANT G	no-co-do-ch	Rubiaceae	<i>Psychotria</i>	sp.	6
PLANT G	pl-la-do-ro-ph-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	7
PLANT G	na-co-do-ph	Myrtaceae	<i>Syzygium</i>	<i>benjaminum</i>	7
PLANT G	me-co-do-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	<i>sayeri</i>	7
PLANT G	no-la-do-ch	Urticaceae	<i>Pilea</i>	<i>papuana</i>	7
PLANT H	me-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>ledermannii</i>	1
PLANT H	pl-la-do-ro-ph-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	1
PLANT H	me-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>densiflora</i>	1
PLANT H	me-co-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>microbotrya</i>	1
PLANT H	me-la-do-ph	Myristicaceae	<i>Horsfieldia</i>	<i>hellwigii</i>	1
PLANT H	no-co-do-ch-li	Rubiaceae	<i>Mussaenda</i>	<i>scratchleyi</i>	1
PLANT H	no-co-do-ch-li	Menispermaceae	<i>Stephania</i>	<i>japonica</i> var. <i>discolor</i>	1
PLANT H	no-la-do-ch	Rubiaceae	<i>Lasianthus</i>	<i>chrysonurus</i>	1
PLANT H	no-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>stipulare</i>	1
PLANT H	no-co-do-ph	Phyllanthaceae	<i>Antidesma</i>	<i>contractum</i>	1
PLANT H	me-la-do-ph	Sapindaceae	<i>Mischocarpus</i>	<i>largifolius</i>	1
PLANT H	ma-la-do-ro-fi-ch	Cyatheaceae	<i>Gymnosphaera</i>	<i>hornei</i>	1
PLANT H	pl-co-is-ro-pv-ph-ad	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	1
PLANT H	no-co-do-ch-li	Vitaceae	<i>Tetrastigma</i>	<i>petrophilum</i>	1
PLANT H	me-co-do-ro-pv-ch	Arecaceae	<i>Heterospatha</i>	<i>elegans</i>	1
PLANT H	me-la-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT H	mi-co-is-pv-ch-ep	Pandanaceae	<i>Freycinetia</i>	<i>angustissima</i>	1
PLANT H	no-co-do-ph	Monimiaceae	<i>Kibara</i>	<i>hartleyi</i>	1

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT H	pl-la-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>montana</i>	1
PLANT H	pl-co-do-ph	Sapotaceae	<i>Planchonella</i>	<i>monticola</i>	1
PLANT H	me-pe-do-ch-li-ep	Piperaceae	<i>Piper</i>	<i>caninum</i>	1
PLANT H	me-la-do-ph	Euphorbiaceae	<i>Macaranga</i>	<i>inermis</i>	1
PLANT H	me-la-do-ph	Apocynaceae	<i>Cerbera</i>	<i>floribunda</i>	1
PLANT H	me-co-do-ch-li	Smilacaceae	<i>Smilax</i>	<i>callophylla</i>	1
PLANT H	no-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>pullei</i>	1
PLANT H	no-la-do-ph	Putranjivaceae	<i>Drypetes</i>	<i>lasiogynoides</i>	1
PLANT H	mi-co-do-ph	Myrtaceae	<i>Xanthomyrtus</i>	<i>polyclada</i>	1
PLANT H	pl-la-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	1
PLANT H	no-la-do-ph-li	Rubiaceae	<i>Schradera</i>	<i>ledermannii</i>	2
PLANT H	no-la-do-ph	Rutaceae	<i>Melicope</i>	<i>rubra</i>	2
PLANT H	me-la-do-ph	Primulaceae	<i>Fittingia</i>	<i>tubiflora</i>	2
PLANT H	me-co-do-ch	Rubiaceae	<i>Psychotria</i>	<i>randiana</i> var. <i>tafaensis</i>	2
PLANT H	me-la-do-ph	Myrtaceae	<i>Syzygium</i>	sp.	2
PLANT H	me-co-do-ph	Rubiaceae	<i>Psychotria</i>	sp.	2
PLANT H	le-la-do-ch	Rubiaceae	<i>Dolianthus</i>	<i>trichanthus</i>	2
PLANT H	no-co-is-ch-li	Goodeniaceae	<i>Scaevola</i>	<i>oppositifolia</i>	2
PLANT H	na-co-do-ph	Cupressaceae	<i>Papuacedrus</i>	<i>papuana</i>	2
PLANT H	mi-co-do-su-ch-li-ep	Gesneriaceae	<i>Aeschynanthus</i>	<i>nummularius</i>	2
PLANT H	me-la-do-ph	Rutaceae	<i>Acronychia</i>	<i>foveata</i>	2
PLANT H	me-la-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>xylophylla</i>	2
PLANT H	pl-co-do-fi-cr	Polypodiaceae	<i>Loxogramme</i>	<i>paltonioides</i>	2
PLANT H	ma-la-do-ph	Meliaceae	<i>Dysoxylum</i>	<i>parasiticum</i>	2
PLANT H	me-co-do-ph	Rubiaceae	<i>Psychotria</i>	<i>chrysantha</i>	2
PLANT H	pl-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>alleniana</i>	2
PLANT H	me-co-do-ph	Melastomataceae	<i>Astronia</i>	<i>papuana</i>	2
PLANT H	mi-pe-is-pv-cr-ep	Orchidaceae	<i>Oberonia</i>	<i>drepanophylla</i>	2
PLANT H	pl-co-do-ph	Actinidiaceae	<i>Saurauia</i>	<i>naumannii</i>	2
PLANT H	me-la-do-ch-li-ep	Ericaceae	<i>Dimorphanthera</i>	<i>inopinata</i>	2
PLANT H	no-la-do-ch-li	Apocynaceae	<i>Alyxia</i>	<i>lamii</i>	2
PLANT H	me-co-do-ph	Phyllanthaceae	<i>Aporosa</i>	<i>carrii</i>	3
PLANT H	me-co-do-ph	Annonaceae	<i>Artabotrys</i>	sp.	3
PLANT H	me-la-do-ph	Euphorbiaceae	<i>Homalanthus</i>	<i>novoguineensis</i>	3
PLANT H	no-la-do-ch	Urticaceae	<i>Elatostema</i>	<i>integrifolium</i>	3

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT H	no-co-do-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	<i>altigenus</i>	3
PLANT H	no-la-do-ch	Rubiaceae	<i>Psychotria</i>	<i>reticulatissima</i>	3
PLANT H	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	sp. 1	4
PLANT H	mi-co-is-pv-ch-li	Pandanaceae	<i>Freycinetia</i>	<i>marginata</i>	4
PLANT H	nc-co-ac-cr-pa	Balanophoraceae	<i>Balanophora</i>	<i>papuana</i>	4
PLANT H	me-co-do-ch	Urticaceae	<i>Cypholophus</i>	<i>nummularis</i>	4
PLANT H	me-co-do-ch	Moraceae	<i>Ficus</i>	<i>adenosperma</i>	4
PLANT H	me-la-do-ph	Primulaceae	<i>Maesa</i>	<i>bismarckiana</i>	5
PLANT H	me-co-do-fi-cr	Dryopteridaceae	<i>Elaphoglossum</i>	<i>novoguineense</i>	5
PLANT H	me-co-do-pv-cr	Araceae	<i>Schismatoglottis</i>	<i>calyptrata</i>	5
PLANT H	no-co-do-pv-ch-ep	Pandanaceae	<i>Freycinetia</i>	<i>decipiens</i>	5
PLANT H	no-la-do-ch-li	Rubiaceae	<i>Uncaria</i>	<i>lanosa</i>	5
PLANT H	no-la-do-hc	Begoniaceae	<i>Begonia</i>	<i>richardsoniana</i>	5
PLANT I	me-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>latissima</i>	1
PLANT I	le-la-do-ch	Rubiaceae	<i>Dolianthus</i>	<i>trichanthus</i>	1
PLANT I	me-la-do-ph	Myristicaceae	<i>Horsfieldia</i>	<i>hellwigii</i>	1
PLANT I	mi-pe-do-li-ad	Moraceae	<i>Ficus</i>	<i>subulata</i>	1
PLANT I	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>wariana</i>	1
PLANT I	me-la-do-ph	Rubiaceae	<i>Pavetta</i>	<i>platyclada</i>	1
PLANT I	me-la-do-ch	Proteaceae	<i>Helicia</i>	sp.	1
PLANT I	na-la-do-ch	Myrtaceae	<i>Xanthomyrtus</i>	<i>scolopacina</i>	1
PLANT I	no-co-do-ch	Rubiaceae	<i>Psychotria</i>	sp.	1
PLANT I	me-la-do-ro-fi-cr	Cyathiaceae	<i>Gymnosphaera</i>	<i>hornei</i>	1
PLANT I	me-co-iso-fi-cr-ep	Hymenophyllaceae	<i>Hymenophyllum</i>	<i>melanosorum</i>	1
PLANT I	me-la-do-ph	Monimiaceae	<i>Stegánthera</i>	<i>stevensii</i>	2
PLANT I	me-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>anomalum</i>	2
PLANT I	plco-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>microbotrya</i>	2
PLANT I	me-co-do-cr	Begoniaceae	<i>Begonia</i>	<i>randiana</i>	2
PLANT I	pl-la-do-ph	Actinidiaceae	<i>Saurauia</i>	<i>naumannii</i>	2
PLANT I	pl-co-is-fi-cr	Thelypteridaceae	<i>Pronephrium</i>	<i>womersleyi</i>	2
PLANT I	pl-la-do-ph	Loganiaceae	<i>Neuburgia</i>	<i>corynocarpa</i>	2
PLANT I	me-la-do-ph	Rubiaceae	<i>Psychotria</i>	sp.	3
PLANT I	pl-co-do-ph	Moraceae	<i>Ficus</i>	<i>pungens</i>	3
PLANT I	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>fuscovellea</i>	3
PLANT I	pl-co-do-fi-cr	Polypodiaceae	<i>Calymmodon</i>	<i>cucullatus</i>	3

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT I	no-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>brevipes</i>	3
PLANT I	pl-la-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>densiflora</i>	4
PLANT I	me-la-do-ph	Rutaceae	<i>Melicope</i>	<i>rubra</i>	4
PLANT I	ma-la-do-ph	Meliaceae	<i>Aglaia</i>	<i>sapindina</i>	4
PLANT I	me-co-do-li-ep	Ericaceae	<i>Dimorphanthera</i>	sp.	4
PLANT I	na-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>buettnerianum</i>	4
PLANT I	ma-la-do-ch-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	5
PLANT I	ma-la-do-ch	Araliaceae	<i>Mackinlaya</i>	<i>schlechteri</i>	5
PLANT I	me-co-do-ph	Monimiaceae	<i>Kibara</i>	<i>hartleyi</i>	6
PLANT I	no-co-do-ch-ep	Piperaceae	<i>Piper</i>	<i>caninum</i>	6
PLANT I	mi-la-do-li	Apocynaceae	<i>Alyxia</i>	<i>lamii</i>	6
PLANT I	me-la-do-li-ep	Melastomataceae	<i>Medinilla</i>	sp.	6
PLANT I	me-la-do-ph	Melastomataceae	<i>Astronia</i>	<i>papuana</i>	6
PLANT I	me-co-do-pv-li	Pandanaceae	<i>Freycinetia</i>	<i>archboldiana</i>	7
PLANT I	no-la-do-ph	Moraceae	<i>Ficus</i>	<i>wassa</i>	7
PLANT I	no-co-do-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	<i>altigenus</i>	7
PLANT J	me-co-is-pv-ch-li	Arecaceae	<i>Calamus</i>	<i>heteracanthus</i>	1
PLANT J	mi-la-do-ch	Rubiaceae	<i>Lasianthus</i>	<i>chrysoneurus</i>	1
PLANT J	me-la-do-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	sp.	1
PLANT J	me-la-do-ph	Stemanuraceae	<i>Medusanthera</i>	<i>laxiflora</i>	1
PLANT J	me-la-do-ph	Lauraceae	<i>Cryptocarya</i>	sp.	1
PLANT J	pl-co-do-ro-pv-ch	Arecaceae	<i>Linospadix</i>	<i>albertisianus</i>	1
PLANT J	me-co-do-ph	Clusiaceae	<i>Garcinia</i>	<i>ledermannii</i>	1
PLANT J	pl-co-do-ph	Rutaceae	<i>Melicope</i>	<i>conjugata</i>	1
PLANT J	me-co-do-ph	Proteaceae	<i>Helicia</i>	<i>hypoglauca</i>	1
PLANT J	no-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>goniopterum</i>	1
PLANT J	me-la-do-ph	Rhamnaceae	<i>Alphitonia</i>	<i>macrocarpa</i>	1
PLANT J	me-co-do-ph	Moraceae	<i>Ficus</i>	<i>wassa</i>	1
PLANT J	me-la-do-ch	Urticaceae	<i>Elatostema</i>	sp.	1
PLANT J	no-co-do-ch-li	Rubiaceae	<i>Mussaenda</i>	<i>scratchleyi</i>	1
PLANT J	le-la-do-ch	Rubiaceae	<i>Dolianthus</i>	sp.	1
PLANT J	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>warriana</i>	1
PLANT J	me-la-do-ch	Clusiaceae	<i>Garcinia</i>	sp.	1
PLANT J	no-la-do-ph-li	Apocynaceae	<i>Alyxia</i>	<i>lamii</i>	1
PLANT J	pl-la-do-ph	Sapindaceae	<i>Guioa</i>	<i>comesperma</i>	1

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT J	me-co-do-ch-li	Fabaceae	<i>Mucuna</i>	<i>platyphylla</i>	1
PLANT J	me-co-do-ch-li	Lamiaceae	<i>Oxera</i>	<i>splendida</i>	2
PLANT J	pl-co-do-ro-pv-hc	Zingiberaceae	<i>Riedelia</i>	<i>corallina</i>	2
PLANT J	pl-la-do-ph	Calophyllaceae	<i>Calophyllum</i>	<i>soulattri</i>	2
PLANT J	me-co-is-ro-pv-ch-ad	Pandanaceae	<i>Pandanus</i>	<i>kaernbachii</i>	2
PLANT J	no-co-do-ph-li	Rubiaceae	<i>Schradera</i>	<i>ledermannii</i>	2
PLANT J	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>hispidissima</i>	2
PLANT J	me-la-do-ro-fi-ch	Thelypteridaceae	<i>Sphaerostephanos</i>	<i>adenostegius</i>	2
PLANT J	no-co-do-ch-li-ep	Piperaceae	<i>Piper</i>	<i>subcaniramum</i>	2
PLANT J	pl-la-do-ph	Actinidiaceae	<i>Saurauia</i>	<i>holotricha</i>	2
PLANT J	pl-la-do-ph	Lauraceae	<i>Litsea</i>	<i>guppyi</i>	2
PLANT J	me-co-do-pv-ph-li-ep	Pandanaceae	<i>Freycinetia</i>	<i>archboldiana</i>	2
PLANT J	pl-co-do-pv-ch-li-ep	Araceae	<i>Rhaphidophora</i>	<i>neoguineensis</i>	2
PLANT J	no-co-do-ph	Lauraceae	<i>Cinnamomum</i>	<i>ledermannii</i>	2
PLANT J	me-co-is-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>brackenridgei</i>	2
PLANT J	me-co-do-ro-pv-ch	Arecaceae	<i>Heterospathe</i>	<i>elegans</i>	2
PLANT J	me-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>grandis</i>	2
PLANT J	me-la-do-ch	Chloranthaceae	<i>Chloranthus</i>	<i>elatior</i>	2
PLANT J	no-co-do-ch-li-ep	Piperaceae	<i>Piper</i>	<i>macropiper</i>	3
PLANT J	me-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>nemorale</i>	3
PLANT J	me-la-do-ph	Myristicaceae	<i>Horsfieldia</i>	<i>hellwigii</i>	3
PLANT J	pl-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>multipaniculata</i>	3
PLANT J	no-la-do-pv-hc-ep	Orchidaceae	<i>Agrostophyllum</i>	<i>superpositum</i>	3
PLANT J	me-la-do-ph	Rutaceae	<i>Acronychia</i>	<i>pedunculata</i>	3
PLANT J	me-co-do-ph	Paracryphiaceae	<i>Sphenostemon</i>	<i>papuanum</i>	3
PLANT J	me-co-do-ph	Annonaceae	<i>Artabotrys</i>	sp.	3
PLANT J	no-co-is-pv-ch-li-ep	Pandanaceae	<i>Freycinetia</i>	<i>angustissima</i>	3
PLANT J	me-la-do-ch-li	Menispermaceae	<i>Stephania</i>	<i>japonica</i>	3
PLANT J	no-la-do-ch-ep	Urticaceae	<i>Procris</i>	<i>grueningii</i>	3
PLANT J	me-la-do-ph	Euphorbiaceae	<i>Claoxylon</i>	<i>paucinerve</i>	4
PLANT J	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>schumanniana</i>	4
PLANT J	no-co-do-ch-li	Urticaceae	<i>Elatostema</i>	<i>mongiensis</i>	4
PLANT J	me-co-is-ro-pv-ch-ad	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	4
PLANT J	me-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>latissima</i>	4
PLANT J	me-la-do-ph	Meliaceae	<i>Aglaia</i>	<i>sapindina</i>	4

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT J	no-la-do-ph	Monimiaceae	<i>Kibara</i>	<i>carii</i>	4
PLANT J	na-la-do-ro-pv-cr	Orchidaceae	<i>Anoectochilus</i>	<i>papuanus</i>	5
PLANT J	pl-co-do-pv-ch-li	Arecaceae	<i>Calamus</i>	<i>heteracanthus</i>	5
PLANT J	me-la-do-ph	Myristicaceae	<i>Myristica</i>	<i>subalulata</i>	5
PLANT J	me-la-do-hc	Araceae	<i>Alocasia</i>	<i>lancifolia</i>	5
PLANT J	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>hellwigii</i>	6
PLANT J	pl-la-do-ro-ch	Arecaceae	<i>Alocasia</i>	<i>lancifolia</i>	6
PLANT J	me-co-do-ph	Pentaphragmaceae	<i>Ternstroemia</i>	<i>cherryi</i>	6
PLANT J	pl-la-do-ch-ep	Melastomataceae	<i>Medinilla</i>	<i>maluensis</i>	6
PLANT J	pl-co-is-ro-fi-ch	Oleandraceae	<i>Oleandra</i>	<i>pilosa</i>	6
PLANT J	mg-co-do-pv-ph	Arecaceae	<i>Caryota</i>	<i>rumphiana</i>	6
PLANT J	pl-la-do-pv-hc	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	6
PLANT J	ma-co-do-pv-ch	Arecaceae	<i>Hydriastele</i>	<i>pinangoides</i>	7
PLANT J	me-la-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>montanum</i>	7
PLANT K	me-la-do-ct-ph	Myristicaceae	<i>Myristica</i>	<i>sabululata</i>	1
PLANT K	na-la-do-ro-ch-li	Apocynaceae	<i>Alyxia</i>	<i>lamii</i>	1
PLANT K	me-co-do-pv-hc	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	1
PLANT K	me-la-do-ch	Euphorbiaceae	<i>Claoxylon</i>	<i>paucinerve</i>	1
PLANT K	ma-co-do-pv-ph	Arecaceae	<i>Gronophyllum</i>	<i>chaunostachys</i>	1
PLANT K	pl-la-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>corallina</i>	1
PLANT K	me-la-do-ct-ph	Lauraceae	<i>Cryptocarya</i>	<i>depressa</i>	1
PLANT K	no-la-do-ct-ch-li-ep	Piperaceae	<i>Piper</i>	<i>caninum</i>	1
PLANT K	me-co-is-pv-ch-ep	Pandanaceae	<i>Freycinetia</i>	<i>angutissima</i>	1
PLANT K	no-co-do-ct-ph	Symplocaceae	<i>Symplocos</i>	<i>conchinchinensis</i>	1
PLANT K	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>decurrens</i>	1
PLANT K	pl-co-do-ch	Meliaceae	<i>Dysoxylum</i>	<i>pettigrewianum</i>	1
PLANT K	ma-co-do-fi-cr	Blechnaceae	<i>Blechnum</i>	<i>vittatum</i>	1
PLANT K	me-la-do-ph	Myrtaceae	<i>Syzygium</i>	sp.	1
PLANT K	pl-co-do-ph	Sapotaceae	<i>Planchonella</i>	<i>firma</i>	1
PLANT K	no-co-do-ct-pv-ch-ad	Poaceae	<i>Nastus</i>	<i>longispicula</i>	1
PLANT K	no-la-do-ct-ph	Rubiaceae	<i>Cyclophyllum</i>	<i>longiflorum</i>	1
PLANT K	pl-la-do-pv-ch-li-ep	Araceae	<i>Epipremnum</i>	<i>papuanum</i>	1
PLANT K	me-co-do-ph	Proteaceae	<i>Helicia</i>	<i>ternifolia</i>	1
PLANT K	no-co-do-ph	Thymelaeaceae	<i>Aquilaria</i>	<i>fillaria</i>	1
PLANT K	no-la-do-ch	Urticaceae	<i>Pilea</i>	<i>melastomoides</i>	1

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT K	me-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	<i>hispidissima</i>	1
PLANT K	me-la-do-ph	Meliaceae	<i>Dysoxylum</i>	<i>papuanum</i>	1
PLANT K	pl-la-do-ct-ph	Myristicaceae	<i>Horsfieldia</i>	<i>hellwigii</i>	2
PLANT K	mg-co-do-ro-pv-ch	Arecaceae	<i>Heterospathe</i>	<i>elegans</i>	2
PLANT K	me-la-do-ct-ph	Calophyllaceae	<i>Calophyllum</i>	<i>collinum</i>	2
PLANT K	no-la-do-ch	Rubiaceae	<i>Ixora</i>	sp.	2
PLANT K	pl-co-is-ro-pv-ch-li-ep	Pandanaceae	<i>Freycinetia</i>	<i>archboldiana</i>	2
PLANT K	me-la-do-ct-ph	Clusiaceae	<i>Garcinia</i>	<i>latissima</i>	1
PLANT K	no-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>grandis</i>	1
PLANT K	pl-la-do-ct-ph	Calophyllaceae	<i>Calophyllum</i>	<i>soulattri</i>	1
PLANT K	no-la-do-ch	Melastomataceae	<i>Medinilla</i>	<i>versteegii</i>	1
PLANT K	no-co-do-ph	Thymelaeaceae	<i>Aquilaria</i>	<i>fillaria</i>	2
PLANT K	me-la-do-ct-ch	Chloranthaceae	<i>Chloranthus</i>	<i>elatior</i>	2
PLANT K	no-la-do-ch	Euphorbiaceae	<i>Euphorbia</i>	<i>plumerioides</i>	2
PLANT K	pl-la-do-ro-ch	Araceae	<i>Alocasia</i>	<i>lancifolia</i>	2
PLANT K	pl-la-do-ct-ph	Lauraceae	<i>Cryptocarya</i>	<i>densiflora</i>	3
PLANT K	me-co-do-pv-ch-li	Arecaceae	<i>Calamus</i>	<i>heteracanthus</i>	3
PLANT K	pl-co-do-pv-ch	Asparagaceae	<i>Cordyline</i>	<i>fruticosa</i>	3
PLANT K	pl-la-do-pv-cr	Zingiberaceae	<i>Alpinia</i>	<i>stenobracteolata</i>	3
PLANT K	me-la-do-ph	Gesneriaceae	<i>Cyrtandra</i>	<i>hellwigii</i>	3
PLANT K	me-co-do-ct-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	sp.	3
PLANT K	me-co-do-ct-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	sp.	4
PLANT K	me-la-do-ch	Monimiaceae	<i>Kibara</i>	<i>carrii</i>	4
PLANT K	no-la-do-ch-li	Apocynaceae	<i>Marsdenia</i>	sp.	4
PLANT K	pl-co-do-ph	Vitaceae	<i>Leea</i>	<i>indica</i>	4
PLANT K	mi-la-do-ch-li	Myrtaceae	<i>Metrosideros</i>	<i>ramiflora</i>	5
PLANT K	no-la-do-ch	Actinidiaceae	<i>Saurauia</i>	sp.	5
PLANT K	no-la-do-ch	Actinidiaceae	<i>Saurauia</i>	<i>purgans</i>	5
PLANT K	me-co-is-ro-pv-ch-ad	Pandanaceae	<i>Pandanus</i>	<i>brosimos</i>	6
PLANT K	no-la-do-ch	Rubiaceae	<i>Ixora</i>	sp.	6
PLANT K	no-co-do-ct-ph	Elaeocarpaceae	<i>Elaeocarpus</i>	<i>altigenus</i>	7
PLANT K	me-la-do-ct-ch-li	Smilacaceae	<i>Smilax</i>	<i>calophylla</i>	7
PLANT K	pi-co-do-ph	Myristicaceae	<i>Myristica</i>	<i>globosa</i>	8
PLANT K	pl-co-do-ct-ph	Moraceae	<i>Ficus</i>	<i>cereicarpa</i>	8
PLANT K	me-co-do-ph	Apocynaceae	<i>Cerbera</i>	<i>floribunda</i>	8

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT L	me-la-do-ch-li	Rubiaceae	<i>Mussaenda</i>	<i>scratchleyi</i>	1
PLANT L	no-la-do-ph	Escalloniaceae	<i>Polyosma</i>	<i>foliolosa</i>	1
PLANT L	mg-co-do-ro-pv-ch	Arecaceae	<i>Heterospathe</i>	<i>elegans</i>	1
PLANT L	ma-la-do-ph	Lecythidaceae	<i>Barringtonia</i>	<i>calyptrocalyx</i>	1
PLANT L	me-pe-do-fi-cr-ep	Oleandraceae	<i>Oleandra</i>	<i>pilosa</i>	1
PLANT L	me-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>alleniana</i>	1
PLANT L	mi-la-do-ph	Rubiaceae	<i>Cyclophyllum</i>	<i>longiflorum</i>	1
PLANT L	me-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>giganthocarpa</i>	1
PLANT L	no-la-do-ch	Gesneriaceae	<i>Cyrtandra</i>	sp.	1
PLANT L	me-la-do-ph	Clusiaceae	<i>Garcinia</i>	<i>latissima</i>	1
PLANT L	pl-la-do-pv-cr	Zingiberaceae	<i>Pleuranthodium</i>	<i>tephrochlamys</i>	1
PLANT L	me-la-do-ph	Melastomataceae	<i>Astronia</i>	<i>papuaana</i>	1
PLANT L	pl-la-do-pv-cr	Zingiberaceae	<i>Hornstedtia</i>	<i>scottiana</i>	1
PLANT L	mg-la-do-ro-fi-ch	Cyatheaceae	<i>Cyathea</i>	<i>contaminans</i>	1
PLANT L	no-la-do-ph	Myrtaceae	<i>Syzygium</i>	sp.	1
PLANT L	me-la-do-ph	Myristicaceae	<i>Horsfieldia</i>	<i>hellwigii</i>	1
PLANT L	pl-co-do-fi-cr-ep	Thelypteridaceae	<i>Metathelypteris</i>	sp.	1
PLANT L	pl-la-do-ph	Moraceae	<i>Ficus</i>	<i>cereicarpa</i>	1
PLANT L	me-co-do-ph	Sapotaceae	<i>Planchonella</i>	<i>firma</i>	1
PLANT L	no-co-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>minutifolia</i>	1
PLANT L	no-co-do-ph	Monimiaceae	<i>Steghanthera</i>	<i>hentyi</i>	1
PLANT L	me-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>pallens</i>	2
PLANT L	mi-co-do-ph	Clusiaceae	<i>Garcinia</i>	<i>schraderi</i>	2
PLANT L	me-co-do-ch	Rubiaceae	<i>Psychotria</i>	<i>crassipedunculata</i>	2
PLANT L	pl-co-do-ph	Sapindaceae	<i>Arytera</i>	<i>densiflora</i>	2
PLANT L	me-la-do-ph	Elaeocarpaceae	<i>Sloanea</i>	<i>pulchra</i>	2
PLANT L	pl-la-do-ph	Euphorbiaceae	<i>Macaranga</i>	<i>inermis</i>	2
PLANT L	pl-co-do-ph	Lauraceae	<i>Litsea</i>	<i>grandis</i>	2
PLANT L	me-co-is-fi-cr-ep	Hymenophyllaceae	<i>Cephalomanes</i>	<i>obscurum</i>	2
PLANT L	me-la-do-pv-cr	Zingiberaceae	<i>Riedelia</i>	<i>microbotrya</i>	2
PLANT L	me-la-do-ph	Rutaceae	<i>Melicope</i>	<i>rubra</i>	2
PLANT L	pl-co-do-ro-ch-ep	Araliaceae	<i>Schefflera</i>	<i>dentata</i>	2
PLANT L	pl-co-do-ph	Meliaceae	<i>Dysoxylum</i>	<i>papuanum</i>	2
PLANT L	no-la-do-ph	Euphorbiaceae	<i>Codiaeum</i>	<i>variegatum</i>	2
PLANT L	ma-la-do-ph	Araliaceae	<i>Polyscias</i>	<i>ledermannii</i>	2

Plot ID	PFTs	Family	Genus	Species	Quadrat
PLANT L	no-co-do-ph-li	Menispermaceae	<i>Stephania</i>	<i>japonica</i>	2
PLANT L	no-co-do-ph	Sapotaceae	<i>Planchonella</i>	<i>firma</i>	2
PLANT L	me-la-do-ph	Myrtaceae	<i>Syzygium</i>	<i>stipulare</i>	2
PLANT L	pi-co-is-pv-hc-ep	Orchidaceae	<i>Taeniophyllum</i>	<i>filiforme</i>	2
PLANT L	pl-co-do-pv-ph-li-ep	Araceae	<i>Epipremnum</i>	<i>papuanum</i>	2
PLANT L	ma-co-do-ro-fi-ch	Cyatheaceae	<i>Sphaerostephanos</i>	<i>unitus</i>	3
PLANT L	me-la-do-ph	Myristicaceae	<i>Myristica</i>	<i>subalulata</i>	3
PLANT L	pl-co-do-ph	Proteaceae	<i>Helicia</i>	<i>latifolia</i>	3
PLANT L	me-co-do-ch-li	Rhamnaceae	<i>Gouania</i>	<i>microcarpa</i>	3
PLANT L	no-la-is-pv-ch-ep	Orchidaceae	<i>Agrostophyllum</i>	<i>majus</i>	3
PLANT L	no-la-do-ch-li	Rosaceae	<i>Rubus</i>	<i>moluccanus</i>	3
PLANT L	pl-co-do-pv-ch	Arecaceae	<i>Linospadix</i>	<i>albertisianus</i>	3
PLANT L	no-la-do-ch	Rubiaceae	<i>Lasianthus</i>	<i>strigosus</i>	3
PLANT L	no-la-do-ph	Lauraceae	<i>Cryptocarya</i>	<i>densiflora</i>	3
PLANT L	pl-la-do-pv-ch	Marantaceae	<i>Phrynium</i>	<i>pedunculatum</i>	4
PLANT L	mg-co-do-ro-fi-cr	Marattiaceae	<i>Ptisana</i>	<i>melanesica</i>	4
PLANT L	pl-la-do-ph	Loganiaceae	<i>Neuburgia</i>	<i>corynocarpa</i>	4
PLANT L	ma-co-do-ro-pv-ch	Arecaceae	<i>Hydriastele</i>	<i>cariosa</i>	4
PLANT L	no-la-do-ph	Actinidiaceae	<i>Saurauia</i>	<i>purgans</i>	4
PLANT L	me-co-do-ph	Proteaceae	<i>Helicia</i>	<i>insculpta</i>	4
PLANT L	pl-la-do-ph	Malvaceae	<i>Sterculia</i>	<i>conwentzii</i>	4
PLANT L	na-la-do-ch	Rubiaceae	<i>Argostemma</i>	<i>bryophyllum</i>	4
PLANT L	no-co-do-ch-li-ep	Piperaceae	<i>Piper</i>	<i>macropiper</i>	4
PLANT L	me-co-do-ph	Apocynaceae	<i>Cerbera</i>	<i>floribunda</i>	4
PLANT L	no-co-do-ch-li	Rubiaceae	<i>Schradera</i>	<i>ledermannii</i>	5
PLANT L	le-la-do-ch	Rubiaceae	<i>Amaracarpus</i>	<i>grandifolius</i> var. <i>humilis</i>	5
PLANT L	no-co-do-pv-ph-li	Smilacaceae	<i>Smilax</i>	<i>calophylla</i>	6
PLANT L	me-co-do-ph	Elaeocarpaceae	<i>Dubouzetia</i>	sp.	6
PLANT L	no-la-do-ph	Monimiaceae	<i>Steganthera</i>	<i>hentyi</i>	6
PLANT L	mi-la-do-ch-li-ep	Urticaceae	<i>Elatostema</i>	sp.	6
PLANT L	pl-la-is-ro-fi-ch	Oleandraceae	<i>Oleandra</i>	<i>pilosa</i>	6
PLANT L	na-la-do-ph	Myrtaceae	<i>Decaspermum</i>	<i>urvillei</i>	6
PLANT L	no-co-do-ph	Nothofagaceae	<i>Trisyngyne</i>	<i>grandis</i>	7
PLANT L	no-co-do-ch-li-ep	Moraceae	<i>Ficus</i>	<i>subulata</i>	7
PLANT L	me-co-do-ph	Malvaceae	<i>Talipariti</i>	<i>albertisii</i>	7

Appendix I.3. Dominance cover/abundance scale used to calculate bryophyte cover in each plot

Cover-abundance	Scale
Cover about 100%	10
Cover > 75%	9
Cover 50–75%	8
Cover 33–50%	7
Cover 25–33%	6
Abundant, cover about 20%	5
Abundant, cover about 5%	4
Scattered, cover small	3
Very scattered, cover small	2
Scarce, cover small	1

Appendix I.4 Plant Functional Types (PFTs)

Plant Functional Types (PFTs) were developed for each species using a string of Plant Functional Elements (PFEs) for each of six vegetation structural attributes (Plant Functional Attributes; PFAs). For example a plant with a platyphyll leaf size, vertical leaf inclination, deciduous leaf chlorotype and a phraenophytic lifeform would have a PFT of pl-ve-de-ph.

Plant Functional Attribute Class	Plant Functional Element Class	Description	
Leaf Size Class	pi	Picophyll	<1–2 mm ²
	le	Leptophyll	2–25 mm ²
	na	Nanophyll	25–225 mm ²
	mi	Microphyll	225–2025 mm ²
	no	Notophyll	2025–4500 mm ²
	me	Mesophyll	4500–18,200 mm ²
	pl	Platyphyll	18,200–36,400 mm ²
	ma	Macrophyll	36,400–180,000 mm ²
	me	Megaphyll	> 180,000 mm ²
Leaf Inclination	ve	Vertical	>30° with leaf tip pointing upwards
	la	Lateral	±30° to horizontal
	pe	Pendulous	>30° below horizontal, leaf tip pointing downwards
	co	Composite	Mixture of inclinations beyond any one class on individual plant
Leaf Chlorotype	do	Dorsiventral	Chlorophyll mainly on the upper side of the leaf
	is	Isobilateral	Chlorophyll equally distributed on both sides of the leaf
	de	Deciduous	Plant loses all or most of its leaves during a season
	ct	Cortic	Chlorophyll is contained within the cortex of the main stem
	ac	Achlorophyllous	Without chlorophyll
Leaf Morphotype	ro	Rosulate	Leaves in a rosette
	so	Solid 3-dimensional	Leaves vestigial or reduced to a green stem
	su	Succulent	When sap is readily expressed when squeezed
	pv	Parallel Veined	Veins parallel e.g. pandanus
	fi	Filicoid	Fern leaf
	ca	Carnivorous	Leaves modified to capture insects

Plant Functional Attribute Class	Plant Functional Element Class	Description	
Life Form	ph	Phanerophytes	Woody plants >2m tall with perenating buds above ground
	ch	Chamaephytes	Woody plants <2m tall with perenating buds on branches at or near the ground
	hc	Hemichrytophytes	Plants with perenating buds at ground level
	cr	Cryptophytes	Plants with perenating organs below ground
	th	Therophytes	Annuals
	li	Liane	Plants with vine-like stems
Aboveground Root Type	ad	Adventitious	Roots growing from an above-ground stem
	ae	Aerating	Pneumatophores in mangrove species
	ep	Epiphytic	Plants supported by other plants e.g. orchids and climbing aroids
	hy	Hydrophytic	Plants in aqueous environments
	pa	Parasitic	Plants feeding on other plants e.g. Loranthaceae.

CHAPTER 2 – FROGS

Stephen Richards and Kyle Armstrong



A new genus and species of frog known only from the PNG LNG Upstream Project Area

SUMMARY

Background and aims

Frogs are commonly used as an indicator group to assess the quality of habitats because their thin, permeable skin and, for many species, aquatic embryonic and larval life stages, make them vulnerable to even subtle changes in both aquatic and terrestrial environments. Recent concern about the decline and disappearance of many frog species globally due to the spread of a deadly chytrid fungus, and concern about the potential impacts of climate change, has also increased the urgency to establish long-term monitoring programs for frogs particularly in tropical montane habitats. To determine whether linear infrastructure created by the ROW is having an impact on local frog populations and communities we trialled two methods of frog monitoring during the 2015 PMA3 surveys in two Biodiversity Assessment Areas (BAAs): Hides Ridge (BAA 1) and on the Agogo Range near Moro (BAA 2):

1. Visual and Audio Encounter Surveys (VAES) were conducted along the first 100 m of ten transects (five in each BAA) established adjacent to the ROW. This involved two people walking slowly along each transect at night counting and identifying the frogs seen and heard on transects at increasing distances (in 20 m sections) from the ROW.
2. Automated sound recording of frog calls was conducted on all 11 transects established in both BAAs by placing acoustic recorders at three different distances from the ROW on each transect (at 5, 70 and 170 m from the forest edge).

This report presents the results of these two survey methods to determine 1) whether there is currently evidence to suggest that the ROW is having an impact on the diversity of frog populations in either BAA, and 2) whether the methods used are suitable for longer term monitoring of frog populations at these sites.

Major results

A total of 37 species of frogs was documented by a combination of the two methods along transects that run perpendicular to the ROW in BAA 1 at Hides Ridge, and BAA 2 on the Agogo Range near Moro. Slightly more than half of all species were detected by both methods, and the remainder by only one or other of the methods.

More than half of the frog species encountered are undescribed ($n = 23$; 62%) but many of these were previously known to occur in the Upstream Project Area. One of the newly discovered species appears to represent an entirely new genus, and is currently known only from BAA 2. Two species are classified as Data Deficient by the IUCN due to the lack of information on their extent of occurrence, status and ecological requirements. The taxonomic status of several species remains uncertain, and at least two call types have not been confidently associated with any species.

Species diversity and composition differed significantly between the two BAAs, with 10 frog species found in BAA 1, 29 species in BAA 2 and only two species (5.4%) shared between them. Analyses of data from both the VAES and the acoustic recorders detected no evidence in either BAA for shifts in species diversity or composition with increasing distance from the ROW.

Conclusions

These results indicate that, to date, establishment of the ROW clearings in BAA 1 on the Hides spine-line and in BAA 2 on the Agogo Range near Moro have had no detectable impacts on local frog populations, and that the biodiversity values of frogs in these areas remain intact.

INTRODUCTION

Amphibians including frogs are excellent indicators of environmental conditions due to their thin, permeable skin and, for many species, exposure to the aquatic environment during their embryonic and larval life stages. These factors make them especially vulnerable to even subtle changes in both aquatic and terrestrial environments. Globally, amphibian populations are in decline due to the spread of a deadly chytrid fungus, and climate change is also likely to be a significant threat to amphibians in the future (Corn 2005).

Frogs are identified as a core taxon in EMPNG's Biodiversity Strategy, and the presence of a distinct assemblage of torrential-stream dwelling treefrogs (Family Hylidae) was partly responsible for upland rainforest streams being recognised as focal habitats. However many frog species in New Guinea do not use streams to breed, instead depositing their eggs on plants or under litter on the forest floor where they hatch directly into froglets without going through a tadpole stage (Anstis et al. 2011). All New Guinean species in the diverse family Microhylidae are known or expected to reproduce this way (Menzies 2006) and as a result this group dominates the frog faunas of karst habitats in Papua New Guinea.

The program for monitoring frogs in the Upstream Project Area was designed to consider these two distinctly different ecological guilds. However, the karst environments of Hides Ridge in BAA 1 and on the Agogo Range near Moro in BAA 2 are characterised by limited flowing water so our efforts focused predominantly on a series of transects through the forest to document the diversity (used here to mean number of species; sometimes also called 'species richness') and composition (which species are present) of microhylid frog communities.

The aims of the 2015 frog survey were to 1) document frog diversity and community composition in both BAAs using quantitative, repeatable sampling techniques to provide baseline data against which future changes in frog diversity and community composition can be measured, 2) assess whether frog diversity and community composition changes with increasing distance from the ROW, and 3) identify species of conservation significance and those that might also be useful targets for population monitoring.

METHODS

Frog surveys in 2015 were conducted in two Biodiversity Assessment Areas (BAAs): on Hides Ridge (BAA 1) between 11–25 June, and on the Agogo Range in the Moro area (BAA 2) between 27 June–8 July (Figure 1 in Executive Summary). Each of these BAAs was divided into two survey 'sites' that differed in elevation:

- Hides Ridge (BAA 1):
 - Transects H1–3: between Wellpad C and Wellpad D, at elevations of 2,100–2,400 m asl.
 - Transects H4–6: between Wellpad E and Wellpad G, at 2,660–2,780 m asl.
- Agogo Range (BAA 2):
 - Transects M1–3: in the vicinity of KP107, at 1,340–1,410 m asl.
 - Transects M4–5: west of Arakubi Quarry and east of the pipeline ROW, at 1,000–1,070 m asl.

Surveys for frogs on transects

Two methods were used to document frogs in a quantitative way along transects—Visual and Audio Encounter Surveys (VAES) conducted along 100 m transects at night; and audio monitoring with acoustic recorders which recorded over a 48 hour period. All but one of the transects (FT5, see below) start at the edge of, and run perpendicular to, the ROW, thereby allowing comparison of species diversity and assemblage composition at increasing distances from the forest edge.

Transect H6 in BAA 1 and transect M5 at Arakubi Quarry in BAA 2 were surveyed using acoustic recorders only because logistical and safety issues prevented night access to conduct the VAESs there. An alternative location for a sixth VAES transect in BAA 1 was not found; accordingly, VAES data was obtained from only five transects in this area. At Arakubi Quarry in BAA 2 a fifth VAES transect (hereafter 'FT5'; see Figure 7 in Executive Summary) was established inside the forest; it commenced 50 m beyond the end of the primary 100 m long VAES transect on M4, and thus 150 m in from the start of the secondary forest cover that abuts the quarry.

Visual and Audio Encounter Surveys (VAES)

VAESs provide counts of the numbers of frogs of each species seen and heard on 100 m transects. Most of the VAES transects start at the edge of, and run perpendicular to, the ROW, and thus allow for comparison of species diversity and assemblage composition at increasing distances from the forest edge. In the case of FT5, the VAES transect starts at a sharp transition from regrowth forest (previously cleared for the quarry) to original forest. Its inclusion in the study will shed light on potential shifts in frog species diversity and composition at increasing distances from a regrowth/primary forest boundary. However, for the purposes of discussion within this report we consider this transect to be providing equivalent information—assessing change in species diversity and composition at increasing distances from a sharp, project-related disturbance boundary.

Coordinates for the beginning and end of each VAES transect are presented in Appendix 2.1. Each 100 m VAES transect was marked at 20 m intervals. Surveys were conducted by two searchers with headlamps and a digital recorder who walked slowly along each transect, noting each frog seen or heard (Figure 2.1). The original objective was to document frogs in a 10-metre wide band along the transect (5 metres on either side of the transect path) but visual detection of small microhylid frogs beyond 2.5 metres proved difficult in the particular forest types in the BAAs, so visual detection was restricted to a 5 m band while the band for acoustic detection remained at 10 m. Each transect was sampled twice on non-consecutive nights to minimise the influence of local weather conditions on frog activity, and whenever possible the first survey each night started approximately 30 minutes after dark and the second survey of the night started by 22:00. A standard set of environmental data (rainfall, temperature etc.) was recorded at the start of each VAES.

Each frog encountered was identified, whether it was seen or heard (or both) was noted, and its location on the transect (which 20 m segment, i.e. distance from the forest edge) was noted. For each species voucher recordings of calls were obtained and a brief description of the call was produced, to permit identification of frogs recorded during the acoustic monitoring component (see Appendices 2.3–2.4), and photographs were taken. A small number of voucher specimens were taken to provide tissue samples for DNA barcoding that will support future efforts to make robust and consistent identifications across successive surveys, as well as to allow formal taxonomic descriptions in the future (further details in Chapter 7). Tissue samples were placed into 95% ethanol and submitted to the Australian Biological Tissue Collection at the South Australian Museum (Appendix 2.5).

VAES transects generally overlap with two acoustic recorders, positioned at 5 m and 70 m from the ROW. This is not the case for Transect 6 in BAA 1 and Transect 5 in BAA 2 for which VAES data were not obtained.

Audio monitoring with acoustic recorders

In addition to the VAES searches, it is possible for non-specialists to obtain information on frog species with relatively little effort by recording their advertisement calls with unattended acoustic recorders. The identification of calls is supported by a resource in preparation that matches them with morphological features and associated DNA barcodes for consistent identification. Unattended acoustic recordings serve to augment the active searches for frogs and they provide standardised recording effort at known distances from the road edge disturbance zone.

The acoustic recorders were placed at three recording sites at increasing distances from the forest edge (5 m, 70 m and 170 m) on transects H1–6 established in BAA 1 and M1–5 in BAA 2 (Figures 2–7 in Executive Summary). Recording units were placed 65 and 100 m apart to reduce the likelihood that an individual frog would be detected by more than one unit. The microphone of the recorder set at the 5 m position on each transect was oriented to maximise reception of

signals from the edge habitat adjacent to the open area over the road. Each transect was surveyed for two consecutive nights, giving a total of 36 recording nights over an 8-night survey period for BAA 1, and 30 recording nights over a 6-night survey period for BAA 2 (Table 2.1).

A summary of the design is presented in Table 2.1 and coordinates for each recording location are presented in Appendix 2.2.

Table 2.1. Summary of the experimental design and frog acoustic recording site placements.

BAA	Elevation	Transect	Distance from forest edge			Total nights
			5 m	70 m	170 m	
BAA 1 Hides Ridge	'2,700 m'	H4—2,700 m (2,681–2,696 m)	2	2	2	36
		H5—2,750 m (2,726–2,756 m)	2	2	2	
		H6—2,730 m (2,725–2,736 m)	2	2	2	
	'2,200 m'	H1—2,150 m (2,148–2,163 m)	2	2	2	
		H2—2,200 m (2,171–2,229 m)	2	2	2	
		H3—2,300 m (2,296–2,327 m)	2	2	2	
BAA 2 Agogo Range	'1,400 m'	M1—1,400 m (1,397–1,405 m)	2	2	2	30
		M2—1,380 m (1,315–1,397 m)	2	2	2	
		M3—1,380 m (1,369–1,389 m)	2	2	2	
	'1,000 m'	M4—1,030 m (995–1,041 m)	2	2	2	
		M5—1,050 m (1,051–1,073 m)	2	2	2	

Recordings were made with Wildlife Acoustics Song Meter SM3 recorders (Figure 2.2), set to make recordings continuously in WAV format at a sampling rate of 48 kHz. By maximising the collection of data through continuous recordings, it provides flexibility in the approach for later analysis, and the opportunity for the data from all surveys to be re-analysed in the future if an improved data processing system is developed.

Audio and visual monitoring of frogs at Wellpad D on Hides Ridge

A small pond adjacent to Wellpad D was identified in the PNG LNG Project Environmental Impact Statement (EIS) as a significant habitat for frogs on Hides Ridge in BAA 1. It provides one of the few habitats for aquatic frogs in BAA 1 and, as well as supporting a population of the Rainbow Treefrog (*Litoria iris*), it is the only known locality for an undescribed, spike-nosed treefrog discovered during the EIS surveys. We conducted one VAES night survey for 30 minutes around the edge of the pond and documented the species present, based on both calls and visual detection. We estimated the abundance of each species based on visual detection only, in categories of 0, 1–10 and >10 and noted the presence and abundance of gelatinous egg masses of the Rainbow Treefrog hanging from low vegetation (0, 1–10, >10 clumps).

An acoustic recorder was also deployed at the pond for two consecutive nights, 20 and 21 June, with the microphone angled across the centre of the pond. The resulting data for analysis were selected using the same methods described for acoustic recorders placed on transects.

Data synthesis and statistical analyses

VAES data

The number of individual frogs seen and heard in each transect interval (0–20, 20–40 m, etc. from the forest edge) was tabulated. For analysis, this was reduced to a table of presence/absence of each species in each transect interval, with species scored as present regardless of whether they were seen or heard. Data from both survey nights on the same transect interval were combined.

Acoustic data

Sixty-six nightly recordings collected from the 11 transects were analysed. Initial attempts at automated recognition (e.g. in MATLAB) were found to be inefficient at rejecting signals from non-target species (mostly insects), and were inadequate for recognising many of the fainter calls of frogs amongst the background noise. Therefore, frog presence was scored by playback of standardised portions of recordings and visual and aural recognition of calls using Adobe Audition software. Using this process the calls of each frog species, most of them confirmed using voucher calls obtained during the VAES surveys, were confirmed by an inspection of calls in a high quality spectrogram view. A proportion of frogs could be heard in the recordings but not observed in spectrograms because some fainter frog calls were obscured by other background noise with overlapping frequencies.

For each 24-hour recording period at each site we analysed five 1-hour sound files, those starting at (or closest to) 19:00 to 23:00 inclusive (recording time 19:00 to 00:00). Within each of these 1-hour files we examined the following three 5-minute sections: 15–20 mins, 35–40 mins and 55–60 mins and noted the presence/absence of calls for each species.

Estimates of Relative Abundance

An additional metric—‘Relative Abundance’—was calculated to provide an indication of ‘commonness’ versus ‘rarity’ of each of the frog species found in the BAAs. It rests on the premise that a common and widely distributed species will be observed in a high proportion of all VAES or acoustic recording sessions, whereas a rare or localised species will be observed only occasionally. It is confounded to a degree by the fact that some frog species may be easier to detect (whether by calls or visually) than others, the effect of which is minimised by maximising sampling effort.

Relative Abundance values were calculated from the presence/absence tabulations and separately for each of the VAES and the acoustic datasets. The metric indicates the proportion of sites that a particular species was recorded at. Exactly how it is calculated depends on how the data is grouped, which in turn depends on the question being asked. For example (using acoustic recording sites), for a given distance from the ROW (e.g. 5 m), a species would have a Relative Abundance of 0.45 if it was recorded on 5 of 11 transects at a distance of 5 m (i.e. across all four elevations combined). Likewise, a species would have a Relative Abundance of 0.45 if it was present in 4 of 9 recording sites on all three transects at one particular elevation (i.e. across all distances from the ROW).

For this study, inter- and intra-specific trends in Relative Abundance were examined by elevation and by distance from the ROW values. This exercise helped to identify species that might be more or less vulnerable to impacts associated with the ROW and also helped identify candidate Indicator Species.

Statistical analysis

Statistical analyses were conducted separately on data obtained from the VAES transects and the acoustic recordings. Analysis of a combined dataset was not attempted at this stage for two reasons; firstly, because there was not 100% compatibility between the two data sets (there was no VAES search conducted at transect H6 in BAA 1 and acoustic sample sites at transect M5 did not correspond with VAES transect FT 5 in BAA 2); and secondly, because we wished to explore the relative contributions of the two datasets to assess the relative utility of each method to meeting the study objectives.

Frog diversity was compared across elevations and distances from the ROW by fitting a Generalised Linear Mixed Model by Maximum Likelihood (Laplace Approximation) to the data. Variation in community composition (i.e. the mix of species found on each transect) was explored for each of the VAES and acoustic recording datasets by calculating the Bray-Curtis Dissimilarity Index and then performing Non-metric Multidimensional Scaling (NMDS). The NMDS is an ordination that grouped sites in two-dimensional space on the basis of the similarity/dissimilarity of their component species. All analyses were conducted using a custom-written [R] language script which can be modified and rerun for subsequent surveys.

DNA barcoding

A genetic framework based on mitochondrial DNA barcodes (see Chapter 7 for a general introduction to this concept) was generated to help confirm the identities and relationships of captured frogs, to provide a genetic perspective on their apparent novelty, and to provide a genetic-based voucher for call types. The barcodes also represent a genetic

basis for consistent identifications for all frogs in future, particularly of individuals that cannot be identified by their calls (e.g. females, froglets) or by using morphological criteria (e.g. eggs, tadpoles, adults of morphologically cryptic species). Tissue samples were sequenced using a single mitochondrial DNA marker (12S rRNA) (see Chapter 7 for details of laboratory methods). Additional sequences were sourced from publicly available data on New Guinea frogs on Genbank (<http://www.ncbi.nlm.nih.gov/genbank/>; Köhler and Günther 2008; Rittmeyer et al. 2012). The resulting sequence alignment was edited and aligned manually in BioEdit version 7.2.5 software (Hall 1999), and a distance matrix and phylogenetic tree (Neighbour Joining phenogram) were constructed in an R script.

To highlight potential species boundaries, the position of the DNA barcoded vouchers was first inspected in the phylogenetic tree. To further support possible species-level differences amongst samples, each representative sequence was assigned to hypothetical species based on their 'barcode gap' using the Automatic Barcode Gap Discovery (ABGD) tool of Puillandre et al. (2011). A barcode gap occurs whenever the genetic divergence among samples from the same species is smaller than divergence among samples from different species. This additional analysis assists in interpreting which samples on the phylogenetic tree can be grouped into species or placed in different species; however, barcode gap detection methods and interpretations of Neighbour-Joining trees are regarded as providing only a preliminary view of species boundaries (Collins and Cruikshank 2012; also see Chapter 7).



Figure 2.1. Spotlighting for frogs on 100 m VAES transects at night



Figure 2.2. Set up of the acoustic frog recorders. Each was placed on a metal star picket underneath an umbrella

RESULTS AND DISCUSSION

The frog species recorded on each transect within the two BAAs is presented in Table 2.2 for the VAES survey and in Table 2.3 for the acoustic survey. A combined species list for each of the four surveyed elevational bands is shown in Table 2.4.

Table 2.2. Summary of species/call type detections for each VAES transect. The sequence of squares is increasing distance from the road (0 to 100 m, left to right in 20 m increments), with a black square indicating a detection of that species, and a grey square an apparent absence.

Species	BAA 2					BAA 1				
	1,000 m asl		1,400 m asl			2,200 m asl			2,700 m asl	
	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5
HYLIDAE*										
<i>Litoria iris</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Litoria</i> sp. 1 'yellow legs'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
LIMNODYNASTIDAE										
<i>Lechriodus aganoposis</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
MICROHYLIDAE										
<i>Austrochaperina</i> sp. 1 'short call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Austrochaperina</i> sp. 2 'long call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Callulops wilhelmanus</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Callulops</i> sp.	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne brevicrus</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne burtoni</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne murruta</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 1 'arboreal'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 2 'tiny'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 3 'buzz call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 4 'montane clicker'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 5 'lowland clicker'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus wempi</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 1 'musical call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 2 'tiny A'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 3 'tiny B'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 4 'rasping call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 5 'peeping call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Copiula</i> sp. 1 '2-note call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■

Species	BAA 2					BAA 1				
	1,000 m asl		1,400 m asl			2,200 m asl			2,700 m asl	
	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5
<i>Hylophorbus</i> sp. 1 'small'	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Hylophorbus</i> sp. 2 'large'	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Liophryne schlaginhaufeni</i>	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Metamagnusia slateri</i>	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Oreophryne anamiatoi</i>	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Oreophryne notata</i>	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Oreophryne oviprotector</i>	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Oreophryne</i> sp. 1 'tiny'	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Oreophryne</i> sp. 2 'ratchet call'	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Oreophryne</i> sp. 3 'slow peeper'	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Oreophryne</i> sp. 4 'yellow spots'	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Oreophryne</i> ? sp. 5 'loud grunter'	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Spenophryne cornuta</i>	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
<i>Xenorhina</i> sp.	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■
Microhylid new genus and species	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■	■ ■ ■ ■ ■

*A recent study (Duellman et al. 2016) places New Guinea treefrogs in the family Pelodyadidae but we retain Hylidae here.

Table 2.3. Summary of species/call type detections at each acoustic recording site. The sequence of squares is increasing distance from the road (5 to 170 m, left to right), with a black square indicating a detection of that species, and a grey square an apparent absence.

Species	BAA2					BAA1					
	1,000 m asl		1,400 m asl			2,200 m asl			2,700 m asl		
	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5	H6
HYLIDAE											
<i>Litoria iris</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Litoria</i> sp. 1 'yellow legs'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
LIMNODYNASTIDAE											
<i>Lechriodus aganoposis</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
MICROHYLIDAE											
<i>Austrochaperina</i> sp. 1 'short call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Austrochaperina</i> sp. 2 'long call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Callulops wilhelmanus</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Callulops</i> sp.	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne brevicrus</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne burtoni</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne murruta</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 1 'arboreal'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 2 'tiny'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 3 'buzz call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 4 'montane clicker'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Choerophryne</i> sp. 5 'lowland clicker'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus wempi</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 1 'musical call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 2 'tiny A'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 3 'tiny B'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 4 'rasping call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Cophixalus</i> sp. 5 'peeping call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Copiula</i> sp. 1 '2-note call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Hylophorbus</i> sp. 1 'small'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Hylophorbus</i> sp. 2 'large'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Liophryne schlaginhaufeni</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Metamagnusia slateri</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Oreophryne anamiatoi</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■

Species	BAA2					BAA1					
	1,000 m asl		1,400 m asl			2,200 m asl			2,700 m asl		
	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5	H6
<i>Oreophryne notata</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Oreophryne oviprotector</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Oreophryne</i> sp. 1 'tiny'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Oreophryne</i> sp. 2 'ratchet call'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Oreophryne</i> sp. 3 'slow peeper'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Oreophryne</i> sp. 4 'yellow spots'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Oreophryne</i> ? sp. 5 'loud grunter'	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Spenophryne cornuta</i>	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
<i>Xenorhina</i> sp.	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■
Microhylid new genus and species	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■	■ ■ ■ ■

Table 2.4. Frog species documented in two elevational bands in BAA 1 at Hides Ridge and in two elevational bands in BAA 2 on the Agogo Range near Moro.

Species	BAA 1 Hides Ridge 2,600–2,800 m asl	BAA 1 Hides Ridge 2,200–2,400 m asl	BAA 2 KP107 1,400 m asl	BAA 2 Arakubi 1,000 m asl	IUCN Status
HYLIDAE					
<i>Litoria iris</i>		X			LC
<i>Litoria</i> sp. 1 'yellow-legs'			X	X	NE
LIMNODYNASTIDAE					
<i>Lechriodus aganoposis</i>		X	X		LC
MICROHYLIDAE					
<i>Austrochaperina</i> sp. 1 'short call'			X		NE
<i>Austrochaperina</i> sp. 2 'long call'				X	NE
<i>Callulops wilhelmanus</i>	X	X			LC
<i>Callulops</i> sp.			X	X	NE
<i>Choerophryne burtoni</i>			X		DD
<i>Choerophryne brevicrus</i>	X	X			NE
<i>Choerophryne murruta</i>			X		NE
<i>Choerophryne</i> sp. 1 'arboreal'		X			NE
<i>Choerophryne</i> sp. 2 'tiny'		X			NE
<i>Choerophryne</i> sp. 3 'buzz call'			X	X	NE
<i>Choerophryne</i> sp. 4 'montane clicker'			X		NE
<i>Choerophryne</i> sp. 5 'lowland clicker'				X	NE
<i>Cophixalus wempi</i>			X	X	NE
<i>Cophixalus</i> sp. 1 'musical call'			X		NE
<i>Cophixalus</i> sp. 2 'tiny A'			X		NE
<i>Cophixalus</i> sp. 3 'tiny B'			X		NE
<i>Cophixalus</i> sp. 4 'rasping call'				X	NE
<i>Cophixalus</i> sp. 5 'peeping call'			X		NE
<i>Copiula</i> sp. 1 '2-note call'				X	NE
<i>Hylophorbus</i> sp. 1 'small'			X		NE
<i>Hylophorbus</i> sp. 2 'large'				X	NE
<i>Liophryne schlaginhaufeni</i>				X	LC
<i>Metamagnusia slateri</i>				X	LC
<i>Oreophryne anamiatoi</i>		X			NE
<i>Oreophryne notata</i>	X	X	X?	X?	DD
<i>Oreophryne oviprotector</i>			X	X	NE
<i>Oreophryne</i> sp. 1 'tiny'		X			NE
<i>Oreophryne</i> sp. 2 'ratchet call'			X	X	NE

Species	BAA 1 Hides Ridge 2,600–2,800 m asl	BAA 1 Hides Ridge 2,200–2,400 m asl	BAA 2 KP107 1,400 m asl	BAA 2 Arakubi 1,000 m asl	IUCN Status
<i>Oreophryne</i> sp. 3 'slow peeper'				X	NE
<i>Oreophryne</i> sp. 4 'yellow-spots'			X	X	NE
<i>Oreophryne?</i> sp. 5 'loud grunter'		X			NE
<i>Sphenophryne cornuta</i>				X	LC
<i>Xenorhina</i> sp.				X	NE
Microhylid new genus and species				X	NE
Totals	3	10	18	19	

Overview of the frog fauna

A total of 37 species of frogs was documented, including 10 species in BAA 1 and 29 species in BAA 2 (Table 2.4).

The frog fauna in both BAAs is dominated by members of the family Microhylidae (34 species, 92% of the fauna), a group characterised by having direct embryonic development that bypasses the aquatic tadpole stage. This reflects the near-lack of permanent water in the karst habitats in both BAAs. One species of aquatic-breeding frog, the Rainbow Treefrog, was abundant in the small pond at Wellpad D. Calls of each species recorded are briefly described (Appendix 2.3) and illustrated (Appendix 2.4) to facilitate future identification of each species.

Elevational trends in frog diversity and community composition

There is a pronounced reduction in frog diversity with increasing elevation (Table 2.5 and Figure 2.3). This pattern is widely repeated in the mountains of New Guinea (e.g. Richards 2007; Richards and Dahl 2011).

Table 2.5. Summary of means \pm standard deviation for frog diversity at each elevation for the two different frog survey methods.

Elevation (m)	Acoustic recordings	Elevation (m)	VAES transects
1,000	6.83 \pm 2.99	1,000	4.0 \pm 2.0
1,400	7.78 \pm 1.09	1,400	4.7 \pm 1.49
2,200	4.33 \pm 0.87	2,200	2.0 \pm 1.20
2,700	1.78 \pm 0.44	2,700	1.7 \pm 0.48

Within BAA 1 there is a particularly sharp pattern of reduction in diversity at the higher elevation sites (~2,600–2,750 m asl, with 3 species) compared to the lower elevation sites (2,100–2,400 m asl, with 10 species). All of the species recorded at the higher elevations in BAA 1 were also found at the lower elevations in that BAA.

The frog fauna in BAA 2 is substantially more diverse than that encountered on Hides Ridge, with nearly three times as many species (29 vs 10). There was also a higher turnover of species between the two sites in BAA 2, with only eight of the 29 species (27.6%) found in BAA 2 occurring at both KP107 (1,400 m asl) and Arakubi (1,000 m asl) despite these sites being in close proximity and having similar numbers of species (18 and 19 respectively). These results suggest that elevation has a greater influence on diversity at higher sites (BAA 1), but more influence on species turnover (composition) at lower sites (BAA 2).

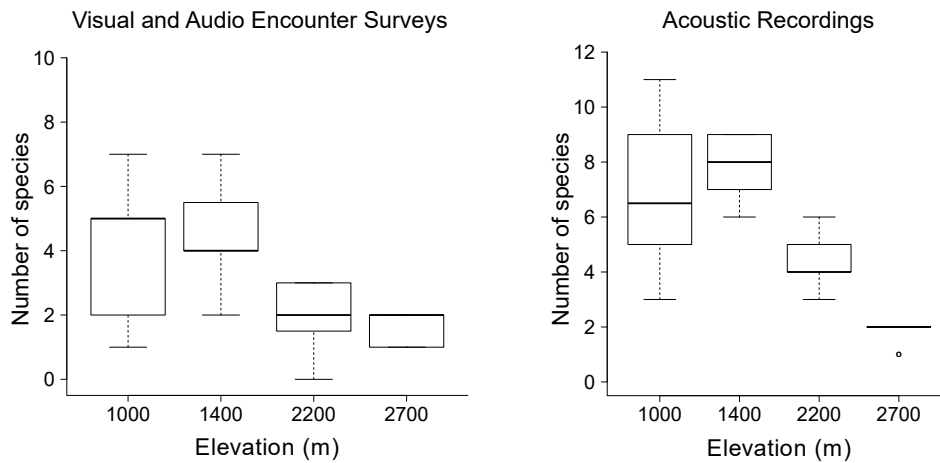


Figure 2.3. Summary of frog diversity (as number of species) at different elevations based on data from VAES transects. Statistical analysis using GLMM confirmed that the diversity of BAA 1 is significantly greater than that of BAA 2 for each of the VAES and acoustic recording datasets, and in each case is not influenced by the distance of observations from the ROW, nor is there a relationship between elevation and distance from ROW (Table 2.6).

It is important to note that the frog communities in BAA 1 are not simply a sub-set of the frogs found in BAA 2, with eight of the 10 species found in BAA 1 not occurring in BAA 2 (Table 2.4). Hides Ridge clearly represents an important habitat for a distinctive suite of high-elevation frogs, several of which are undescribed or known from few or no other localities.

Table 2.6. Summary of the tests of the Generalised Linear Mixed Model1 (values from the Analysis of Deviance table; Type III Wald chi-square tests) and post hoc pairwise comparisons to test for the influence on frog diversity of elevation and distance from the ROW for each of the acoustic recording and the VAES data sets (only significant pairs shown; values are elevations in metres; Significance codes: '*' <0.05 '**' <0.01 '***' <0.001).

Acoustic recordings	Chi-square	df	P	Pairwise
Elevation	7.22	3	0.065 ^{NS}	1,000 > 2,700*** 1,400 > 2,200* 1,400 > 2,700*** 2,200 > 2,700*
Distance	0.04	2	0.98 ^{NS}	—
Distance*Elevation	0.90	6	0.99 ^{NS}	—
VAES transects				
Elevation	3.22	3	0.36 ^{NS}	1,000 > 2,200 . 1,000 > 2,700 . 1,400 > 2,200** 1,400 > 2,700**
Distance	0.99	4	0.91 ^{NS}	—
Distance*Elevation	3.08	12	0.99 ^{NS}	—

¹ Model coded in [R] as: `glmer(total_richness.t ~ dist + elev + dist*elev + (1 | transect), family=poisson(), data = y)`
 #Species diversity values transformed prior to analysis by adding 1 in each case.

Multi-dimensional Scaling (NMDS) ordinations of species composition based on each of the VAES transect and acoustic recording datasets also emphasise the strong differentiation in the frog communities of each of the elevational zones in BAA 2 and between these and the BAA 1 frog communities (Figure 2.4). Interestingly, the ordination based on acoustic recordings also showed a consistent difference between species composition of the higher and lower Hides Ridge sites, while those based on nocturnal VAES searches were not differentiated. This probably reflects the lower number of species encountered during nocturnal searches than with acoustics recorders at the lower (~2,200 m asl) Hides Ridge site and that the frog community at the highest elevation site (~2,700 m asl) in BAA 1 is entirely a subset of the species occurring at this lower site.

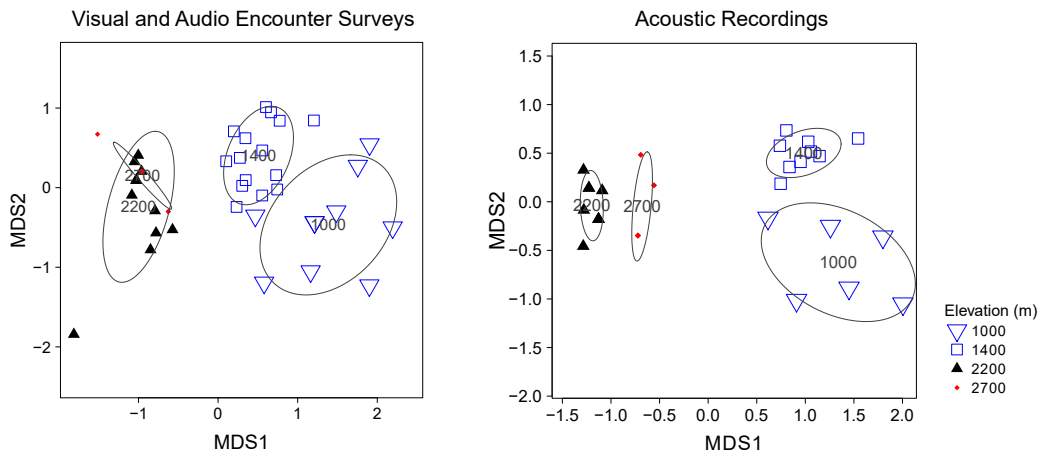


Figure 2.4. Multi-dimensional Scaling (NMDS) ordinations summarising patterns of species composition at different elevations within the BAAs (confidence ellipses are one standard deviation).

New and undescribed species

More than half of the frog species encountered are undescribed ($n = 23$; 62%), and they occurred at all elevations except the highest band in BAA 1 (>2,600 m asl; Table 2.4). Many of these were previously known to occur in the Upstream Project Area (Richards 2002) but at least two species appear to be entirely new to science. One of the newly discovered species may represent an entirely new genus, and is currently known only from BAA 2. A tiny frog of the morphologically conservative genus *Oreophryne* (*O. sp. 1* 'tiny') that was found only at the lower elevation band in BAA 1 was identified to genus by DNA barcoding. Although calls were not heard, the similar small size and morphology of the two captured animals suggest that they are the same species. DNA barcoding of the larger co-occurring species *Oreophryne notata* is required to confirm definitively that they are not juveniles of that species but given a number of consistent morphological differences we tentatively conclude that these tiny frogs represent a species new to science. Confirming this identification will be a priority during the 2017 survey. Brief summaries of the new and undescribed species are presented below.

Family Hylidae

Litoria sp. 1 'yellow-legs' (Figure 2.10)

A beautiful, moderately small (males to ~32 mm) and slender treefrog with yellow colouration in the thighs. This species was previously known only from the Moro area and Gobe Ridge in the Kikori Basin. During this survey several individuals were observed in forest adjacent to Arakubi Quarry and calls were heard at KP107. It is illustrated in Richards (2002) as *Litoria sp. nov. 8* and is currently being described by S. Richards. It is possibly a restricted range species found only in the Kikori River catchment.

Family Microhylidae

Studies on the taxonomic status of microhylid frogs encountered during the 2015 PMA3 survey are ongoing but several species are known or suspected to be undescribed. Comments on these are provided below.

Austrochaperina sp. 1 'fast call' (Figure 2.11)

A medium-sized (females to 30 mm), ground-dwelling frog with short legs that was found only at KP107. The call tentatively associated with this species (no males were seen calling) is a series of rapid yapping notes. Studies are ongoing to determine its taxonomic status but this species appears to be undescribed and, if so, it will have a known distribution restricted to BAA 2.

Choerophryne spp. (Figures 2.12–2.13)

Five of the eight species of these small (SVL normally <25 mm) microhylid frogs that were encountered are undescribed. However all of these have been previously documented from other sites in the Kikori Basin or further afield. *Choerophryne sp. 2* 'tiny' is one of the smallest frogs known from New Guinea (adult SVL ~11 mm) and it is so far known from just one other site in the central cordillera.



Figure 2.5. The Rainbow Treefrog, *Litoria iris*



Figure 2.6. This small pond at Wellpad D on Hides Ridge provides an important breeding site for the Rainbow Treefrog. Several gelatinous egg masses belonging to this species can be seen hanging from leaves in the top left foreground.

Cophixalus spp. (Figures 2.14–2.15)

Five of the six species of this genus that were encountered, all of them in BAA 2, are undescribed. All five are known to occur at other sites in the Kikori Basin.

Copiula sp. 1. '2-note call'

This moderate-sized (~35 mm) species is undescribed but it is known to occur outside of the BAAs to the west of the Kikori Basin (Richards, unpublished data). It is known in the BAAs only from calls detected by the acoustic recorders in BAA 2.

Hylophorbus spp. (Figure 2.16)

Two species of this taxonomically difficult genus were encountered in BAA 2 – one at KP107 and one at Arakubi Quarry. Both are probably undescribed, but without confirmation of call structure, identification to species is difficult. A call attributable to this genus was detected on the acoustics recorders at Arakubi and we tentatively associate it with the species captured there. Although DNA barcoding confirms the presence of two distinct species in BAA 2 further DNA comparisons with other populations, and information on calls of both species, are required to confirm whether they are endemic to the BAAs.

Oreophryne spp. (Figures 2.17–2.18)

Four species of this taxonomically difficult genus are undescribed; a very small species found only in BAA 1 (*Oreophryne* sp.1 'tiny') and three moderate-sized species encountered in BAA 2. Two of the species from BAA 2 (*Oreophryne* sp. 3 'slow peeper' and *Oreophryne* sp. 4 'yellow-spots') are currently being described from elsewhere in the Kikori Basin (Günther and Richards, in press). The species listed in Table 2.2 as '*Oreophryne?* sp. 5 'loud grunter' is, based on its call (no animal was seen), new to science and probably represents an additional undescribed *Oreophryne* species. Obtaining a voucher specimen is a high priority to confirm its taxonomic status.

Microhylid new genus and species (Figure 2.19)

This tiny species (SVL<13 mm) is new to science and was discovered in the forest adjacent to Arakubi Quarry in BAA 2 where individuals were spotted hopping in the litter on the forest floor. The call is unknown. DNA barcoding revealed that this species does not belong in any existing genus of microhylid frogs in New Guinea.

Species of conservation significance (IUCN-Listed)

Choerophryne burtoni (IUCN Data Deficient) (Figure 2.20)

Originally described from near Moran, this small (males <13 mm), long-snouted frog is now known from a number of additional sites in the mountains of south-central PNG (Kraus 2010, Richards and Dahl 2011). It was common along transects at KP107 in BAA 2 where its conspicuous calls were heard regularly along transects after rain. Relative abundance data from both VAES and audio recorders (see below) also indicate that this species may be sensitive to edge effects so it may be an appropriate target for long-term monitoring.

Oreophryne notata (IUCN Data Deficient) (Figure 2.21)

This is a small (<18 mm) frog with a distinct, pale upturned 'U' mark on the lip. It is an arboreal species found in mossy high-elevation forest in south-central Papua New Guinea. Its loud and distinctive 'peeping' call and relatively high abundance on the Hides Ridge make it a candidate for long-term acoustic monitoring there.

Frogs at Wellpad D on Hides Ridge

Extremely large numbers of the Rainbow Treefrog (Figure 2.5) were present around the small pond at Wellpad D and their gelatinous egg masses were observed hanging from fringing vegetation. Several egg masses are visible in the top-left corner of Figure 2.6. Calls of this species were recorded on 100% of the audio segments analysed, and frogs and egg masses were both present in the highest abundance class (>10). No other pond-breeding frogs were observed at this site but several calls that are slightly atypical of those known for the Rainbow Treefrog (Appendices 2.3–2.4) were detected on the acoustic recorder. These may represent an undescribed, spike-nosed treefrog that was discovered at (and is still known only from) this site during the EIS surveys. No individuals of this new species were seen at the pond in 2015, and its call remains unknown. Rediscovery and formal description of this poorly known species is a high priority for future surveys.

DNA barcoding

Of the 22 voucher specimens taken, DNA barcodes were generated from 20 of them. Their relationships with described and previously barcoded species are presented in Figure 2.7 along with their 13 putative species groupings.

The DNA barcoding significantly improved our ability to accurately identify several species, and contributed greatly to our understanding of both the diversity and composition of frog assemblages in both BAAs, and of their conservation significance. For example DNA barcoding revealed that a tiny unidentified microhylid frog from Arakubi Quarry does not belong with any known genus of that family in New Guinea. This species is known only from transect FT5, so documenting its broader distribution and population status is a high priority.

The DNA results also supported the notion that, given the lack of acoustic information, the three *Hylophorbus* specimens encountered represent two different species, one from KP107 and one from Arakubi. Many members of this genus are difficult to distinguish morphologically, requiring access to comparative call data or genetic information. Similarly, the DNA barcoding revealed that a tiny frog encountered in BAA 1 represents a species of the genus *Oreophryne* that is probably undescribed; and if so is currently known only from Hides Ridge, and that at least two species of *Oreophryne* with acoustically similar 'rattling' calls occur at KP107.

Two results presented in this tree should be treated with some caution. *Choerophryne* sp. 3 'buzz call' and *Choerophryne* sp. 4 'montane clicker' are morphologically and acoustically distinct species so although their extreme proximity in the tree in Figure 2.7 might indicate that they are related genetically, it is also possible that their proximity is due to a mix-up of tissue samples; accordingly, this result needs to be re-tested with fresh tissue samples. A similar explanation probably accounts for the anomalous placement of *Austrochaperina* sp. 1 'fast call' as a close relative of *Oreophryne* species.

The DNA barcodes establish a framework for consistent identifications across surveys and a way of conforming the allocation of call types, specimens and names. It is especially useful given that many of the frog taxa encountered on the survey are either known to science but undescribed, or completely new.

Influence of the ROW on species diversity, community composition and relative abundances

Local environmental changes close to the ROW (collectively termed 'edge effects'), including lower humidity and greater extremes of temperature, might be expected to reduce frog diversity there or result in changes to community structure with more 'climate tolerant' frogs replacing forest-interior species closer to the ROW. We analysed the VAES and acoustic recording data in various ways to explore the potential relationship between distance from ROW and each of frog species diversity and community composition.

Graphical summaries of species diversity recorded at increasing distances from the ROWs on each of the VAES transects, and by acoustic recordings, are shown in Figure 2.8. Only at Arakubi Quarry at c. 1000 m asl in BAA 2 is there any suggestion of an increasing trend in species diversity with increasing distance from the ROW (or secondary forest edge in the case of FT5) and this is observed only in the VAES dataset and not matched in the acoustic recordings (Figure 2.8). A reverse trend, with an apparent drop in diversity with increasing distance from the ROW, is shown in the acoustic survey data from the 2,200 m asl elevational band. Again, this trend is evident in only one of the two datasets, and is not statistically significant.

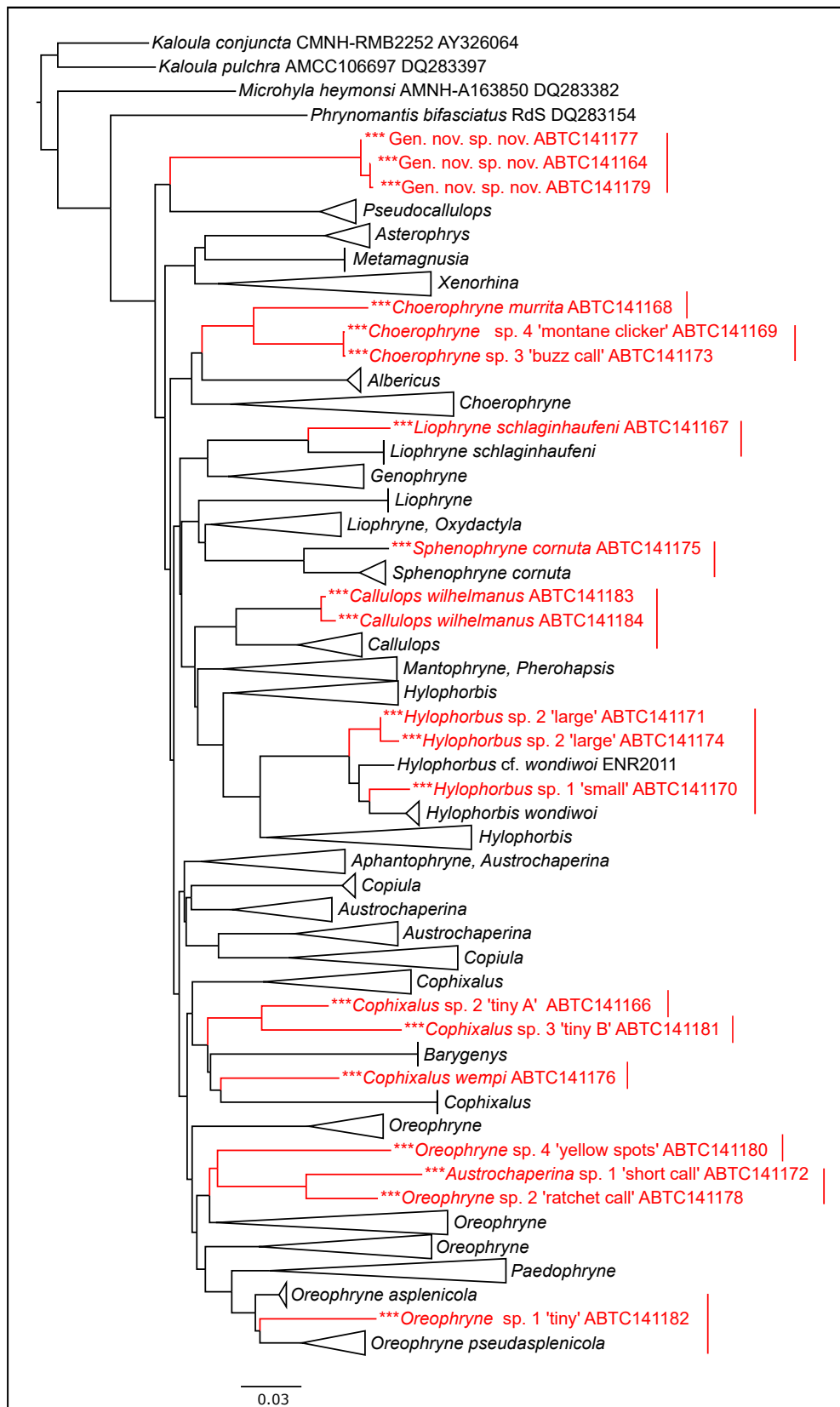


Figure 2.7. Neighbour Joining distance phenogram showing the relationship of DNA-barcoded captures on the 2015 PMA3 survey to other taxa with available sequence (Köhler and Günther 2008; Rittmeyer et al. 2012). Larger clades have been collapsed (to triangles) to save space—these contain one or more species of the named genera; vertical bars represent groupings identified by the ABGA analysis as likely to represent single species (Puillandre et al. 2011; further details in Chapter 7). In two cases this is contradicted by differences in call type or morphology.

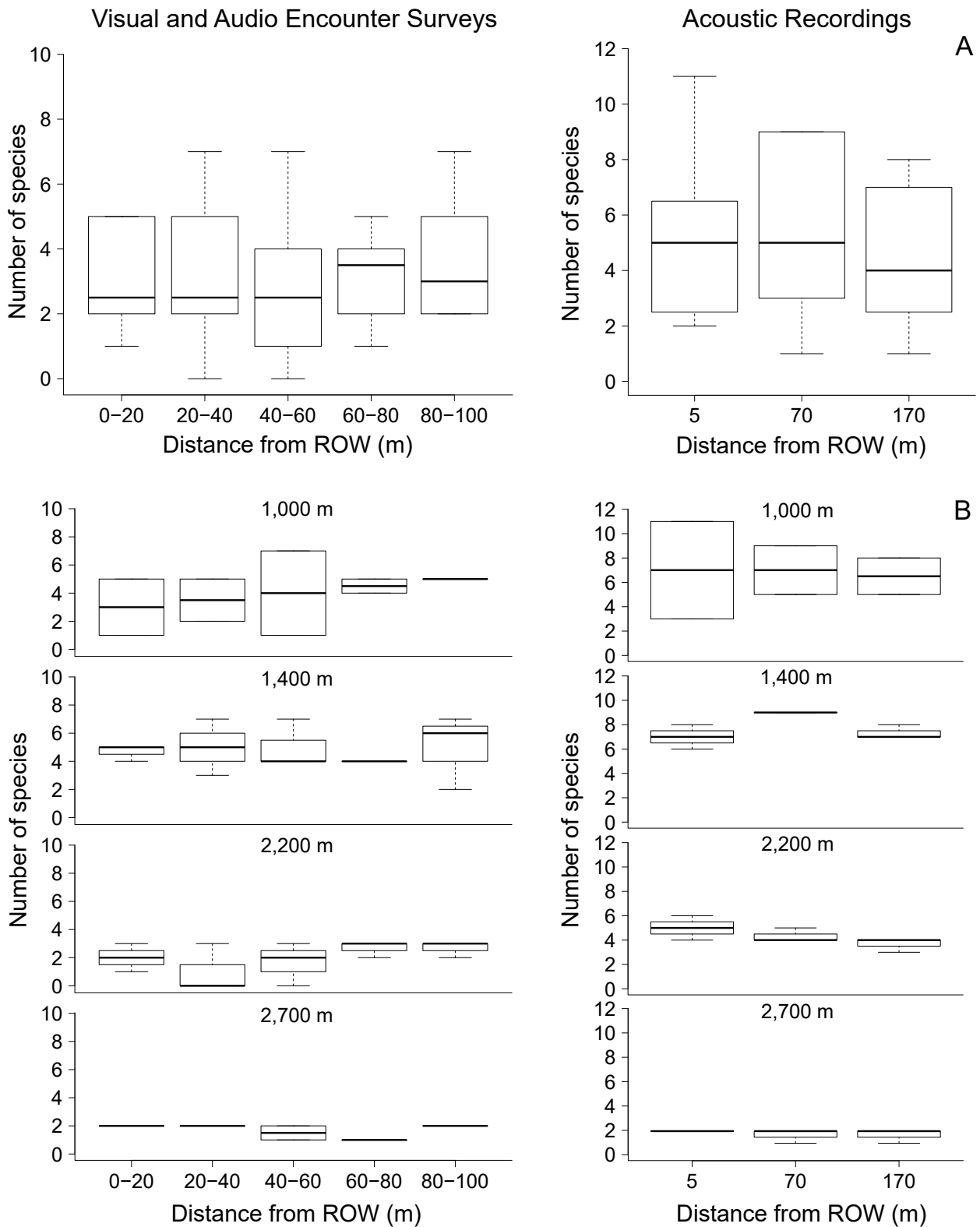


Figure 2.8. Summary of frog diversity (as number of species) at different distances from the ROW based on data from VAES transects (left column) and the acoustic survey (right column). For each of the two series, the uppermost graphs (A) are pooled across all distances, while those below are for each of the elevational zones (B). See figure 2.3 for explanation of boxplots.

The lack of evidence for a strong impact of the ROW on frog communities in BAA 1 and BAA 2 is further supported by the results of NMDS ordination analyses based on the VAES and acoustic recording datasets, neither of which shows any differentiation of frog communities based on distance from the ROW (Figure 2.9)

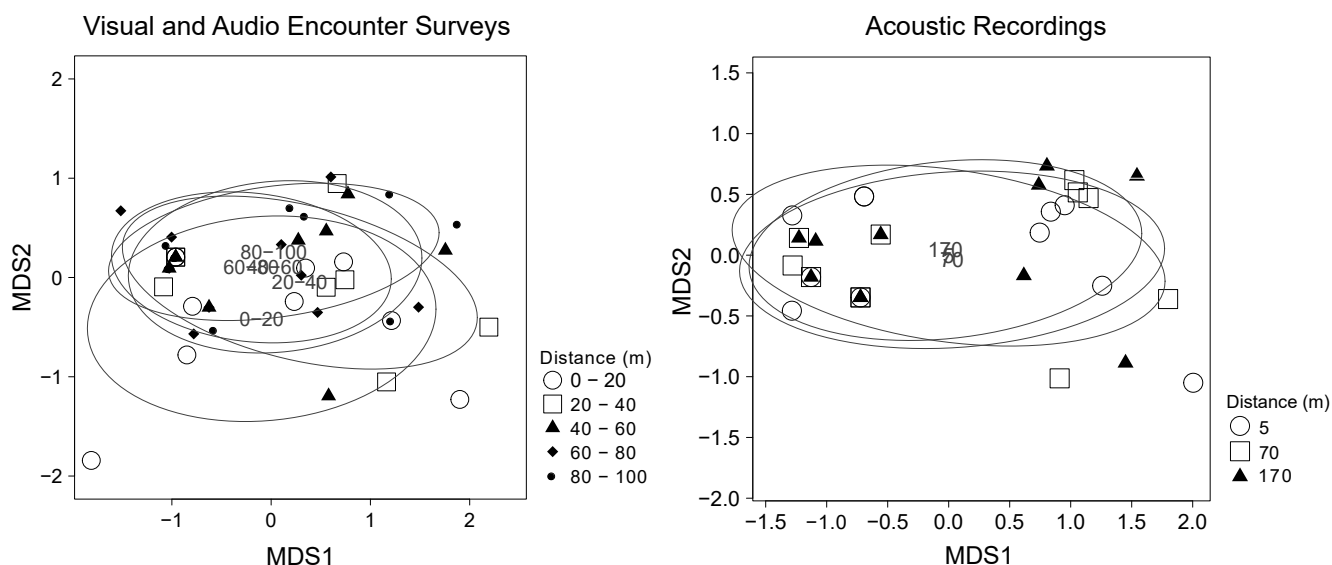


Figure 2.9. Multi-dimensional Scaling (NMDS) ordinations summarising patterns of species composition at different distances from the ROW based on each of the VAES transect (left) and acoustic recording (right) datasets (confidence ellipses are one standard deviation).

Further confirmation that the ROW has had little, if any, impact to date on species occurrences in either of the BAAs comes from the statistical analysis using the GLMM (Table 2.6). This found no significant influence of distance from ROW on species diversity, whether measured by the VAES transect method or acoustic recordings. Nor is there any evidence of an interaction between the two main factors of elevation and distance.

These analysis have been based on presence/absence data and are relatively insensitive to impacts associated with the ROW that have altered the relative commonness or rarity of different species but without causing actual species losses from the communities. Relative Abundance data is expected to be more sensitive to such changes, as it allows for a species to be still present but at reduced numbers due to deleterious impacts from being near the ROW, or to be present in higher than normal numbers if it is advantaged by the ROW conditions.

Table 2.7 shows the Relative Abundance data derived from each of the VAES transect and acoustic recording datasets.

Table 2.7. Relative Abundance values (blue heat-scale) and trend for increasing distances (m) from the ROW based on data from VAES transects and acoustic recordings.

Species	Visual and Audio Encounter Surveys					Acoustic Recordings				
	1,000	1,400	2,200	2,700	Trend 1,000 ⇄ 2,700	1,000	1,400	2,200	2,700	Trend 1,000 ⇄ 2,700
HYLIDAE										
<i>Litoria iris</i>	0	0	0	0	↔	0	0	0.1	0	↗↘
<i>Litoria</i> sp. 1 'yellow legs'	0.4	0.1	0	0	↘	0.3	0.8	0	0	↗↘
LIMNODYNASTIDAE										
<i>Lechriodus aganoposis</i>	0	0	0.1	0	↗↘	0	0	0	0	↔
MICROHYLIDAE										
<i>Austrochaperina</i> sp. 1 'short call'	0	0.1	0	0	↗↘	0	0.1	0	0	↗↘

Species	Visual and Audio Encounter Surveys					Acoustic Recordings				
	1,000	1,400	2,200	2,700	Trend 1,000 ⇄ 2,700	1,000	1,400	2,200	2,700	Trend 1,000 ⇄ 2,700
<i>Austrochaperina</i> sp. 2 'long call'	0	0	0	0		0.3	0	0	0	
<i>Callulops wilhelmanus</i>	0	0	0	0		0	0	0.1	0.2	
<i>Callulops</i> sp.	0	0.1	0	0		0.2	0.2	0	0	
<i>Choerophryne brevicrus</i>	0	0	0.5	0.8		0	0	0.6	0.6	
<i>Choerophryne burtoni</i>	0	0.3	0	0		0	0.3	0	0	
<i>Choerophryne murruta</i>	0	0.3	0	0		0	0.7	0	0	
<i>Choerophryne</i> sp. 1 'arboreal'	0	0	0.3	0		0	0	1	0	
<i>Choerophryne</i> sp. 2 'tiny'	0	0	0.2	0		0	0	0.1	0	
<i>Choerophryne</i> sp. 3 'buzz call'	0.5	0.4	0	0		0.5	1	0	0	
<i>Choerophryne</i> sp. 4 'montane clicker'	0	0.7	0	0		0	0.9	0	0	
<i>Choerophryne</i> sp. 5 'lowland clicker'	0.1	0	0	0		0	0	0	0	
<i>Cophixalus wempi</i>	0.1	0.1	0	0		0	0	0	0	
<i>Cophixalus</i> sp. 1 'musical call'	0	0.3	0	0		0	0.8	0	0	
<i>Cophixalus</i> sp. 2 'tiny A'	0	0.1	0	0		0	0	0	0	
<i>Cophixalus</i> sp. 3 'tiny B'	0	0	0	0		0	0.3	0	0	
<i>Cophixalus</i> sp. 4 'rasping call'	0.1	0	0	0		0.2	0	0	0	
<i>Cophixalus</i> sp. 5 'peeping call'	0	0	0	0		0	0.2	0	0	
<i>Copiula</i> sp. 1 '2-note call'	0	0	0	0		0.3	0	0	0	
<i>Hylophorbus</i> sp. 1 'small'	0	0.1	0	0		0	0.1	0	0	
<i>Hylophorbus</i> sp. 2 'large'	0.2	0	0	0		0.7	0	0	0	
<i>Liophryne schlaginhaufeni</i>	0.3	0	0	0		0.3	0	0	0	
<i>Metamagnusia slateri</i>	0.3	0	0	0		0.5	0	0	0	
<i>Oreophryne anamiatoi</i>	0	0	0.1	0		0	0	0.4	0	
<i>Oreophryne notata</i>	0.1	0.6	0.7	0.9		0.5	0.9	1	1	
<i>Oreophryne oviprotector</i>	0.1	0	0	0		0.8	0	0	0	
<i>Oreophryne</i> sp. 1 'tiny'	0	0	0.1	0		0	0	0	0	
<i>Oreophryne</i> sp. 2 'ratchet call'	0.1	0.5	0	0		0	0.4	0	0	
<i>Oreophryne</i> sp. 3 'slow peeper'	0	0	0	0		0.5	0	0	0	
<i>Oreophryne</i> sp. 4 'yellow spots'	0.6	1	0	0		1	1	0	0	
<i>Oreophryne</i> ? sp. 5 'loud grunter'	0	0	0.1	0		0	0	1	0	
<i>Spelopryne cornuta</i>	0.8	0	0	0		0.5	0	0	0	
<i>Xenorhina</i> sp.	0	0	0	0		0.2	0	0	0	
Microhylid new genus and species	0.3	0	0	0		0	0	0	0	

Relative Abundance for each species at different elevations showed few trends with either survey method because most species were restricted entirely or predominantly to one of the four elevational bands (Table 2.4). However inspection of the patterns of Relative Abundance of each species according to distance from the ROW (summarised in the miniature 'sparkline' plots) reveals some patterns that are consistent across the two survey methods. Several species, for example *Choerophryne burtoni* and *Liophryne sclaginhaufeni*, were recorded moderately often by both methods at distances of greater than 20 m from the ROW but were not recorded at the very edge of the forest. Other trends are apparent only from one of the two datasets. From the acoustic recordings it appears that *Callulops wilhelmanus* and *Litoria iris* may be confined to or most abundant immediately alongside the ROWs, while *Litoria* sp. 1 'yellow legs' and *Cophixalus* sp. 5 'peeping call' may be less common or absent in close proximity to the ROW. From the VAES dataset, species that may be more abundant close to the ROW include *Choerophryne* sp. 3 'buzz call' and *Oreophryne?* sp. 5 'loud grunter', while *Cophixalus wempi* and *Choerophryne brevicrus* appear to be more abundant at greater distances from the ROW although these patterns are relatively weak.

One species, the high-elevation microhylid frog *Callulops wilhelmanus*, was detected only by acoustic recorders at the closest (5 m) distance from the ROW at transects H2, H4 and H5 (Table 2.5). Based on the intensity of their vocalisations this species occurs at extremely high densities on the rocky verges of the ROW but is absent or occurs only at low density in the forest. This strong pattern was supported by casual observations in the field. Most members of this genus occupy small tunnels and gaps between rocks and roots on steep slopes and on Hides Ridge *C. wilhelmanus* appears to have benefitted from the creation of structurally similar habitat along the ROW. This species may be among the few frogs that has clearly benefitted from construction of the ROW.

These patterns might be used as a basis for selecting a number of key 'Indicator Species', i.e. some that might increase in response to ROW impacts and some that might decrease. However, there are grounds for caution in premature selection of species for this purpose. For example, *Choerophryne* sp. 3 'buzz call' was detected more often close to the ROW in the VAES surveys (as noted above) but it was found to be equally abundant at all distances from the ROW in the acoustic survey. While it is clear that further data are needed before these Relative Abundance values can be used to full advantage, early indications are that this approach holds promise of being a sensitive indicator of subtle changes in the frog communities and as a potential criterion for selecting useful key indicator species.

Comments on efficacy of the two survey methods employed

Frogs are extremely sensitive to local climatic conditions, and the activity levels and calling behaviour of each species are influenced differently by changes in temperature, humidity and rainfall. On any given night some species will vocalise strongly while others sit on vegetation but do not call. Although these differences in behaviour are by no means random, they do introduce a potential element of stochasticity into datasets of the kind reported here because the results are likely to be influenced by inherently variable climatic factors. By using two methods for frog survey we hoped to achieve the highest possible species detection rates during surveys and thereby minimise any such stochastic effects.

As reported above, slightly more than one half of frog species were detected by both methods used and slightly less than one quarter by each of the individual methods (Table 2.8). It is relevant to consider whether failure to detect frogs using one or other of the two alternative methods represents an inherent limitation in that method with regard to detection ability for that particular species, or whether it could simply be stochasticity. If the latter, it is possible that the additional species might be detected by each of the methods in the future. Alternatively, if there is a reason to consider that a particular frog species is not being detected because of a limitation in one or other of the methods, then this might prompt an adjustment in the sampling protocol.

This issue might be explored statistically by examining the effect of sampling method on likelihoods of species detection, while controlling for all other fixed and random effects. However, this test will be more powerful with the enlarged dataset from a second survey and when full compatibility has been attained between the VAES and acoustic datasets. In the interim, we note that both methods appear to have made similarly important contributions to knowledge of the frog fauna and are likely to remain important for achieving survey and monitoring completeness in future phases of PMA3.

Interestingly, and despite differences in the particular species detected by each of the two methods, it is clear from both the statistical results and the patterns observed in the summary boxplots and NMDS plots (Figures 2.8–2.9) that the two methods were both sensitive to the same general patterns within the frog fauna, most notably the influence of elevation on species diversity, and the apparent absence of any major change in species occurrences associated with ROW impacts. In this regard, it is possible that either method alone might be adequate for detecting future changes in the overall frog community. This question should be reconsidered following at least one more survey period, after which it will be possible to test alternative views with far greater statistical power.

Table 2.8. Correspondence between methods of detection for each species (--: not detected by either method; +-: detected only on VAES surveys; ++: detected only on acoustic recordings; ++: detected with both methods of survey; no correspondence for transect H6 (because no VAES transect undertaken). Overall: 20.8% acoustic only; 16.7% transect only; 62.5% both survey means; summarised by elevation (m asl) across transects.

Species	BAA 2					BAA 1						Combined transects					
	1,000		1,400			2,200			2,700			1,000	1,400	2,200	2,700		
	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5	H6						
HYLIDAE																	
<i>Litoria iris</i>	--	--	--	--	--	--	--	+-	--	--	-					+-	
<i>Litoria</i> sp. 1 'yellow legs'	++	++	+-	++	+-	--	--	--	--	--	-	++	++				
LIMNODYNASTIDAE																	
<i>Lechriodus aganoposis</i>	--	--	--	--	--	-+	--	--	--	--	-					-+	
MICROHYLIDAE																	
<i>Austrochaperina</i> sp. 1 'short call'	--	--	--	++	--	--	--	--	--	--	-		++				
<i>Austrochaperina</i> sp. 2 'long call'	--	+-	--	--	--	--	--	--	--	--	-	+-					
<i>Callulops wilhelmanus</i>	--	--	--	--	--	--	+-	--	+-	+-	-					+-	+-
<i>Callulops</i> sp.	--	+-	-+	+-	++	--	--	--	--	--	-	+-	++				
<i>Choerophryne brevicrus</i>	--	--	--	--	--	+-	++	++	++	++	+					++	++
<i>Choerophryne burtoni</i>	--	--	++	++	--	--	--	--	--	--	-		++				
<i>Choerophryne murruta</i>	--	--	++	--	+-	--	--	--	--	--	-		++				
<i>Choerophryne</i> sp. 1 'arboreal'	--	--	--	--	--	++	++	++	--	--	-					++	
<i>Choerophryne</i> sp. 2 'tiny'	--	--	--	--	--	-+	--	++	--	--	-					++	
<i>Choerophryne</i> sp. 3 'buzz call'	++	++	++	++	++	--	--	--	--	--	-	++	++				
<i>Choerophryne</i> sp. 4 'montane clicker'	--	--	++	++	++	--	--	--	--	--	-		++				
<i>Choerophryne</i> sp. 5 'lowland clicker'	--	-+	--	--	--	--	--	--	--	--	-	-+					
<i>Cophixalus wempi</i>	-+	--	--	-+	--	--	--	--	--	--	-	-+	-+				
<i>Cophixalus</i> sp. 1 'musical call'	--	--	++	++	+-	--	--	--	--	--	-		++				
<i>Cophixalus</i> sp. 2 'tiny A'	--	--	-+	--	--	--	--	--	--	--	-		+-				
<i>Cophixalus</i> sp. 3 'tiny B'	--	--	--	--	+-	--	--	--	--	--	-		+-				
<i>Cophixalus</i> sp. 4 'rasping call'	--	++	--	--	--	--	--	--	--	--	-	++					
<i>Cophixalus</i> sp. 5 'peeping call'	--	--	+-	+-	--	--	--	--	--	--	-		+-				

Species	BAA 2					BAA 1						Combined transects			
	1,000		1,400			2,200			2,700			1,000	1,400	2,200	2,700
	M4	M5	M1	M2	M3	H1	H2	H3	H4	H5	H6				
<i>Copiula</i> sp. 1 '2-note call'	--	+-	--	--	--	--	--	--	--	--	--	+-			
<i>Hylophorbus</i> sp. 1 'small'	--	--	--	++	--	--	--	--	--	--	--		++		
<i>Hylophorbus</i> sp. 2 'large'	+-	++	--	--	--	--	--	--	--	--	--	++			
<i>Liophryne schlaginhaufeni</i>	--	++	--	--	--	--	--	--	--	--	--	++			
<i>Metamagnusia slateri</i>	++	++	--	--	--	--	--	--	--	--	--	++			
<i>Oreophryne anamiatoi</i>	--	--	--	--	--	+-	++	--	--	--	--			++	
<i>Oreophryne notata</i>	+-	++	++	++	++	++	++	++	++	++	+	++	++	++	++
<i>Oreophryne oviprotector</i>	+-	++	--	--	--	--	--	--	--	--	--	++			
<i>Oreophryne</i> sp. 1 'tiny'	--	--	--	--	--	--	--	-+	--	--	--			-+	
<i>Oreophryne</i> sp. 2 'ratchet call'	--	-+	++	++	-+							-+	++		
<i>Oreophryne</i> sp. 3 'slow peeper'	--	+-	--	--	--	--	--	--	--	--	--	+-			
<i>Oreophryne</i> sp. 4 'yellow spots'	++	++	++	++	++	--	--	--	--	--	--	++	++		
<i>Oreophryne</i> ? sp. 5 'loud grunter'	--	--	--	--	--	+-	++	++	--	--	--			++	
<i>Spenophryne cornuta</i>	++	++	--	--	--	--	--	--	--	--	--	++			
<i>Xenorhina</i> sp.	--	+-	--	--	--	--	--	--	--	--	--	+-			
Microhylid new genus and species	--	-+	--	--	--	--	--	-	--	--	--	-+			

CONCLUSIONS

1. The forests at Hides Ridge in BAA 1 and on the Agogo Range near Moro in BAA 2 continue to support a high diversity of frog species. Diversity at these sites is typical of assemblages documented at similar elevations elsewhere on mainland New Guinea (e.g. Richards 2007; Richards and Dahl 2011) suggesting that no major declines or losses have been experienced within these communities.
2. More than half of the frogs documented during this survey are undescribed and many of these are known to date only from the Kikori Basin; at least one new species is currently known only from BAA 1 and another (which also represents a new genus) is known only from BAA 2.
3. Quantitative surveys of frog communities at different distances from the ROW during this survey have provided a baseline for future monitoring of this important group of animals. There was no evidence of any difference in species diversity or composition with increasing distance from the ROW.
4. Preliminary results of species abundance identified several species that appear to be consistently more or less commonly encountered close to the ROWs, with the two outcomes probably in approximately equal proportion. These species may be useful targets for monitoring of ecologically sensitive species.
5. Overall, the results from the first monitoring survey suggest that, in relation to frogs, the biodiversity values of the Upstream Project Area have been retained to date.

REFERENCES

- Anstis, M., Parker, F., Hawkes, T., Morris, I. & Richards, S.J. 2011. Direct development in some Australopapuan microhylid frogs of the genera *Austrochaperina*, *Cophixalus* and *Oreophryne* (Anura: Microhylidae) from northern Australia and Papua New Guinea. *Zootaxa* 3052: 1–50.
- Collins, R. A. & Cruikshank, R. H. 2012, The seven deadly sins of DNA barcoding. *Molecular Ecology Resources* doi: 10.1111/1755-0998.12046
- Corn, P.S. 2005. Climate change and amphibians. *Animal Biodiversity and Conservation* 28: 59–67.
- Duellman, W. E., Marion, A. B. & Hedges, S. B. 2016. Phylogenetics, classification, and biogeography of the treefrogs (Amphibia: Anura: Arboranae). *Zootaxa* 4104: 1–109.
- Günther, R. & Richards, S.J. (in press). Description of two new species of the microhylid genus *Oreophryne* from southern Papua New Guinea. *Vertebrate Zoology*
- Köhler, F. & Günther, R. 2008. The radiation of microhylid frogs (Amphibia: Anura) on New Guinea: A mitochondrial phylogeny reveals parallel evolution of morphological and life history traits and disproves the current morphology-based classification. *Molecular Phylogenetics and Evolution* 47: 353–365.
- Kraus, F. 2010. More range extensions for Papuan reptiles and amphibians. *Herpetological Review* 41: 246–248.
- Menzies, J.I. 2006. *The frogs of New Guinea and the Solomon Islands*. Pensoft, Sofia-Moscow, 346 pp.
- Puillandre, N., Lambert, A., Brouillet, S. & Achaz, G. 2011. ABGD, Automatic Barcode Gap Discovery for primary species delimitation. *Molecular Ecology* 21:1864–1877. URL: <http://www.wabi.snv.jussieu.fr/public/abgd/abgdweb.html>
<http://www.wabi.snv.jussieu.fr/public/abgd/>
- Richards, S.J. 2002. *Rokrok: An illustrated guide to frogs of the Kikori Integrated Conservation and Development Project area (Moro, Gobe and Kopi), Papua New Guinea*. WWF-South Pacific.
- Richards, S.J. 2007. Herpetofauna of the Kaijende Highlands, Enga Province, Papua New Guinea. Pp 40–46 In: Richards, S.J. (editor). *A rapid biodiversity assessment of the Kaijende Highlands, Enga Province, Papua New Guinea*. RAP Bulletin of Biological Assessment 45. Conservation International. Arlington, Virginia.
- Richards, S.J. & Dahl, C. 2011. Herpetofauna of the Strickland Basin and Muller Range, Papua New Guinea. Pp 190–197 In: Richards, S.J. and Gamui, B.G. (editors). (2011). *Rapid Biological Assessments of the Nakanai Mountains and the upper Strickland Basin: surveying the biodiversity of Papua New Guinea's sublime karst environments*. RAP Bulletin of Biological Assessment 60. Conservation International. Arlington, VA.
- Rittmeyer, E.N., Allison, A., Gründler, M.C., Thompson, D.K. & Austin, C.C. 2012. Ecological guild evolution and the discovery of the world's smallest vertebrate. *PLOS One* <http://dx.doi.org/10.1371/journal.pone.0029797>
- Sueur J., Aubin T. & Simonis C. 2008. Seewave: a free modular tool for sound analysis and synthesis. *Bioacoustics*: 18: 213–226.

Undescribed frogs encountered during the survey



Figure 2.10. *Litoria* sp. 1. 'yellow legs'



Figure 2.11. *Austrochaperina* sp. 1 'fast call'



Figure 2.12. *Choerophryne* sp. 2 'tiny'



Figure 2.13. *Choerophryne* sp. 4 'montane clicker'



Figure 2.14. *Cophixalus* sp 1. 'musical call'



Figure 2.15. *Cophixalus* sp. 2 'tiny A'

Undescribed and IUCN Data Deficient frogs encountered during the survey



Figure 2.16. *Hylophorbus* sp. 1 'small'



Figure 2.17. *Oreophryne* sp. 1 'tiny'



Figure 2.18. *Oreophryne* sp. 4. 'yellow spots'



Figure 2.19. A new genus and species of frog from BAA 2



Figure 2.20. *Choerophryne burtoni* (IUCN Data Deficient)



Figure 2.21. *Oreophryne notata* (IUCN Data Deficient)

APPENDICES

Appendix 2.1 Start and finish points for the ten 100 m VAES frog survey transects in BAA 1 and BAA 2.

BAA 1	Start	Finish
H1	S5.97242 E142.75320	S5.97304 E142.75284
H2	S5.96907 E142.75124	S5.96914 E142.75045
H3	S5.94380 E142.74182	S5.94459 E142.74188
H4	S5.91842 E142.69533	S5.91919 E142.69496
H5	S5.91627 E142.69284	S5.91652 E142.69208
BAA 2	Start	Finish
M1	S6.44025 E143.22417	S6.44025 E143.22339
M2	S6.44063 E143.22559	S6.44130 E143.22540
M3	S6.44166 E143.22717	S6.44231 E143.22658
M4	S6.46203 E143.25664	S6.46181 E143.25580
FT5*	S6.46179 E143.25532	S6.46154 E143.25457

*FT5 is a replacement transect for M5 which could not be accessed at night.

Appendix 2.2 Frog recording site locations in BAA 1 on Hides Ridge and BAA 2 on the Agogo Range near Moro. Coordinates in WGS84 datum.

Elevation category	Transect	Site	Latitude	Longitude	Elevation (m asl)
1,000	M4	M4_005	S6.462013	E143.256616	1,017
1,000	M4	M4_070	S6.461926	E143.256018	1,030
1,000	M4	M4_170	S6.461667	E143.255006	1,041
1,000	M5	M5_005	S6.461944	E143.250132	1,052
1,000	M5	M5_070	S6.462124	E143.250560	1,057
1,000	M5	M5_170	S6.461528	E143.251531	1,056
1,400	M1	M1_005	S6.440230	E143.224085	1,403
1,400	M1	M1_070	S6.440240	E143.223590	1,398
1,400	M1	M1_170	S6.440079	E143.222562	1,408
1,400	M2	M2_005	S6.440718	E143.225566	1,395
1,400	M2	M2_070	S6.441409	E143.225425	1,378
1,400	M2	M2_170	S6.442099	E143.224895	1,391
1,400	M3	M3_005	S6.441778	E143.227103	1,379
1,400	M3	M3_070	S6.442142	E143.226678	1,375
1,400	M3	M3_170	S6.443061	E143.226314	1,392
2,200	H1	H1_005	S5.972520	E142.753279	2,163
2,200	H1	H1_070	S5.972856	E142.752890	2,155
2,200	H1	H1_170	S5.973729	E142.752471	2,151
2,200	H2	H2_005	S5.969087	E142.751274	2,167
2,200	H2	H2_070	S5.969068	E142.750669	2,187
2,200	H2	H2_170	S5.969126	E142.749804	2,217
2,200	H3	H3_005	S5.943807	E142.741784	2,289
2,200	H3	H3_070	S5.944572	E142.741865	2,284
2,200	H3	H3_170	S5.945233	E142.741622	2,322
2,700	H4	H4_005	S5.918423	E142.695320	2,695
2,700	H4	H4_070	S5.919144	E142.694951	2,702
2,700	H4	H4_170	S5.919827	E142.694924	2,692
2,700	H5	H5_005	S5.916343	E142.692853	2,751
2,700	H5	H5_070	S5.916471	E142.692311	2,749
2,700	H5	H5_170	S5.916749	E142.691230	2,731
2,700	H6	H6_005	S5.913796	E142.690169	2,733
2,700	H6	H6_070	S5.914176	E142.689647	2,737
2,700	H6	H6_170	S5.914911	E142.688983	2,729

Appendix 2.3 Brief descriptions of each frog call recorded during Phase I. Definitions follow the table.

Species	Call structure
HYLIDAE	
<i>Litoria iris</i>	Multi-pulsed notes; short, harsh 'chip' or longer 'buzz' repeated intermittently and often in rapid succession.
<i>Litoria</i> sp. 1 'yellow legs'	Call a single multi-pulsed note, a scratchy 'chirp' repeated relatively slowly.
LIMNODYNASTIDAE	
<i>Lechriodus aganoposis</i>	—
MICROHYLIDAE	
<i>Austrochaperina</i> sp. 1 'short call'	Call with c. 10 rapidly repeated multi-pulsed notes, uttered intermittently and lasting about 1.5 seconds.
<i>Austrochaperina</i> sp. 2 'long call'	Call a long 'call train' of multi-pulsed notes 'yap yap yap' lasting more than 10 seconds
<i>Callulops wilhelmanus</i>	Call up to c. 20 deep, multi-pulsed barking notes, repeated intermittently
<i>Callulops</i> sp.	Call with c. 4 deep multi-pulsed barking notes, repeated intermittently.
<i>Choerophryne brevicrus</i>	Call a single multi-pulsed note, lasting more than 0.3 seconds and uttered singly or repeated at a relatively low rate
<i>Choerophryne burtoni</i>	Call with c. 6 multi-pulsed notes, uttered singly or in long series separated by at least several seconds.
<i>Choerophryne murrita</i>	Call a single tone, 'peep' repeated continuously at relatively low rates.
<i>Choerophryne</i> sp. 1 'arboreal'	Call a single multi-pulsed note, a short (c. 0.1 seconds) 'buzz' or 'ank', repeated for long periods at slow to fast rates.
<i>Choerophryne</i> sp. 2 'tiny'	Call a single multi-pulsed note, a rapid 'clicking' repeated continuously for long periods, mostly during the day.
<i>Choerophryne</i> sp. 3 'buzz call'	Call a single multi-pulsed note, a short 'buzz' lasting c. 0.4 seconds and repeated continuously at a relatively low rate.
<i>Choerophryne</i> sp. 4 'montane clicker'	Call with c. 25+ single-pulse notes; a series of distinct "clicks" lasting c. 1 second and becoming more rapid at the end of the call.
<i>Choerophryne</i> sp. 5 'lowland clicker'	Call with c. 18 single-pulse notes; a series of distinct "clicks" lasting more than 3 seconds and repeated at a relatively low rate.
<i>Cophixalus wempi</i>	—
<i>Cophixalus</i> sp. 1 'musical call'	Call with 3–6 tonal notes, the first note >10 times as long as successive notes, repeated for several minutes
<i>Cophixalus</i> sp. 2 'tiny A'	—
<i>Cophixalus</i> sp. 3 'tiny B'	—
<i>Cophixalus</i> sp. 4 'rasping call'	Call with two or more different multi-pulsed notes; a harsh 'buzz', often in couplets, and repeated for up to several minutes.
<i>Cophixalus</i> sp. 5 'peeping call'	Call a single tone, repeated in a long call train at a high rate.

Species	Call structure
<i>Copiula</i> sp. 1 '2-note call'	Call with two loud, harsh, multi-pulsed notes, repeated for long periods.
<i>Hylophorbus</i> sp. 1 'small'	—
<i>Hylophorbus</i> sp. 2 'large'	—
<i>Liophryne schlaginhaufeni</i>	Call a single multi-pulsed note; a loud 'chirp' repeated up to c. 10 times with long silent periods between.
<i>Metamagnusia slateri</i>	Call with <10 loud, rather melodious notes repeated intermittently.
<i>Oreophryne anamiatoi</i>	Call up to c. 20 rapidly-produced multi-pulsed notes; a harsh 'rattle' lasting about 3 seconds and repeated intermittently.
<i>Oreophryne notata</i>	Call up to c. 20 rapidly-produced tonal notes 'peep peep peep...' repeated intermittently.
<i>Oreophryne oviprotector</i>	Call up to c. 20 rapidly-produced multi-pulsed notes; a short, harsh 'rattle' lasting about 1 second and repeated intermittently.
<i>Oreophryne</i> sp. 1 'tiny'	—
<i>Oreophryne</i> sp. 2 'ratchet call'	—
<i>Oreophryne</i> sp. 3 'slow peeper'	Call a single tonal note, repeated about 8-12 times 'peep...peep...' at a relatively slow rate.
<i>Oreophryne</i> sp. 4 'yellow spots'	Call up to c. 50 rapidly-produced multi-pulsed notes; a harsh 'rattle' lasting more than 2 seconds and repeated intermittently.
<i>Oreophryne(?)</i> sp. 5 'loud grunter'	A loud, harsh 'grunt' uttered singly or with several notes in quick succession.
<i>Sphenophryne cornuta</i>	Calls start with a series of intermittent 'pop' sounds followed by 1-3 long calls each containing >60 rapidly-produced multi-pulsed notes lasting several seconds
<i>Xenorhina</i> sp.	Call a series of melodious, unpulsed 'hoot' notes, repeated slowly for several seconds with both intensity and pitch increasing during the series.
Microhylid new genus and species	—

Definitions

Call—a discrete group of notes, or a single note, which are separated by silence.

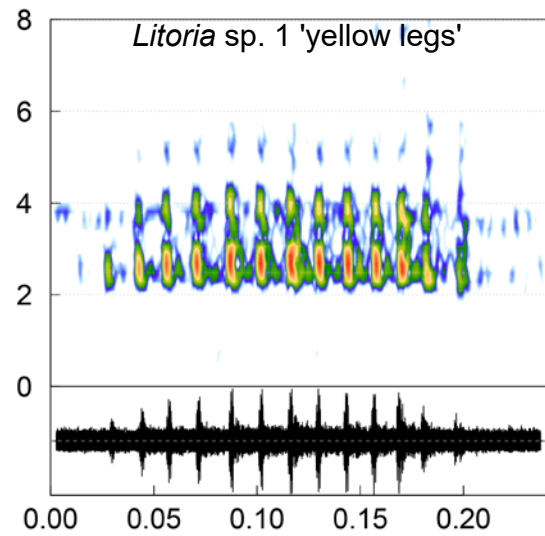
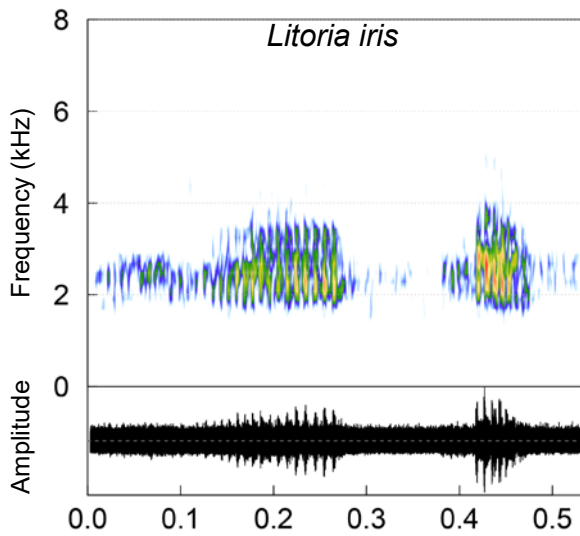
Call train—a group of calls that is repeated regularly over a period of seconds or minutes with intervals between call trains much longer than intervals between calls.

Note—One distinct component of a call, separated by silence.

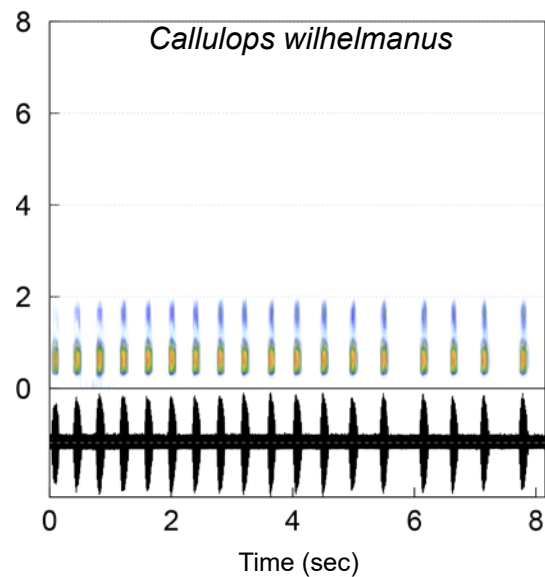
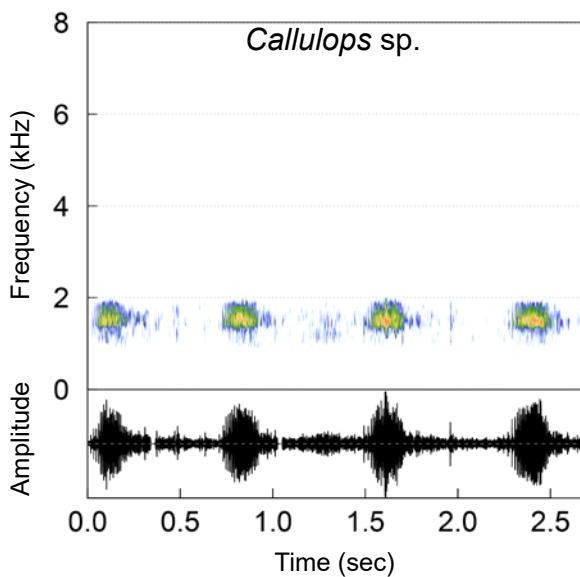
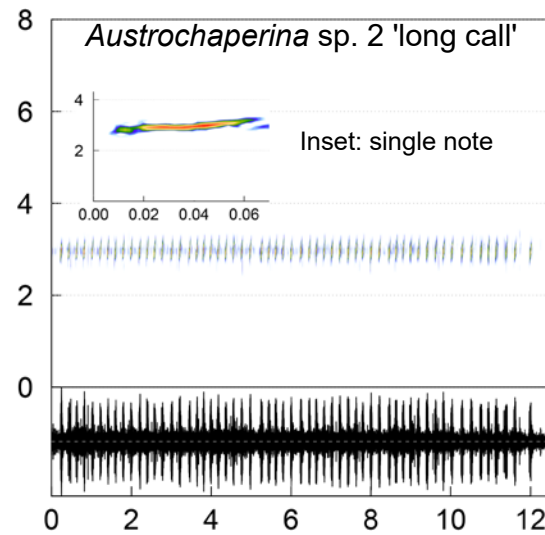
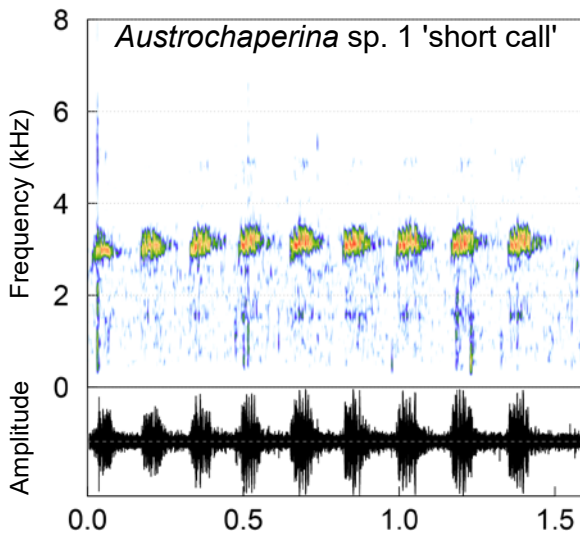
Pulse—periods of amplitude within each note.

Appendix 2.4 Examples of calls for each frog species recorded during the 2015 survey. Note that the time scale differs for each call; illustrated with seewave version 2.0.2 (Sueur et al. 2008).

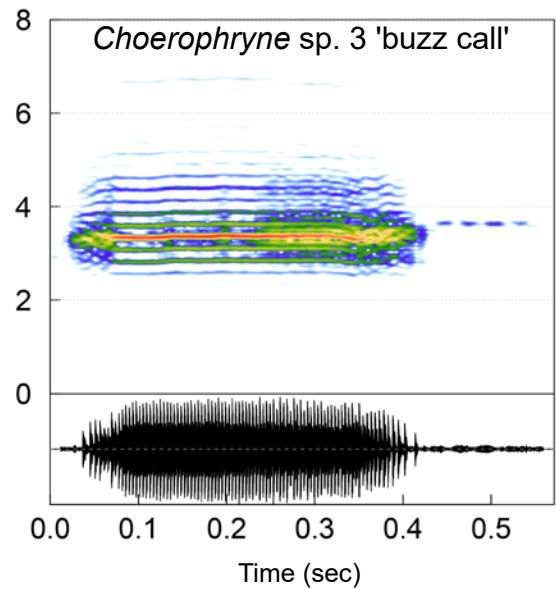
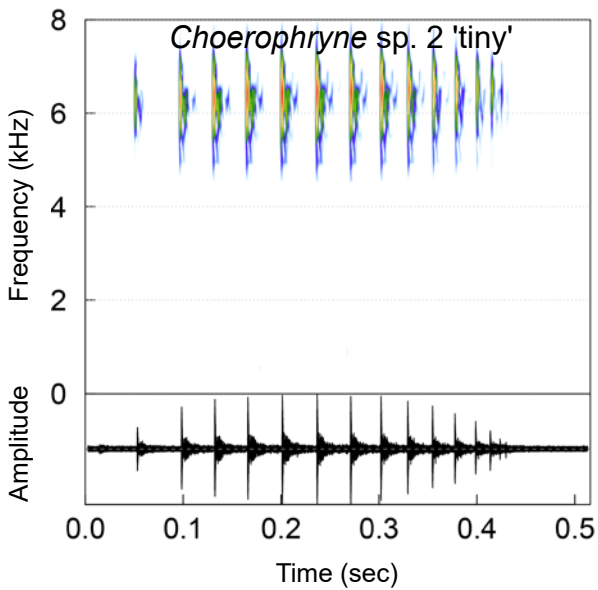
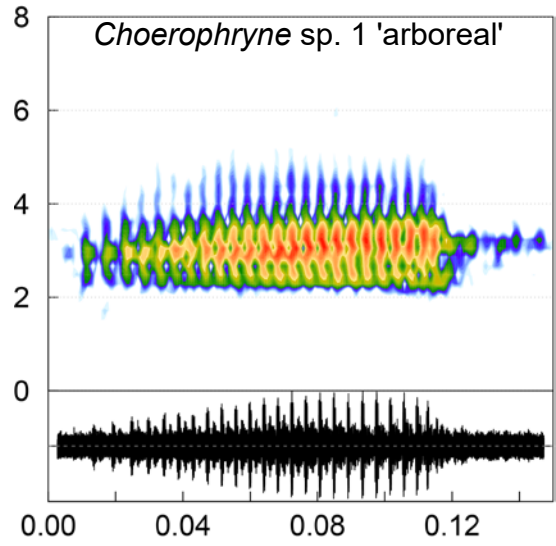
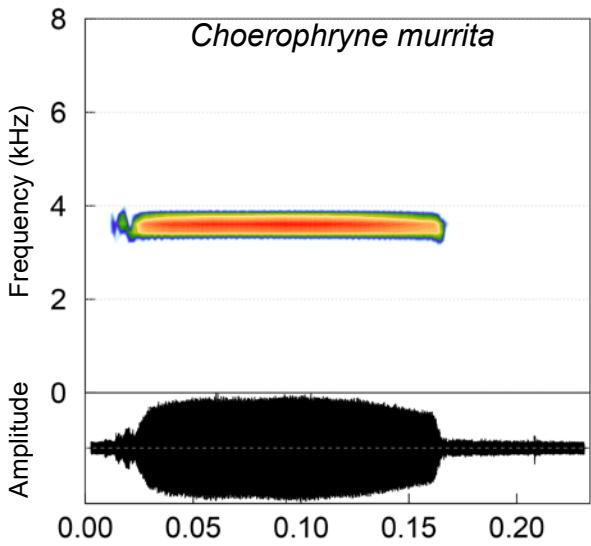
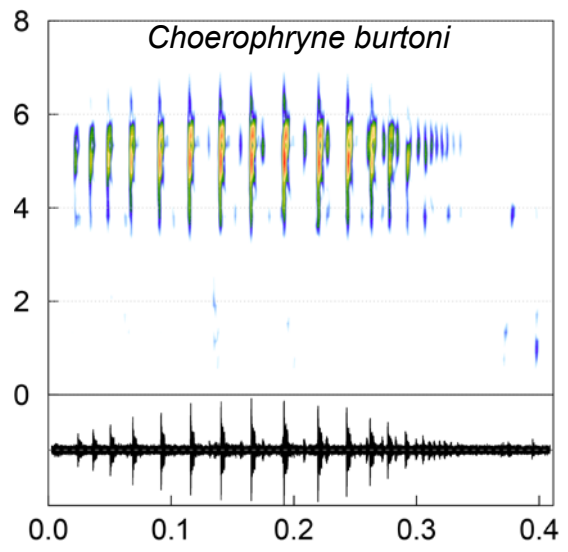
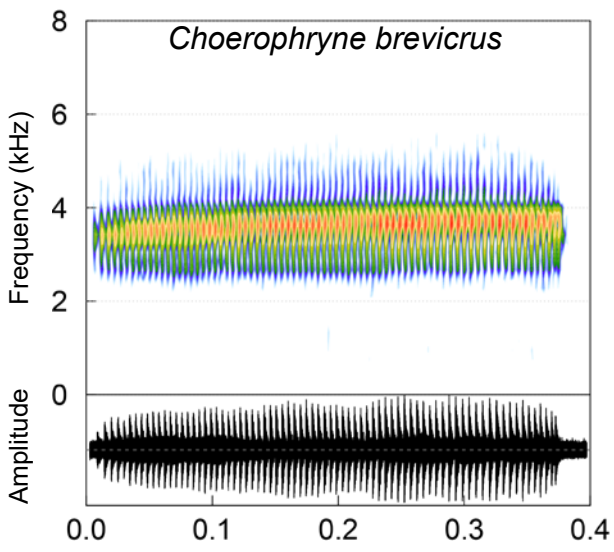
HYLIDAE



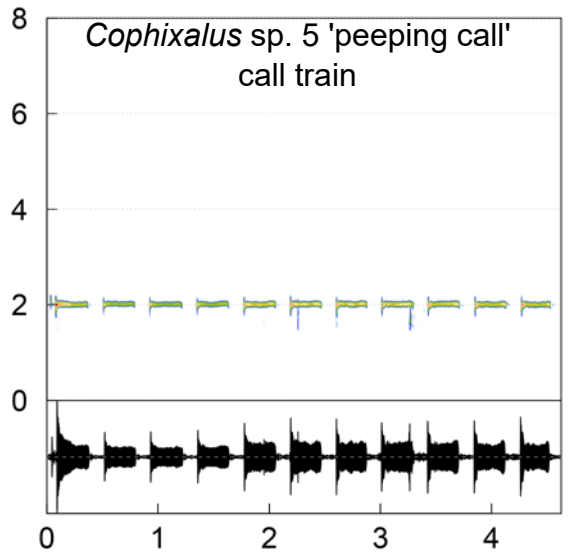
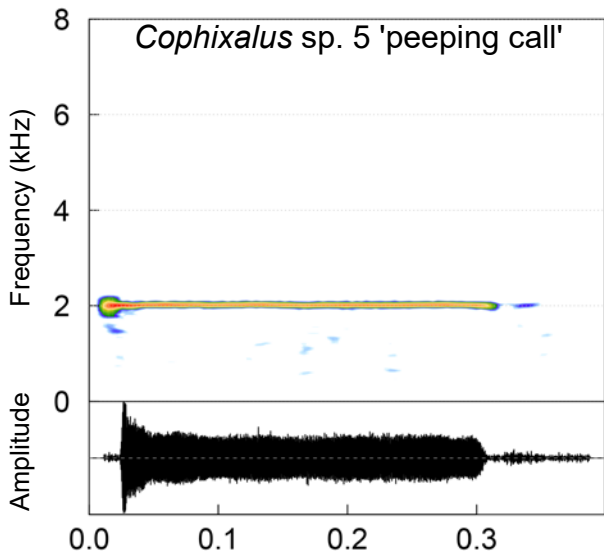
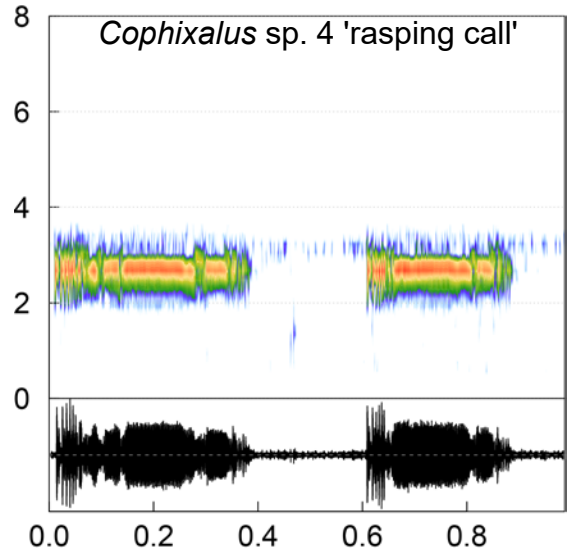
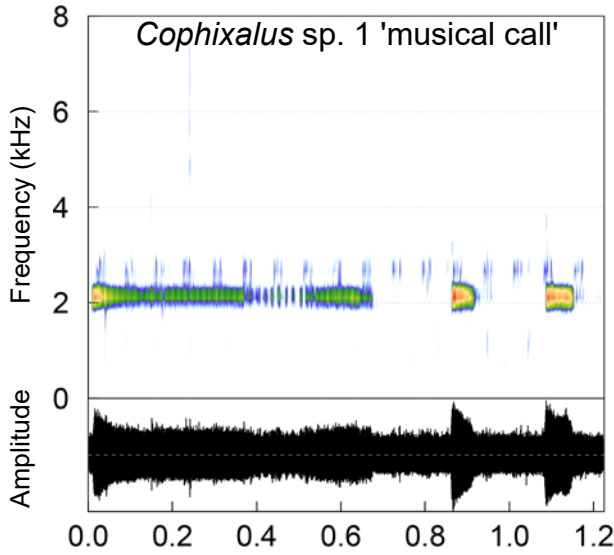
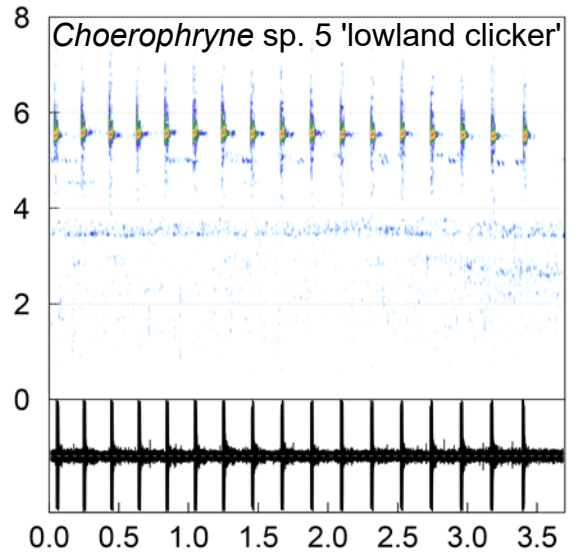
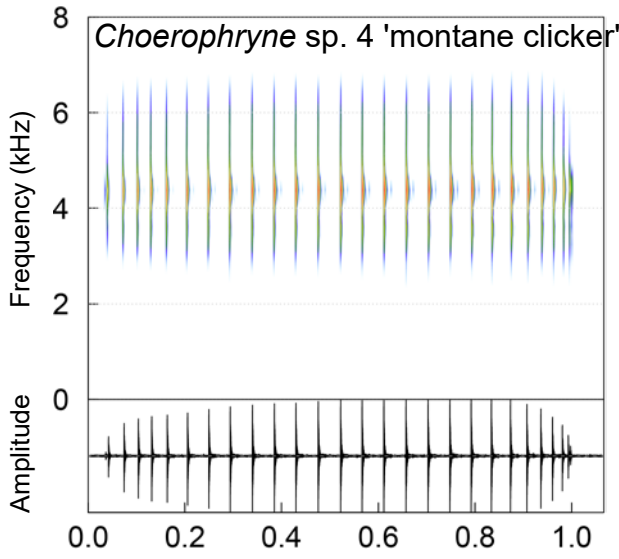
MICROHYLIDAE



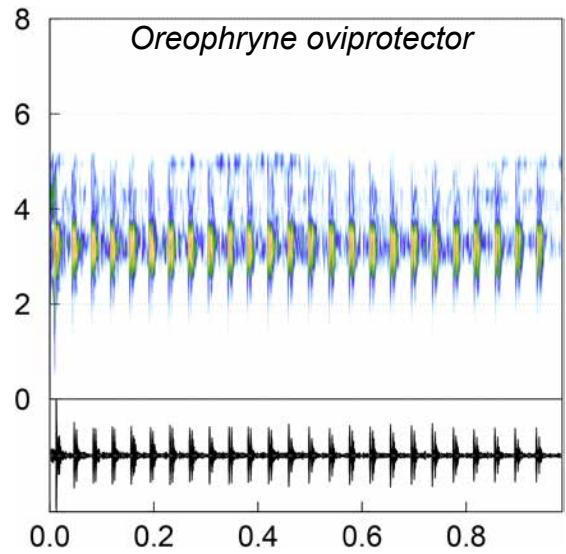
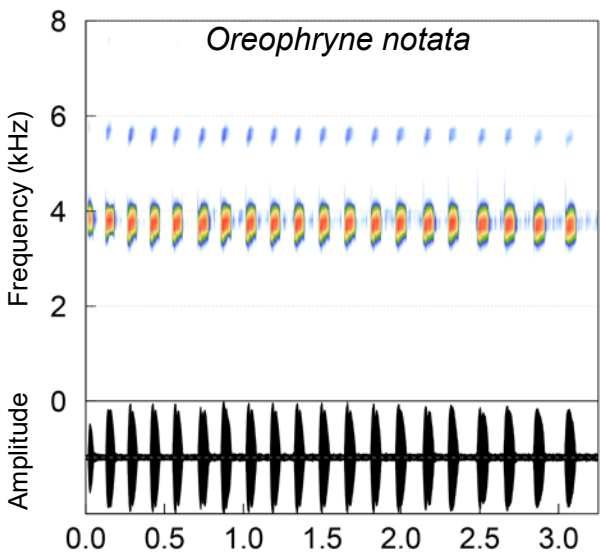
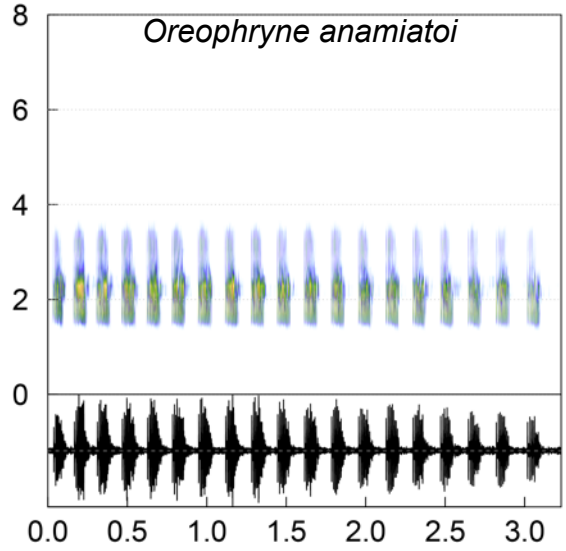
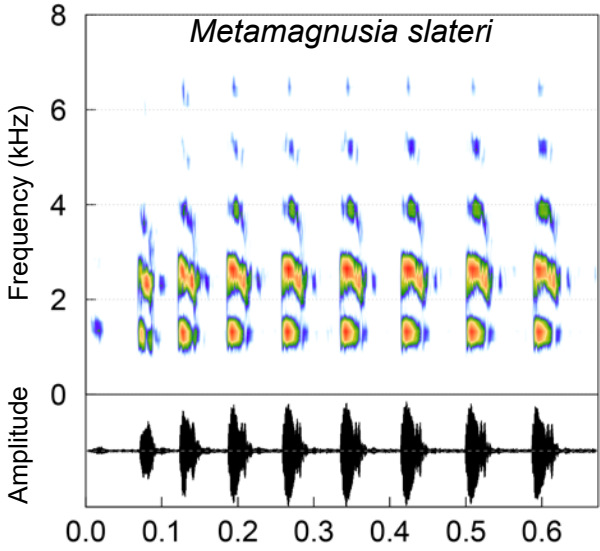
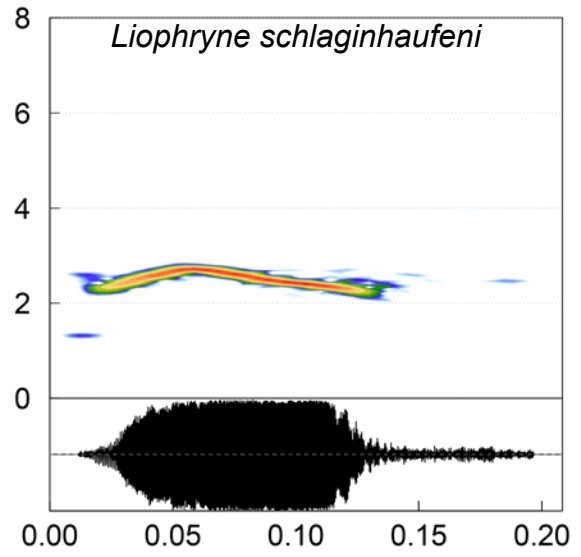
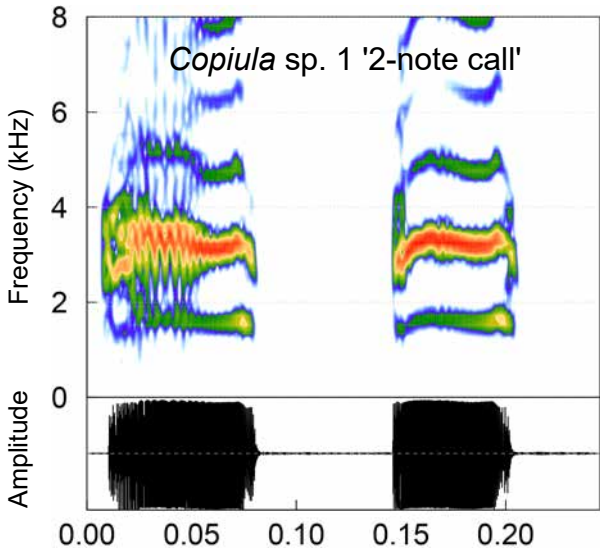
MICROHYLIDAE



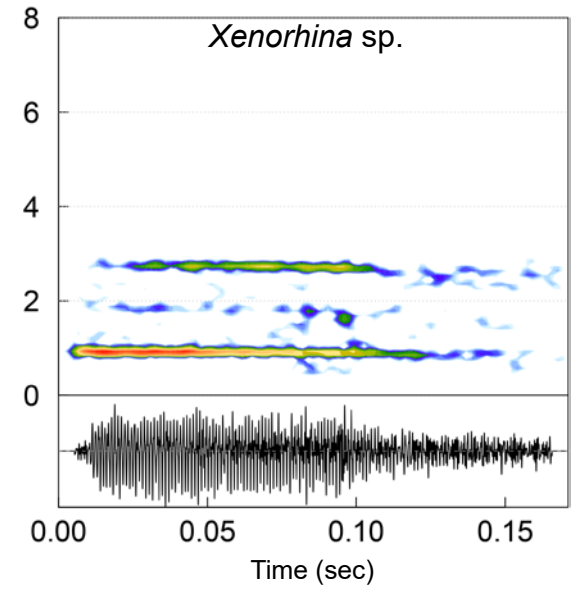
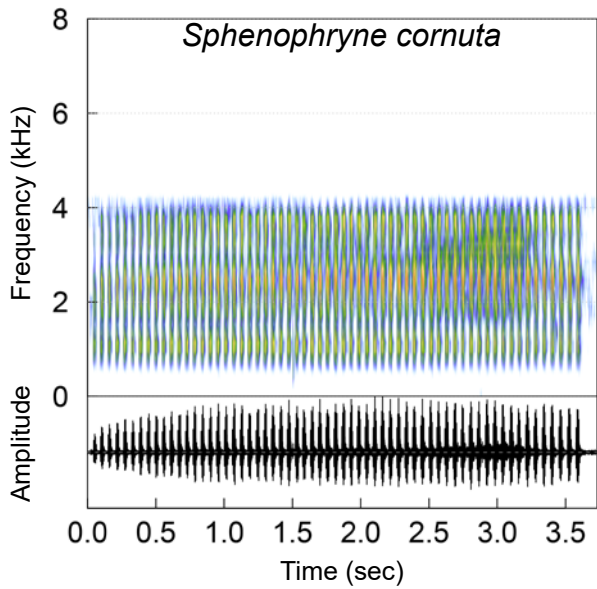
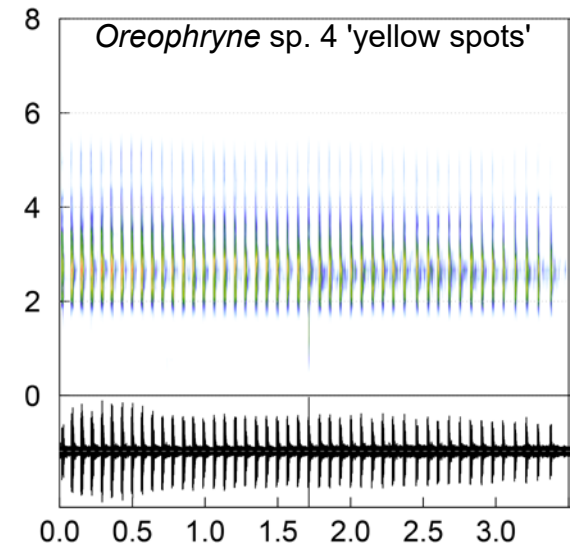
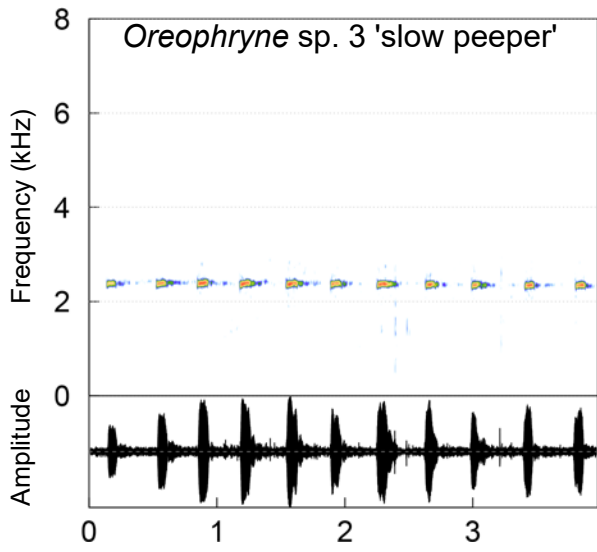
MICROHYLIDAE



MICROHYLIDAE



MICROHYLIDAE



Appendix 2.5 Frog voucher specimens submitted to the Australian Biological Tissue Collection (ABTC) and DNA barcoded.

ABTC No.	Identification	Family	Location	Field No.	Latitude	Longitude
ABTC141164	Microhylid new genus and species	Microhylidae	M5	14930	S6.46168	E143.25494
ABTC141165	<i>Litoria</i> sp. 1 'yellow-legs'	Hylidae	M5	14931	S6.46168	E143.25494
ABTC141166	<i>Cophixalus</i> sp. 2 'tiny A'	Microhylidae	M1	14932	S6.44027	E143.22372
ABTC141167	<i>Liophryne schlaginhaufeni</i>	Microhylidae	M5	14933	S6.46168	E143.25494
ABTC141168	<i>Choerophryne murruta</i>	Microhylidae	M1	14934	S6.44027	E143.22372
ABTC141169	<i>Choerophryne</i> sp. 4 'montane clicker'	Microhylidae	M3	14936	S6.44191	E143.22696
ABTC141170	<i>Hylophorbus</i> sp. 1 'small'	Microhylidae	M2	14937	S6.44096	E143.2256
ABTC141171	<i>Hylophorbus</i> sp. 2 'large'	Microhylidae	M5	14938	S6.46168	E143.25494
ABTC141172	<i>Austrochaperina</i> sp. 1 'short call'	Microhylidae	M2	14939	S6.44096	E143.2256
ABTC141173	<i>Choerophryne</i> sp. 3 'buzz call'	Microhylidae	M1	14940	S6.44027	E143.22372
ABTC141174	<i>Hylophorbus</i> sp. 2 'large'	Microhylidae	M5	14941	S6.46168	E143.25494
ABTC141175	<i>Sphenophryne cornuta</i>	Microhylidae	M5	14942	S6.46168	E143.25494
ABTC141176	<i>Cophixalus wempi</i>	Microhylidae	M4	14943	S6.46197	E143.25613
ABTC141177	Microhylid new genus and species	Microhylidae	M5	14945	S6.46168	E143.25494
ABTC141178	<i>Oreophryne</i> sp. 4 'yellow-spots'	Microhylidae	M1	14955	S6.44027	E143.22372
ABTC141179	Microhylid new genus and species	Microhylidae	M5	14947	S6.46168	E143.25494
ABTC141180	<i>Oreophryne</i> sp. 4 'yellow-spots'	Microhylidae	M3	14946	S6.44191	E143.22696
ABTC141181	<i>Cophixalus</i> sp. 3 'tiny B'	Microhylidae	M3	14956	S6.44191	E143.22696
ABTC141182	<i>Oreophryne</i> sp. 1 'tiny'	Microhylidae	H3	15095	S5.94416	E142.74176
ABTC141183	<i>Callulops wilhelmanus</i>	Microhylidae	H5	15097	S5.91624	E142.69281
ABTC141184	<i>Callulops wilhelmanus</i>	Microhylidae	H5	15098	S5.91624	E142.69281
ABTC141185	<i>Oreophryne anamiatoi</i>	Microhylidae	H2	15274	S5.96908	E142.75079

CHAPTER 3 – BIRDS

Iain Woxvold and Leo Legra



The Crested Satinbird, a strikingly coloured bird newly reported from the Kikori Basin and adjacent PNG LNG Project areas during the 2015 survey

SUMMARY

Background and aims

Birds are suitable for monitoring because, compared to many other biotic groups, their taxonomy is well understood and they are relatively easy to detect. Three methods of bird monitoring were trialled during the 2015 PMA3 surveys at Hides Ridge (Biodiversity Assessment Area (BAA) 1) and the Moro area (Agogo Range; BAA 2):

1. A mist netting program designed to monitor insectivorous birds of the forest understorey, a group that includes species sensitive to disturbance and fragmentation of tropical habitat.
2. A pilot study to test the effectiveness of camera traps in monitoring changes in terrestrial bird (and mammal) populations, a group that includes a variety of species of conservation significance (including hunting-sensitive, IUCN listed, rare and restricted range species).
3. Automated sound recording of three iconic birds-of-paradise resident on Hides Ridge—the King of Saxony Bird-of-paradise (*Pteridophora albertisi*), Black Sicklebill (*Epimachus fastosus*) and Brown Sicklebill (*E. mayeri*). These vocally conspicuous species are often targeted by hunters for their elaborate plumes.

This report presents the results of the mist netting and automated sound recording studies. Results of the camera trapping pilot study are presented in a separate report (Chapter 4). Data from these three monitoring studies are combined with the results of previous surveys to update our knowledge of bird diversity in this sector of the PNG LNG Project area.

Major results

Mist nets were deployed at increasing distances from linear infrastructure clearings along three transects on Hides Ridge in BAA 1 and one transect at KP107 on the Agogo Range near Moro in BAA 2. Terrain, weather and logistic constraints limited mist netting activities and forced alteration of the original survey design. Across all sites, 115 birds from 35 species were captured, including 66 individuals from 17 species of understorey insectivore. Visual exploration of the dataset (via boxplots) revealed no relationship between capture rate and distance from Project infrastructure among species-groups of interest (families/genera). Data were too few to explore patterns at the species level or to perform statistical analyses.

Automated sound recorders were deployed along six transects in BAA 1 and five transects in BAA 2. Among the three bird-of-paradise species that were monitored acoustically on Hides Ridge, each was seen at the forest edge within 30 m of Project infrastructure, but statistical analysis (multilevel mixed models) of the acoustic dataset revealed that each species was significantly less likely to vocalise at positions next to the road/ROW than in forest 170 m from linear clearings. This pattern was strongest for the IUCN Vulnerable Black Sicklebill. In addition to monitoring birds-of-paradise, acoustic data from all sound recorders (in both BAAs) were screened more generally for the vocalisations of birds not detected by other methods.

Combining results from all studies, 175 bird species were recorded during the PMA3 surveys (BAA 1—81 species; BAA 2—110 species), including 34 bird species not previously recorded on Hides Ridge, 10 species not previously recorded in the Moro area, and nine species not previously reported for any site previously surveyed within the Kikori Basin or adjacent areas. Bird species richness was inversely related to elevation, consistent with patterns of diversity elsewhere. New elevation records are reported for eight species.

Conclusions

The PMA3 results corroborate prior assessments that both BAAs represent special areas for birds, supporting numerous rare, conservation listed, hunting-sensitive and restricted range species. While mist netting is a powerful tool that has been used successfully in other tropical environments, under the present conditions the mist netting program will be discontinued in favour of the alternate bird monitoring studies. Proximal causes of the apparent partial avoidance of forest edge by birds-of-paradise on Hides Ridge are unknown. Prior to initiating management strategies, we recommend that additional data from subsequent surveys be analysed to gain further insight into spatial and temporal patterns among these species.

INTRODUCTION

The limestone forests of Hides Ridge (Hela Province) and the Agogo Range (Southern Highlands Province) have respectively been surveyed previously for birds by Woxvold and Crome (2005) and Diamond and Bishop (2003). Each of these areas was recognised for supporting notable biodiversity values, and both are currently the subject of multi-disciplinary studies initiated in 2015 under the PMA3 biodiversity monitoring program.

Birds are a suitable choice of taxon for examining trends in local wildlife populations because they are taxonomically well known and relatively easy to detect. However, monitoring New Guinea avifauna can be challenging—most forest species are heard far more often than seen, so that accurate ‘direct’ census techniques require a rare expertise in bird-call recognition, and a number of major bird groups, most notably frugivores and nectarivores (e.g. columbids, parrots, honeyeaters, some birds-of-paradise), are unpredictably nomadic in response to changes in food availability. In tropical forest environments, suitable bird monitoring techniques effectively remove the risk of observer bias and focus on resident, territorial species that are expected to be present all year round.

Three methods of bird monitoring were trialled during the 2015 PMA3 surveys.

First, a mist netting program was designed to monitor insectivorous birds of the forest understorey. This group of birds is moderately diverse, includes mostly sedentary species and is known to be sensitive to disturbance and fragmentation of tropical forest habitat (e.g. Lambert and Collar 2002; Johns 1996; Thiollay 1997; Peh et al. 2005; Edwards et al. 2009). They are readily captured in mist nets, providing opportunity for photography and individual banding to remove observer bias.

Second, a pilot study was trialled to test the efficacy of camera traps in monitoring terrestrial birds and mammals. Terrestrial birds and mammals are an excellent candidate monitoring group because they include a number of ‘charismatic’, hunting- and/or disturbance-sensitive species, many of which are IUCN Threatened or Near Threatened. While many of these are large, they often occur at naturally low densities and/or are difficult to detect due to their avoidance of humans. Additionally, terrestrial birds include a variety of insectivorous species that form a subset of those understorey taxa targeted by the mist netting study.

Finally, automated sound recording was used to monitor Hides Ridge populations of three iconic and hunting-sensitive birds-of-paradise—the King of Saxony Bird-of-paradise (*Pteridopora albertisi*), Black Sicklebill (*Epimachus fastosus*) and Brown Sicklebill (*E. mayeri*). Adult males of these species are specifically targeted by hunters for their elaborate plumes which are used for ceremonial purposes or sold on (Frith and Beehler 1998; Frith and Frith 2009). The IUCN Vulnerable Black Sicklebill has the longest feathers of any species of bird-of-paradise and is one of PNG’s rarest birds (Beehler 1993). Both the King of Saxony Bird-of-paradise and the Brown Sicklebill are restricted-range species (Stattersfield et al. 1998). All three species are conspicuously vocal, so that automated sound recorders provide an effective and unbiased technique for monitoring population trends over time and space.

Here we report the results of the mist netting and automated sound recording studies, and update our knowledge of the bird communities present on Hides Ridge and the Agogo Range based on the results of these studies and more general observations. Results of the pilot camera trapping study are presented separately in Chapter 4.

METHODS

Study areas

Bird surveys were conducted in two Biodiversity Assessment Areas (BAAs): on Hides Ridge (BAA 1) during 11–25 June, and on the Agogo Range in the Moro area (BAA 2) during 27 June–8 July. Each of these BAAs was divided into two survey ‘sites’ that differed in elevation:

- Hides Ridge (BAA 1):
 - WP C–D: between Wellpad C and Wellpad D, at elevations of 2,100–2,400 m asl.
 - WP E–G: between Wellpad E and Wellpad G, at 2,660–2,780 m asl.
- Moro area (BAA 2):
 - Arakubi: west of Arakubi Quarry and east of the pipeline ROW, at 1,000–1,070 m asl.
 - KP107: on the Agogo Range in the vicinity of KP 107, at 1,340–1,410 m asl.

Survey methods

Survey effort was focused on the establishment and running of a mist netting program and the deployment of camera traps. Total effort for each of these activities is shown in Table 3.1. In addition to the main survey program, incidental bird records were collected at all sites throughout the survey period. Acoustic data for monitoring birds was extracted from automated sound recorders deployed by Kyle Armstrong and Stephen Richards as part of a separate study (Chapter 2).

Table 3.1. Mist netting and camera trap survey effort.

Method	Hides		Moro	
	WP C–D	WP E–G	Arakubi	KP107
Mist netting				
No. nets	10	21	0	10
Net hours	93.5	162	0	99.75
Camera trapping				
No. camera traps	12	9	6	18
Camera trap hours	1,638.5	1,515.5	1,037.25	3,643.75

Mist netting

Mist nets (9 m x 31 mm mesh; Figure 3.3) were deployed along three transects on Hides Ridge (H3 at WP C–D, H4 and H6 at WP E–G) and one transect (M3) at KP 107 (see Figures 2–4 in Executive Summary). On each transect 5–6 netting stations were established at increasing distances from linear infrastructure clearings. Mist nets were deployed in pairs at each netting station where terrain permitted (19/22 stations) with a total of 10–11 mist nets on each transect. Mist netting was restricted to one transect on each netting day (n = 6). Nets were opened shortly after dawn and closed prior to 4:30 pm or earlier in the event of heavy rain. Two transects were operated for a single day, and two transects were operated on a second day when rain interrupted the first day's netting.

All mist netted birds were measured, photographed, blood sampled (70% ethanol), banded with an individually number metal leg ring (Australian Bird and Bat Banding Scheme) and released at the site of capture. The location of each net and the dates and times of operation are presented in Appendix 3.2.

Camera trapping

Camera trap deployment and analysis methods are described in Chapter 4.

Automated sound recordings

Sound recording units (Wildlife Acoustics Song Meter SM3) were deployed along six transects on Hides Ridge (three each at the WP C–D and WP E–G sites) and five transects in the Moro area (three at KP107 and two at Arakubi) according to the sampling design described in Chapter 2. Acoustic data used to monitor vocally conspicuous birds-of-paradise was collected only from recorder arrays deployed on Hides Ridge. Birds-of-paradise were not monitored in BAA 2 because the only vocally conspicuous species present there that is commonly hunted for its plumes was the Raggiana Bird-of-paradise (*Paradisaea raggiana*). This species is still widespread and common across much of southern PNG and is known to persist in many populous and disturbed areas.

In addition to monitoring birds-of-paradise, acoustic data from all sound recorders (in both BAAs) were screened more generally for the vocalisations of birds not detected by other methods.

Analysis

Mist netting

Mist netting data for individual species and target species-groups (e.g. understory insectivores) were too few to perform detailed statistical analyses. Rather, the potential effects of Project infrastructure on capture rates of taxa of interest were explored visually by plotting the distribution of capture rates (number of captures/mist net hours) at varying distances from the nearest infrastructure clearing. Boxplots were generated to show the median, interquartile range and outlier capture rates within each of six 'distance classes': (D1) 0–30 m; (D2) 30–60 m; (D3) 60–90 m; (D4) 90–120 m; (D5) 120–150 m; (D6) 150+ m.

Camera trapping

Data from the camera trapping pilot study are analysed in Chapter 4. Pertinent records of birds detected during the camera trapping study are incorporated into the species lists presented here.

Automated sound recordings

Bird-of-paradise acoustic data were logged from automated sound recorders located 5 m and 170 m from Project infrastructure (road/ROW) on each of the six transects (H1–H6) in BAA 1. Data were collected from two days of recording at each of the 12 recording positions. For each day of recording, data were logged from 90-second sound bites at the start of every 10-minute period within each of two 2.5-hour time 'blocks': AM (06:30–09:00) and PM (15:30–18:00). This sampling strategy is based on detailed analysis of call rates from a representative set of Hides Ridge acoustic data recorded throughout the diurnal cycle (06:00 to 18:00) and is in accordance with published information on the timing and frequency of vocalisations from the target species (Frith and Beehler 1998). The following data were recorded from each 90-second sound bite: (a) the presence/absence (1/0) of calls of each of the three target species, and (b) the level of rainfall ranked as absent (0), light (1), moderate (2) or heavy (3) using recorded examples for reference. Where moderate or heavy rain interrupted the start of a 10-minute block, the earliest 90-second sound bite of light rain, or the lightest available period of rain, was screened. Potential terrain effects were tested by measuring the distance of each recorder from the nearest high point (peak) in the local landscape (in the karst terrain on Hides Ridge these were never more than 250 m away).

We examined the influence of distance from Project infrastructure on the likelihood/frequency of bird-of-paradise vocalisations using multilevel mixed modelling procedures in MLwiN 2.35 (Rasbash et al. 2015). This approach allows within-period/site patterns to be examined while taking into account the nested relationship of repeated sampling of individual birds. The probability that each species would vocalise in any given sound bite was examined using a binomial response model (vocalise or not) with the penalised quasilielihood (PQL) estimation procedure (Rasbash et al. 2015). Three-level models were used to analyse the vocal behaviour of (a) Brown Sicklebill, (b) King of Saxony Bird-of-paradise and (c) all birds-of-paradise (three species pooled), with repeated sampling within individual 2.5-hour time blocks (level one) nested within transect (level two) and site (WP C–D/WP E–G; level three). Black Sicklebill behaviour was analysed using a two-level model (time block within transect); this species was not recorded at the WP E–G site which is outside its elevational range, thus negating the requirement for a third 'site' level.

This method of hierarchical modelling is interactive, with the investigator determining the order in which explanatory variables are added or removed. Final models were derived using backward elimination of non-significant explanatory variables and their interactive terms. In summary tables, the model effect estimate is provided for each variable where $P < 0.05$.

Conventions

Nomenclature (common and scientific names) and family arrangements follow the International Ornithological Congress (IOC) World Bird List (version 6.1) (Gill and Donsker 2016). Where species are mentioned in the text the scientific name appears with the common name on first mention and only the common name is used thereafter.

Species appearing in square brackets (in text, tables and appendices) were only provisionally identified to species level—though not definitively identified, encounters are considered most likely to have involved the species named.

RESULTS AND DISCUSSION

Overall bird results

All birds recorded in 2015, and those recorded on Hides Ridge in 2005 and during preclearance surveys, are listed in Appendix 3.1 along with their conservation status.

Combining results from all survey methods, Table 3.2 lists the number of bird species recorded in 2015 at each of the four survey sites. One hundred and seventy-five (175) bird species (including provisional records) were recorded at all sites, including 81 on Hides Ridge and 110 in the Moro area. The number of bird species recorded at each site was inversely proportional to elevation, consistent with patterns of diversity across New Guinea (Diamond 1972; Beehler 1982) and tropical regions elsewhere (Corlett and Primack 2011).

Table 3.2. The number of bird species recorded in 2015 at each survey site and BAA.

Hides (BAA 1)		Moro (BAA 2)	
WP C–D	WP E–G	Arakubi	KP 107
72	44	82	77
81		110	

The 2015 surveys registered 34 bird species not previously recorded on Hides Ridge (Woxvold and Crome 2005: see below) and 10 species not previously recorded in the Moro area (Diamond and Bishop 2003) (Appendix 3.1). Nine species recorded during the 2015 surveys have not previously been reported for any site surveyed within the Kikori Basin or adjacent areas (during EIS, WWF or related surveys) (Table 3.3; Appendix 3.1; Figures 3.5–3.8). Eight of these are permanent resident species that are rare, secretive and/or restricted to high elevation forest habitats. In most cases their omission from prior checklists is attributable to limited search effort in high elevation forest and the greater use of camera traps during the 2015 surveys. The White-faced Heron (*Egretta novaehollandiae*) is an uncommon Australian-breeding migrant.

Appendix 3.1 includes a revision of records collected from the 'Hides 3' area (= Wellpad D) on Hides Ridge in 2005 (Woxvold and Crome 2005). Knowledge of vocalisations and the distribution of New Guinea birds, including both geographic and elevational ranges, has progressed greatly in the decade since that survey. The list is here revised based on reanalysis of the original sound recordings and on reinterpretation of sightings reported by others to Woxvold in 2005.

Table 3.3. Bird species newly reported from the Kikori Basin and adjacent PNG LNG Project areas during the 2015 surveys.

Scientific Name	English name	Hides (BAA 1)		Moro (BAA 2)		Method
		WP C-D	WP E-G	Arakubi	KP107	
<i>Egretta novaehollandiae</i>	White-faced Heron			X		s
<i>Rallidula rubra</i>	Chestnut Forest Rail	X	X			h
<i>Gymnocrex plumbeiventris</i>	Bare-eyed Rail				X	c
<i>Scolopax rosenbergii</i>	New Guinea Woodcock	X				c
<i>Gallinula beccarii</i>	Bronze Ground Dove		X		X	s,h,c
<i>Psittacula modesta</i>	Modest Tiger Parrot		X			s
<i>Cnemophilus macgregorii</i>	Crested Satinbird		X			s,m
<i>Daphoenositta miranda</i>	Black Sittella	X	X			s
<i>Erythrura papuana</i>	Papuan Parrotfinch		X			m

^A Method of detection listed as seen (s), heard (h), mist netted (m) and/or photographed by camera trap (c).

Conservation listed bird species

Conservation listed species recorded on Hides Ridge (2005–2015) and in the Moro area (2015) are listed in Table 3.4 and examples are shown in Figures 3.9–3.14.

Seventeen conservation listed bird species were recorded in 2015, including four species listed by the IUCN as Vulnerable (Papuan Eagle *Harpyopsis novaeguineae*, Pesquet’s Parrot *Psittrichas fulgidus*, Black Sicklebill *Epimachus mayeri*) or Near Threatened (Ribbon-tailed *Astrapia Astrapia mayeri*). One additional species—Archbold’s Bowerbird (*Archboldia papuensis*)—recorded on Hides Ridge during preconstruction surveys is listed as Near Threatened.

Sixteen species Protected under PNG law were recorded in 2015 and a further four Protected species were recorded on Hides Ridge in 2005 (Table 3.4). All birds-of-paradise (Paradisaeidae) and all satinbirds (Cnemophilidae—formerly included within Paradisaeidae) are Protected under PNG law, and these two bird families make up 17 of the 21 Protected species recorded at these survey areas.

Table 3.4. Conservation listed bird species recorded at Hides Ridge during 2005–2015 and in the Moro area in 2015.

Scientific Name	English Name	Status		Hides			Moro	
		IUCN	PNG	2005+	WP C-D	WP E-G	Arakubi	KP107
<i>Harpyopsis novaeguineae</i>	Papuan Eagle	VU	P		X			
<i>Probosciger aterrimus</i>	Palm Cockatoo		P				X	
<i>Psittrichas fulgidus</i>	Pesquet’s Parrot	VU	P				X	X
<i>Rhyticeros plicatus</i>	Blyth’s Hornbill	LC	P				X	
<i>Archboldia papuensis</i>	Archbold’s Bowerbird	NT		X				
<i>Cnemophilus loriae</i>	Loria’s Satinbird	LC	P		X	[X]		
<i>Cnemophilus macgregorii</i>	Crested Satinbird	LC	P			X		
<i>Loboparadisea sericea</i>	Yellow-breasted Satinbird	LC	P	[X]				
<i>Manucodia chalybatus</i>	Crinkle-collared Manucode	LC	P					[X]
<i>Phonygamus keraudrenii</i>	Trumpet Manucode	LC	P				[X]	
<i>Paradigalla brevicauda</i>	Short-tailed Paradigalla	LC	P	X				
<i>Astrapia mayeri</i>	Ribbon-tailed <i>Astrapia</i>	NT	P		X	X		
<i>Parotia carolae</i>	Queen Carola’s Parotia	LC	P					X
<i>Parotia lawesii</i>	Lawes’s Parotia	LC	P	X				
<i>Pteridophora alberti</i>	King of Saxony Bird-of-paradise	LC	P		X	X		
<i>Lophorina superba</i>	Superb Bird-of-paradise	LC	P	X				
<i>Ptiloris magnificus</i>	Magnificent Riflebird	LC	P				X	
<i>Epimachus fastosus</i>	Black Sicklebill	VU	P		X			
<i>Epimachus mayeri</i>	Brown Sicklebill	LC	P		X	X		
<i>Drepanomis albertisi</i>	Black-billed Sicklebill	LC	P		X			
<i>Diphyllodes magnificus</i>	Magnificent Bird-of-paradise	LC	P				X	X
<i>Paradisaea raggiana</i>	Raggiana Bird-of-paradise	LC	P				X	X

Mist netting

For each species mist netted, Table 3.5 lists the number of captures and their preferred food sources and foraging strata. Combining results from all sites in both BAAs, 115 individuals from 35 bird species were captured in mist nets. Seventy-eight (78) birds from 24 species were captured along the three mist net transects on Hides Ridge in BAA 1, and 37 birds from 11 species were captured along the single mist net transect at KP107 in BAA 2. There was a complete turnover in species captured in nets at Hides Ridge and at KP107 (no species captured at both BAAs).

The mist netting study targeted those species that (a) include invertebrates as the major component of their diet and (b) occupy (solely or predominantly) the lower forest strata, including the ground, understorey and mid-storey levels (see Table 3.5). Here termed 'understorey insectivores', 17 such species were mist netted in 2015 (Table 3.5; examples shown in Figures 3.15–3.20). Understorey insectivore capture rates were inversely proportional to elevation—the most captures were made at KP107 (1,360–1,380 m asl; 34 captures from nine species on one transect), fewer at WP C–D (2,320–2,370 m asl; 19 captures from eight species on one transect) and the fewest at WP E–G (2,675–2,715 m asl; 13 captures from eight species on two transects).

Figure 3.1A shows the rate of capture of all understorey insectivores at varying distances from the forest edge when data from all species and sites are pooled. Considering this dietary guild as a whole, there was no indication that understorey insectivores preferentially occupy forest away from Project infrastructure—multiple individuals were mist netted in all distance classes, including within 30 m of the road/ROW.

However, individual taxa respond differently to various environmental variables and some taxa may be more sensitive to edge effects than others. Within the understorey insectivore guild, we explored capture rates among species within each of the three most commonly captured families/genera—mouse warblers and scrubwrens (*Acanthizidae*), Australasian robins (*Petroicidae*) and long-billed berrypeckers (*Melanocharitidae*: *Oedistoma* and *Toxorhamphus*) (Figures 3.1B–D). Again no clear patterns emerge—multiple individuals were captured in almost all distance classes, and where absences were recorded these may be an artefact of under-sampling. Data were too few to sensibly explore patterns at the species level.

Terrain, weather and logistic issues combined to constrain mist netting activities and force alteration of the original survey design. The difficult terrain (limestone karst) limited the number of transects that could be established and restricted their arrangement to one side (rather than both sides) of linear infrastructure routes, disallowing examination of 'barrier effects'. The difficult terrain also increased the time taken to deploy mist nets. Once transects were established, logistic and weather constraints limited the amount of time spent operating mist nets and restricted the amount of data that could be collected (the original proposal was for surveys to be conducted outside of the rainy season while based in camps located at the survey sites). Although deployment of mist nets on established transects will take less time during subsequent visits, additional netting sites are still needed if the full sampling protocol is to be achieved and the overall set-up time (for established and new netting transects combined) is expected to take longer than that expended during the Phase 1 surveys. Moreover, logistic and weather issues are unlikely to change for subsequent survey phases, again limiting the time available to operate mist nets.

In conclusion, although mist netting is a powerful tool that has been used successfully in other tropical environments to investigate a suite of ecological questions relevant to the present study, the karstic landscapes at BAA 1 and BAA 2 and inclement weather experienced during Phase 1 severely constrained data collection. For these reasons, and in light of the favourable results obtained from the other monitoring studies (camera trapping pilot study and acoustic bird-of-paradise monitoring), the mist netting program be discontinued in favour of these alternate bird monitoring programs.

Table 3.5. Birds mist netted in 2015 on Hides Ridge and at KP107, their food sources and occurrence in various forest strata. Understorey insectivores are marked with an asterisk (*).

Scientific Name	English Name	HIDES		MORO	Total captures	Food ^A	Strata ^B
		WP C-D	WP E-G	KP107			
<i>Cacomantis flabelliformis</i>	Fan-tailed Cuckoo		1		1	i	gumc
<i>Collocalia esculenta</i>	Glossy Swiftlet	1			1	i	a
<i>Caligavis subfrenata</i>	Black-throated Honeyeater		1		1	inf	(um)c
<i>Meliphaga mimikae</i>	Mottle-breasted Honeyeater*			4	4	if(n)	um
<i>Melipotes fumigatus</i>	Common Smoky Honeyeater	1	9		10	f(i)	umc
<i>Melidectes belfordi</i>	Belford's Melidectes		1		1	in(f)	(um)c
<i>Ptiloprora guisei</i>	Rufous-backed Honeyeater	1			1	i(fn)	umc
<i>Ptiloprora perstriata</i>	Grey-streaked Honeyeater		7		7	ifn	umc
<i>Melilestes megarhynchus</i>	Long-billed Honeyeater*			5	5	ivn(f)	um(c)
<i>Crateroscelis robusta</i>	Mountain Mouse-warbler*	1			1	i	gu
<i>Sericornis papuensis</i>	Papuan Scrubwren*	2	1		3	i	um(c)
<i>Sericornis nouhuysi</i>	Large Scrubwren*	1	2		3	i	u(m)
<i>Sericornis perspicillatus</i>	Buff-faced Scrubwren*	5			5	i	um(c)
<i>Sericornis arfakianus</i>	Grey-green Scrubwren*			1	1	i	um
<i>Cnemophilus macgregorii</i>	Crested Satinbird		2		2	f	(g)umc
<i>Melanocharis nigra</i>	Black Berrypecker			1	1	fi	um(c)
<i>Melanocharis versteri</i>	Fan-tailed Berrypecker	5	8		13	fi	um(c)
<i>Oedistoma iliolophus</i>	Dwarf Longbill*			11	11	in(f)	u(mc)
<i>Toxorhamphus poliopterus</i>	Slaty-headed Longbill*			8	8	in	um(c)
<i>Ptilorrhoa castanonota</i>	Chestnut-backed Jewel-babbler*			1	1	i	g
<i>Coracina montana</i>	Black-bellied Cuckooshrike			1	1	fi	(um)c
<i>Rhagologus leucostigma</i>	Mottled Whistler	1			1	f(i)	um(c)
<i>Pachycephala modesta</i>	Brown-backed Whistler		1		1	i(f)	(um)c
<i>Pachycephala soror</i>	Sclater's Whistler*	3			3	i	um(c)
<i>Colluricincla megarhyncha</i>	Little Shrikethrush*			1	1	i(f)	um(c)
<i>Rhipidura atra</i>	Black Fantail*	3			3	i	um
<i>Rhipidura albolimbata</i>	Friendly Fantail*		3		3	i	um(c)
<i>Pteridophora alberti</i>	King of Saxony Bird-of-paradise		1		1	f(i)	(u)mc
<i>Diphyllodes magnificus</i>	Magnificent Bird-of-paradise			1	1	fi	gumc
<i>Heteromyias albispecularis</i>	Ashy Robin*	4			4	i	gu
<i>Poecilodryas albonotata</i>	Black-throated Robin		1		1	i	(u)mc

Scientific Name	English Name	HIDES		MORO	Total captures	Food ^A	Strata ^B
		WP C–D	WP E–G	KP107			
<i>Peneothello sigillata</i>	White-winged Robin*		5		5	i(f)	u
<i>Tregellasia leucops</i>	White-faced Robin*			3	3	i	um
<i>Microeca papuana</i>	Canary Flyrobin	1	5		6	i	umc
<i>Erythrura papuana</i>	Papuan Parrotfinch		1		1	f	umc
No. individuals		29	49	37	115		
No. species		13	16	11	35		

^A Food items: i—invertebrates (including insects); n—nectar; f—fruit (including seeds); v—vertebrates. Food items are listed in order of preference.

Non-preferred (occasionally consumed) food items appear in brackets. Data from Coates (1985, 1990).

^B Foraging strata: g—ground; u—understorey (below c. 3–5 m; varies with forest stature); m—mid-storey (3–5 m to lower canopy); c—canopy;

a—aerial. Strata are listed from ground up. Non-preferred (occasionally occupied) strata appear in brackets. Data from Coates (1985, 1990).

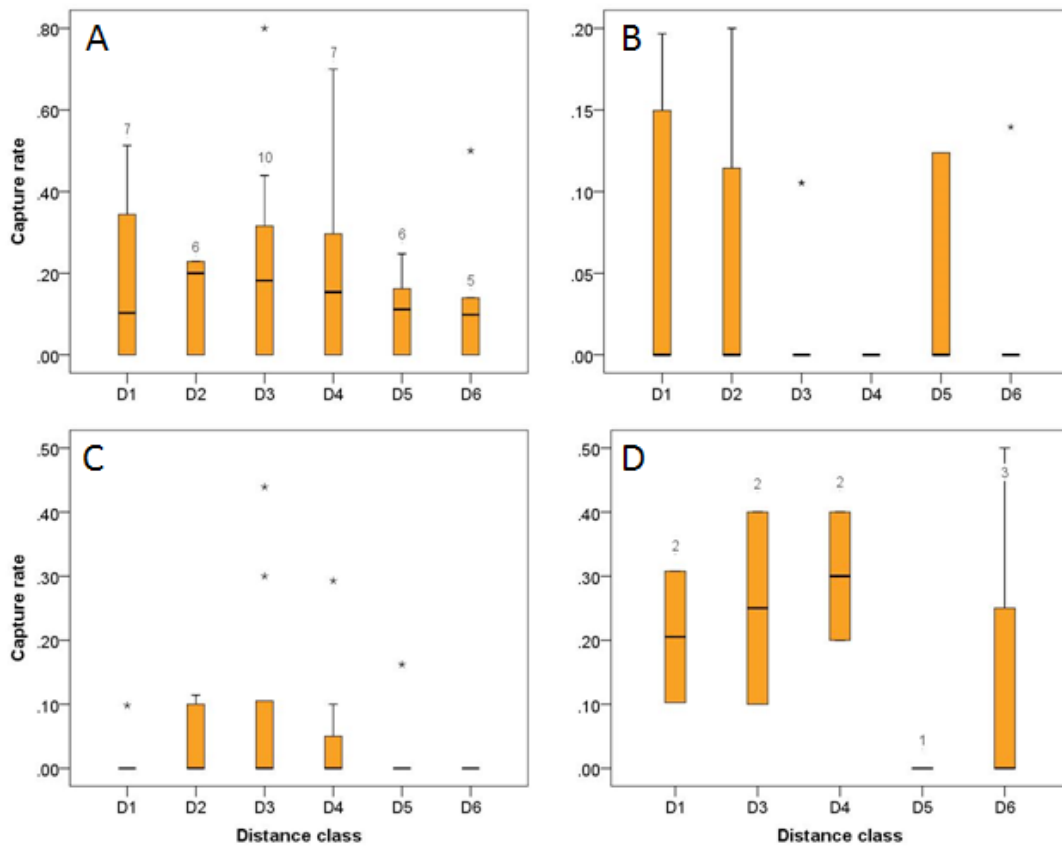


Figure 3.1. Capture rates for understorey insectivores in each of six distance classes: A—all species combined; B—mouse warblers and scrubwrens (Acanthizidae); C—Australasian robins (Petroicidae); D—long-billed berrypeckers (Melanocharitidae: *Oedistoma* and *Toxorhamphus*). Distance from Project infrastructure increases from D1 to D6. Figures 3.1A–C include results from all sites. Figure 3.1D includes data only from KP107 (Hides Ridge being above the normal range of long-billed berrypeckers). The number of mist nets in each distance class is shown atop each boxplot in Figures 3.1A and 3.1D (the same sample sizes apply to all boxplots in Figures 3.1A–C). Outliers are indicated with a star.

Camera trapping

Birds photographed by camera trap are incorporated into the species lists presented in Appendix 3.1. Detailed results of the pilot camera trapping study are presented in Chapter 4. Briefly, combining results from all sites, 133 camera trap 'events' were detected from 28 bird species. There was a near-complete turnover in species composition among birds camera trapped in BAA 1 and BAA 2, with only the Pheasant Pigeon (*Otidiphaps nobilis*) camera trapped at both locations.

Despite extensive prior survey effort (e.g. Diamond and Bishop 2003; Woxvold and Crome 2005; Woxvold 2008), three bird species were recorded for the first time in the Kikori Basin by camera trapping—the Bare-eyed Rail (*Gymnocrex plumbeiventris*; Figure 3.5) and Russet-tailed Thrush (*Zoothera heinei*; Figure 3.8) at KP107, and the New Guinea Woodcock (*Scolopax rosenbergii*) at WP C–D on Hides Ridge.

Automated sound recordings

Sound recordings of Birds-of-paradise on Hides Ridge revealed that birds were much less likely to be heard during periods of moderate or heavy rain (all species: $P \leq 0.001$). Rainfall reduces detectability both by suppressing calling behaviour and by making calling birds less audible. We therefore restricted analyses to a reduced dataset collected during periods of light or no rain (Table 3.6).

All bird-of-paradise species recorded on Hides Ridge in 2015 were observed to utilise forest edge as well as interior forest habitats and both the Brown Sicklebill and the King of Saxony Bird-of-paradise were seen displaying within c. 30 m of the road. Black Sicklebills and Ribbon-tailed Astrapias were also encountered at the forest edge adjacent to the road or ROW. These observations are consistent with prior reports of habitat use for these species (Frith and Beehler 1998; Frith and Frith 2009).

However, while edge environments are utilised by these species on Hides Ridge, analysis of sound recordings suggests that both sicklebill species and the King of Saxony Bird-of-paradise prefer interior forest environments—controlling for other spatial, temporal and weather factors (see below), each of these species vocalised significantly less often at positions close to Project infrastructure clearings (analysed individually and collectively; Table 3.6; Figure 3.2). This pattern was strongest for Black Sicklebills (detected at the WP C–D site only), which were more than twice as likely to be heard at positions 170 m from linear clearings.

The proximal causes of this pattern are unknown. In each of these species, territories of at least some adult males (which are responsible for the advertising calls analysed here), span or abut these linear clearings (as evidenced by display sites and/or overflights). Are these birds spending less time near the forest edge or simply vocalising less often at these sites? Are these behaviours influenced by differences in resource availability, susceptibility to predation (including hunting), human activity (for example traffic noise), or availability of females in edge environments? Any one or a combination of these factors may lead to partial avoidance of linear clearings. Prior to developing/initiating management recommendations or further investigations, additional data from the proposed 2017 survey be analysed to gain further insight into potential spatial influences as well as possible temporal patterns.

A number of other variables were correlated with patterns in calling behaviour. Black Sicklebills and King of Saxony Birds-of-paradise were more likely to be recorded near terrain high points ('distance from peak' in Table 3.6), Black Sicklebills called more frequently in the afternoon ('period') and the King of Saxony Birds-of-paradise were less likely to be heard in light rain (compared with no rain) (Table 3.6). The King of Saxony Bird-of-paradise has the quietest call of the three monitored species, and it is possible that even light rain reduced the detectability of this species' call.

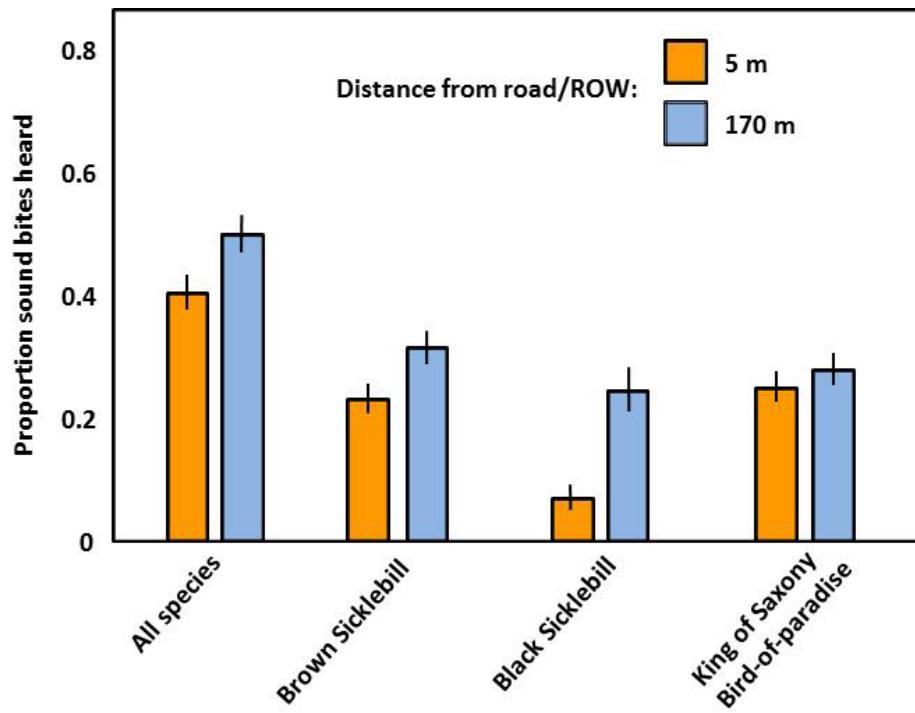


Figure 3.2. The proportion (\pm standard error) of sound bites in which birds-of-paradise were heard calling as a function of distance from Project infrastructure (road/ROW). Birds from all species (analysed individually and collectively) vocalised significantly more frequently at sites 170 m from Project infrastructure than at sites adjacent to linear clearings.

Table 3.6. Multilevel model summaries of factors influencing the likelihood of vocalisation by birds-of-paradise. Models include only those sound bites during which ‘no’ or ‘light’ rain were recorded (‘moderate’ and ‘heavy’ rain periods excluded). Sample sizes (‘n’) show total number of sound bites/transects/sites used in each model. For significant categorical factors (A:B), the final model estimate indicates the relative effect of the first category (A) compared with the second (B); for example, a significant negative model estimate for Rain (light:none) indicates that birds are less likely to be heard calling during light rain than during periods with no rain.

Dependent variable	Explanatory variable	χ^2	df	P	Final model estimate (±s.e.)
All three birds-of-paradise n = 580/6/2	Distance from road/ROW (170:5 m)	9.43	1	0.002	0.572 (0.186)
	Distance from peak			ns	
	Period (AM:PM)			ns	
	Rain (light:none)	4.681	1	0.031	-0.449 (0.207)
Brown Sicklebill n = 580/6/2	Distance from road/ROW (170:5 m)	8.088	1	0.004	0.617 (0.217)
	Distance from peak			ns	
	Period (AM:PM)			ns	
	Rain (light:none)			ns	
Black Sicklebill n = 283/3 (one site)	Distance from road/ROW (170:5 m)	13.513	1	<0.001	2.385 (0.649)
	Distance from peak	5.663	1	0.017	0.013 (0.006)
	Period (AM:PM)	9.415	1	0.002	-1.156 (0.377)
	Rain (light:none)			ns	
King of Saxony Bird-of-paradise n = 580/6/2	Distance from road/ROW (170:5 m)	8.432	1	0.004	0.687 (0.237)
	Distance from peak	11.293	1	0.001	0.013 (0.004)
	Period (AM:PM)			ns	
	Rain (light:none)	8.734	1	0.003	-0.724 (0.245)

Range extensions

New elevation records are reported for eight species:

- Pheasant Pigeon *Otidiphaps nobilis* – singles photographed at two camera traps at 2,260 m asl on Hides Ridge. Previously reported from as high as 2,050 m asl on the Saruwaged Range, Huon Peninsula (Freeman et al. 2013).
- White-crowned Cuckoo *Cacomantis leucolophus* – heard and call recorded at c. 2,250 m asl on Hides Ridge, previously reported from as high as 1,800 m asl (Woxvold et al. 2015).
- Papuan Boobook *Ninox theomacha* – one recorded by automated sound recorder located at 2,750 m asl on Hides Ridge, previously reported from as high as 2,500 m (Beehler and Pratt 2016).
- Eclectus Parrot *Eclectus roratus* – one heard calling at c. 2,275 m asl on Hides Ridge, previously reported from as high as 1,900 m asl.
- Orange-breasted Fig Parrot *Cyclopsitta guillemittii* – party of five seen at close quarters on Agogo Range at 1,385 m on 29 June and again at 1,360 m asl on 6 July. Previously reported from as high as 1,100 m asl.

- Papuan Black Myzomela *Myzomela nigrita* – one male seen at a flowering *Syzigium* at 1,360 m asl on 5 July. Previously reported from as high as 1,250 m asl (Coates 1990).
- Green-backed Honeyeater *Glycichaera fallax* – one seen at a flowering *Syzigium* at 1,360 m asl on 5 and 6 July. Previously reported from as high as 1,200 m asl (Coates 1990; 1,300 m in Beehler & Pratt 2016).
- Crested Pitohui *Ornorectes cristatus* – one camera trapped at 1,380 m asl at KP107 on the Agogo Range. Previously reported from as high as 1,300 m asl (Coates 1990).

Special areas

BAA I (Hides Ridge)

The forests along Hides Ridge are a special area for birds as they support numerous rare, conservation listed, hunting-sensitive and restricted range species (Crome et al. 2008; this study). The high elevation and rugged karst terrain have long protected the Hides Ridge bird community from hunting and agricultural practices that threaten montane faunal communities in many other parts of PNG.

Hunting is a major factor in the population decline of large and elaborately plumed birds in montane New Guinea. Three IUCN listed hunting-sensitive species have been recorded on Hides Ridge—Papuan Eagle (VU), Black Sicklebill (VU) and Ribbon-tailed Astrapia (NT). All are specifically targeted by hunters for their meat and/or plumes and are now rare or extirpated from the vicinity of many settled areas.

A notable feature of the Hides Ridge bird community was the ease with which four species of elaborately plumed bird-of-paradise—the Black Sicklebill, Brown Sicklebill, Ribbon-tailed Astrapia and King of Saxony Bird-of-paradise—were seen along the access road and pipeline ROW. This suggests that the construction of linear infrastructure in this previously remote landscape has not yet resulted in the loss of these birds from potentially vulnerable roadside territories. Analysis of the 2015 automated sound recorder data suggest that the three vocally conspicuous species occur (or at least vocalise) more commonly in interior forest away from the infrastructure edge. Local residents are venturing at least as far as the Wellpad C area, and further study is warranted to monitor the ongoing status of these easily detectable species.

In addition to hunting-sensitive species, numerous rare and poorly known montane taxa are now known to occur on Hides Ridge, including Meyer's Goshawk (*Accipiter meyerianus*), New Guinea Woodcock (*Scolopax rosenbergii*), Archbold's Bowerbird (*Archboldia papuensis*), Orange-crowned Fairywren (*Clytomyias insignis*), Papuan Logrunner (*Orthonyx novaeguineae*), Yellow-breasted Satinbird (*Looparadisaea sericea*), Black Sittella (*Daphoenositta miranda*), Black Sicklebill and Papuan Parrotfinch (*Erythrura papuana*). Two of these—Archbold's Bowerbird and the Black Sicklebill—have been listed among PNG's rarest bird species (Beehler 1993). Archbold's Bowerbird has not been encountered directly, but was detected by L. Legra during preconstruction surveys through the discovery of a bower at 2,480 m asl at a site along the current Project road approximately 1.6 km west-northwest of transect 3 in the Wellpad C–D area (at WGS84 54S 691367E 9343439N; Figure 3.10).

Rates of endemism are particularly high in New Guinea's montane forest environments. Sixteen restricted range bird species (sensu BirdLife International) are now known to occur on Hides Ridge (Table 3.7).

Forest above 2,400 m asl on Hides Ridge, including that in the Wellpad E–G area, is isolated from nearby areas of comparable habitat on the Muller and Karius ranges. This area supports isolated populations of at least two mid-upper montane bird species—Grey-streaked Honeyeater (*Ptiloprora perstriata*) and the restricted range and nationally Protected Crested Satinbird (*Cnemophilus macgregorii*). Habitat loss/degradation is proportionally higher for these 'island' populations than for those at lower elevations that extend unbroken into surrounding areas.

Table 3.7. Restricted range bird species recorded on Hides Ridge.

Scientific Name	English name
<i>Rallicula rubra</i>	Chestnut Forest Rail
<i>Psittacella modesta</i>	Modest Tiger Parrot
<i>Archboldia papuensis</i>	Archbold's Bowerbird
<i>Ptiloprora guisei</i>	Rufous-backed Honeyeater
<i>Ptiloprora perstriata</i>	Grey-streaked Honeyeater
<i>Melidectes belfordi</i>	Belford's Melidectes
<i>Cnemophilus loriae</i>	Loria's Satinbird
<i>Cnemophilus macgregorii</i>	Crested Satinbird
<i>Loboparadisea sericea</i>	Yellow-breasted Satinbird
<i>Daphoenositta miranda</i>	Black Sittella
<i>Eulacestoma nigropectus</i>	Wattled Ploughbill
<i>Paradigalla brevicauda</i>	Short-tailed Paradigalla
<i>Astrapia mayeri</i>	Ribbon-tailed Astrapia
<i>Parotia lawesii</i>	Lawes's Parotia
<i>Pteridophora alberti</i>	King of Saxony Bird-of-paradise
<i>Epimachus meyeri</i>	Brown Sicklebill

BAA 2 (Agogo Range, Moro area)

The rugged limestone forests around KP 107 and the Arakubi Quarry support similar biodiversity values to those recorded on Hides Ridge, including a number of rare, conservation listed, hunting-sensitive and restricted range species.

The IUCN Vulnerable Pesquet's Parrot (*Psitttrichas fulgidus*) was recorded at both sites in 2015, with 10 Pesquet's Parrots seen in a single fruiting fig (*Ficus* sp.) near Arakubi Quarry on 27 June. Surveys by Jared Diamond and David Bishop during the period 1998–2003 have also confirmed the presence of the IUCN Vulnerable Papuan Eagle from the Moro area (Diamond and Bishop 2003).

Of note also is the presence of the Greater Melampitta (*Melampitta gigantea*; Figure 3.13) at KP107. This is one of New Guinea's most enigmatic birds, being restricted to rugged limestone country where it roosts and nests below ground (the world's only passerine to do so) and it is known from only five localities in PNG (Coates 1990; Boles 2007). First recorded in the area by Diamond and Bishop (2003), Greater Melampittas were heard on multiple occasions at KP107, with camera trapping subsequently proving a useful tool for detecting this restricted range species (Chapter 4). Other rare or elusive species recorded in BAA 2 include the Bare-eyed Rail (*Gymnocrex plumbeiventris*; Figure 3.5), Bronze Ground Dove (*Gallicolumba beccarii*; Figure 3.6) and Russet-tailed Thrush (*Zoothera heinei*; Figure 3.8). Despite extensive prior surveys around Moro and at other sites in the Kikori Basin each of these species was newly reported for the region in 2015. Terrestrial insectivores such as the Bare-eyed Rail and Russet-tailed Thrush belong to the bird guilds most sensitive to degradation of tropical forest habitat. High camera trapping rates for these species indicates that this technique is suitable for monitoring these shy and normally silent species (Chapter 4).

CONCLUSIONS

- 1) The 2015 PMA3 survey results corroborate prior assessments that the Hides Ridge and Agogo Range forests represent special areas for birds through their support of numerous rare, conservation listed, hunting-sensitive and restricted range species.
- 2) By combining a variety of modern 'rapid assessment' survey techniques, including camera trapping, automated sound recording, mist netting and direct encounter methods, the PMA3 surveys have also improved our knowledge of the diversity of bird communities resident in the Kikori basin.
- 3) While mist netting is a powerful tool that has been used successfully in other tropical environments, terrain, weather and logistic constraints severely constrained data collection via this technique.
- 4) Analysis of acoustic data from automated sound recorders deployed on Hides Ridge in BAA 1 indicated that the King of Saxony Bird-of-paradise, Black Sicklebill and Brown Sicklebill were each significantly less likely to vocalise at positions next to the road/ROW than in forest 170 m from linear clearings. The reasons for this partial avoidance behaviour are unknown.

REFERENCES

- Beehler, B. M. 1982. Ecological structuring of forest bird communities in New Guinea. Pp. 837–860 in Gressitt, J. L. (ed.) *Biogeography and Ecology of New Guinea*. Monographiae Biologicae, Vol. 42. Dr W. Junk Publishers, The Hague.
- Beehler, B. M. 1993. Biodiversity and conservation of the warm-blooded vertebrates of Papua New Guinea. Pp. 77–155 in Beehler, B. M. (ed.) *Papua New Guinea Conservation Needs Assessment* (Volume 2). Biodiversity Support Program, Washington, D. C.
- Beehler, B. M. & Pratt, T. K. 2016. *Birds of New Guinea: Distribution, Taxonomy, and Systematics*. Princeton, New Jersey: Princeton University Press.
- Boles, W. E. 2007. Eupetidae (Jewel-babblers and allies). Pp. 348–73 in del Hoyo, J., Elliott, A. & Christie, D. (eds) *Handbook of the Birds of the World. Volume 12: Picathartes to Tits and Chickadees*. Lynx Edicions, Barcelona.
- Coates, B. J. 1985. *The Birds of Papua New Guinea, Including the Bismarck Archipelago and Bougainville*. Volume I, Non-Passerines. Dove Publications, Alderley, Queensland.
- Coates, B. J. 1990. *The Birds of Papua New Guinea, Including the Bismarck Archipelago and Bougainville*. Volume II, Passerines. Dove Publications, Alderley, Queensland.
- Crome, F. H. J. et al. 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: *The PNG LNG Project Environmental Impact Statement*. Prepared by Coffey Natural Systems for Esso Highlands Limited.
- Diamond, J. M. 1972. *Avifauna of the Eastern Highlands of New Guinea*. Nuttall Ornithological Club, Cambridge, Massachusetts.
- Diamond, J. M. & Bishop, K. D. 2003. Seasonality in birds in the Kikori River catchment: year-2003 Studies. WWF KICDP area Report.
- Edwards D. P., Ansell F. A., Ahmad A. H., Nlius R. & Hamer K. C. 2009. The value of rehabilitating logged rainforest for birds. *Conservation Biology* 6: 1,628–1,633.
- Freeman, B. G., Class, A., Mandeville, J., Tomassi, S. & Beehler, B. M. 2013. Ornithological survey of the mountains of the Huon Peninsula, Papua New Guinea. *Bulletin of the British Ornithologists' Club*. 133: 4–18.
- Frith, C. B. & B. M. Beehler. 1998. *The Birds of Paradise: Paradisaeidae*. Oxford University Press, Oxford.

- Frith, C. B. & Frith, D. W. 2009. Paradisaeidae (Birds-of-paradise). Pp. 404–493 in del Hoyo, J., Elliott, A. and Christie, D. (eds) *Handbook of the Birds of the World. Volume 14: Bush-shrikes to Old World Sparrows*. Lynx Edicions, Barcelona.
- Gill, F. & Donsker, D. (eds.) 2016. *IOC World Bird List* (v 6.1). <http://www.worldbirdnames.org/>
- Johns, A. G. 1996. Bird population persistence in Sabahan logging concessions. *Biological Conservation* 75: 3–10.
- Lambert, F. R. & Collar, N. J. 2002. The future for Sundaic lowland forest birds: long-term effects of commercial logging and fragmentation. *Forktail* 18: 127–146.
- Peh, K. S.-H., de Jong, J., Sodhi, N. S., Lim, S. L.-H. & Yap, C. A.-M. 2005. Lowland rainforest avifauna and human disturbance: persistence of primary forest birds in selectively logged forests and mixed-rural habitats of southern Peninsular Malaysia. *Biological Conservation* 123: 489–505.
- Rasbash, J., Browne, W., Healy, M., Cameron, B. & Charlton, C. 2015. *MLwiN*. Version 2.35. Centre for Multilevel Modelling, University of Bristol.
- Stattersfield, A. J., Crosby, M. J., Long, A. J. & Wege, D. C. 1998. *Endemic Bird Areas of the World*. BirdLife International, Cambridge, UK.
- Thiollay, J.-M. 1997. Disturbance, selective logging and bird diversity: a Neotropical forest study. *Biodiversity and Conservation* 6: 1,155–1,173.
- Woxvold, I. A. 2008. Avifauna of the Upstream Portion of the PNG LNG Project, Southern Highlands and Western Provinces, Papua New Guinea. Unpublished report to Coffey Natural Systems. Annex 8 in: Crome, F. H. J. et al. 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: *The PNG LNG Project Environmental Impact Statement*. Prepared by Coffey Natural Systems for Esso Highlands Limited.
- Woxvold, I. A. & Crome, F. H. J. 2005. A report on the Avifauna of the Papua New Guinea Gas project area. Unpublished report to Enesar Consulting Py Ltd.. Annex 7 in: Crome, F. H. J. et al. 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: *The PNG LNG Project Environmental Impact Statement*. Prepared by Coffey Natural Systems for Esso Highlands Limited.
- Woxvold, I. A., Ken, B. & Aplin, K. P. 2015. Results of a bird survey of the Ok Tedi headwaters area, Western Province, Papua New Guinea. Chapter 8 in: *A rapid biodiversity assessment of the Hindenburg Wall region, Western Province, Papua New Guinea* (S. Richards and N. Whitmore, eds.). PNGSDP, WCS, PNG Department of Environment and Conservation.

Bird survey techniques, team and species newly recorded for the Kikori basin



Figure 3.3. A mist net erected in moss forest on Hides Ridge



Figure 3.4. The bird team releasing a netted bird after examination



Figure 3.5. Bare-eyed Rail



Figure 3.6. Bronze Ground Dove



Figure 3.7. Modest Tiger Parrot



Figure 3.8. Russet-tailed Thrush

Conservation listed and restricted range bird species



Figure 3.9. Papuan Eagle (IUCN Vulnerable; PNG Protected)

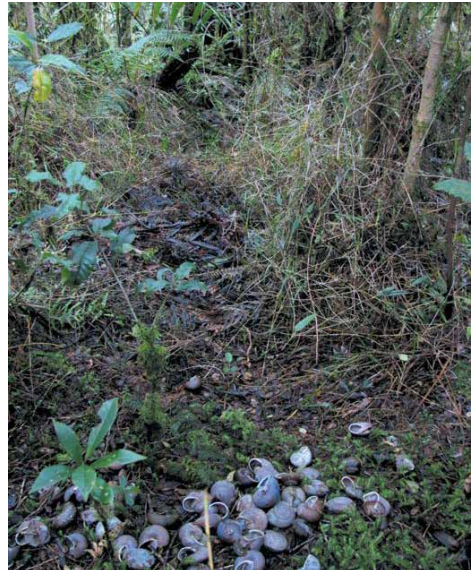


Figure 3.10. Archbold's Bowerbird bower (IUCN Near Threatened)



Figure 3.11. King of Saxony Bird-of-paradise (PNG Protected; IUCN Near Threatened)



Figure 3.12. Magnificent Bird-of-paradise (PNG Protected)



Figure 3.13. Greater Melampitta (restricted range)



Figure 3.14. Belford's Melidectes (restricted range)

Understorey insectivores captured in mist nets



Figure 3.15. Long-billed Honeyeater



Figure 3.16. Papuan Scrubwren



Figure 3.17. Grey-green scrubwren



Figure 3.18. Chestnut-backed Jewel-babbler



Figure 3.19. Ashy Robin



Figure 3.20. White-faced Robin

APPENDICES

Appendix 3.1. Bird species recorded on Hides Ridge and in the Moro area in 2015, and on Hides Ridge in 2005 and during preclearance surveys.

Scientific Name	English name	Status		Hides (BAA 1)			Moro (BAA 2)		New records ¹	Method ²
		IUCN	PNG	2005	WP C-D	WP E-G	Arakubi	KP107		
CASUARIIDAE										
<i>Casuarius bennetti</i>	Dwarf Cassowary	NT		X	X		X	X		
MEGAPODIIDAE										
<i>Aepyodius arfakianus</i>	Wattled Brushturkey							X		
<i>Talegalla jobiensis</i>	Collared Brushturkey						[X]	X	mo	c
<i>Megapodius decollatus</i>	New Guinea Scrubfowl				X		X	X	hr,mo	h,c
ARDEIDAE										
<i>Egretta novaehollandiae</i>	White-faced Heron						X		mo,k	s
ACCIPTRIDAE										
<i>Henicopernis longicauda</i>	Long-tailed Honey Buzzard			X						
<i>Harpyopsis novaeguineae</i>	Papuan Eagle	VU	P		X				hr	c
<i>Accipiter melanochlamys</i>	Black-mantled Goshawk			X						
<i>Accipiter poliocephalus</i>	Grey-headed Goshawk							X		
<i>Accipiter meyerianus</i>	Meyer's Goshawk			X						
<i>Haliastur indus</i>	Brahminy Kite			X	X		X	X		
RALLIDAE										
<i>Rallicula rubra</i>	Chestnut Forest Rail				X	X			hr,k	h
<i>Rallicula forbesi</i>	Forbes's Forest Rail			X	X					
<i>Gymnocrex plumbeiventris</i>	Bare-eyed Rail							X	mo,k	c
SCOLOPACIDAE										
<i>Scolopax rosenbergii</i>	New Guinea Woodcock				X				hr,k	c
COLUMBIDAE										
<i>Macropygia amboinensis</i>	Slender-billed Cuckoo-Dove						X	X		
<i>Macropygia nigrirostris</i>	Bar-tailed Cuckoo-Dove			X	X	X				
<i>Reinwardtoena reinwardtsi</i>	Great Cuckoo-Dove			X			X	X		
<i>Henicophaps albifrons</i>	New Guinea Bronzewing							X		
<i>Gallicolumba rufigula</i>	Cinnamon Ground Dove						X	X		
<i>Gallicolumba beccarii</i>	Bronze Ground Dove					X		X	hr,mo,k	s,h,c

Scientific Name	English name	Status		Hides (BAA 1)			Moro (BAA 2)		New records ¹	Method ²
		IUCN	PNG	2005	WP C-D	WP E-G	Arakubi	KP107		
<i>Otidiphaps nobilis</i>	Pheasant Pigeon				X		X	X	hr	c
<i>Ptilinopus perlatus</i>	Pink-spotted Fruit Dove						X			
<i>Ptilinopus ornatus</i>	Ornate Fruit Dove			X				[X]		
<i>Ptilinopus superbus</i>	Superb Fruit Dove						X			
<i>Ptilinopus pulchellus</i>	Beautiful Fruit Dove						X			
<i>Ptilinopus rivoli</i>	White-bibbed Fruit Dove			X	X	X	[X]	X		
<i>Ducula chalconota</i>	Rufescent Imperial Pigeon			X	X					
<i>Ducula zoeae</i>	Zoe's Imperial Pigeon						X	X		
<i>Gymnophaps albertisii</i>	Papuan Mountain Pigeon			X	X			X		
CUCULIDAE										
<i>Centropus bernsteini/phasianinus</i>	Black-billed/Pheasant Coucal						X		mo	s
<i>Chrysococcyx ruficollis</i>	Rufous-throated Bronze Cuckoo				X	X			hr	h
<i>Chrysococcyx meyerii</i>	White-eared Bronze Cuckoo						X	X		
<i>Cacomantis leucolophus</i>	White-crowned Cuckoo				X		X		hr	h
<i>Cacomantis castaneiventris</i>	Chestnut-breasted Cuckoo						X			
<i>Cacomantis flabelliformis</i>	Fan-tailed Cuckoo					X			hr	h,m
<i>Cacomantis flabelliformis/castaneiventris</i>	Fan-tailed/Chestnut-breasted Cuckoo			X						
TYTONIDAE										
<i>Tyto tenebricosa</i>	Sooty Owl							X		
STRIGIDAE										
<i>Ninox theomacha</i>	Papuan Boobook				X	X	X	X	hr	h
PODARGIDAE										
<i>Podargus ocellatus</i>	Marbled Frogmouth							X		
CAPRIMULGIDAE										
<i>Eurostopodus archboldi/Caprimulgus macrurus</i>	Archbold's/Large-tailed Nightjar			X						
AEGOTHELIDAE										
<i>Aegotheles insignis</i>	Feline Owlet-nightjar				X	X			hr	h
<i>Aegotheles albertisi</i>	Mountain Owlet-nightjar				X	X			hr	h
APODIDAE										
<i>Collocalia esculenta</i>	Glossy Swiftlet			X	X	X	X	X		

Scientific Name	English name	Status		Hides (BAA 1)			Moro (BAA 2)		New records ¹	Method ²
		IUCN	PNG	2005	WP C-D	WP E-G	Arakubi	KP107		
<i>Aerodramus [hirundinaceus]</i>	[Mountain] Swiftlet			X	X	X	X			
CORACIIDAE										
<i>Eurystomus orientalis</i>	Oriental Dollarbird						X			
ALCEDINIDAE										
<i>Melidora macrorrhina</i>	Hook-billed Kingfisher						X			
<i>Clytoceyx rex</i>	Shovel-billed Kookaburra				X				hr	h
<i>Dacelo gaudichaud</i>	Rufous-bellied Kookaburra						X			
<i>Todirhamphus sanctus</i>	Sacred Kingfisher						X	X		
<i>Syma megarhyncha</i>	Mountain Kingfisher				X				hr	h
<i>Syma megarhyncha/toro-toro</i>	Mountain/Yellow-billed Kingfisher						X			
BUCEROTIDAE										
<i>Rhyticeros plicatus</i>	Blyth's Hornbill		P				X			
CACATUIDAE										
<i>Probosciger aterrimus</i>	Palm Cockatoo		P				X			
<i>Cacatua galerita</i>	Sulphur-crested Cockatoo						X			
PSITTACIDAE										
<i>Psittarchas fulgidus</i>	Pesquet's Parrot	VU	P				X	X		
<i>Micropsitta bruijnii</i>	Red-breasted Pygmy Parrot				X				hr	s
<i>Trichoglossus haematodus</i>	Coconut Lorikeet						X	X		
<i>Lorius lory</i>	Black-capped Lory						X	X		
<i>Chamosyna wilhelminae</i>	Pygmy Lorikeet							X		
<i>Chamosyna papou</i>	Papuan Lorikeet			X	X	X				
<i>Oreopsittacus arfaki</i>	Plum-faced Lorikeet					X			hr	s
<i>Neopsittacus musschenbroekii</i>	Yellow-billed Lorikeet			X	X					
<i>Psittacella modesta</i>	Modest Tiger Parrot					X			hr,k	s
<i>Geoffroyus geoffroyi</i>	Red-cheeked Parrot						X			
<i>Geoffroyus simplex</i>	Blue-collared Parrot						X	X		
<i>Eclectus roratus</i>	Eclectus Parrot				X		X	X	hr	h
<i>Alisterus chloropterus</i>	Papuan King Parrot			X	X		X			
<i>Cyclopsitta gulemitertii</i>	Orange-breasted Fig Parrot							X		
<i>Cyclopsitta diophthalma</i>	Double-eyed Fig Parrot			?						

Scientific Name	English name	Status		Hides (BAA 1)			Moro (BAA 2)		New records ¹	Method ²
		IUCN	PNG	2005	WP C-D	WP E-G	Arakubi	KP107		
PITTIDAE										
<i>Erythropitta erythrogaster</i>	Red-bellied Pitta							X		
<i>Pitta sordida</i>	Hooded Pitta						X			
PTILONORHYNCHIDAE										
<i>Ailuroedus melanotis</i>	Spotted Catbird							X		
<i>Archboldia papuensis</i>	Archbold's Bowerbird	NT		X						
<i>Amblyornis macgregoriae</i>	MacGregor's Bowerbird				X				hr	b
MALURIDAE										
<i>Malurus alboscapulatus</i>	White-shouldered Fairywren						X	X		
<i>Clytomyias insignis</i>	Orange-crowned Fairywren			X	X					
MELIPHAGIDAE										
<i>Myzomela nigrita</i>	Papuan Black Myzomela							X		
<i>Glycichaera fallax</i>	Green-backed Honeyeater							X		
<i>Ptiloprora guisei</i>	Rufous-backed Honeyeater			X	X					
<i>Ptiloprora perstriata</i>	Grey-streaked Honeyeater					X			hr	s,m
<i>Xanthotis polygrammus</i>	Spotted Honeyeater							X		
<i>Xanthotis flaviventer</i>	Tawny-breasted Honeyeater						X	X		
<i>Melilestes megarhynchus</i>	Long-billed Honeyeater							X		
<i>Melipotes fumigatus</i>	Common Smoky Honeyeater			X	X	X				
<i>Timeliopsis fulvigula</i>	Olive Straightbill			X						
<i>Caligavis subfrenata</i>	Black-throated Honeyeater				X	X			hr	h,m
<i>Caligavis obscura</i>	Obscure Honeyeater						X	X		
<i>Melidectes belfordi</i>	Belford's Melidectes			X	X	X				
<i>Meliphaga mimikae</i>	Mottle-breasted Honeyeater							X		
<i>Meliphaga sp.</i>							X			
ACANTHIZIDAE										
<i>Pachycare flavogriseum</i>	Goldenface						X			
<i>Crateroscelis murina</i>	Rusty Mouse-warbler						X	X		
<i>Crateroscelis robusta</i>	Mountain Mouse-warbler			X	X	X				
<i>Sericornis papuensis</i>	Papuan Scrubwren			X	X	X				

Scientific Name	English name	Status		Hides (BAA 1)			Moro (BAA 2)		New records ¹	Method ²
		IUCN	PNG	2005	WP C-D	WP E-G	Arakubi	KP107		
<i>Sericornis nouhuysi</i>	Large Scrubwren			X	X	X				
<i>Sericornis perspicillatus</i>	Buff-faced Scrubwren			X	X					
<i>Sericornis arfakianus</i>	Grey-green Scrubwren							X	mo	m
<i>Gerygone ruficollis</i>	Brown-breasted Gerygone			X	X					
<i>Gerygone cinerea</i>	Ashy Gerygone			?						
<i>Gerygone chloronota</i>	Green-backed Gerygone						X			
<i>Gerygone palpebrosa</i>	Fairy Gerygone						X			
ORTHONYCHIDAE										
<i>Orthonyx novaeguineae</i>	Papuan Logrunner			X	X					
CNEMOPHILIDAE										
<i>Cnemophilus loriae</i>	Loria's Satinbird		P		X	[X]			hr	h
<i>Cnemophilus macgregorii</i>	Crested Satinbird		P			X			hr,k	s,m
<i>Loboparadisea sericea</i>	Yellow-breasted Satinbird		P	[X]						
MELANOCHARITIDAE										
<i>Melanocharis nigra</i>	Black Berrypecker						X	X		
<i>Melanocharis versteri</i>	Fan-tailed Berrypecker			X	X	X				
<i>Melanocharis striativentris</i>	Streaked Berrypecker			?						
<i>Oedistoma iliolophus</i>	Dwarf Longbill						X	X		
<i>Oedistoma pygmaeum</i>	Pygmy Longbill						X	X		
<i>Toxorhamphus novaeguineae</i>	Yellow-bellied Longbill						[X]			
<i>Toxorhamphus poliopterus</i>	Slaty-headed Longbill							X		
PARAMYTHIIDAE										
<i>Oreocharis arfaki</i>	Tit Berrypecker				X				hr	h
PSOPHODIDAE										
<i>Ptilorrhoa leucosticta</i>	Spotted Jewel-babbler			X	X					
<i>Ptilorrhoa castanonota</i>	Chestnut-backed Jewel-babbler						X	X		
MACHAERIRHYNCHIDAE										
<i>Machaerirhynchus nigripectus</i>	Black-breasted Boatbill			X	X	X				
ARTAMIDAE										
<i>Artamus maximus</i>	Great Woodswallow					X	X		hr	s
<i>Peltops montanus</i>	Mountain Peltops				X		X	X	hr	h
<i>Cracticus quoyi</i>	Black Butcherbird						X	X		

Scientific Name	English name	Status		Hides (BAA 1)			Moro (BAA 2)		New records ¹	Method ²
		IUCN	PNG	2005	WP C-D	WP E-G	Arakubi	KP107		
RHAGOLOGIDAE										
<i>Rhagologus leucostigma</i>	Mottled Whistler			X	X					
CAMPEPHAGIDAE										
<i>Coracina caeruleogrisea</i>	Stout-billed Cuckooshrike						X	X		
<i>Coracina longicauda</i>	Hooded Cuckooshrike			X	X	X				
<i>Coracina incerta</i>	Black-shouldered Cicadabird							[X]		
<i>Coracina schisticeps</i>	Grey-headed Cuckooshrike						X	X		
<i>Coracina montana</i>	Black-bellied Cuckooshrike			X	X			X		
<i>Lalage leucomela</i>	Varied Triller						X	X		
NEOSITTIDAE										
<i>Daphoenositta papuensis</i>	Papuan Sittella			X	X					
<i>Daphoenositta miranda</i>	Black Sittella				X	X			hr,k	s
EULACESTOMIDAE										
<i>Eulacestoma nigropectus</i>	Wattled Ploughbill			X	[X]					
OREOICIDAE										
<i>Aleadryas rufinucha</i>	Rufous-naped Whistler			X	X	X				
<i>Ornorectes cristatus</i>	Crested Pitohui						X	X		
PACHYCEPHALIDAE										
<i>Melanorectes nigrescens</i>	Black Pitohui				X	X			hr	h
<i>Pachycephala hyperythra</i>	Rusty Whistler							X		
<i>Pachycephala modesta</i>	Brown-backed Whistler			X	X	X				
<i>Pachycephala simplex</i>	Grey Whistler						X	X		
<i>Pachycephala soror</i>	Sclater's Whistler			X	X					
<i>Colluricincla megarhyncha</i>	Little Shrikethrush						X	X		
ORIOLIDAE										
<i>Pitohui dichrous</i>	Hooded Pitohui						X	X		
<i>Oriolus szalayi</i>	Brown Oriole						X			
RHIPIDURIDAE										
<i>Rhipidura leucophrys</i>	Willie Wagtail				X		X	X	hr	s
<i>Rhipidura rufiventris</i>	Northern Fantail						X			
<i>Rhipidura atra</i>	Black Fantail			X	X					
<i>Rhipidura hyperythra</i>	Chestnut-bellied Fantail						X			

Scientific Name	English name	Status		Hides (BAA 1)			Moro (BAA 2)		New records ¹	Method ²
		IUCN	PNG	2005	WP C-D	WP E-G	Arakubi	KP107		
<i>Rhipidura albolimbata</i>	Friendly Fantail			X	X	X				
<i>Rhipidura brachyrhyncha</i>	Dimorphic Fantail			X		X				
MONARCHIDAE										
<i>Symposiachrus axillaris</i>	Black Monarch			?				X		
<i>Monarcha frater</i>	Black-winged Monarch							X		
<i>Carterornis chrysomela</i>	Golden Monarch						X			
<i>Arses telescopthalmus</i>	Friiled Monarch						X	X		
CORVIDAE										
<i>Corvus tristis</i>	Grey Crow						X			
MELAMPITTIDAE										
<i>Melampitta lugubris</i>	Lesser Melampitta			X	X	X				
<i>Melampitta gigantea</i>	Greater Melampitta						X	X		
IFRITIDAE										
<i>Ifrita kowaldi</i>	Blue-capped Ifrit			X	X	X				
PARADISAEIDAE										
<i>Manucodia chalybatus</i>	Crinkle-collared Manucode		P					[X]		
<i>Phonygammus keraudrenii</i>	Trumpet Manucode		P				[X]		mo	s
<i>Paradigalla brevicauda</i>	Short-tailed Paradigalla		P	X						
<i>Astrapia mayeri</i>	Ribbon-tailed Astrapia	NT	P	X	X	X				
<i>Parotia carolae</i>	Queen Carola's Parotia		P					X		
<i>Parotia lawesii</i>	Lawes's Parotia		P	X						
<i>Pteridophora alberti</i>	King of Saxony Bird-of-paradise		P	X	X	X				
<i>Lophorina superba</i>	Superb Bird-of-paradise		P	X						
<i>Ptiloris magnificus</i>	Magnificent Riflebird		P				X			
<i>Epimachus fastosus</i>	Black Sicklebill	VU	P	X	X					
<i>Epimachus meyeri</i>	Brown Sicklebill		P	X	X	X				
<i>Diphyllodes magnificus</i>	Magnificent Bird-of-paradise		P				X	X		
<i>Paradisaea raggiana</i>	Raggiana Bird-of-paradise		P				X	X		
PETROICIDAE										
<i>Heteromyias albispecularis</i>	Ashy Robin				X	X			hr	h,m
<i>Poecilodryas albonotata</i>	Black-throated Robin				X	X			hr	h,m
<i>Peneothello sigillata</i>	White-winged Robin			[X]		X				

Scientific Name	English name	Status		Hides (BAA 1)			Moro (BAA 2)		New records ¹	Method ²
		IUCN	PNG	2005	WP C-D	WP E-G	Arakubi	KP107		
<i>Peneothello cyanus</i>	Slaty Robin			X	X					
<i>Peneothello bimaculata</i>	White-rumped Robin						X	X		
<i>Tregellasia leucops</i>	White-faced Robin							X		
<i>Pachycephalopsis polio-soma</i>	White-eyed Robin						X	X		
<i>Microeca papuana</i>	Canary Flyrobin			X	X	X				
<i>Eugerygone rubra</i>	Garnet Robin			X	X	X				
<i>Drymodes supercilialis</i>	Northern Scrub Robin						X	X		
<i>Amalocichla incerta</i>	Lesser Ground Robin			X	X					
HIRUNDINIDAE										
<i>Hirundo tahitica</i>	Pacific Swallow						X	X		
ZOSTEROPIDAE										
<i>Zosterops minor</i>	Black-fronted White-eye						X	X		
STURNIDAE										
<i>Mino dumontii</i>	Yellow-faced Myna						X			
TURDIDAE										
<i>Zoothera heinei</i>	Russet-tailed Thrush							X	mo	c
<i>Turdus poliocephalus</i>	Island Thrush			X						
DICAEIDAE										
<i>Dicaeum geelvinkianum</i>	Red-capped Flowerpecker						X	X		
NECTARINIIDAE										
<i>Leptocoma sericea</i>	Black Sunbird						X	X		
ESTRILDIDAE										
<i>Erythrura papuana</i>	Papuan Parrotfinch					X			hr,k	m
<i>Erythrura</i> sp.	Blue-faced/Papuan Parrotfinch				X				hr	h

¹ New records indicate birds recorded for the first time in 2015 at Hides Ridge (hr), the Moro area (mo) or for all of the Kikori Basin (k) and adjacent areas (including Mount Bosavi, Mount Moran, Mount Sisa) as surveyed previously during EIS, WWF or related surveys.

² Method of detection listed as seen (s), heard (h), mist netted (m) and/or photographed by camera trap (c).

Appendix 3.2. The location and operation times of mist nets at BAA 1 and BAA 2.

Site/Transect/ Net no.	Coordinates	Time open	Time closed	Time open	Time closed
BAA 1					
Transect H6		19/06/2015			
1	S5.91372° E142.69007°	6:45	16:15		
2	S5.91375° E142.69001°	6:45	16:15		
3	S5.91409° E142.68971°	7:00	15:50		
4	S5.91421° E142.68965°	7:00	15:50		
5	S5.91438° E142.68947°	7:15	15:30		
6	S5.91441° E142.68946°	7:15	15:30		
7	S5.91481° E142.68911°	7:25	15:15		
8	S5.91483° E142.68897°	7:25	15:15		
9	S5.91532° E142.68879°	7:35	14:45		
10	S5.91542° E142.68885°	7:35	14:45		
Transect H3		21/06/2015		22/06/2015	
1	S5.94349° E142.73941°	6:50	10:00	7:00	14:00
2	S5.94359° E142.73941°	6:50	10:00	7:00	14:00
3	S5.94380° E142.73963°	7:00	10:00	7:00	14:00
4	S5.94392° E142.73968°	7:00	10:00	7:00	14:00
5	S5.94431° E142.73952°	7:15	10:30	7:15	13:30
6	S5.94441° E142.73950°	7:15	10:30	7:15	13:30
7	S5.94454° E142.73918°	7:25	10:40	7:20	13:05
8	S5.94447° E142.73904°	7:25	10:40	7:20	13:05
9	S5.94500° E142.73889°	7:40	10:45	7:30	12:30
10	S5.94499° E142.73877°	7:40	10:45	7:30	12:30
Transect H4		24/06/2015			
1	S5.91849° E142.69529°	6:45	16:10		
2	S5.91873° E142.69510°	7:00	15:45		
3	S5.91887° E142.69502°	7:00	15:45		
4	S5.91918° E142.69498°	7:10	15:00		
5	S5.91937° E142.69503°	7:10	15:00		
6	S5.91978° E142.69512°	7:20	15:00		
7	S5.91987° E142.69512°	7:20	15:00		
8	S5.92025° E142.69520°	7:35	14:05		
9	S5.92046° E142.69530°	7:35	14:05		
10	S5.92093° E142.69498°	7:50	14:00		
11	S5.92078° E142.69492°	7:50	14:00		

Site/Transect/ Net no.	Coordinates	Time open	Time closed	Time open	Time closed
BAA 2					
Transect M3		3/07/2015		4/07/2015	
1	S6.44254° E143.22645°	6:50	12:15	6:55	11:15
2	S6.44181° E143.22711°	6:50	12:15	6:55	11:15
3	S6.44208° E143.22669°	7:00	12:30	7:00	11:30
4	S6.44213° E143.22663°	7:00	12:30	7:00	11:30
5	S6.44254° E143.22645°	7:15	12:40	7:10	11:45
6	S6.44264° E143.22641°	7:15	12:40	7:10	11:45
7	S6.44290° E143.22625°	7:20	12:45	7:20	12:00
8	S6.44338° E143.22618°	7:35	12:50	7:25	12:10
9	S6.44341° E143.22612°	7:35	12:50	7:25	12:10
10	S6.44363° E143.22593°	7:40	12:55	7:30	12:25

**CHAPTER 4 – CAMERA TRAP MONITORING OF
TERRESTRIAL BIRDS AND MAMMALS: A PILOT STUDY**

Iain Woxvold and Ken Aplin



The Forest Wallaby *Dorcopsulus* cf. *vanheurni* is a hunting-sensitive species

SUMMARY

Background and aims

Terrestrial birds and mammals are suitable for monitoring because they include a variety of species that are targeted by hunters, are sensitive to forest disturbance or to invasive species impacts, or are otherwise indicative of ecosystem health (for example top-order predators). Wildlife most at risk in Papua New Guinea (PNG) include a variety of 'charismatic' species such as wallabies, cassowaries and tree kangaroos, a number of which are listed by the IUCN as Threatened or Near Threatened with extinction. While many of these are large, they often occur at naturally low densities and are difficult to detect due to their avoidance of humans.

Camera traps are increasingly used to monitor terrestrial wildlife populations, and are particularly useful for detecting species occurring at naturally low density that are wary of humans; as a non-invasive, continuous sampling tool they provide a practical and unbiased method for sampling rare and elusive species. Here we describe the results of a pilot study conducted in June–July 2015 to test the effectiveness of camera traps in meeting the following objectives:

1. To monitor trends (increase/decrease) in wildlife populations in two Biodiversity Assessment Areas (BAAs) established on Hides Ridge (BAA 1) and on the Agogo Range near Moro (BAA 2).
2. To improve our understanding of bird and mammal diversity within the PNG LNG Upstream Project Area.

Major results

Twenty-one camera traps were deployed in BAA 1 and 24 in BAA 2 for a period of 5–9 days each. Data were logged for each species by counting the number of independent images ('events') taken by each camera. Event rates were used to generate a 'relative abundance index' (RAI) for individual species or species-groups of interest.

Combining data from both BAAs, 49 species (21 mammals, 28 birds) were photographed in 366 camera trap events. Most species were photographed on multiple occasions, including six mammals in more than 15 events and 10 birds in at least six events. Priority monitoring targets photographed on multiple occasions include the hunting-sensitive forest wallaby *Dorcopsulus cf. vanheurni* and a variety of marsupial carnivores, giant rats, large terrestrial hunting-sensitive birds and terrestrial insectivorous birds.

Species of conservation significance recorded on camera traps include Western Montane Tree Kangaroo (*Dendrolagus notatus*; IUCN Endangered), Papuan Eagle (*Harpyopsis novaeguineae*; IUCN Vulnerable), the forest wallaby *Dorcopsulus cf. vanheurni* (IUCN Near Threatened), New Guinea Quoll (*Dasyurus albopunctatus*; IUCN Near Threatened), Woolley's Three-striped Dasyure (*Myoictis leucura*; IUCN Data Deficient) and Greater Melampitta (*Melampitta gigantea*; restricted range). Despite extensive previous survey effort in the region, this pilot camera trapping study detected three mammal species and three bird species not previously recorded in the Kikori Basin.

Conclusions

These results clearly demonstrate the utility of camera trapping for documenting the true diversity of rare and elusive vertebrate fauna within large areas of forest. Moreover, given the brevity of this pilot study, it is predicted that statistically useful datasets will be collected for a variety of priority monitoring taxa under an expanded sampling protocol. Based on these results an expanded camera trapping program incorporating 40 cameras will be deployed for a period of 10–13 weeks in each BAA. Data obtained from such a program will provide a statistically robust dataset for detecting changes in populations of a group of conservation-significant species that is otherwise difficult to monitor.

INTRODUCTION

As a remotely operated, static sampling tool camera traps bring many advantages to wildlife monitoring studies (Pettorelli et al. 2010; O'Connell et al. 2011; Srbek-Araujo and Chiarello 2013):

- They run continuously for long periods without maintenance (up to 3+ months with the Reconyx cameras used in this program).
- They are particularly effective at sampling rare and elusive species.
- They are non-invasive and result in minimal environmental disturbance.
- They provide quantitative data that are sufficiently robust for use in statistical analysis.
- They eliminate observer bias, making the program suitable for transfer to different practitioners. They provide a cost effective method for conducting long-term monitoring programs.

Because of these benefits camera traps are increasingly used as an efficient and effective tool for monitoring terrestrial animal populations (O'Connell et al. 2011). For example, camera trap studies have been used to examine the influence of roads or edge effects on animal behaviour and abundance (Srbek-Araujo and Chiarello 2013), to compare use of different habitats (Pettorelli et al. 2010), to examine the impacts of hunting and disturbance (Datta et al. 2008; Jenks et al. 2011), to monitor feral animal populations (Bengsen et al. 2011a, b), to test the effectiveness of wildlife corridors (Gregory et al. 2014), or simply to detect the presence of rare and elusive species.

Terrestrial birds and mammals, particularly those that are hunted, are an excellent candidate monitoring group because changes in hunting pressure and the impacts of invasive species (including dogs) are among the most important processes to be considered during impact assessment for any major development in PNG forest environments. Species most at risk include a variety of 'charismatic' terrestrial birds and mammals, a number of which are IUCN Threatened or Near Threatened. While many of these are large, they often occur at naturally low densities and/or are difficult to detect due to their avoidance of humans. Examples include the Critically Endangered Long-beaked Echidna (*Zaglossus bartoni*), Endangered tree kangaroos (*Dendrolagus* spp.), Near Threatened forest wallabies (*Dorcopsulus* spp.) and cassowaries (*Casuarius* spp.).

Smaller birds and mammals that are not specifically targeted by hunters may also be sensitive to the impacts of invasive species or disturbance. For example, in other tropical regions insectivorous birds of the forest understorey are known to be sensitive to habitat degradation and fragmentation (e.g. Lambert 1992; Lambert and Collar 2002; Johns 1996; Thiollay 1997; Peh et al. 2005; Edwards et al. 2009). Though not well studied in New Guinea, many terrestrial birds found in the PNG LNG Upstream Project Area feed mainly on invertebrates and may be similarly susceptible to changes in the forest environment (for example through edge effects).

We will use camera trap arrays to meet two main objectives:

- First, to improve our understanding of bird and mammal diversity present in sampling areas—at the simplest level we anticipate that camera trapping will detect a number of rare and elusive species that are typically missed during rapid assessment biodiversity surveys.
- Second, to monitor population trends (increase/decrease) in target species over time and space (for example in relation to proximity to existing project facilities/infrastructure).

Here we describe the results of a pilot camera trapping study conducted in June–July 2015 to test the effectiveness of camera traps in detecting and monitoring wildlife populations within the Upstream Project Area.

METHODS

Study areas

The 2015 pilot camera trapping study was conducted in two Biodiversity Assessment Areas (BAAs). Camera traps (Reconyx PC850) were deployed in BAA 1 at Hides Ridge during 16–25 June, and in BAA 2 on the Agogo Range near Moro during 28 June–8 July. Each of the main survey areas was divided into two survey 'sites' that differed in elevation:

- Hides Ridge (BAA 1):
 - WP C–D: between Wellpad C and Wellpad D, at elevations of 2,160–2,365 m above sea level (asl).
 - WP E–G: between Wellpad E and Wellpad G, at 2,670–2,720 m asl.
- Moro area (BAA 2):
 - Arakubi: west of Arakubi Quarry and east of the pipeline ROW, at 1,020–1,045 m asl.
 - KP107: on the Agogo Range in the vicinity of KP 107, at 1,350–1,400 m asl.

Survey methods

Survey effort at these sites is shown in Table 4.1, and the position of camera traps is mapped in Figures 4, 6 and 7 of the Executive Summary.

Camera traps were deployed in forest at increasing distances from linear infrastructure clearings. Most camera traps were placed at least 50 m apart and at least 50 m from transects operated by other survey programs. Each camera trap was fixed to a tree at 10–20 cm above the ground to maximise the detectability of small as well as medium-sized and large bird and mammal species, and oriented along an animal trail or a confluence of trails that showed recent sign of animal activity. Trapping stations were not baited and most units were positioned away from obvious feeding stations (e.g. clusters of fallen fruit). Camera traps were programmed to take three images per trigger and to minimise the time delay between successive triggers (<2 seconds). All camera traps were deployed as soon as practical and left undisturbed (no visits) until collection on the last day of survey at each site. The positions of each camera trap and the dates and times that they were deployed are presented in Appendix 4.1.

Table 4.1. Camera trap survey effort.

	BAA 1 (Hides)		BAA 2 (Moro)	
	WP C–D	WP E–G	Arakubi	KP107
No. camera traps	12	9	6	18
Camera trap hours	1,638.5	1,515.5	1,037.25	3,643.75

Analysis

Camera trap data were logged for each species by counting the number of independent images (= 'events') taken by each camera. Images of the same species were considered independent when taken more than 30 minutes apart or where multiple individuals were recognisable within a single photograph or among photographs taken less than 30 minutes apart. Birds were identified by Woxvold and mammals by Aplin.

Photographic event rates were used to generate a 'relative abundance index' (RAI) for each camera for individual species or species-groups of interest. RAIs were calculated as: Number of events/camera trap hours x 100.

The potential effects of Project infrastructure on the presence/abundance of taxa of interest were explored visually by plotting the distribution of RAIs at varying distances from the nearest infrastructure clearing. Boxplots were generated to show the median, interquartile range and outlier RAIs within each of five 'distance classes': (D1) 0–50 m; (D2) 50–100 m; (D3) 100–200 m; (D4) 200–300 m; (D5) 300–400+ m.

Data from the pilot study are insufficient to perform the detailed statistical analyses (generalised additive mixed models) that will be applied to datasets collected from the full sampling design proposed for subsequent surveys.

Conventions

Where species are referred to in the text, the scientific name appears with the English name on first mention. For species whose identity and taxonomy are certain, only the English name is used in the text thereafter. The scientific name is used persistently in photographs and tables, and in the text for species whose identity or taxonomy are not well known (for example because photographs are insufficient to identify an animal to species level or where their relationship with closely related taxa is still under investigation).

RESULTS AND DISCUSSION

Overall results

Combining data from all four sites, 49 species were photographed in a total of 366 camera trap events. The number of events and cameras recording individual species at each site is presented in Appendix 4.2. Table 4.2 summarises the results for mammals and birds at each site.

Among mammals, 21 species were photographed in 236 camera trap events across all sites. Eight of the photographed taxa (38.1%) were recorded in both BAAs. The highest mammal diversity (14 species) was recorded at KP107 in BAA 2. Event rates (RAIs) were highest at Arakubi and KP107 in BAA 2 and lowest in the Wellpad E–G area on Hides Ridge in BAA 1 (Table 4.2).

Among birds, 28 species were photographed in 133 camera trap events across all sites. The highest number of bird species and the highest RAIs were recorded at KP107 in BAA 2 and in the Wellpad C–D area on Hides Ridge in BAA 1 (Table 4.2). There was a near-complete turnover in species composition among birds camera trapped at Hides Ridge and the Agogo Range, with only the Pheasant Pigeon (*Otidiphaps nobilis*) camera trapped at both BAAs (Appendix 4.2).

Notable mammal species recorded by camera trap are described in Chapter 5, and notable bird species in Chapter 3.

Table 4.2. Summary camera trap results for mammals and birds at each survey site.

	Hides		Moro		Totals
	WP C–D	WP E–G	Arakubi	KP107	
MAMMALS					
No. events	42	17	45	132	236
RAI*	2.56	1.12	4.34	3.62	3.01
No. species	9	10	9	14	21
BIRDS					
No. events	23	4	13	93	133
RAI*	1.40	0.26	1.25	2.55	1.70
No. species	9	3	6	17	28

* Calculated across all taxa within each group (mammals/birds).

Taxa suitable for camera trap monitoring

Monitoring population trends across time and space requires multiple photographs of individual target species from different cameras. Figures 4.1 and 4.2 show the number of events recorded for each mammal and bird species respectively.

Notwithstanding taxonomic uncertainties (the native rodents *Rattus* cf. *niobe* and *Paramelomys* spp. each represent more than one biological species that cannot be distinguished from the images; see Chapter 5), more than half of the mammal taxa recorded by camera trap were photographed on at least four independent occasions, with six species recorded in more than 15 events and two species in more than 40 events. Among birds, more than half of the species recorded were photographed more than once, with 10 species recorded in at least six events and two species in 17 events.

Given the brief operational period of camera trap arrays during this pilot study (5–9 nights per camera compared to the 2–3-month deployment period recommended for the full monitoring program), these results suggest that camera trapping presents a suitable monitoring approach for a variety of taxa that were frequently or regularly photographed. Examples are discussed below.

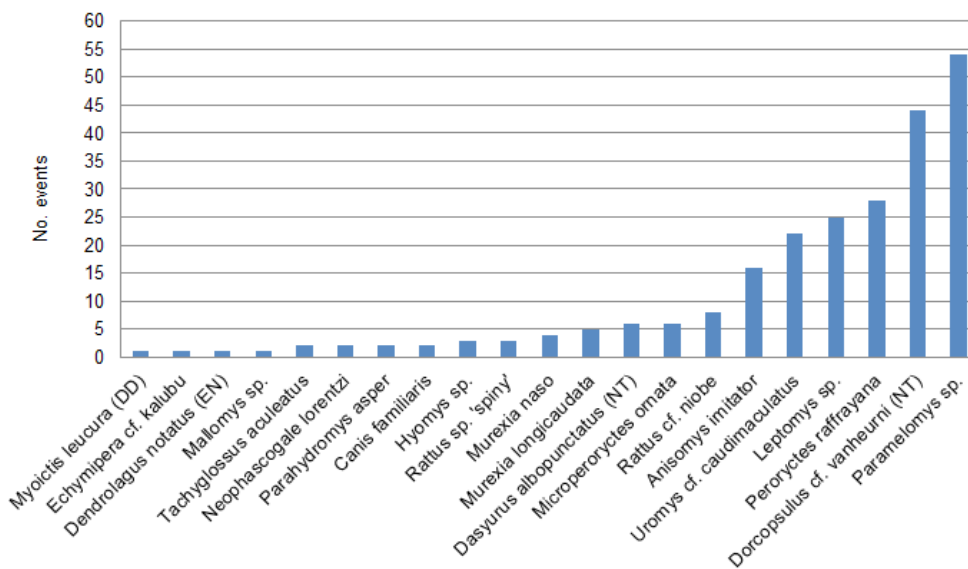


Figure 4.1. Number of camera trap events recorded for each mammal species. The following IUCN listings are indicated: EN—Endangered; NT—Near Threatened; DD—Data Deficient.

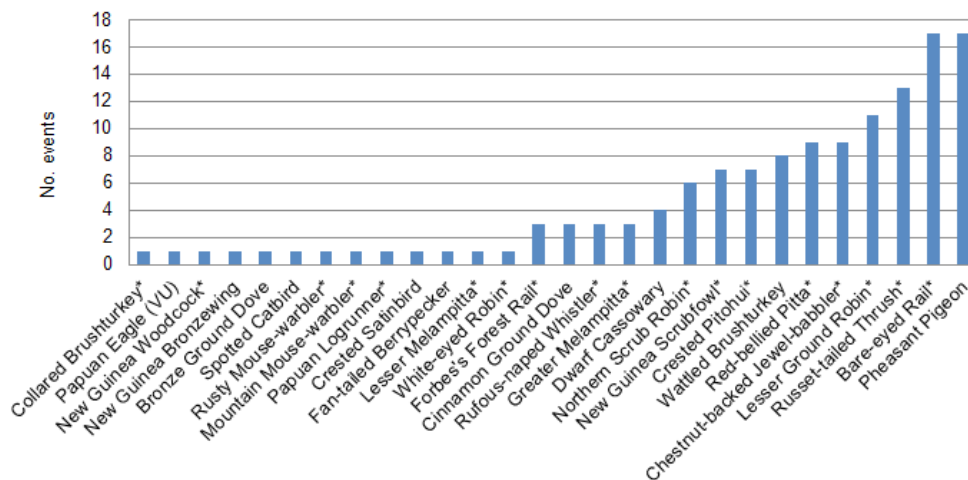


Figure 4.2. Number of camera trap events recorded for each bird species. The following IUCN listings are indicated: VU—Vulnerable. Species marked with an asterisk (*) include invertebrates as the major component of their diet.

Mammals

The following mammal taxa camera trapped on at least four occasions are considered to be priority monitoring targets due to their conservation status, hunting sensitivity and/or their ecological position (for example apex predators). Given the frequency of encounters, it is anticipated that statistically useful datasets will be acquired for these taxa under the full sampling protocol.

Forest wallaby (*Dorcopsulus cf. vanheurni*) (Figure 4.8). Populations of this IUCN Near Threatened wallaby are thought to be declining due to hunting and predation by dogs. This hunting-sensitive species was one of the most frequently imaged animals during the pilot study, with 44 events recorded across 16 cameras at all four survey sites (Appendix 4.2).

Figure 4.3 shows the distribution of RAIs for *Dorcopsulus cf. vanheurni* in each of the five distance classes. No wallabies were photographed within 100 m of an infrastructure clearing. While this pattern is suggestive of an ‘edge effect’ it may be an artefact of under-sampling. A more conclusive analysis will in future be possible with data from the full recommended sampling design.

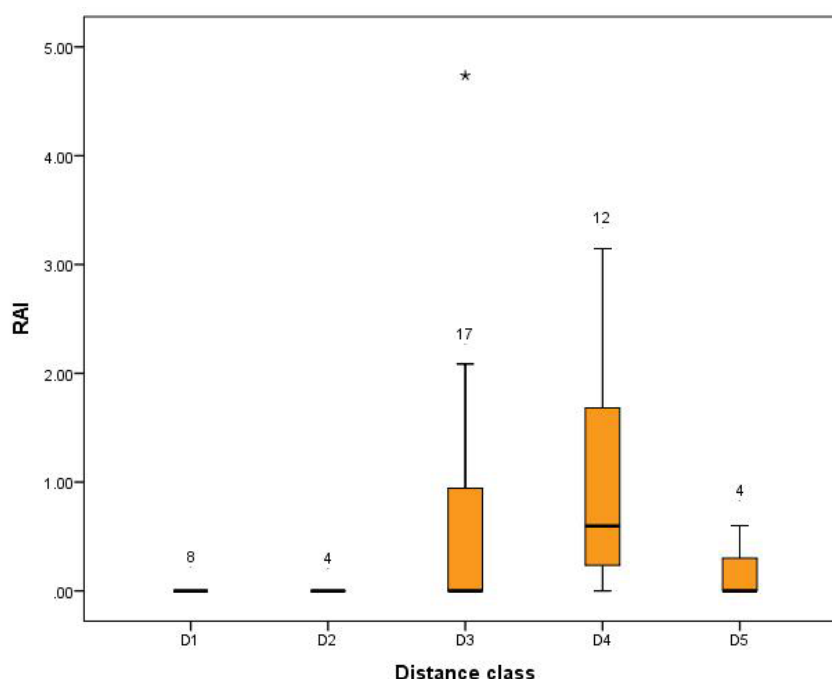


Figure 4.3. RAIs for *Dorcopsulus cf. vanheurni* in each of five distance classes. Distance from Project infrastructure increases from D1 to D5. The number of cameras in each distance class is shown atop each boxplot (the same sample sizes apply to all subsequent boxplot figures). Outliers are indicated with a star.

Marsupial carnivores. Five marsupial carnivores were photographed during the pilot study—the New Guinea Quoll (*Dasyurus albopunctatus*; IUCN Near Threatened), Long-nosed Murexia (*Murexia naso*), Short-furred Murexia (*M. longicaudata*), Woolley’s Three-striped Dasyure (*Myoictis leucura*; IUCN Data Deficient) and Speckled Dasyure (*Neophascogale lorentzi*). Despite their diminutive size, these species are New Guinea’s apex native mammalian predators—weighing less than 1 kg, the New Guinea Quoll (Figure 4.9) is the island’s largest native mammalian carnivore. As apex predators their abundance, both individually and as a group, is a good indicator of the abundance of their prey (birds, reptiles, small mammals and invertebrates) and thus of overall ecosystem health.

Figure 4.4 shows the distribution of pooled RAIs for all marsupial carnivores across the five distance classes. Multiple individuals were photographed in most distance classes, including within 50 m of infrastructure edge at two different sites. Additional data will allow more detailed analysis of patterns both across the group and within species.

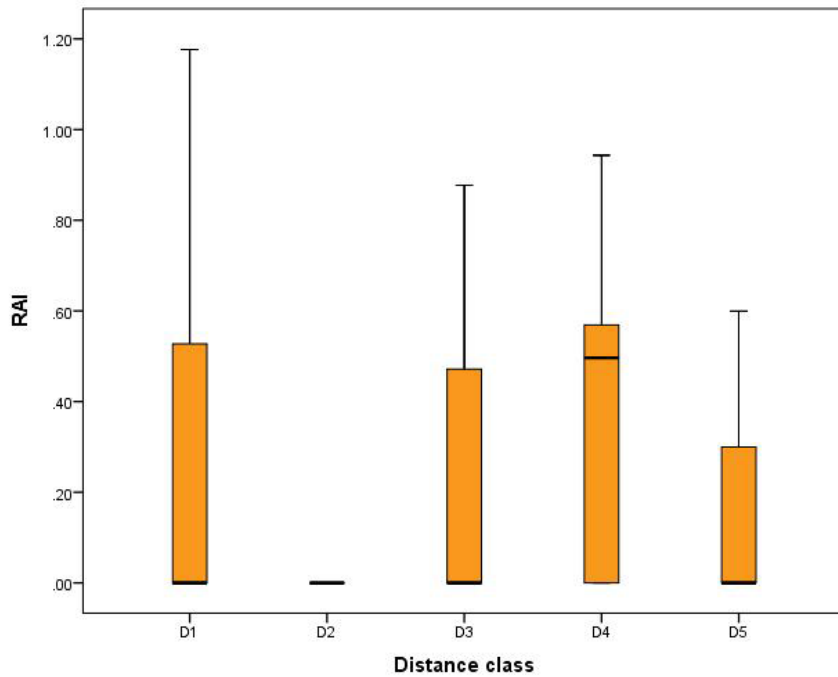


Figure 4.4. RAIs for marsupial carnivores in each of five distance classes.

Giant rats. The montane forests of PNG host a remarkable diversity of ‘giant’ rats, adults of which typically weigh 1–2 kg. All are herbivorous but little is yet known about their individual ecologies. Four species were imaged on camera traps, the most frequently recorded being White-tailed Giant Rat (*Uromys cf. caudimaculatus*) (22 events, 6 cameras, Arakubi and KP107 in BAA 2) and the Uneven-toothed Rat (*Anisomys imitator*) (16 events, 6 cameras, Wellpad C–D area in BAA 1 and KP107 in BAA 2; Figure 4.10). The high diversity of these specialised herbivores is another good indicator of the continuing robustness of these ecosystems.

Figure 4.5 shows the distribution of pooled RAIs for all giant rats across distance classes. Fewer events were recorded within 50 m of an infrastructure edge (D1), though this may be an artefact of under-sampling. A more conclusive analysis will in future be possible with data from full sampling protocols.

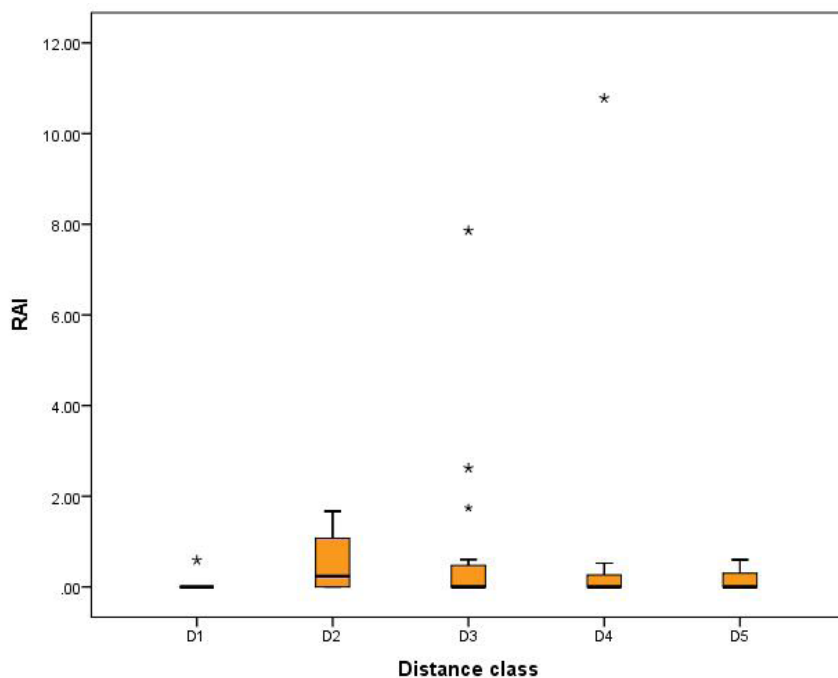


Figure 4.5. RAIs for giant rats in each of five distance classes.

Other frequently camera trapped mammals. Other mammals camera trapped at high frequency during the pilot study include Raffray’s Bandicoot (*Peroryctes raffrayana*; 28 events, 13 cameras, three sites) (Figure 4.11) and the native rats *Paramelomys* spp. (54 events, 18 cameras, all sites) and *Leptomys* sp. (25 events, 11 cameras at KP107). Raffray’s Bandicoot is a target for snaring by hunters, though its small size means that it is not a specific target for long-distance hunting forays. The native rats are not specifically targeted by hunters and are the subject of a separate monitoring study (Chapter 5). These species are not identified as target species for the camera trapping study and are not analysed further here. However, given that the high frequency of records may result in a statistically useful dataset, their populations may be analysed in future for potential effects of spatial and temporal variables of interest in support of other studies.

Birds

Most of the 15 bird species camera trapped on at least three occasions are considered to be suitable monitoring targets due to their hunting sensitivity and/or their ecological position within the ‘terrestrial insectivore’ dietary guild. Given the frequency of encounters, it is anticipated that statistically useful datasets will be acquired for a variety of target taxa.

Terrestrial hunting-sensitive birds. Four bird species susceptible to hunting were photographed on multiple occasions—Dwarf Cassowary (*Casuarius bennetti*), New Guinea Scrubfowl (*Megapodius decollatus*; Figure 4.18), Wattled Brushturkey (*Aepyptodius arfakianus*) and Pheasant Pigeon (*Otidiphaps nobilis*). The Collared Brushturkey (*Talegalla jobiensis*) was photographed once. All are medium-sized or large terrestrial species that are susceptible to trapping, direct capture or capture by dogs. The New Guinea Scrubfowl, Wattled Brushturkey and Collared Brushturkey are also ‘mound-building’ species (family Megapodiidae) whose eggs are regularly harvested from nest mounds (Jones et al. 1995; Sinclair et al. 2010). The Dwarf Cassowary (Figure 4.12) is heavily hunted in some areas; previously listed as Near Threatened by the IUCN, it has recently been reclassified as Least Concern as it remains secure in remote mountainous regions. It was photographed on four occasions (three cameras) at both sites in BAA 2, and the stability of the population in both BAAs will be actively monitored. The Pheasant Pigeon (Figure 4.17) was the most frequently camera trapped bird species with 17 events recorded on 10 cameras at three sites.

Figure 4.6 shows the distribution of pooled RAIs for all terrestrial hunting-sensitive birds across distance classes. Fewer events were recorded within 100 m of an infrastructure edge (D1 and D2 combined), though this may be an artefact of under-sampling. Additional data will allow more detailed analysis of patterns both across the group and within species.

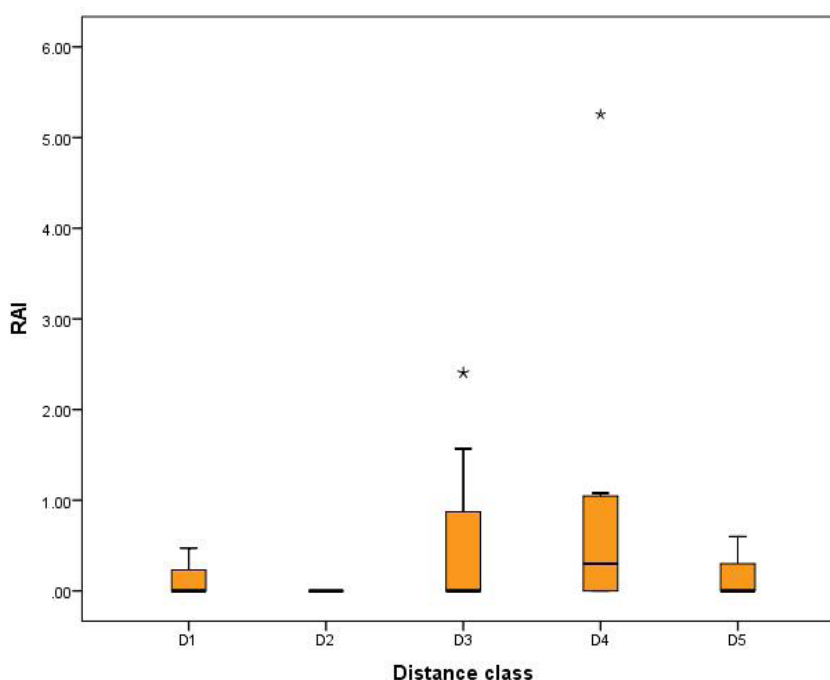


Figure 4.6. RAIs for terrestrial hunting-sensitive birds in each of five distance classes.

Terrestrial insectivores. Eleven species camera trapped on at least three occasions include invertebrates as the major component of their diet. Multiple species were recorded at each site, providing an opportunity to analyse data across species within a single dietary guild. Relevant taxa include five of the six most frequently photographed bird species (at least nine events)—Bare-eyed Rail (*Gymnocrex plumbeiventris*), Red-bellied Pitta (*Erythropitta erythrogaster*; Figure 4.19), Chestnut-backed Jewel-babbler (*Ptilorrhoa castanonota*), Lesser Ground Robin (*Amalocichla incertae*) and Russet-tailed Thrush (*Zoothera heinei*).

Of particular note within this dietary guild is the Greater Melampitta (*Melampitta gigantea*). This ‘restricted-range’ species is one of New Guinea’s most enigmatic birds, being restricted to rugged limestone country and known from only five localities in PNG (Coates 1990; Boles 2007). First recorded in the Agogo Range by Diamond and Bishop (2003), Greater Melampittas were photographed on three occasions (three cameras) at KP 107.

Figure 4.7 shows the distribution of pooled RAIs for all terrestrial insectivores (the 18 species marked as such in Figure 4.2) across distance classes. Across the group as a whole there is currently no evidence of an edge effect—multiple individuals were photographed in all distance classes, including within 50 m of infrastructure edge at two different sites. Additional data will allow more detailed analysis of patterns both across the group and within species.

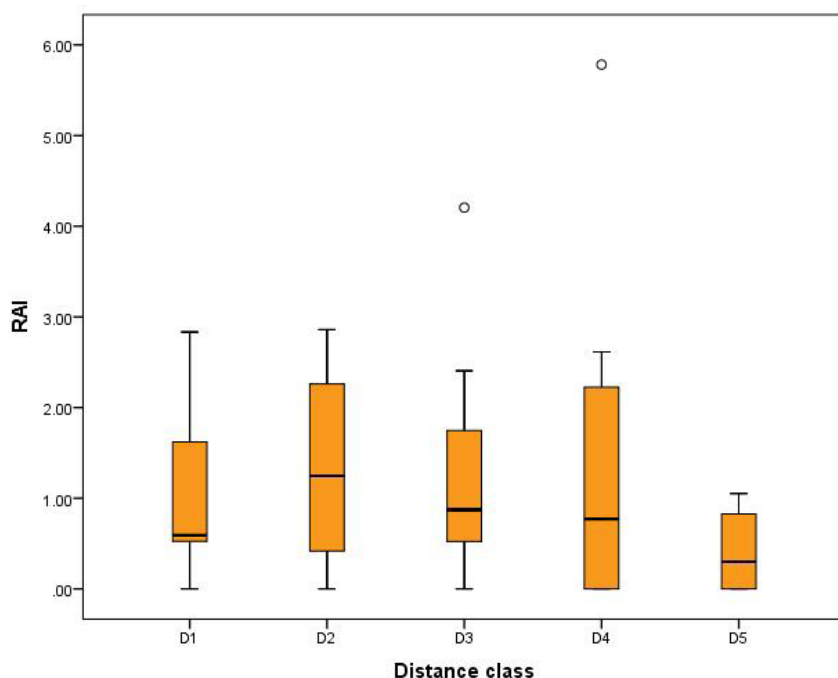


Figure 4.7. RAIs for terrestrial insectivores in each of five distance classes.

Occasionally camera trapped target species

In addition to the regularly photographed taxa described above, a number of mammal species camera trapped once or twice during the pilot study are considered suitable for monitoring due to their conservation status, hunting sensitivity and/or their ecological position. It is anticipated that camera trapping will continue to provide useful information on the presence of these species in the BAAs, though datasets suitable for statistical analysis of individual species may not be acquired at the current rate of recording.

Western Montane Tree Kangaroo (*Dendrolagus notatus*) (Figure 4.14). All tree kangaroo species are Protected under PNG law and are highly susceptible to hunting. This IUCN Endangered species is found in montane forest throughout the central ranges of PNG but in many areas its populations have been seriously depleted. One individual was camera trapped at 2,670 m asl in the Wellpad E–G area in BAA 1. This record indicates the continued presence of this highly sensitive and iconic species on Hides Ridge. This shy species is rarely recorded by direct search methods, and it is hoped that future camera trap monitoring will provide further information on its presence and abundance at this and other sites.

Short-beaked Echidna (*Tachyglossus aculeatus*) (Figure 4.15). Normally considered an 'Australian' species, the short-beaked Echidna is widely distributed in the southern lowlands of PNG but is rarely recorded in the highlands. It was photographed on two cameras at KP107 and Arakubi in BAA 2. Nothing is known about the ecology of this species in rainforest habitat and the Agogo Range population may provide an opportunity to obtain information that might assist in its wider conservation in PNG.

Wild/Domestic Dog (*Canis familiaris*). This invasive predator is implicated as a causal factor in the population declines of a variety of native species, including the forest wallaby *Dorcopsulus cf. vanheurni* known to be present in both BAAs. Two dogs were photographed, one in the Wellpad C–D area on Hides Ridge and one at KP107 in the Moro area. Monitoring the distribution and abundance of dogs in these areas will provide information useful in interpreting potential population shifts in locally occurring native species.

Species recorded for the first time in the Kikori Basin

Despite extensive prior survey effort (e.g. Hartshorn et al. 1995; Leary and Seri 1997; Diamond and Bishop 2003; Mamu et al. 2005; Woxvold and Crome 2005; Mamu 2008; Woxvold 2008), three mammal species and three bird species were recorded for the first time in the Kikori Basin, detected exclusively by this pilot camera trapping study (Table 4.3).

Newly recorded mammals include the Short-beaked Echidna, Speckled Dasyure and Woolley's Three-striped Dasyure. None of these species appears to be especially common, as would be expected from their high trophic level. The record of the Speckled Dasyure is a particularly significant range extension and the first occurrence of the species from the southern limestone mountains of PNG.

Among birds, two of the new records for the Kikori Basin are the Bare-eyed Rail (17 events) and the Russet-tailed Thrush (13 events), both of which appear to be fairly common at KP107 in BAA 2. Although this area had previously been surveyed on multiple occasions by two extremely competent ornithologists (Diamond and Bishop 2003), both of these birds are very elusive and their vocalisations remain unknown. The third new bird record for the basin is the New Guinea Woodcock (*Scolopax rosenbergii*), a rare and secretive inhabitant of montane forest; one was photographed in the Wellpad C–D area on Hides Ridge.

These results clearly demonstrate the utility of camera trapping in documenting the true diversity of rare and elusive vertebrate fauna. Continuing and expanding the program is predicted to detect the presence of a number of additional taxa.

Table 4.3. Mammals and birds (no. events) recorded for the first time in the Kikori Basin during the camera trapping pilot study.

Scientific Name	English Name	IUCN	Hides		Moro	
			WP C–D	WP E–G	Ara-kubi	KP107
MAMMALS						
<i>Tachyglossus aculeatus</i>	Short-beaked Echidna				1	1
<i>Myoictis leucura</i>	Woolley's Three-striped Dasyure	DD				1
<i>Neophascogale lorentzi</i>	Speckled dasyure			2		
BIRDS						
<i>Gymnocrex plumbeiventris</i>	Bare-eyed Rail					17
<i>Scolopax rosenbergii</i>	New Guinea Woodcock		1			
<i>Zoothera heinei</i>	Russet-tailed Thrush					13

CONCLUSIONS

1. The 2015 camera trapping pilot study was undertaken as an adjunct activity to other bird and mammal monitoring studies in order to examine the efficacy of this tool for monitoring wildlife populations in the PNG LNG Upstream Project Area.
2. Despite the limited number of camera traps used (6–18 per site), and their limited period of deployment (5–9 nights per camera at each site), nearly 50 bird and mammal species were recorded, 20 of which were photographed in at least five independent events. Photographed species also include a variety of rare and elusive taxa, some of which were not previously known to occur in the Kikori Basin.
3. Many of the taxa recorded are considered to be suitable monitoring targets due to their conservation status (for example IUCN Threatened or Near Threatened), hunting sensitivity, ecological position (for example apex predators) and/or their potential sensitivity to forest disturbance and associated edge effects (for example avian terrestrial insectivores).
4. Initial data exploration (using boxplots) suggests that some of these taxa may be less common close to Project infrastructure—for example the forest wallaby *Dorcopsulus cf. vanheurni* and large terrestrial hunting-sensitive birds. However, these initial patterns may be an artefact of under-sampling—more detailed analysis of a larger dataset is required.
5. These results demonstrate the efficacy of camera traps in documenting rare and elusive taxa, and suggest that statistically useful datasets may reasonably be expected from the full recommended sampling design.

REFERENCES

- Bengsen, A., Butler, J. & Masters, P. 2011a. Estimating and indexing feral cat population abundances using camera traps. *Wildlife Research* 38: 732–739.
- Bengsen, A., Leung, L. K.-P., Lapidge, S. J. & Gordon I. J. 2011b. Using a general index approach to analyse camera-trap abundance indices. *The Journal of Wildlife management* 75: 1222–1227.
- Boles, W. E. 2007. Eupetidae (Jewel-babblers and allies). Pp. 348–373 in (del Hoyo, J., Elliott, A. & Christie, D. eds) *Handbook of the Birds of the World. Volume 12: Picathartes to Tits and Chickadees*. Lynx Edicions, Barcelona.
- Coates, B. J. 1990. *The Birds of Papua New Guinea, Including the Bismarck Archipelago and Bougainville*. Volume II, Passerines. Dove Publications, Alderley, Queensland.
- Diamond, J. M. & Bishop, K. D. 2003. *Seasonality in birds in the Kikori River catchment: year-2003 Studies*. WWF KICDP area Report.
- Datta, A., Anand, M. O. & Naniwadekar, R. 2008. Empty forests: large carnivore and prey abundance in Namdapha National park, north-east India. *Biological Conservation* 141: 1429–1435.
- Edwards D. P., Ansell F. A., Ahmad A. H., Nlius R. & Hamer K. C. 2009. The value of rehabilitating logged rainforest for birds. *Conservation Biology* 6: 1628–1633.
- Gregory, T., Rueda, F. C., Deichmann, J., Kolowski, J. & Alonso, A. 2014. Arboreal camera trapping: taking a proven method to new heights. *Methods in Ecology and Evolution* 5: 443–451.
- Hartshorn, G. S., et al. 1995. *Field survey of biodiversity in the Kikori River Basin, Papua New Guinea*. WWF KICDP Area Report, 1995.

- Jenks, K. E., Chanteap, P., Damrongchainarong, K., Cutter, P., Cutter, P., Redford, T., Lynam, A. J., Howard, J. & Leimgruber, P. 2011. Using relative abundance indices from camera-trapping to test wildlife conservation hypotheses – an example from KhaoYai National Park, Thailand. *Tropical Conservation Science* 4: 113–131.
- Johns, A. G. 1996. Bird population persistence in Sabahan logging concessions. *Biological Conservation* 75: 3–10.
- Jones, D. N., Dekker, R. W. R. J. & Roselaar, C. S. 1995. *The megapodes: Megapodiidae*. Oxford University Press, Oxford.
- Lambert, F. R. 1992. The consequences of selective logging for Bornean lowland forest birds. *Phil. Trans. R. Soc. London Series B* 335: 443–457.
- Lambert, F. R. & Collar, N. J. 2002. The future for Sundaic lowland forest birds: long-term effects of commercial logging and fragmentation. *Forktail* 18: 127–146.
- Leary, T. & Seri, L. 1997. An annotated checklist of mammals recorded in the Kikori River Basin, Papua New Guinea. *Science in New Guinea* 23: 79-100.
- Mamu, T., Gebia, O., Enoch, I., Kuduk, M. & Ona, A. 2005. Report for an assessment survey of terrestrial mammals for PNG Gas Project, Papua New Guinea. Annex 3 in: Crome, F. H. J. et al. 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: The PNG LNG Project Environmental Impact Statement. Prepared by Coffey Natural Systems for Esso Highlands Limited.
- Mamu, T. 2008. Environmental Impact Study of Terrestrial Mammals for the PNG LNG Project, Papua New Guinea. Annex 4 in: Crome, F. H. J. et al. 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: The PNG LNG Project Environmental Impact Statement. Prepared by Coffey Natural Systems for Esso Highlands Limited.
- O'Connell, A. F., Nichols, J. D. & Karanth, K. U. (eds.) 2011. *Camera traps in animal ecology: methods and analyses*. Springer.
- Peh, K. S.-H., de Jong, J., Sodhi, N. S., Lim, S. L.-H., & Yap, C. A.-M. 2005. Lowland rainforest avifauna and human disturbance: persistence of primary forest birds in selectively logged forests and mixed-rural habitats of southern Peninsular Malaysia. *Biological Conservation* 123: 489–505.
- Pettorelli, N., Lobora, A. L., Msuha, M. J., Foley, C. & Durant, S. M. 2010. Carnivore biodiversity in Tanzania: revealing the distribution patterns of secretive mammals using camera traps. *Animal Conservation* 13: 131–139.
- Sinclair, J. R., Tuke, L. & Opiang, M. 2010. What the locals know: comparing traditional and scientific knowledge of megapodes in Melanesia. Pp. 115–137 in Tidemann, S. & Gosler, A. (eds) *Ethno-ornithology: birds, indigenous peoples, culture and society*. Earthscan, London.
- Srbek-Araujo, A. C. & Chiarello, A. G. 2013. Influence of camera-trap sampling design on mammal species capture rates and community structures in southeastern Brazil. *Biota Neotropica* 13: 51–62.
- Thiollay, J.-M. 1997. Disturbance, selective logging and bird diversity: a Neotropical forest study. *Biodiversity and Conservation* 6: 1155–1173.
- Woxvold, I. A. & Crome, F. H. J. 2005. A report on the Avifauna of the Papua New Guinea Gas project area. Annex 7 in: Crome, F. H. J. et al. 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: The PNG LNG Project Environmental Impact Statement. Prepared by Coffey Natural Systems for Esso Highlands Limited.
- Woxvold, I. A. 2008. Avifauna of the upstream portion of the PNG LNG Project, Southern highlands and Western Provinces, Papua New Guinea. Annex 8 in: Crome, F. H. J. et al. 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: The PNG LNG Project Environmental Impact Statement. Prepared by Coffey Natural Systems for Esso Highlands Limited.

Mammals and birds photographed by camera traps



Figure 4.8. Adult and juvenile forest wallabies (*Dorcopsulus* cf. *vanheurni*) photographed at KP107.



Figure 4.9. New Guinea Quoll (*Dasyurus albopunctatus*) camera trapped at KP107.



Figure 4.10. Uneven-toothed Rat (*Anisomys imitator*) camera trapped in the Wellpad C-D area on Hides Ridge.



Figure 4.11. Raffray's Bandicoot (*Peroryctes raffrayana*) camera trapped at KP107.



Figure 4.12. Dwarf Cassowary (*Casuaris bennetti*) camera trapped at KP107.



Figure 4.13. Crested Pitohui (*Ornorectes cristatus*).

Mammals and birds photographed by camera traps



Figure 4.14. Western Montane Tree Kangaroo (*Dendrolagus notatus*) camera trapped at Wellpad E–G area on Hides Ridge.



Figure 4.15. Short-beaked Echidna (*Tachyglossus aculeatus*) camera trapped at KP107.



Figure 4.16. Northern Scrub Robin (*Drymodes superciliaris*)



Figure 4.17. Pheasant Pigeon (*Otidiphaps nobilis*)



Figure 4.18. New Guinea Scrubfowl (*Megapodius decollatus*)



Figure 4.19. Red-bellied Pitta (*Erythropitta erythrogaster*)

Appendix 4.1. Location and timing of camera traps.

BAA/Site/ camera number	Coordinates	Elevation (m asl)	Time on	No. nights	Hours run
BAA 1					
WP C–D					
C1	S5.94120° E142.74162°	2,255	20/6, 16:00	5	114.50
C2	S5.94212° E142.74254°	2,255	20/6, 16:35	5	114.25
C4	S5.94204° E142.74181°	2,270	20/6, 09:45	5	120.50
C5	S5.94156° E142.74221°	2,260	20/6, 10:10	5	120.50
C14	S5.97472° E142.75131°	2,170	16/6, 15:45	6	143.50
C16	S5.94149° E142.74173°	2,260	20/6, 15:45	5	114.75
C17	S5.94132° E142.74188°	2,255	20/6, 16:00	5	114.50
C18	S5.94192° E142.74266°	2,250	20/6, 16:45	5	114.00
C19	S5.94517° E142.73832°	2,340	16/6, 16:35	9	209.25
C22	S5.94219° E142.74153°	2,280	20/6, 10:30	5	119.75
C23	S5.94462° E142.73850°	2,365	16/6, 16:00	9	209.75
C24	S5.97487° E142.75180°	2,175	16/6, 16:15	6	143.25
Subtotal				70	1,638.50
WP E–G					
C7	S5.91817° E142.69460°	2,700	16/6, 13:45	7	169.00
C8	S5.91543° E142.68810°	2,715	16/6, 10:30	7	168.75
C9	S5.92140° E142.69424°	2,670	16/6, 12:55	7	165.75
C10	S5.91525° E142.68859°	2,720	16/6, 11:00	7	168.25
C11	S5.91610° E142.69183°	2,715	16/6, 12:00	7	170.00
C12	S5.91552° E142.68769°	2,700	16/6, 10:45	7	168.75
C13	S5.91621° E142.69187°	2,720	16/6, 12:15	7	169.75
C15	S5.92106° E142.69442°	2,670	16/6, 12:30	7	166.25
C20	S5.91819° E142.69444°	2,700	16/6, 13:50	7	169.00
Subtotal				63	1,515.50
BAA 2					
KP107					
C1	S6.44309° E143.22673°	1,360	28/6, 15:05	9	212.00
C2	S6.44367° E143.22473°	1,385	28/6, 14:40	9	212.00
C3	S6.43911° E143.22143°	1,400	29/6, 13:35	8	191.50
C4	S6.44350° E143.22541°	1,375	28/6, 14:15	9	212.50
C6	S6.43791° E143.22418°	1,370	29/6, 10:30	9	216.00

BAA/Site/ camera number	Coordinates	Elevation (m asl)	Time on	No. nights	Hours run
C7	S6.43822° E143.22087°	1,395	29/6, 14:15	8	190.75
C8	S6.43765° E143.22134°	1,390	29/6, 14:45	8	190.00
C10	S6.43903° E143.22121°	1,405	29/6, 15:05	8	190.00
C11	S6.43901° E143.22233°	1,390	29/6, 11:20	8	193.00
C13	S6.43862° E143.22390°	1,355	29/6, 10:40	9	216.00
C16	S6.43733° E143.22282°	1,370	29/6, 12:15	8	191.75
C17	S6.44361° E143.22560°	1,365	28/6, 14:05	9	212.75
C18	S6.44280° E143.22759°	1,350	28/6, 15:30	9	211.75
C19	S6.43728° E143.22286°	1,370	29/6, 12:50	8	191.25
C20	S6.43671° E143.22161°	1,375	29/6, 14:35	8	190.25
C21	S6.43776° E143.22260°	1,380	29/6, 13:00	8	191.25
C22	S6.44285° E143.22676°	1,350	28/6, 13:05	9	214.00
C23	S6.43944° E143.22364°	1,380	29/6, 09:45	9	217.00
Subtotal				153	3,643.75
Arakubi					
C5	S6.46149° E143.25227°	1,040	30/6, 15:25	8	185.25
C9	S6.46285° E143.25436°	1,030	1/7, 10:45	7	166.50
C12	S6.46157° E143.25244°	1,035	30/6, 15:20	8	185.50
C14	S6.46227° E143.25308°	1,045	1/7, 10:05	7	167.00
C15	S6.46307° E143.25506°	1,020	1/7, 11:00	7	166.25
C24	S6.46281° E143.25381°	1,035	1/7, 10:30	7	166.75
Subtotal				44	1,037.25
Total				260	6,196.50

Appendix 4.2. Camera trap records for all bird and mammal species from sites in the Hides Ridge and Moro area AAs.

Numbers show the number of independent photographic 'events' for each species (see Methods) and the number of camera traps where more than one event was recorded. Conservation status is given for species: (1) listed by the IUCN as (in descending order of conservation status) Endangered (EN), Vulnerable (VU), Near Threatened (NT) or Data Deficient (DD), and; (2) Protected (P) under PNG law. RAIs are summarised for each site as: total number of events/total camera trap hours x 100.

Scientific Name	English Name	Status		Hides (BAA 1)		Moro (BAA 2)		Totals
		IUCN	PNG	WP C-D	WP E-G	Arakubi	KP107	
MAMMALS								
<i>Tachyglossus aculeatus</i>	Short-beaked Echidna					1	1	2(2)
<i>Dasyurus albopunctatus</i>	New Guinea Quoll	NT			1	2(2)	3(3)	6(6)
<i>Murexia naso</i>	Long-nosed Murexia			3(3)	1			4(4)
<i>Murexia longicaudata</i>	Short-furred Murexia					2(2)	3(2)	5(4)
<i>Myoictis leucura</i>	Woolley's Three-striped Dasyure	DD					1	1
<i>Neophascogale lorentzi</i>	Speckled dasyure				2(1)			2(1)
<i>Echymipera cf. kalubu</i>	An Echymipera					1		1
<i>Microperoryctes ornata</i>	Eastern Striped Bandicoot			3(3)	1		2(2)	6(6)
<i>Peroryctes raffrayana</i>	Raffray's Bandicoot			3(3)	3(3)		22(7)	28
<i>Dendrolagus notatus</i>	Western Montane Tree Kangaroo	EN	P		1			1
<i>Dorcopsulus cf. vanheurni</i>	A forest wallaby	NT		2(1)	2(2)	6(4)	34(9)	44(16)
<i>Anisomys imitator</i>	Uneven-toothed Rat			15(5)			1	16(6)
<i>Hyomys sp.</i>	A white-eared giant rat			2(2)	1			3(3)
<i>Leptomys sp.</i>	A Leptomys						25(11)	25(11)
<i>Mallomys sp.</i>	A Woolly Giant Rat					1		1
<i>Parahydromys asper</i>	Waterside Rat						2(2)	2(2)
<i>Paramelomys spp.</i>	Several Paramelomys species			12(3)	2(1)	10(4)	30(10)	54(18)
<i>Rattus cf. niobe</i>	Native rats			1	3(2)		4(3)	8(6)
<i>Rattus sp. 'spiny'</i>	An undescribed native rat					3(1)		3(1)
<i>Uromys cf. caudimaculatus</i>	White-tailed Giant Rat					19(3)	3(3)	22(6)
<i>Canis familiaris</i>	Wild/Domestic Dog			1			1	2(2)
No. events				42	17	45	132	236
RAI				2.56	1.12	4.34	3.62	3.01
No. species				9	10	9	14	21
BIRDS								
<i>Casuarus bennetti</i>	Dwarf Cassowary					3(2)	1	4(3)
<i>Aepyodius arfakianus</i>	Wattled Brushturkey						8(5)	8(5)
<i>Talegalla jobiensis</i>	Collared Brushturkey						1	1
<i>Megapodius decollatus</i>	New Guinea Scrubfowl			1		4(1)	2(1)	7(3)
<i>Harpyopsis novaeguineae</i>	Papuan Eagle	VU	P	1				1

Scientific Name	English Name	Status		Hides (BAA 1)		Moro (BAA 2)		Totals
		IUCN	PNG	WP C-D	WP E-G	Arakubi	KP107	
<i>Rallicula forbesi</i>	Forbes's Forest Rail			3(2)				3(2)
<i>Gymnocrex plumbeiventris</i>	Bare-eyed Rail						17(7)	17(7)
<i>Scolopax rosenbergii</i>	New Guinea Woodcock			1				1
<i>Henicophaps albifrons</i>	New Guinea Bronzewing						1	1
<i>Gallicolumba rufigula</i>	Cinnamon Ground Dove					1	2(1)	3(2)
<i>Gallicolumba beccarii</i>	Bronze Ground Dove						1	1
<i>Otidiphaps nobilis</i>	Pheasant Pigeon			2(2)		1	14(7)	17(10)
<i>Erythropitta erythrogaster</i>	Red-bellied Pitta						9(5)	9(5)
<i>Ailuroedus melanotis</i>	Spotted Catbird						1	1
<i>Crateroscelis murina</i>	Rusty Mouse-warbler						1	1
<i>Crateroscelis robusta</i>	Mountain Mouse-warbler			1				1
<i>Orthonyx novaeguineae</i>	Papuan Logrunner			1				1
<i>Cnemophilus macgregorii</i>	Crested Satinbird				1			1
<i>Melanocharis versteri</i>	Fan-tailed Berrypecker			1				1
<i>Ptilorrhoa castanonota</i>	Chestnut-backed Jewel-babbler					2(2)	7(5)	9(7)
<i>Aleadryas rufinucha</i>	Rufous-naped Whistler			1	2(2)			3(3)
<i>Ornorectes cristatus</i>	Crested Pitohui						7(5)	7(5)
<i>Melampitta lugubris</i>	Lesser Melampitta				1			1
<i>Melampitta gigantea</i>	Greater Melampitta						3(3)	3(3)
<i>Pachycephalopsis poliosoma</i>	White-eyed Robin						1	1
<i>Drymodes superciliaris</i>	Northern Scrub Robin					2(2)	4(3)	6(5)
<i>Amalocichla incerta</i>	Lesser Ground Robin			11(5)				11(5)
<i>Zoothera heinei</i>	Russet-tailed Thrush						13(9)	13(9)
No. events				23	4	13	93	133
RAI				1.40	0.26	1.25	2.55	1.70
No. species				9	3	6	17	28

CHAPTER 5 – NON-VOLANT MAMMALS (RODENTS AND MARSUPIALS)

Ken Aplin and Muse Opiang



The Speckled Dasyure, *Neophascogale cf. lorentzi* is a poorly-known marsupial that was encountered in the forests on Hides Ridge

SUMMARY

Backgrounds and aims

The non-volant mammal fauna of New Guinea is a good target group for environmental monitoring because it is moderately diverse, relatively well-known, includes species of variable sensitivity to disturbance (some even benefiting), is relatively easy to survey using well-proven methods, and includes several species of conservation significance. The contemporary non-volant mammal assemblage also includes a range of exotic species that might themselves have deleterious impacts on the native mammal community and general habitat condition.

The principal aims of the non-volant mammal study are: 1) to monitor the specific impact of the linear right-of-way (ROW) infrastructure on the non-volant mammal communities, as an indicator of more general ROW impacts; 2) to assess the usefulness of non-volant mammal communities more broadly as potential indicators of change in habitat quality in each of the BAAs; and 3) to monitor the status of exotic mammal species in each of the BAAs.

Other objectives that align with the broader aims of the Biodiversity Strategy are: 1) to contribute to knowledge of small mammal diversity and distributions within each of the BAAs; 2) to identify non-volant mammal species of conservation concern (including new or undescribed species) within each of the BAAs and, where practicable, determine their special sensitivities; and 3) to contribute to knowledge of the local ecology of exotic non-volant mammals within each of the BAAs, and, where practicable, determine their potential vulnerabilities.

Major results

Twenty-eight species of non-volant mammals were recorded in BAA 1 and BAA 2 by a combination of trapping and deployment of camera traps during the 2015 field surveys. A further 21 species are represented in a 'modern' owl roost assemblage that was collected in BAA 1 in 2011. The non-volant mammal community appears to be substantially if not wholly intact in both BAAs, at least in terms of species inventories for terrestrial and scansorial (ground dwellers that also climb) mammals. The status of arboreal mammals was not assessed in any systematic manner.

Four of the non-volant mammals recorded from the BAAs are of conservation concern: *Dendrolagus notatus* – IUCN Endangered and PNG Fauna Act Protected; *Dorcopsulus cf. vanheurni* – IUCN Near Threatened; *Dasyurus albopunctatus* – IUCN Near Threatened; and *Myoictis leucura* – IUCN Data Deficient.

The use of genetic methods for species delineation and identification proved invaluable, as it revealed the presence of morphologically cryptic species in each of the rodent genera *Rattus* and *Paramelomys*. Accurate documentation of species diversity is not only important for biodiversity conservation but it also increases the utility of the mammal community as an indicator of environmental change. Genetic comparisons also demonstrated a close relationship between many of the species captured in the BAAs and other regional populations. However, two of the species detected by genetic analysis are currently known only from the study sites—*Paramelomys cf. rubex* B from KP107 in BAA 2 on the Agogo Range and *Paramelomys cf. mollis* C from BAA 1 on Hides Ridge. It is possible that one or both of these species will be shown to occur elsewhere through further genetic analysis of regional samples already in hand.

The following species are either known to be undescribed or are potentially undescribed (prefixed * i.e. they lack a prior scientific name): **Dorcopsulus cf. vanheurni*; *Rattus cf. niobe* B and *Rattus cf. niobe* D; *Paramelomys cf. mollis* A and/or *Paramelomys cf. mollis* C; *Paramelomys cf. rubex* A; **Rattus* sp. 'spiny'; and *Uromys cf. caudimaculatus*.

Other results of special note include the confirmed survival in BAA 1 of the Endangered Western Montane Tree Kangaroo (*Dendrolagus notatus*) and its occurrence within 200–250m of the ROW; the occurrence of the Near Threatened Small Forest Wallaby (*Dorcopsulus cf. vanheurni*) in both BAAs and its apparent high population density in BAA 2; and the occurrence of the Speckled Dasyure (*Neophascogale cf. lorentzii*) in BAA 1 (a range extension and the first record of this species off the central cordillera of New Guinea).

Statistical analysis of the mammal trapping results indicate that rodents of the genus *Paramelomys* are less common within 100–150 m of the ROWs in both BAAs, whereas the abundance of native *Rattus* species appears to be unaffected by proximity of the ROW. The actual cause of any impact (e.g. increased noise or sunlight, depletion of food resources) is not known.

Two of the nine sites investigated in 2015 appear to host less diverse small mammal faunas than expected: 1) transect H5 in the upper elevational zone in BAA 1 where numerous large trees have fallen in recent years, most likely due to strong winds; and 2) Arakubi Quarry in BAA 2 where low trap capture rates and the apparent absence or low numbers of species that were expected to occur at this elevation may reflect the long history of disturbance at this infrastructure site.

Comparison of the 2015 trapping results with the owl roost mammal assemblage collected on Hides Ridge in 2011 (prior to construction of the ROW) reveals some notable differences in composition that might be indicative of more pervasive changes in the small mammal community. Most notably, this includes a possible increase in the relative abundance of disturbance tolerant species of the genus *Rattus* over a range of less tolerant rodent species. Further data is needed to confirm and interpret these differences—firstly from within BAA 1 to establish the extent of any changes; and secondly from more remote ‘control’ sites to determine whether any changes are related to the ROW rather than an unrelated external factor such as climate change.

Invasive rodents (Pacific Rat, *Rattus exulans*) were detected close to the ROW at KP107 in BAA 2 but were not detected in BAA 1. However, a second species of invasive rodent (Black Rat, *Rattus rattus*) was recorded at the Hides Gas Conditioning Plant; this species represents a potential biosecurity risk.

Feral dogs are active across the full elevational range in BAA 1. They appear to use the ROW to facilitate movement across the rugged landscape and are preying on the IUCN Near Threatened Small Forest Wallaby and possibly other species of conservation concern. Increased predation on native herbivores could potentially lead to a cascade of wider indirect impacts on plant and animal communities.

Conclusions

The non-volant mammal community appears to be substantially if not wholly intact in both BAAs and there is evidence for the local persistence of populations of mammal species of high conservation value and considerable sensitivity. Even so, trapping results from the first survey revealed subtle ROW impacts on some elements of the non-volant mammal fauna in both BAAs. Additionally, in BAA 2 an exotic rodent species was detected along the margin of the ROW. On a more general level, comparison of the 2015 survey results for BAA 1 with the contents of a pre-construction bone deposit hints at a possibly more general shift toward disturbance tolerant species at the expense of more sensitive species on Hides Ridge.

The potential cause/s of the documented and/or suspected impacts remains unclear. However, one possible factor worthy of closer scrutiny is increased wild dog predation on the larger herbivorous mammals with an associated ecological cascade, potentially related to improved dog access along the ROW. Spread of exotic rodent species is more likely a symptom rather than a cause of changes in the mammal community but this balance could shift if their spread is not managed.

In addition to continuing the current mammal sampling regime, the following additional actions may be appropriate:

1. Establish a second trap-line at Arakubi Quarry to provide trap-line replication for the lower elevational band in BAA 2;
2. Further investigate the possible extent of habitat changes in the lower elevational band in BAA1 by resampling the owl roost site for remains accumulated since 2011, or if this is not possible, by some targeted trapping for key species.
3. Investigate potential regional ‘control’ sites that would allow for more precise differentiation between ROW impacts (and any other project impacts) and broader changes due to external factors including climate change.
4. Continue with a genetic approach to species delineation and identification.

INTRODUCTION

The non-volant (non-flying) native mammal fauna of New Guinea includes members of three different groups—the ancient egg-laying monotremes (the echidnas), the pouched marsupials (including tree kangaroos, cuscuses and bandicoots), and the placental mammals (all rats and mice but including many highly specialized forms; bats and humans also belong to this group). Almost all of New Guinea’s non-volant mammal species occur nowhere else in the world and many are confined to specific habitat types or geographic features such as particular mountain ranges (Flannery 1995).

Although New Guinea’s mammals have attracted scientific interest since the early 1800s, large areas of the island are still biologically unexplored. Not surprisingly, new species of mammals turn up regularly, with 15 species described in the last decade alone (Aplin 2015).

Most of New Guinea’s non-volant mammals are sensitive to environmental disturbance and many are of conservation concern. However, a few species seem to benefit from disturbance, most notably some of the native rodents. This mixture of disturbance-sensitive and disturbance-tolerant species makes the non-volant mammals especially valuable as environmental indicators. Fortunately, they are also relative easy to monitor through standard methods such as live-capture and camera trapping.

New Guinea also supports populations of a range of exotic mammals. Some of these, including the pig, dog and Pacific Rat, arrived in prehistoric times. Others, such as the cat, deer, and several other kinds of rats and mice, came to New Guinea during the colonial period. Most of the exotic species are still spreading, often by first colonizing disturbed habitats and later expanding into more natural habitats. The threats posed by these exotic species to natural environments include habitat destruction, competition with native animals for resources, predation on native species, and the introduction of new parasites and diseases into naïve animal communities.

Roadways and other ROWs can facilitate the rapid dispersal of exotic mammals. In the case of exotic rodents, dispersal might occur either through repeated small scale natural movements or by long-distance carriage in freight or vehicles. Populations of exotic rodents that become established along the ROW are likely to interact with native species creating the potential for pathogen transfer into naïve animal communities. Feral dogs, cats and pigs may use the more open conditions along ROWs to disperse into previously unoccupied areas or to access previously remote areas on a more regular basis.

Study objectives

The overall aim of this study was to document and interpret observed changes in non-volant mammal species diversity and abundance in order to provide informed advice about potential project-related impacts.

To achieve this aim the study has six major objectives:

1. To document small mammal diversity (used here to mean the simple tally of different species; this is sometime given the more formal name of Species Richness) and abundances within each of the BAAs.
2. To identify non-volant mammal species of conservation significance (including new or undescribed species) within each of the BAAs and, where practicable, determine their special sensitivities.
3. To monitor the status of exotic mammal species in each of the BAAs.
4. To contribute to knowledge of the local ecology of exotic non-volant mammals within each of the BAAs, and, where practicable, determine their potential vulnerabilities.
5. To monitor the specific impact of the linear right-of-way (ROW) infrastructure on the non-volant mammal communities, as an indicator of more general ROW impacts.
6. To assess the usefulness of non-volant mammal communities more broadly as potential indicators of change in habitat quality in each of the BAAs.

METHODS

Overview of methods

Two field methods and three analytical methods were used in this study of non-volant mammals.

- Field methods
 - live trapping along the permanent transects
 - camera trapping
- Analytical methods
 - analysis of owl roost prey remains
 - genetic analysis
 - population analysis

Each of these methods is expected to provide information of relevance to one or more of the objectives. The relationship between objectives and methods is shown in Table 5.1 and discussed below.

Table 5.1. The survey and analytical methods and their relevance to each of the study objectives. ++ = a primary source of information; + = a secondary source of information; - = no relevant information.

Survey Methods	Transect trap-lines	Camera traps	Owl roost remains	Genetic analysis	Population analysis
Objective 1 (general mammal inventory)	++	++	++	++	-
Objective 2 (identify species of conservation concern)	++	++	+	++	+
Objective 3 (status of exotics)	++	++	+	++	+
Objective 4 (ecology and vulnerabilities of exotics)	++	++	-	++	++
Objective 5 (specific ROW impacts)	++	++	+	-	+
Objective 6 (general habitat condition/impacts)	++	++	++	+	+

Objective 1 (general mammal inventory)

All of the major methods employed during this study contribute to the inventory of the non-volant mammal communities of BAA 1 and BAA 2. For BAA 1 this information is supplemented by knowledge generated during the EIS studies and from the analysis of the owl roost deposit at c. 2,065 m asl. Although the latter source is judged to be 'modern', it may contain species that are no longer present and were possibly absent by the time of the EIS studies. For this reason, species known only from the owl roost are treated as potential but unconfirmed members of the contemporary mammal community.

Genetic analysis also plays a significant role in the species inventory process. One aspect of this role is the detection of morphologically cryptic species, with several examples already found during this study. Another is determination of the degree of genetic relatedness of populations in the BAAs compared with other regional populations. The rationale and limitations of these approaches are discussed in Chapter 7.

Objective 2 (identify species of conservation concern)

Species of conservation concern are identified principally by comparing the species inventory for each study area with three listings:

1. The PNG *Fauna (Protection and Control) Act 1996*.
2. The International Union for the Conservation of Nature (IUCN) *Red List of Threatened Species*.
3. Appendices I and II of the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES).

For mammals that are thought to be closely related to but distinct from species currently placed in a threatened category by the IUCN we adopt the general principle that, pending a formal assessment by the IUCN, for the purposes of this report they warrant a level of consideration at least equal to that of the related species. Additional insights into the conservation values of populations within the BAAs will come from the genetic analysis of these populations compared with those in surrounding regions.

Objective 3 (status of exotic mammals)

The most significant exotic mammals encountered thus far or likely to occur in BAA 1 and BAA 2 are rodents, feral dogs and feral pigs. Trapping (for rats) and camera trapping (all taxa) are appropriate tools for studying these species. Genetic methods also represent a powerful tool for investigating the process and outcome of biological invasions.

Some relevant data on exotic rodents was obtained from transect trapping in BAA 1.

Information on the status and impacts of feral dogs was obtained during the transect trapping in BAA 1 and through the collection of dog scats along the ROW. Future camera trapping activities are expected to generate much valuable data on the distribution and abundance of feral dogs and pigs.

Objective 4 (ecology and vulnerabilities of exotic species)

Information on the ecology of exotic rodents and feral dogs is expected to come from the trapping transects and camera trapping. Genetic methods might also be used to monitor population trends in feral dogs and to investigate their diet and movements (see Chapter 7). For exotic rodents, population analysis will provide important insights into their ecology and will help to identify vulnerabilities including the most appropriate timing of control activities.

Objective 5 (specific ROW impacts)

The existence of the ROW and vehicle operations along it might impact on the local mammal community in various direct and indirect ways. Potential direct impacts include a reduction or absence of suitable food resources and shelter close to the ROW, road mortality, and restrictions on individual movements. Potential indirect impacts include increased predation along the ROW due to greater accessibility by predators such as owls, quolls and dogs, and altered patterns of competition for resources due to ROW impacts on other leaf, seed and fruit eating species such as certain bats and birds.

The key questions to be addressed for this objective are firstly, whether or not there are observable changes in the mammal community (manifest either in species abundance or reproductive activity) that are more pronounced in proximity to the ROW rather than further away from the ROW; and secondly, whether these changes are confined to the mammal community or are indicative of wider changes in habitat condition. These questions can be addressed at any stage during the history of the ROW and there is no necessity to have pre-construction data.

For the 2015 survey period this objective was investigated using live-trapping on permanent transects in each of BAA 1 and BAA 2. This method is outlined below. Results from the trap-lines primarily inform on populations of smaller mammals, particularly the native rodents.

A preliminary camera trapping survey in 2015 demonstrated the potential value of this method for analyzing ROW impacts (Chapter 4). The expanded program, to begin in 2017, will produce robust data on population trends across all groups of terrestrial and scansorial mammals, from the smaller rodents to larger species such as quolls, bandicoots, wallabies and tree kangaroos.

Population analysis (as measured by age structure, level of breeding activity etc.) is an additional source of relevant information on potential ROW impacts. A species might be present in an impacted context as a result of dispersal but be non-functional in a biological sense due to local failure of breeding systems. This can be assessed by examining variation along trapping transects in population parameters such as individual maturity and reproductive activity. Furthermore, to interpret any changes in abundance through time it is necessary to control for the timing of breeding activity. For example, an increase in population density of a species may simply be due to the coincident emergence of numerous young animals from nests to join the free ranging population (many of which typically do not survive to adulthood). Variation caused by such factors will be obvious from examination of age profiles.

Objective 6 (assess change to general habitat condition)

It is possible that the construction and subsequent existence of the ROW and associated facilities has had more pervasive impacts on the mammal community. If such changes have occurred they are less likely to be detected by transect-based methods because they might be manifest much further from the ROW.

Change on a broader spatial scale potentially could occur through various direct and indirect impacts.

Potential direct impacts on a mammal community might include:

- The loss of critical habitat needed to support a viable regional population.
- Excessive mortality during the construction phase that reduced the viability of a regional population.

Potential indirect impacts on a mammal community might include:

- A regional change in population dynamics following a change in the level of predation. This might be due to decline or loss of key native predators, a change (either increase or decrease) in human hunting activity, or a change in the intensity of dog predation.
- The introduction and spread of novel wildlife diseases that have entered the region with exotic animal species such as rodents.

The key questions here are firstly, whether or not there has been any regional scale change in the mammal community since the commencement of the Project, and secondly, whether any such changes have been caused by direct or indirect impacts of the Project (the alternative being that they reflect even more widespread changes brought about by external factors such as climate change).

The ideal context to answer these questions is a 'BACI' experimental approach ('Before/After and Control/Impact'; Underwood 1991). As the name suggests, this approach requires data from before and after an impact, and additionally, requires parallel before and after data from 'control' sites that are environmentally comparable but remained unaffected by the main impact. The BACI approach is the only way to be certain that any observed changes were caused by project activities rather than some unrelated, regional scale effect (such as climate change) and it represents a standard ecological approach to identifying biotic changes and speculating on their causality.

There is some information on the pre-construction small mammal community of Hides Ridge (BAA 1) but none for the Agogo Range (BAA 2). The information for Hides Ridge comes from two sources:

- a survey conducted between 24 April and 1 May 2005 around the Hides 3 well site, at an elevation of 2,163 m. This was carried out in preparation for the PNG LNG EIS.
- A bone deposit accumulated by owls in a small cave at c. 2,065 m asl on Hides Ridge. This was located and collected in 2011 during a pre-clearance survey and analysed by Aplin in 2014 (see Appendix 5 for a full account of the site and its contents).

Two approaches can be taken to detect broader-scale changes (i.e. those that might extend beyond the spatial scale of the transects) for sites that lack data on the pre-construction mammal community.

The first is to compare the contemporary mammal community across each of the the two BAAs with a view to detecting any inconsistencies between sites. The second is to compare the mammal community with broader regional records with a view to detecting any significant omissions in the BAA communities. In each case the logic is that studies of variability within the present mammal community might provide clues about the processes that have generated the pattern.

In the longer term the survey process started in 2015 will generate a post-construction baseline that can be used to monitor any changes in the regional fauna from that point forward. The potential future use of genetic methods to investigate population history is discussed in Chapter 7.

Detail of methods

Transect trap-lines

Eleven permanent survey transects were established during the 2015 survey, six in BAA 1 on Hides Ridge (H1–H6) and five in BAA 2 on the Agogo Range near Moro (M1–M5). These sample the elevational range of each BAA and provide replication at each of the sampled elevations. The locations and elevations of permanent transects are provided in the Executive Summary.

Trap-lines of standardized design and length were established on each of the six transects in BAA 1 and on four of the five transects in BAA 2 (M1-4). Establishment of a transect trap-line involved the marking of trapping positions with numbered metal tags and the GPS recording of these positions. Transect M5 (used for studies of frogs and bats) was too far from the access point at Arakubi Quarry to establish a trap-line in 2015; an alternative site will be identified in 2017.

The design of a standard transect trap-line is shown in Figure 5.1. In brief, a trap-line consists of a series of live traps set at regular and increasing distances from the ROW, with some supplementary sampling along the roadside to increase the chances of detecting exotic small mammals using the ROW for dispersal. As much as was possible each trap-line was established with its long axis oriented perpendicular to the ROW and maintained a more-or-less constant elevation along its full length. The rugged terrain of both Hides Ridge and the Agogo Range made it difficult to meet this ideal but sites were selected to approximate these conditions as closely as possible.

The length of the transect trap-line was standardized at 240–250 m straight line distance from the ROW. This length was dictated by landscape conditions on Hides Ridge in BAA 1 where the extremely rugged terrain constrained the practical dimensions of the trap-lines.

The precise location of all trap-line elements is documented in Appendix 5.1.

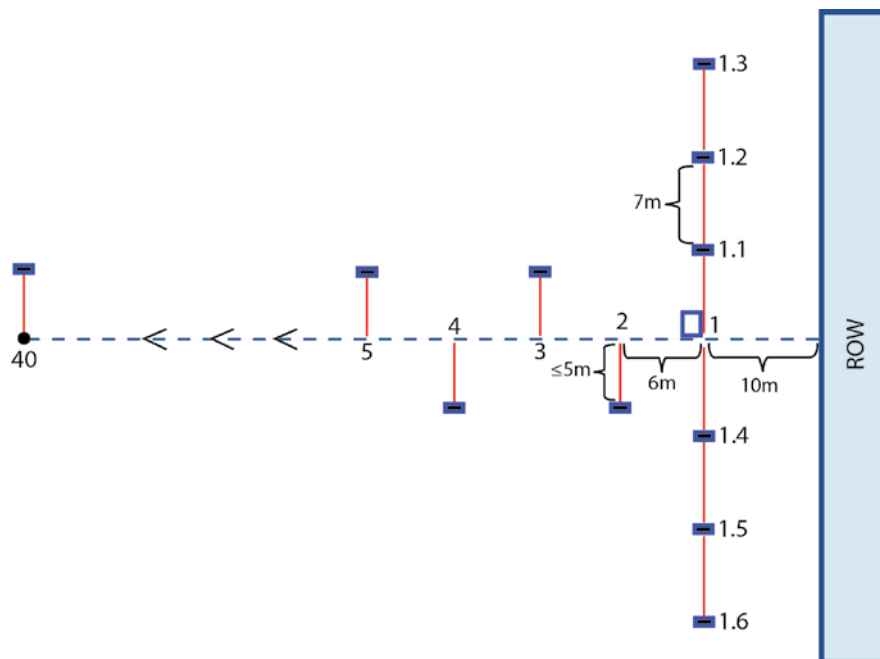


Figure 5.1. Design of a transect trap-line. ROW = right of way; open rectangle = large Elliott trap; closed rectangle = medium-sized Elliott trap. The central access path is represented by the dashed line. Trap positions are located at 6 m intervals along the transect access path. Traps are placed on alternate sides of the access path, and no more than 5 m to the right or left. Large Elliott traps are placed at positions 1, 11, 21 and 31. Medium-sized Elliott traps are placed at all other positions. Six medium-sized Elliott traps are placed parallel to the ROW to provide additional sampling of the most heavily impacted 'edge' habitat.



Figure 5.2. An Elliott live trap hidden among mossy roots and leaf litter of the forest floor.

Operation of a trap-line involved the setting of baited live capture traps (Elliott traps; see Figure 5.2) at each of the marked trapping positions. Each trap-line contained four large Elliott Traps and 42 medium-size Elliott Traps. Traps were baited with a mixture of peanut butter and rolled oats mixed with water in BAA 1 and with blocks of raw sweet potato in BAA 2.

During the 2015 survey trap-lines were operated on transects H1-H3 and H5-H6 in BAA 1 and on transects M1-M3 and M4. The trap-line on transect H4 was established but not operated due to time constraints. A record was kept of the time taken to perform each major task on each of the trap-lines. This was done to allow for effective planning of future sampling activities. These data are shown in Appendix 5.2.

Some problems were encountered during the operation of the trap-lines. In BAA 2 ant infestation emerged as a serious problem but this was resolved by changing the bait type to sweet potato. In BAA 1 there was interference to traps by feral dogs and to a lesser extent by people. On trap-lines M1 and M2 interference by feral dogs reached such extreme levels as to prompt early closure.

Animal handling and data collection

Captured animals were examined, sampled and recorded on site and released immediately at the point of capture.

Small mammals can be difficult to identify due to changes in appearance that occur during growth and maturation. This is especially so in New Guinea where many closely related species coexist in the same area. In addition, in any location in New Guinea there is a strong possibility of encountering undescribed mammal species. For these reasons, comprehensive DNA sampling of all captured individuals was carried out in 2015. This approach also guarantees the veracity of current and future species identifications (see Chapter 7 for a full account of the methodology).

DNA sampling was usually done by removal of a tail clip. Where this was not possible a hair sample was taken instead. Tail or hair clips also served to identify previously captured animals. A small number of captured animals were removed from site and humanely euthanased to allow for more comprehensive taxonomic investigations. Individual age and reproductive condition were noted for every captured mammal.

Camera trapping

The camera trapping activities in 2015 and recommendations for future camera trap monitoring are described in Chapter 4. Mammal encounters were scored as separate 'events' if a gap of at least 30 minutes occurred between images of the same species. The following values were calculated for each site: 1) the total number of 'events' for each species, 2) the number of camera positions that recorded at least one event, and 3) a Relative Abundance Index (RAI) across all cameras. The RAI is calculated as follows:

$RAI = \text{number of events} \times 100 / \text{hours of imaging}$

Owl roost prey remains

The owl roost deposit was collected by Mr Steve Hamilton in 2011 from a small cave at c. 2,065 m asl on Hides Ridge (see Appendix 5.5 for details). The sample was studied by Ken Aplin in 2014 and judged to be modern based on the occurrence of five complete pellets (a regurgitated ball of fur and bones) and the general condition of the other remains which showed signs of rapid biogenetic breakdown.

Species identifications were carried out on jaws, teeth and other cranial remains. Photographs and measurements were taken of important specimens. For each species a count was made of the identified elements and a 'minimum number of individuals' (MNI) value calculated for each species. The MNI value is the smallest number of individuals required to account for all of the remains of the species; e.g. 3 right dentaries; 2 left dentaries; 2 left maxillae: MNI = 3.

Other casual observations

These include a few sightings of mammals made during the day, one record from a road kill, and species recorded from bones in feral dog scats collected along the road verge on Hides Ridge. These observations are tabulated in Appendix 5.4.

Data analysis

Captures were scored as 'novel' (i.e. first capture) or 'recaptures', with the latter indicated by the prior tail or hair clips. Trapping success was calculated as the total number of captures per trap-night (one trap set for one night = one trap-night). The percentage of recaptures was calculated as the number of recaptures divided by the number of released individuals (i.e. excluding the small number removed from the trap-lines for vouchering purposes).

Capture rates on the various transects at each site were examined in more detail using a Linear Model that compared the results from one arbitrarily selected transect with every other transect from that site (i.e., H1 was compared with H2–H3, H5–H6 and with M1–M4). This analysis tests whether the capture rate on each trap-line (e.g. H2) differs from that observed on the first transect (H1), whilst taking into account the other fixed effect of Trapping Day (i.e. first day, second day etc.).

The relationship between trapping results and distance from the ROW was analysed in two ways. An initial exploratory analysis divided the trap-line into five blocks, each containing 8 traps within a 50 m zone. The number of individuals captured (i.e. excluding recaptures) was summed for all *Rattus* and *Paramelomys* species. Insufficient data were available for other mammal groups. The distribution of captures at varying distance from the ROW was examined visually by examining graphs for various groups of species.

A more sophisticated analysis was performed using Generalized Linear Mixed Models (GLMMs) – a powerful family of methods that can explore datasets with a combination of 'fixed' and 'random' effects as well as a variety of different kinds of variables (i.e. categorical, interval and continuous), and data in various forms (e.g. dichotomous, counts) and with varied distributions (e.g. normal, Poisson, binomial). 'Fixed' effects in this case include the elevational band of the transect, the distance of each trap from the ROW, and the sampling period. 'Random' in this context equates to natural variability and can include such parameters as transect identity and, in a situation where numerous recaptures were made, individual animal identity.

In this first phase of the study the GLMM analyses were used to test whether the distance of the trap from the ROW influenced the likelihood of a capture in the trap, whilst taking into account the other fixed and random effects. Insufficient captures were made to support analysis of individual species but this should become possible after future surveys. As an interim measure the GLMM analyses were conducted with data grouped in two ways: 1) by grouping all novel captures (i.e. excluding recaptures); and 2) by grouping the novel captures into three categories – all *Rattus* species, all *Paramelomys* species, all other captures.

GLMMs are also ideally suited to analysis of longitudinal datasets where sets of observations are not independent of each other but are related through time. After the 2017 sampling period it will be possible to incorporate the fixed factor *year* into the analysis.

Usage of scientific and common names

The scientific names used in this report attempt to follow the usage of the current IUCN Red List (<http://www.redlist.org/>). However, for some groups of New Guinean mammals this listing is known to be an underestimate of the true species diversity. In some cases this is due to the presence of morphologically distinctive forms that have been collected since the last critical taxonomic studies; in others it is due to the likely presence of morphologically 'cryptic' species that differ in subtle anatomical features and require the application of genetic methods for confident discrimination.

Where a taxon cannot be unambiguously identified to a currently recognised species, its scientific name contains 'cf' (which means 'compare') followed by the name of the most similar taxon. For example, a species listed as *Rattus cf. niobe* would most closely resemble true *R. niobe* but would be different in ways suggestive of a distinct and currently unrecognized species. When there is more than one such taxon, they are given a sequential letter code – thus *Rattus cf. niobe A* and *Rattus cf. niobe B* are two different species, both of which resemble *R. niobe* (and each other) more than any other species.

The common names used in this report are also derived from the IUCN Red List (<http://www.redlist.org/>). Some of these conflict with common names used in the major works on New Guinea mammals by Menzies and Dennis (1979), Flannery (1995), Menzies (2011) and Zachos (2015), but usage of names also differs among these sources. There is no 'legal' system of arbitration for usage of common names equivalent to that governing the use of scientific names so we have adopted the most widely available terminology for use in this report.

RESULTS AND DISCUSSION

General results

Trap-line establishment and operation

Trap-lines were established on all six transects in BAA 1 and on four of the five transects in BAA 2.

BAA 1: The six trap-lines were clustered in two groups at contrasting lower and higher elevations. One group of three trap-lines was established on transects H1–H3 at elevations of 2,100–2,400 m asl; the other group of three trap-lines were established on transects H4–H6 at elevations of 2,600–2,800 m asl. Five of the six trap-lines were operated during the 2015 survey with a maximum of four trap-lines under simultaneous operation.

BAA 2: Three trap-lines were established on transects M1–M3 at elevations of 1,300–1,400 m asl near KP107 on the Agogo Range. One trap-line was established on transect M4 at Arakubi Quarry, with an elevational range of 1,050 m–1,150 m asl.

The scheduling of trap-line operation and the time-budgets are detailed in Appendix 5.2. Individual trap-lines were operated for a minimum of two nights and a maximum of nine nights (mean = 6.22). The number of trap-lines that could be run simultaneously by the team of two people was four but with the benefit of greater experience this can probably be increased to five or six trap-lines.

Trapping results

A total of 178 mammals was captured on the nine trap-lines, including 62 in BAA 1 and 112 in BAA 2. The taxonomic identity of all captures is summarized in Tables 5.2 and 5.3 for BAA 1 and in Tables 5.4 and 5.5 for BAA 2. For each site the captures are presented separately for total captures and for novel captures only (i.e. excluding recaptures). Examples of some of these species are illustrated in Figures 5.11–5.16.

Table 5.2. BAA 1 trap-lines - all captures

Transect	<i>Rattus cf. niobe B</i>	<i>Paramelomys cf. rubex A</i>	<i>Paramelomys cf. mollis A</i>	<i>Paramelomys cf. mollis C</i>	<i>Dasyurus albopunctatus</i>	<i>Microperoryctes ornata</i>
H6	11	6	1	-	-	-
H5	6	-	-	-	-	-
H3	3	1	3	1	1	-
H2	9	1	1	-	-	-
H1	14	3	-	-	-	1

Table 5.3. BAA 1 trap-lines - novel captures only

Transect	<i>Rattus cf. niobe B</i>	<i>Paramelomys cf. rubex A</i>	<i>Paramelomys cf. mollis A</i>	<i>Paramelomys cf. mollis C</i>	<i>Dasyurus albopunctatus</i>	<i>Microperoryctes ornata</i>
H6	11	6	1	-	-	-
H5	6	-	-	-	-	-
H3	3	1	3	1	1	-
H2	8	1	1	-	-	-
H1	14	3	-	-	-	1

Table 5.4. BAA 2 trap-lines – all captures.

Transect Line	<i>Rattus cf. niobe D</i>	<i>Rattus sp. 'spiny'</i>	<i>Rattus exulans</i>	<i>Paramelomys cf. rubex B</i>	<i>Paramelomys cf. lorentzii</i>	<i>Paramelomys platyops</i>	<i>Uromys cf. caudimaculatus</i>	<i>Dasyurus albopunctatus</i>
M1	20	-	2	1	1	-	-	-
M2	23	-	1	4	5	-	1	-
M3	27	-	1	9	1	-	-	-
M4		13		1		1		1

Table 5.5. BAA 2 trap-lines – novel captures only.

Transect Line	<i>Rattus cf. niobe D</i>	<i>Rattus sp. 'spiny'</i>	<i>Rattus exulans</i>	<i>Paramelomys cf. rubex B</i>	<i>Paramelomys cf. lorentzii</i>	<i>Paramelomys platyops</i>	<i>Uromys cf. caudimaculatus</i>	<i>Dasyurus albopunctatus</i>
M1	13	-	2	1	1	-	-	-
M2	13	-	1	4	2	-	1	-
M3	14	-	1	8	1	-	-	-
M4	-	10	-	1	-	1	-	1

Table 5.6. Summary of trapping results for sites in BAA 1.

Trap-line	Captures	Trap nights	Trap success
H6	18	322	5.6%
H5	6	322	1.9%
High elevation sites	24	644	3.7%
H3	11	90	12.2%
H2	8	229	3.5%
H1	19	230	8.3%
Low elevation sites	38	549	6.9%

Table 5.7. Summary of trapping results for sites in BAA 2. Results are shown separately for the entire trapping period and for the period after switching to raw sweet potato.

Trap-line	All nights / both baits			Nights with sweet potato bait		
	Total captures	Total trap nights	Trap success	Total captures	Total trap nights	Trap success
M1	25	322	7.80%	22	230	9.60%
M2	35	368	9.50%	21	230	9.10%
M3	29	276	10.50%	27	230	11.70%
Total KP107	89	966	9.20%	70	690	10.10%
M4 (Arakubi Quarry)	16	420	3.80%	13	300	4.30%

Capture and recapture rates

Capture rates (Tables 5.6 and 5.7) were highest (average 9.2% overall, 10.1% using sweet potato) at the mid-elevations transects at KP107 (M1-M3 at 1,300–1,400 m asl) and show an overall pattern of decline with increasing elevation (average 6.9% at H1–H3 at 2,100–2,300 m asl; average 3.7% at H5–H6 at 2,600–2,800 m asl). However, the capture rate was also low (4.3%) at the Arakubi Quarry transect (M4), even after switching to the sweet potato bait to avoid ant infestation (Table 5.7).

The GLMM analysis gave a slightly different perspective on the trapping results. It tested whether capture likelihoods at each trap-line was significantly different from that observed at transect H1 (selected arbitrarily), whilst taking into account other factors including the day on which captures were made. Three trap-lines had significantly lower capture likelihoods than H1—H2, H5 and M4 (Arakubi Quarry)—but on no trap-line was the capture likelihood significantly higher. Low capture likelihoods on transect H2 might be explained by the exceptionally high disturbance of this site by feral dogs, while for transects H5 and M4 there are other indicators that these sites have experienced higher than average levels of disturbance in the recent past (see below).

Recaptures were rare on the trap-lines in BAA 1 but quite common on the BAA 2 trap-lines (Table 5.8). The difference is most clearly observed between the two forms of *R. cf. niobe* (2.9% recaptures for *R. cf. niobe* B at Hides Ridge vs 44.1% for *R. cf. niobe* D on the Agogo Range) but it is also indicated in the results for the other species of *Rattus* and *Paramelomys*. Interestingly, both sexes of *R. cf. niobe* D had high recapture rates (68.4% for males; 100% for females).

Recapture rate might be expected to be influenced by overall capture rate. Although this does appear to be the case (Table 5.8), even species with relatively low capture rates at the Agogo Range sites (e.g. *Rattus* sp. 'spiny' and *Paramelomys* spp.) still had recapture rates in excess of those observed at Hides Ridge.

The reason for the strong contrast in recapture rates between the two survey sites is not clear. Different baits were used at the two sites and it is possible that sweet potato baits are more likely to produce recaptures than the peanut butter/oats mix. However, if the sweet potato bait was more attractive it might be asked why overall capture rates were not also higher on all of the Agogo Range transects where instead overall capture rates on transect M4 at Arakubi Quarry were among the lowest recorded. A second possible explanation is that the species found at the lower elevation sites are behaviourally more susceptible to recaptures, and by chance, just happen to be so across the two genera. A third is that the rodent community on the Agogo Range as a whole was under greater food stress such that all individuals were more inclined to enter the traps. Of the three options, the last seems most likely although no evidence for differences in food availability (seeds, fruiting etc) between the sites were noted in the field.

Table 5.8. Recapture rates for each of the two BAAs, calculated separately for each species and for the combined captures. Recapture % is calculated using the number released rather than the total number captured, as vouchered animals by definition could not be recaptured. Two captured individuals are excluded from this analysis because they escaped before their recapture status could be determined.

Species	Total captures	Number released	Number recaptured	Recaptures as % of releases	Capture rate
BAA 1 (Hides Ridge)					
<i>Rattus cf. niobe</i> B	43	33	1	3.0%	3.6%
<i>Paramelomys cf. rubex</i> A	11	9	0	0.0%	0.9%
<i>Paramelomys cf. mollis</i> A	5	3	0	0.0%	0.4%
<i>Paramelomys cf. mollis</i> C	1	1	0	0.0%	0.1%
All species	60	46	1	2.1%	5.0%
BAA 2 (Agogo Range)					
<i>Rattus cf. niobe</i> D	70	69	30	43.5%	5.0%
<i>Rattus</i> sp. 'spiny'	12	10	3	30.0%	1.0%
<i>Paramelomys cf. lorentzii</i>	7	2	2	100%	0.4%
<i>Paramelomys platyops</i>	1	1	0	0.0%	0.1%
<i>Paramelomys cf. rubex</i> B	15	14	1	7.7%	1.1%
All species	105	97	36	37.1%	7.6%

Species discrimination and identification

All but four captures were of small rodents belonging to two genera—*Paramelomys* and *Rattus*. These genera are readily distinguished in the hand by the nature of the tail, which appears almost naked in *Paramelomys* but quite hairy in *Rattus*. However, identification to species level within each genus is notoriously difficult because the various species do not differ greatly in external appearance. It is also likely that both genera contain more species than are currently recognised (see Robins et al. 2014 for *Rattus*). We therefore employed genetic methods to assist with species delineation and identification (see Appendix 5.3 for a full account of these results).

For the genus *Rattus* the molecular analysis identified six genetic groups in contrast to the four groups provisionally distinguished on morphological criteria. One major finding was that the small-bodied, soft furred species identified as *Rattus* cf. *niobe* from BAA 1 (Figure 5.15) and BAA 2 very likely represent two different species; neither is likely to be true *R. niobe* that was first described from mid-elevations in the Owen Stanley Range. The morphologically distinctive *Rattus* sp. 'spiny' from Arakubi Quarry (Figure 5.16) was confirmed as a distinct species.

Genetic comparison of the PMA3 *Rattus* samples with others drawn from across New Guinea found that all of them are more widely distributed. Significantly, *Rattus* sp. 'spiny' from Arakubi Quarry was shown to be closely related to a morphologically similar population discovered recently on the P'nyang Range of Western Province. The Black Rat from HGCP gave a genetic signal indicative of Lineage II of Aplin et al. (2011). This lineage originated in East Asia but has spread to various parts of the world including Papua New Guinea, Australia and U.S.A. The precise genetic type found at HGCP has not previously been recorded in Papua New Guinea and it may be the product of a novel introduction during Project activities.

For *Paramelomys* the molecular analysis identified six genetic groups compared with four identified on morphological criteria. All small-bodied *Paramelomys* were provisionally identified as *Paramelomys* cf. *rubex* (Figure 5.14) but the samples from each of BAA 1 and BAA 2 proved genetically distinct. They almost certainly represent two different species and neither is likely to be true *P. rubex*. The genetic type found in BAA 1 (*P. cf. rubex* A) is represented in samples from elsewhere in Papua New Guinea but that from BAA 2 (*P. cf. rubex* B) is currently known only from this locality.

The larger-bodied *Paramelomys* were tentatively identified on morphological criteria as *P. cf. mollis* (in BAA 1; Figure 5.12), *P. platyops* (Arakubi Quarry; Figure 5.13) and *P. cf. lorentzii* (in BAA 2). The molecular analysis found four genetic groups including two groups within *P. cf. mollis*. One of these (*P. cf. mollis* A; Figure 5.12) is widespread in our broader sampling but the other (*P. cf. mollis* C) is a unique lineage currently known only from transect H3 in BAA 1. The genetic analysis confirmed the identity of *P. cf. lorentzii* and *P. platyops* and indicated that both taxa are widespread in southern New Guinea.

For the few captures of other genera, genetic comparisons were made with samples from other regional populations. Our single sample of Speckled Dasyure (*Neophascogale* cf. *lorentzii* (illustrated on the cover page) was compared with one from Enga Province and found to be minimally divergent. Similarly, our single sample of a white-eared giant rat (*Hyomys* sp.) in BAA 1 was found to be weakly divergent from samples from Southern Highlands Province and West Sepik Province but it is presently unclear whether these represent *H. goliath* or *H. dammermani*; until this is resolved, the BAA 1 populations is listed as *Hyomys* sp.

Our single sample of another giant rat, *Uromys* cf. *caudimaculatus*, is minimally divergent from a sample from Mt Karimui in Chimbu Province. Together these are deeply divergent from samples from localities in Central Province and West Sepik Province. Other studies in progress suggest that there are several species in the *Uromys caudimaculatus* group in New Guinea but it is not yet clear what any of them should be called.

Camera traps captured images of rodents of the genera *Leptomys* and *Mallomys* but the images are not diagnostic for any particular species. Captures will be required to establish the species identity of these populations.

Taxonomic notes are provided in Appendix 5.3 for all other groups where there is taxonomic ambiguity.

Camera trapping results

A detailed analysis of camera trapping results is contained in Chapter 4. We limit our analysis to some observations on species composition and relative abundances of mammals across the four main elevational zones in BAA 1 and BAA 2. The relevant data are summarised in Table 5.9.

Table 5.9. Summary of camera trapping results for each of the four elevational zones surveyed in BAA 1 and BAA 2. Results are presented as three values for each species: 1) number of 'events'; 2) number of camera trap positions that recorded events; and 3) RAI values for all camera positions pooled.

Taxon recorded	BAA 2: Arakubi (1,020-1,045m asl)			BAA 2: KP107 (1,350-1,405m asl)			BAA 1: H1-H3 (2,160-2,365m asl)			BAA 1: H5-6 (2,670-2,720m asl)		
	6 CTs, 44 nights, 1,037.25 hrs			18 CTs, 153 nights, 3,643.75			12 CTs, 70 nights, 1,638.5 hrs			9 CTs, 63 nights, 1,515.5 hrs		
	# events	# CTs	RAI	# events	# CTs	RAI	# events	# CTs	RAI	# events	# CTs	RAI
<i>Tachyglossus aculeatus</i>	1	1	0.096	1	1	0.027						
<i>Dasyurus albopunctatus</i>	2	2	0.193	3	3	0.082				1	1	0.066
<i>Murexia longicaudata</i>	2	2	0.193	3	2	0.082						
<i>Murexia naso</i>							3	3	0.183	1	1	0.066
<i>Myoictis leucura</i>				1	1	0.027						
<i>Neophascogale cf. lorentzii</i>										2	1	0.132
<i>Echymipera cf. kalubu</i>	1	1	0.096									
<i>Microperoryctes ornata</i>				2	2	0.055	3	3	0.183	1	1	0.066
<i>Peroryctes raffrayana</i>				22	7	0.604	3	3	0.183	3	3	0.198
<i>Dendrolagus notatus</i>										1	1	0.066
<i>Dorcopsulus cf. vanheurni</i>	6	4	0.578	34	9	0.933	2	1	0.122	2	2	0.132
<i>Anisomys imitator</i>				1	1	0.027	15	5	0.915			
<i>Hyomys sp.</i>							2	2	0.122	1	1	0.066
<i>Leptomys sp.</i>				25	11	0.686						
<i>Mallomys sp.</i>	1	1	0.096									
<i>Parahydromys asper</i>				2	2	0.055						
<i>Paramelomys spp.</i>	10	4	0.964	30	10	0.823	12	3	0.732	2	1	0.132
<i>Rattus cf. niobe</i>				4	3	0.110	1	1	0.061	3	2	0.198
<i>Rattus sp. spiny</i>	3	1	0.289									
<i>Uromys cf. caudimaculatus</i>	19	3	1.831	3	3	0.082						
<i>Canis familiaris</i>				1	1	0.027	1	1	0.061			

Table 5.10. The non-volant mammal fauna of BAA 1 and BAA 2. Shaded cells indicate a confirmed species occurrence. Taxa marked with an * were recorded during the 2015 survey. Other records come from identification of owl roost remains and from EIS survey work on Hides Ridge. Three taxa were reported differently by Mamu et al. (2005): *Lorentzimys cf. nouhuysi* was reported as *Pogonomys loriae*; *Pseudochirops cupreus* as *P. corinnae*; and *Uromys anak* as *Xenuromys barbatus*– all were re-identified from photographs included in Crome et al. (2008).

Scientific name	English Name	BAA 2		BAA 1	
		Arakubi Quarry 1,050 – 1,150 m	KP107 1,300 – 1,400 m	H1-H3 2,100 – 2,300 m	H5-H6 2,600 – 2,800 m
<i>Tachyglossus aculeatus</i>	Short-beaked Echidna	*	*		
<i>Dasyurus albopunctatus</i>	New Guinea Quoll	*	*	*	*
<i>Murexia longicaudata</i>	Long-tailed Murexia	*	*		
<i>Murexia cf. habbema</i>	Lake Habbema Murexia				
<i>Murexia melanurus</i>	Black-tailed Murexia				
<i>Murexia naso</i>	Long-nosed Murexia			*	*
<i>Myoictis leucura</i>	Woolley's Three-striped Dasyure		*		
<i>Neophascogale cf. lorentzii</i>	Speckled Dasyure				*
<i>Echymipera cf. kalubu</i>	Common Echymipera	*			
<i>Microperoryctes ornata</i>	Ornate Bandicoot		*	*	*
<i>Peroryctes raffrayana</i>	Raffray's Bandicoot		*	*	*
<i>Distoechurus cf. pennatus</i>	Pen-tailed Possum				
<i>Cercartetus cf. caudatus</i>	Long-tailed Pygmy Possum				
<i>Petaurus cf. breviceps</i>	Sugar Glider				
<i>Pseudochirulus larvatus</i>	Painted Ringtail Possum				
<i>Pseudochirulus mayeri</i>	Pygmy Ringtail Possum				
<i>Pseudochirops cupreus*</i>	Coppery Ringtail Possum				
<i>Phalanger carmelitae</i>	Mountain Cuscus				
<i>Phalanger sericeus</i>	Silky Cuscus				
<i>Dorcopsulus cf. vanheurni</i>	Small Forest Wallaby	*	*	*	*
<i>Dendrolagus notatus</i>	Western Montane Tree Kangaroo				*
<i>Abeomelomys sevia</i>	Menzies' Mouse				
<i>Anisomys imitator</i>	Uneven-toothed Rat		*	*	
<i>Chiruromys vates</i>	Lesser Tree Mouse				
<i>Hyomys sp.</i>	a White-eared Giant Rat			*	*
<i>Leptomys sp.</i>	a Leptomys		*		
<i>Lorentzimys cf. nouhuysi*</i>	Long-footed Tree Mouse				
<i>Mallomys</i>	a Woolly Giant Rat	*			
<i>Melomys cf. dollmani</i>	Long-tailed Melomys				

Scientific name	English Name	BAA 2		BAA 1	
		Arakubi Quarry 1,050 – 1,150 m	KP107 1,300 – 1,400 m	H1-H3 2,100 – 2,300 m	H5-H6 2,600 – 2,800 m
<i>Melomys cf. rufescens</i>	Black-tailed Melomys				
<i>Parahydromys asper</i>	Waterside Rat		*		
<i>Paramelomys cf. lorentzii</i>	Lorentz's Paramelomys		*		
<i>Paramelomys cf. mollis</i> A	Thomas's Paramelomys			*	*
<i>Paramelomys cf. mollis</i> B	Thomas's Paramelomys				*
<i>Paramelomys platyops</i>	Lowland Paramelomys	*			
<i>Paramelomys cf. rubex</i> A	Mountain Paramelomys			*	*
<i>Paramelomys cf. rubex</i> B	Mountain Paramelomys	*	*		
<i>Protochromys cf. fellowsi</i>	Red-bellied Mosaic-tailed Rat				
<i>Pogonomys cf. macrourus</i>	Chestnut Tree Mouse				
<i>Pogonomys cf. loriae</i>	Large Tree Mouse				
<i>Rattus exulans</i>	Pacific rat		*		
<i>Rattus cf. niobe</i> B	Moss Forest Rat			*	*
<i>Rattus cf. niobe</i> D	Moss Forest Rat	*	*		
<i>Rattus</i> sp. 'spiny'	An undescribed rat	*			
<i>Rattus steini</i>	Small Spiny Rat				
<i>Rattus cf. verecundus</i>	Slender Rat				
<i>Uromys anak</i> *	Black-tailed Giant Rat				
<i>Uromys cf. caudimaculatus</i>	White-tailed Giant Rat	*	*		
<i>Canis familiaris</i>	Feral dog		*	*	*
Total species recorded		11	16	32	13

Results for specific objectives

Species inventory (Objective 1)

The non-volant mammal fauna of BAA 1 and BAA 2 is summarized in Table 5.10, with separate entries for each of the two elevational bands sampled in each BAA.

The number of species recorded in each elevational band during the 2015 survey ranged from 11 to 16. The highest number was recorded in BAA 2 on transects M1 to M3 on the Agogo Range, and the lowest number on transect M4 (Arakubi Quarry) in BAA 2.

Eleven species were recorded during the 2015 survey in the lower elevational band in BAA 1 (2,100 – 2,300 m asl). An additional 21 species were documented from the owl roost sample (see also Appendix 5.5) and from the EIS survey carried out at Hides 3 in 2005 (Mamu et al. 2005). Notably, most of these species are arboreal animals that are unlikely to be detected either by trapping or camera trapping at ground level. Other species that might be expected to occur at this elevational zone on Hides Ridge, based on broader regional records, are the Long-fingered Triok (*Dactyloxax palpator*), one or two species of Woolly Rats (*Mallomys* spp.), and several shrew mice (*Pseudohydromys* spp.). The full non-volant mammal community at this elevation thus may be 37 species or more.

Fewer species are expected at the upper elevations in BAA 1 due the general trend of declining mammal diversity at higher elevations across New Guinea.

The lower montane habitats represented in BAA 2 are likely to support even higher mammal diversity than that documented in BAA 1.

Some of the observed contrasts in species composition between the four elevational bands align with elevational limits observed more broadly across New Guinea. Species that occur exclusively at BAA 2 and are elsewhere restricted to elevations below c.1500 m asl include: the Short-beaked Echidna (*Tachyglossus aculeatus*), two dasyurid marsupials (*Murexia longicaudata* and *Myoictis leucura*), a bandicoot (*Echymipera* cf. *kalubu*), and five rodents (*Leptomys* spp., *Parahydromys asper*, *Paramelomys* cf. *lorentzii* and *P. platyops*, and *Uromys* cf. *caudimaculatus*).

Species that are exclusive to the BAA 1 sites and which are elsewhere confined to upper montane habits (typically above 2,000 m asl) include: *Murexia naso*, *Neophascogale* cf. *lorentzii*, *Hyomys* sp., and *Paramelomys* cf. *mollis* A. Several pairs of species appear to show elevational replacement, in which a closely related species replaces another as elevation changes. Examples are the two species that resemble *Rattus niobe* (*R.* cf. *niobe* D at BAA 2 replaced by *R.* cf. *niobe* B at BAA 1) and the two that resemble *Paramelomys rubex* (*P.* cf. *rubex* A in BAA 2 replaced by *P.* cf. *rubex* B in BAA 1). *Paramelomys* cf. *lorentzii* and *P. platyops* also appear to be replaced at higher elevations by the two similar-sized *Paramelomys*—*P.* cf. *mollis* A and *P.* cf. *mollis* C.

Species of conservation concern (Objective 2)

Four of the mammals recorded from the BAAs are of conservation concern:

- *Dendrolagus notatus* – IUCN **Endangered** and PNG Fauna Act **Protected**;
- *Dorcopsulus* cf. *vanheurni* – IUCN **NearThreatened**;
- *Dasyurus albopunctatus*– IUCN **NearThreatened**; and
- *Myoictis leucura* – IUCN **Data Deficient**.

Dendrolagus notatus, the Western Montane Tree kangaroo, was encountered only once (by camera trap) in BAA 1 and the size and extent of the local population is unknown. It is possible that this species also occurs in BAA 2, especially in the vicinity of KP107 where habitat appears to be suitable. All New Guinean tree kangaroos are thought to exist in low population densities with largely exclusive territories measuring 10 ha or more. With such low population densities, the likelihood of detecting them during any localized survey is very small and camera traps appear to be the best method for monitoring this rare species.

Dorcopsulus cf. *vanheurni* (*D. vanheurni* is IUCN Near Threatened) is a small forest wallaby that was detected on camera traps at all elevations in both BAAs. Although this undescribed species occurs across a broad elevational range (at least 1,000 m to 2,600 m asl), it appears to be more abundant at lower elevations. The remains of this species were noted in several feral dog scats collected along the ROW in BAA 1.

Dasyurus albopunctatus, the New Guinea Quoll, was recorded in both BAAs and in three of the four elevational bands surveyed. This species is one of New Guinea's top level predators and it appears to be relatively uncommon throughout its range.

Myoictis leucura, Woolley's Three-striped Dasyure, is a medium-sized carnivorous marsupial that is known from scattered localities along the southern foot-hills and slopes of the central cordillera of New Guinea. Although it has been recorded at several sites over the past few years (Aplin, unpublished data), it is nowhere very common. Unlike the majority of marsupials, species of *Myoictis* are often active during the day, and this is probably related to their predation on diurnal birds.

Other species recorded in 2015 that may prove to be of special conservation concern are:

- *Paramelomys cf. mollis C*, a new species currently known only from transect H3 in BAA 1; and
- *Paramelomys cf. rubex B*, a new species currently known only from KP107 and Arakubi Quarry in BAA 2.

It is possible that genetic analysis of as yet unanalysed samples available from elsewhere in Papua New Guinea might identify additional populations of one or both of these species, and their conservation status will depend on whether they occur outside of these localities. However as small rodents, neither is likely to be sensitive to major threats other than habitat degradation and/or loss.

The following species are either known to be undescribed (i.e. they lack a prior scientific name; prefixed *) or are potentially undescribed:

- **Dorcopsulus cf. vanheurni*;
- *Rattus cf. niobe B* and *Rattus cf. niobe D*;
- *Paramelomys cf. mollis A* or *Paramelomys cf. mollis C*;
- *Paramelomys cf. rubex A*;
- **Rattus* sp. 'spiny'; and
- *Uromys cf. caudimaculatus*.

Exotic mammal species (Objectives 3 and 4)

The Pacific Rat (*Rattus exulans*) was trapped on several transects at KP107 but only within 10–15 m of the road verge.

The Black Rat (*Rattus rattus*) was recorded at HGCP. An example of this species was found dead in the compound which is baited for rodent control.

Dog activity was detected in both BAAs. While it is possible that these were domestic dogs (in BAA 1 these might have belonged either to communities around Komo or staff of the OSL camp), there are several reasons to believe that they were members of a feral population (i.e. entirely free-living):

1. Where dog footprints were observed they were not accompanied by any signs of human activity.
2. In BAA 1 there was no obvious decline in the level of dog activity away from human settlements.
3. In BAA 1 the trap-lines were being visited by dogs on consecutive nights, suggestive of locally resident animals rather than transient visitors.

The presence of forest wallaby (*Dorcopsulus cf. vanheurni*) bones in the dog scats from the upper elevational band in BAA 1 is significant as it confirms predation of this Near Threatened marsupial. Feral dogs in New Guinea also commonly consume a variety of other vertebrates including possums and cuscuses, giant rats and bandicoots. Too few scats were found to provide any quantitative analysis of prey items.

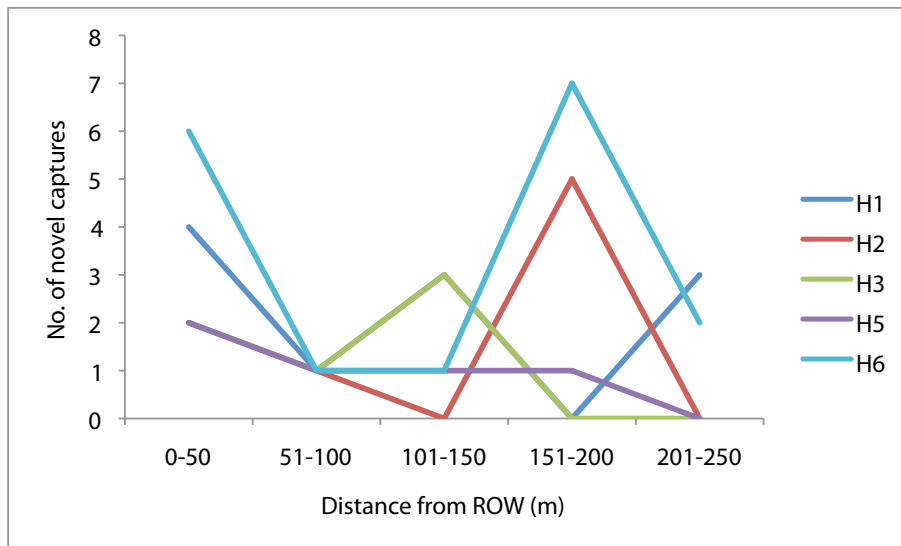


Figure 5.3. BAA 1 - trends in trap captures (all species combined) with increasing distance from the ROW (traps grouped in 50m intervals).

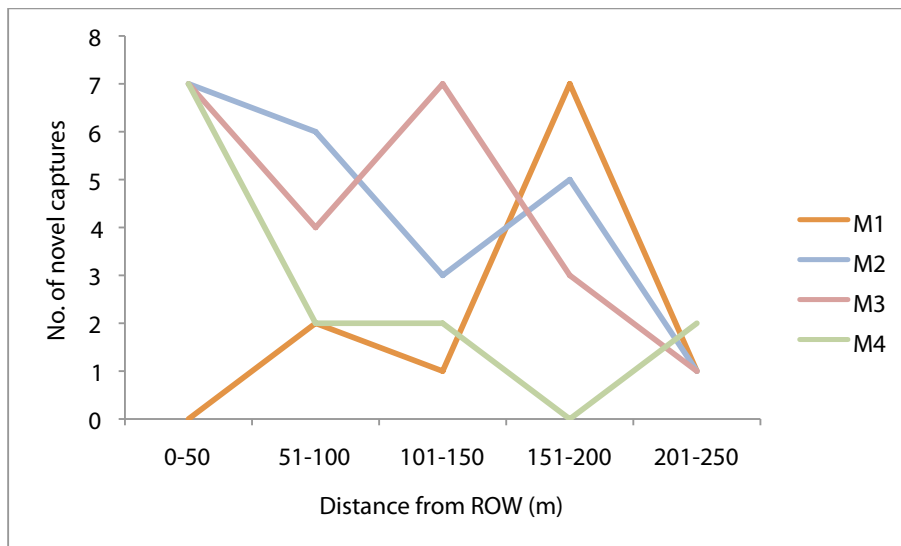


Figure 5.4. BAA 2 - trends in trap captures (all species combined) with increasing distance from the ROW (traps grouped in 50 m intervals).

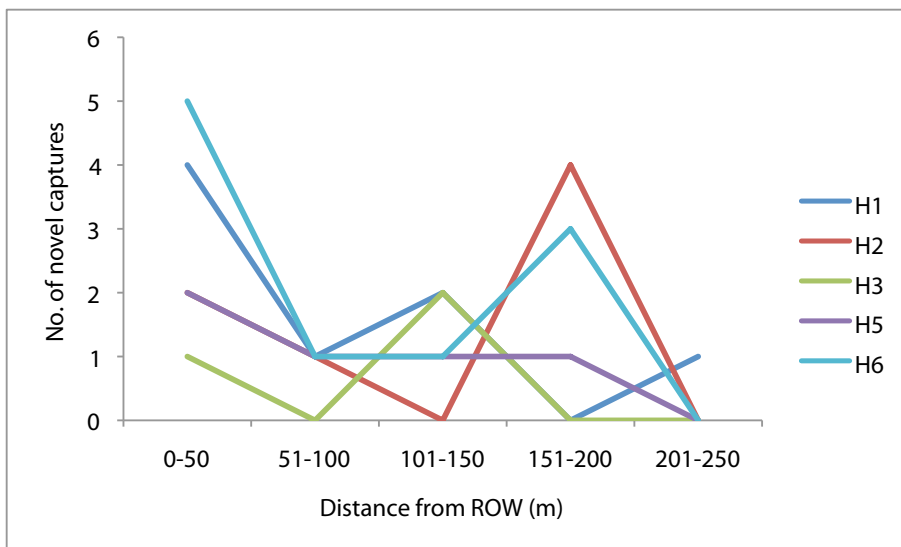


Figure 5.5. BAA 1 - trends in trap captures of *Rattus* spp. with increasing distance from the ROW (traps grouped in 50 m intervals).

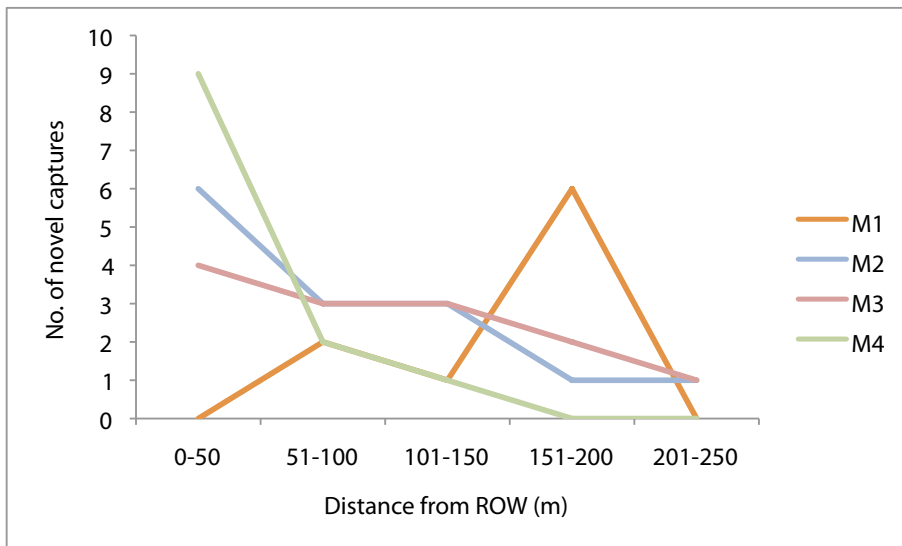


Figure 5.6. BAA 2 - trends in trap captures of *Rattus* spp. with increasing distance from the ROW (traps grouped in 50 m intervals).

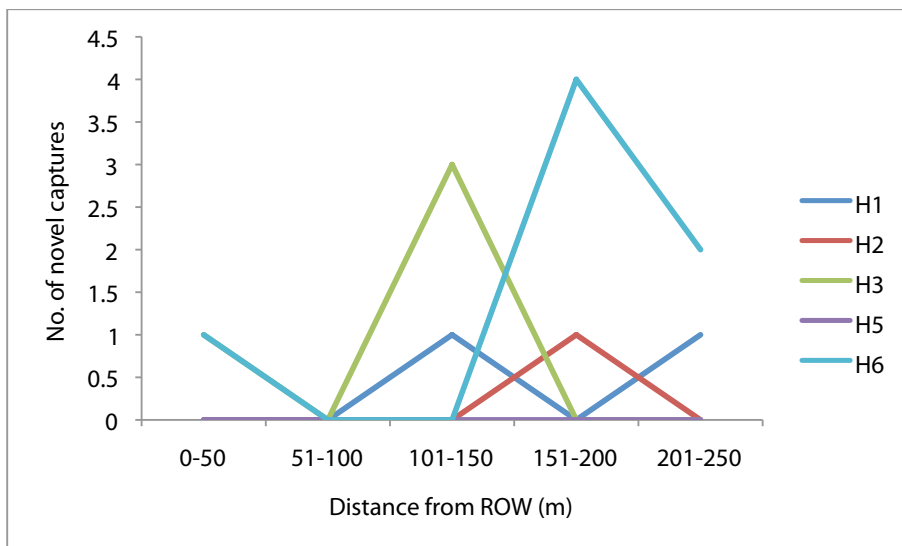


Figure 5.7. BAA 1 - trends in trap captures of *Paramelomys* species with increasing distance from the ROW (traps grouped in 50 m intervals).

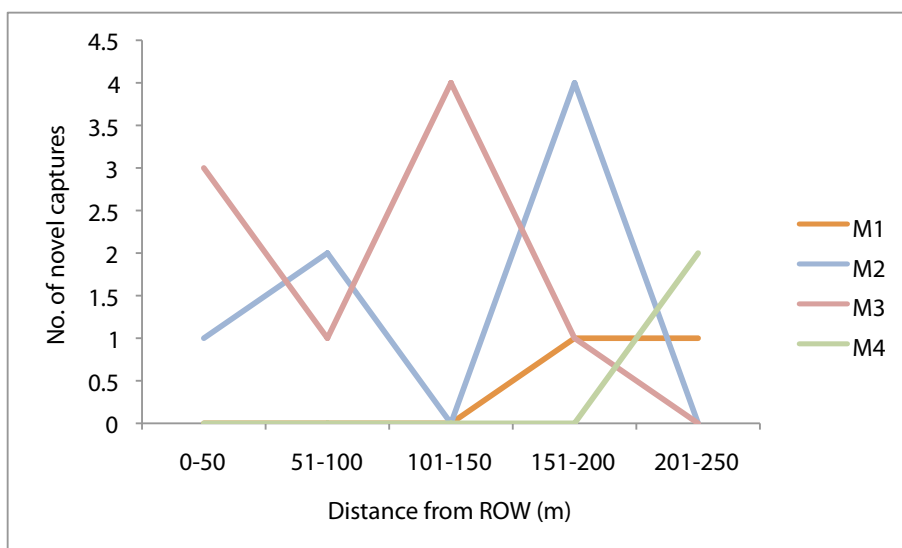


Figure 5.8. BAA 2 - trends in trap captures of *Paramelomys* species with increasing distance from the ROW (traps grouped in 50 m intervals).

ROW impacts (Objective 5)

Specific ROW impacts (those related directly to the existence and/or operation of the ROW) should be manifest as trends that are correlated with distance from the ROW.

When results are pooled for all species there is no obvious trend in either BAA 1 (Figure 5.3) or BAA 2 (Figure 5.4) in the novel captures of small mammals at increasing distance from the ROW. For *Rattus* species, six out of nine transects showed the highest number of captures within 50 m of the ROW (Figures 5.5 and 5.6); however, several transects also showed peaks in captures of *Rattus* at distances greater than 100 m from the ROW. By contrast, *Paramelomys* spp. shows a more consistent pattern of few captures within 100 m of the ROW and more captures at greater distances (Figure 5.7 and 5.8).

The statistical analysis using GLMM (see Appendix 5.6 for details) allowed for more rigorous testing of these trends by testing whether the likelihood of capture was random with respect to distance from the ROW or was more likely either closer to or further from the ROW.

For all species combined, the GLMM analysis found a slight but significant increase in capture likelihood for traps that were closer to the ROW rather than further from the ROW. It also revealed that novel captures tended to occur more often earlier in the trapping period (i.e. fewer new individuals were captured as the trapping continued on a site). For BAA 2 where recapture rates were high, this is probably indicative of trap saturation (i.e. captures of a high proportion of the total resident population). In BAA 1 recapture rates were very low and it is unlikely that all (or a majority) of resident individuals were trapped; trap avoidance following capture also seems likely in BAA 1.

GLMM analysis of captures for each of the two commonly captured rodent genera demonstrated that *Paramelomys* was more likely to be captured at greater distances from the ROW than closer to the ROW (see Appendix 5.6) while, for *Rattus*, the likelihood of capture appears not to be influenced random by distance from the ROW.

In summary, the GLMM results indicate that capture likelihood (and by inference, population densities) of *Paramelomys* spp. is lower in proximity to the ROW. Interestingly, the fact that a response was detected indicates that the impact may be at least partially restricted to the zone sampled by the transects (i.e. within c. 150–250m) of the ROW. Whether the impact is entirely contained within this zone or extends further into flanking forests cannot be answered from the present data.

The results for *Rattus* suggest that populations of *Rattus* spp. are not consistently advantaged or disadvantaged by proximity to the ROW. Rather, the captures appear to be patchy within many of the sites, with a strong suggestion of local 'hot-spots' in population density. This is not unexpected given the general characterization of *Rattus* spp. as 'disturbance' specialists—i.e. able to respond to local, short term pulses in resources such as often occur in association with phenomena such as tree fall and land slips (Dwyer 1984; Aplin and Ford 2010).

General habitat quality and potential indicators of change (Objective 6)

The mammal community in each of the BAAs appears to be largely intact, with no major gaps in trophic or taxonomic representation in at least three of the four elevational bands (transect M4, the Arakubi Quarry site, may be an exception – see below).

More specific indicators of general ecosystem health include:

- The presence at all sites of one or more of the largest, locally occurring herbivores (*Dorcopsulus* cf. *vanheurni* and *Dendrolagus notatus*);
- The presence at all sites of the largest native carnivore (New Guinea Quoll, *Dasyurus albopunctatus*) as well as 2–3 species of small carnivorous/insectivorous marsupials and rodents (*Murexia* spp., *Myoictis leucura*, *Leptomys* sp., *Parahydromys asper*);
- Mammal capture rates that are consistent with results obtained using similar methods in other recent surveys in southern Papua New Guinea (Aplin, unpublished data);
- The absence of exotic rodent species apart from along the very edge of the ROW at KP107; and

- The presence of a variety of small to large-bodied rodents including some species that are thought to possess specialized diets such as *Anisomys imitator*, *Hyomys* sp., *Leptomys* sp. and *Parahydromys asper*. None of these species are known to occur in degraded habitats anywhere within their broad geographic ranges.

Comparison of the mammal communities within each of the BAAs hints at some possible variation in habitat condition within each of the BAAs.

Within BAA 1 the composition of trap captures varied considerably among the transects (Figure 5.9). Transect H3 stands out for its high diversity and evenness of composition (i.e. no species is dominant). At the other extreme, transect H5 produced captures of only one rodent species, *Rattus* cf. *niobe* B; interestingly, this transect was characterised by numerous fallen trees and related disturbance, presumably a result of strong winds. The implication from these data is that *Rattus* cf. *niobe* B is relatively more disturbance tolerant than any of the species of *Paramelomys* that occur in BAA 1.

Within BAA 2 the three transects at KP107 all produced similar captures in which *R. cf. niobe* D was dominant and two species of *Paramelomys* were captured in smaller numbers (Figure 5.10). *Rattus exulans* also occurred on all three transects in this elevation band though all captures of this exotic species were made within a few meters of the roadside clearing.

Despite its close proximity to the KP107 site, the lower elevation transect M4 at Arakubi Quarry produced a very different rodent assemblage. The most frequently captured species at this site was the undescribed *Rattus* sp. 'spiny', which was not encountered elsewhere in BAA 1 or BAA 2. Most captures of this species were made within the regrowth habitat that fringes Arakubi Quarry, and only one was made within original forest habitat. Two species of *Paramelomys* were captured exclusively in the forest habitat. One of these species (*P. cf. rubex* B) was also captured at KP107 but the other, the Lowland *Paramelomys* (*P. platyops*) was not caught anywhere else in BAA 2 or in BAA 1.

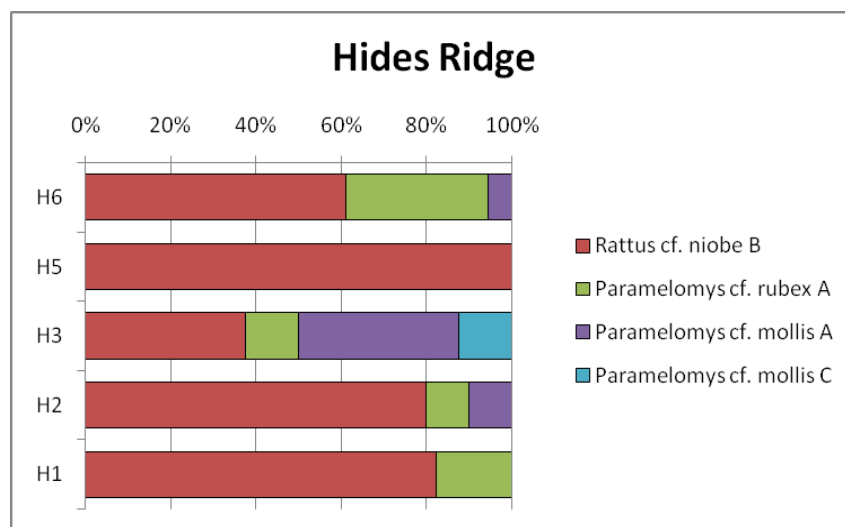


Figure 5.9. Composition of the small rodent captures made on each transect in BAA 1. The plotted values exclude recaptured individuals.

There are two potential indicators that habitat condition at Arakubi Quarry is inferior to that at the nearby KP107 transects. The first is that overall capture rate at this site is considerably lower (3.8% of trap nights vs 9.5–10.5% for KP107) with the majority of captures made in the first 100 m of transect which passed through scrub and secondary forest. The second is the apparent absence at this site of several species that were confirmed present at KP107 and were expected at Arakubi Quarry based on their elevational ranges elsewhere. The most notable absences are Lorentz's *Paramelomys* (*Paramelomys* cf. *lorentzii*), the omnivorous Raffray's Bandicoot (*Peroryctes raffrayana*), and the carnivorous rodent *Leptomys* sp., all of which were captured or imaged at moderate to high frequency at KP107 but were not detected at Arakubi Quarry (Table 5.9).

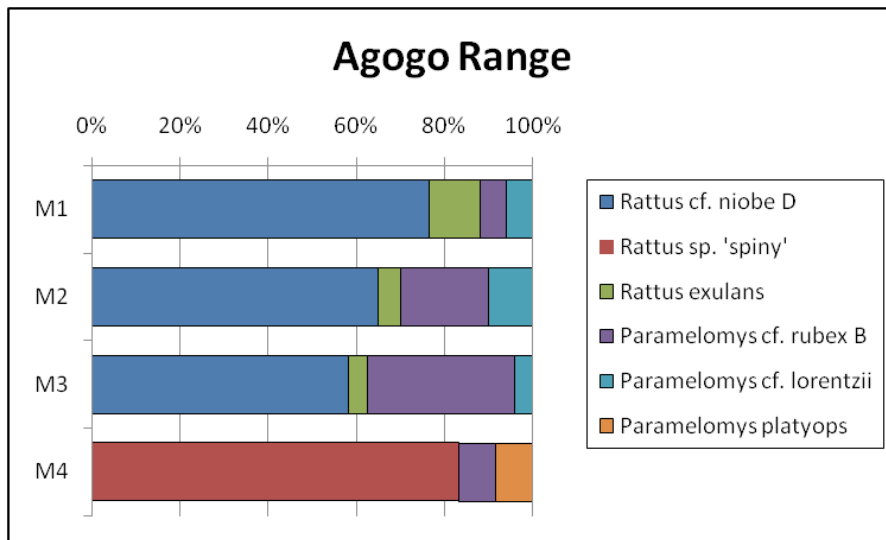


Figure 5.10. Composition of the small rodent captures made on each transect on the Agogo Range. The plotted values are exclusive of recaptured individuals.

For the lower elevation band in BAA 1 it is also possible to assess potential changes to habitat condition by comparing the 2015 survey results with information on the pre-construction mammal community. As mentioned in Methods (above) this historical information comes from two sources:

- The EIS survey conducted between 24 April and 1 May 2005 around the Hides 3 well site (now Wellpad D), at an elevation of 2,163 m asl; and
- A 'modern' owl roost sample from a small cave adjacent to the ROW at an elevation of c. 2,065 m asl.

The species lists for each of these sources are given in Table 5.10.

The 2005 EIS survey recorded 10 mammal species by direct observation including trapping. Unfortunately, trap capture statistics were not reported so no quantitative comparisons with the 2015 results are possible.

Six of the mammal species recorded in 2005 were not detected during the 2015 survey. All but one of these is exclusively or primarily arboreal and thus unlikely to be detected with the methods used in 2015. The exception is *Uromys anak*, a large scansorial rodent that was trapped in 2005 at the Hides 3 locality. Although this species can be trapped and also imaged by camera traps set on the ground, it is not particularly common anywhere within its range. It will most likely be detected in BAA 1 during future surveys.

The owl roost sample was collected and analyzed in a way that provides information on relative abundances of the various species (see Appendix 5.5 for details of methods). As such, it represents an excellent 'benchmark' for the pre-construction environment in the lower elevational band in BAA 1.

The owl roost sample contains many more species of small mammals than were trapped or imaged in 2015, including a range of additional terrestrial, scansorial and arboreal species. As is often the case with owl roost samples in New Guinea (Ken Aplin, unpublished data), the BAA 1 sample is dominated by the remains of arboreal rodents. In this case, the most common arboreal taxa are species of *Pogonomys*, *Chiruromys vates* and *Abeomelomys sevia*. These species may still be abundant in this area; unless special methods are employed to detect them (e.g. placement of traps or camera traps in the canopy) they are commonly underrepresented in survey results. On the other hand, the owl roost sample also contains a number of terrestrial and scansorial species, all of which can be trapped using standard methods. Some of these were indeed trapped in 2015 but others were not detected, despite an expectation that they would be found. Most notable among these potentially 'missing' taxa are *Rattus steini* and *R. verecundus*, *Protochromys fellowsi* and *Melomys* spp.

One possible explanation for the 'missing' species is that they reach their elevational limits at or below the elevation of the owl roost (2,065 m asl) and thus never occurred on the transects. This might be the case with *Rattus steini* and

Melomys cf. rufescens among the terrestrial/scansorial taxa, and also for *Chiruromys vates* and *Distoechurus cf. pennatus* among the arboreal taxa. For each of these taxa, occurrence at 2,065 m already represents an unusually high elevation record. In a similar way, the marsupial *Neophascogale cf. lorentzii*, which was detected on transects H5 and H6 but not in the owl roost sample, may reach its lower elevational limit on Hides Ridge above the owl roost—in fact there are few records of this species below 2,500 m anywhere across its wider geographic range.

Table 5.11. Comparison of the pre- and post-construction mammal fauna of the lower elevations of BAA 1 (2,100–2,400 m asl) as documented from various sources. Taxa from the Hides 3 survey that are marked with an * were reported as different taxa by Mamu et al. (2005; see Table 5.3 caption). Codes for ‘Habitus’; are: A = arboreal; S = scansorial; T = terrestrial.

Species	Habitus	Owl Roost 2011	Hides 3 2005	PMA3 2015
<i>Dasyurus albopunctatus</i>	S			+
<i>Murexia cf. habbema</i>	S	+		
<i>Murexia melanurus</i>	S	+		
<i>Murexia naso</i>	S	+		+
<i>Neophascogale cf. lorentzii</i>	S			+
<i>Microperoryctes ornata</i>	T	+	+	+
<i>Peroryctes raffrayana</i>	T			+
<i>Distoechurus cf. pennatus</i>	A	+		
<i>Cercartetus cf. caudatus</i>	A	+		
<i>Petaurus cf. breviceps</i>	A	+	+	
<i>Pseudochirulus larvatus</i>	A	+		
<i>Pseudochirulus mayeri</i>	A	+		
<i>Pseudochirops cupreus</i>	A		+	
<i>Phalanger carmelitae</i>	A		+	
<i>Phalanger sericeus</i>	A		+	
<i>Dorcopsulus cf. vanheurni</i>	T			+
<i>Abeomelomys sevia</i>	A	+		
<i>Chiruromys vates</i>	A	+		
<i>Hyomys sp.</i>	S			+
<i>Lorentzimys cf. nouhuysi</i>	A	+	+	
<i>Melomys cf. dollmani</i>	S	+		
<i>Melomys cf. rufescens</i>	S	+	+	
<i>Paramelomys cf. mollis</i>	T	+		+
<i>Paramelomys cf. rubex</i>	T	+	+	+
<i>Protochromys fellowsi</i>	T	+		
<i>Pogonomys cf. macrourus</i>	A	+		
<i>Pogonomys cf. loriae</i>	A	+		
<i>Rattus cf. niobe</i>	T	+	+	+
<i>Rattus steini</i>	T	+		
<i>Rattus cf. verecundus</i>	T	+		
<i>Uromys anak</i>	S		+	
Total species recorded		23	10	8

To compare the owl roost sample and the 2015 survey results in a more quantitative way it is necessary to control for the different modes of collection of the two assemblages—one derived from ground trapping and camera trapping, and the other from hunting by an aerial predator. While this cannot be done in any definitive way, a reasonable first step is to limit the comparison to terrestrial and scansorial species (i.e. only counting those species that might be reasonably expected to enter live traps set on the ground). This comparison is shown in Table 5.12.

Table 5.12. Quantitative comparison of the terrestrial/scansorial mammals found in the owl roost (i.e. pre-construction sample) and recorded during the 2015 survey (post-construction) by trapping and camera trapping. Contrasts that may indicate changes in species abundances in the environment are highlighted in grey.

Taxon	Owl Roost	Owl Roost %	Trapping (H1-3)	Trapping %	Camera Trapping
<i>Murexia naso</i>	2	2.1%			*
<i>Murexia melanurus</i>	3	3.2%			
<i>Murexia cf. habbema</i>	2	2.1%			
<i>Microperoryctes ornata</i>	1	1.1%	100.0%	2.8%	*
<i>Melomys cf. dollmani</i>	12	12.8%			
<i>Melomys cf. rufescens</i>	9	9.6%			
<i>Protochromys cf. fellowsi</i>	2	2.1%			
<i>Melomys</i> or <i>Protochromys</i>	28	29.8%			
<i>Paramelomys cf. mollis</i>	12	12.8%	500.0%	13.9%	*
<i>Paramelomys cf. rubex</i>	6	6.4%	500.0%	13.9%	*
<i>Rattus cf. niobe</i>	12	12.8%	2500.0%	69.4%	*
<i>Rattus steini</i>	2	2.1%			
<i>Rattus cf. verecundus</i>	3	3.2%			
Total for all taxa	94		3600.0%		

After limiting the comparisons in this way, the most notable differences between the owl roost sample and the 2015 survey results are the higher than expected rate of capture of *Rattus cf. niobe*, a disturbance tolerant species (Dwyer 1984; Aplin and Ford 2014), and the lower than expected captures of *Paramelomys cf. rubex*, *Melomys* spp. and *Protochromys cf. fellowsi*, all of which are more typically found in less disturbed contexts in montane habitats (Flannery 1995; Aplin, unpublished data). These apparent differences in small mammal abundance raise the possibility that more pervasive changes in habitat quality have occurred in the lower elevational band on Hides Ridge. This possibility requires further investigation, firstly to confirm or refute that such changes have occurred, and secondly, to determine the scale and causality of any changes. The first issue might be resolved in one of two ways. One way would be to recover and analyse owl roost remains deposited in the same cave since the creation of the ROW. This method would eliminate uncertainties related to differences in selection between owl predation and trapping. The second option is to conduct additional trapping and camera trapping activities in a range of habitats around the owl roost site. This will not remove the potential selection biases but will determine whether or not some of the ‘missing’ species still occur in the lower elevational band in BAA 1.

The second issue will be more difficult to resolve—establishing causality of an ecological change is often a complex undertaking. In this case the key question to ask is whether any changes in the mammal community and wider habitat are related to the installation and operation of the ROW or to unrelated external factors, such as climate change. To make this determination with any certainty it will be necessary to obtain data from one or more ‘control’ sites—localities that are more remote from the influence of the project infrastructure but are at comparable elevations and support equivalent plant and animal communities.

CONCLUSIONS

1. The non-volant mammal community appears to be substantially if not wholly intact in both BAAs, at least in terms of species inventories for terrestrial and scansorial mammals. The status of arboreal mammals was not assessed in any systematic fashion in 2015.
2. The confirmed survival in BAA 1 of the Endangered Western Montane Tree Kangaroo (*Dendrolagus notatus*) and its occurrence within 200–250m of the ROW is a notable finding given the acknowledged sensitivity of all tree kangaroos to disturbance and their high status value for hunting.
3. The occurrence of the Near Threatened Small Forest Wallaby (*Dorcopus cf. vanheurni*) in both BAAs identifies the upper Kikori Basin as a potential conservation stronghold for this undescribed species. Contrary to expectation, the highest population densities appear to be present at the lower altitudes in BAA 2 rather than in BAA 1. This may be due to predation by feral dogs in BAA 1 (see below).
4. The trapping program produced evidence that some small ground mammals are less common in close proximity to the ROW although the casual mechanism (e.g. noise, depletion of food resources) is not known. In contrast, a small number of native species, most notably members of the genus *Rattus*, appear to adapt well to the loss of forest cover along the road margin which has produced a distinctive habitat type.
5. Two of the nine transects investigated in 2015 show localized deterioration of habitat condition – 1) Transect Line H5 in the upper elevational zone in BAA 1 which has suffered from extensive tree falls in recent times, presumably during high winds; and 2) Arakubi Quarry in BAA 2 that has experienced a long history of disturbance associated with extraction of quarry materials. Both localities show lower than expected diversity with some anticipated species being uncommon or absent.
6. Comparison of the 2015 trapping results for the lower elevational band in BAA 1 with data from pre-construction times reveals some notable points of contrast that hint at potentially broader changes within the small mammal community.
7. Data from 'control' sites that are further away from the influence of the ROW would best help to determine whether or not these changes are related to the installation and operation of the ROW or to unrelated external factors, such as climate change.
8. Invasive rodents (Pacific Rat, *Rattus exulans*) were detected close to the ROW at KP107 in BAA 2 but were not detected in BAA 1. However, a second species of invasive rodent, the Black Rat (*Rattus rattus*) was recorded at HGCP; this species is identified as a potential short-term biosecurity risk to BAA 1 and a longer term risk at a wider regional level.
9. Feral dogs are active across the full elevational range in BAA 1 They appear to use the ROW to move across the rugged landscape and are predating the Near Threatened Small Forest Wallaby and probably other species of conservation concern as well. Predation on native herbivores could potentially lead to wider indirect impacts on plant and animal communities.

REFERENCES

- Aplin, K. 2015. Chapter 8. Ongoing discovery of mammal diversity in New Guinea. Pp. 137-142 in Bryan, J. E. & Shearman, P. L. (eds) *The State of the Forests of Papua New Guinea 2014: Measuring change over the period 2002-2014*. University of Papua New Guinea, Port Moresby.
- Aplin, K. P. & Ford, F. 2013. Chapter 10. Murine rodents: late but highly successful invaders. Pp. 196-240 in Prins, H. H. and Gordon, I. J. (eds.). *Invasion Biology and Ecological Theory: Insights from a Continent in Transformation*. Cambridge University Press, Cambridge.
- Aplin, K. P. & Kale, E. 2011. Non-volant mammals of the Muller Range, Papua New Guinea. Pp. 210-221 in Richards, S. J. & Gamui, B. G. (eds) *Rapid Biological Assessments of the Nakanai Mountains and the upper Strickland Basin: surveying the biodiversity of Papua New Guinea's sublime karst environments*. RAP Bulletin of Biological Assessment 60. Conservation International, Arlington, Virginia, U.S.A.
- Aplin K.P., Suzuki H., Chinen, A. A., Chesser, R. T., ten Have, J., Donnellan, S. C., Austin, J., Frost, A., Gonzalez, J.-P.,Herbreteau, V., Catzeflis, F., Soubrier, J., Fang, Y.-P., Robins, J., Matisoo-Smith, E., Bastos, A. D. S., Maryanto, I., Sinaga, M. H., Denys, C., Yap, G., Van Den Bussche, R. A., Conroy, C., Rowe, K. & Cooper, A. 2011. Multiple geographic origins of commensalism and complex dispersal history of black rats. *PLoS One* 6: e26357.
- Crome, F. H. J. *et al.* 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: *The PNG LNG Project Environmental Impact Statement*. Prepared by Coffey Natural Systems for Esso Highlands Limited.
- Dwyer, P. D. 1984. From garden to forest: small rodents and plant succession in Papua New Guinea. *Australian Mammalogy* 7: 29-36.
- Flannery, T. F. 1995. *The Mammals of New Guinea*. Revised Edition. Reed Books, Chatswood, NSW.
- ICZN 1999. *International Code of Zoological Nomenclature*. 4th Edition. The International Trust for Zoological Nomenclature 1999.
- Mamu, T., Gebia, O., Enoch, I., Namu, R., Kuduk, M. & Ona, A. 2006. Report for an Assessment Survey of Terrestrial Mammals for Papua New Guinea Gas Project, Papua New Guinea. Prepared by *WWF Kikori Integrated Conservation and Development Project* for Enesar Consulting Pty Ltd, June 2006. Included as 'Annex 03. Biodiversity survey results: Non volant mammals at Hides, Nogoli and Benaria in 2005' in the Papua New Guinea LNG Project Environmental Impact Statement Part II. Existing Environment, prepared by Coffey Natural Systems Pty Ltd for Esso Highlands Ltd, January 2009
- Menzies, J. I. 2011. *A Handbook of New Guinea's Marsupials and Monotremes*. 2nd Edition. University of Papua New Guinea Press, Port Moresby, P.N.G.
- Menzies, J. I. & Dennis, E. 1979. *Handbook of New Guinea rodents*. Handbook No. 6, Wau Ecology Institute, Wau, Papua New Guinea.
- Richards, S. J. & Gamui, B. G. (eds) 2011. *Rapid Biological Assessments of the Nakanai Mountains and the upper Strickland Basin: surveying the biodiversity of Papua New Guinea's sublime karst environments*. RAP Bulletin of Biological Assessment 60. Conservation International, Arlington, Virginia, U.S.A.
- Robins, J. H., Tintinger, V., Aplin, K. P., Hingston, M., Matisoo-Smith, E., Penny, D., & Lavery, S. D. 2014. Phylogenetic Species identification in *Rattus* highlights rapid radiation and morphological similarity of New Guinean species. *PloS one*, 9: e98002.
- Zachos, F. E. 2015. *Handbook of the Mammals of the World. Vol. 5. Monotremes and Marsupials*. Lynx Edicions, Barcelona.

Some small mammals captured during the non-volant mammals survey



Figure 5.11. An Ornate Bandicoot (*Microperoryctes ornata*) trapped on transect H1 in BAA1.



Figure 5.12. A Thomas's Paramelomys (*Paramelomys* cf. *mollis* A) trapped on transect H3 in BAA 1.



Figure 5.13. A Lowland Paramelomys (*Paramelomys platyops*) trapped at Arakubi Quarry in BAA 2.



Figure 5.14. A Mountain Paramelomys (*Paramelomys* cf. *rubex* A) trapped on transect H3 in BAA 1



Figure 5.15. A Moss Forest Rat (*Rattus* cf. *niobe* B) trapped on transect H1 in BAA 1.



Figure 5.16. An undescribed species of Rattus (*Rattus* sp. 'spiny') trapped at Arakubi Quarry in BAA 2.

APPENDICES

Appendix 5.1. GPS data (WGS84 datum) for the start point of each transect and for each trapping station.

Type of traps: SE - small Elliott; LE - large Elliott.

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 1 H1	H1-0	Start Point	S5.97239	E142.75336	2156 m
BAA 1 H1	H1-1	LE	S5.97237	E142.75331	2176 m
BAA 1 H1	H1-2	SE	S5.97245	E142.75330	2167 m
BAA 1 H1	H1-2.1	SE	S5.97247	E142.75331	2167 m
BAA 1 H1	H1-2.2	SE	S5.97248	E142.75340	2167 m
BAA 1 H1	H1-2.3	SE	S5.97250	E142.75342	2169 m
BAA 1 H1	H1-2.4	SE	S5.97244	E142.75332	2164 m
BAA 1 H1	H1-2.5	SE	S5.97243	E142.75330	2165 m
BAA 1 H1	H1-2.6	SE	S5.97237	E142.75320	2163 m
BAA 1 H1	H1-3	SE	S5.97240	E142.75328	2174 m
BAA 1 H1	H1-4	SE	S5.97241	E142.75328	2172 m
BAA 1 H1	H1-5	SE	S5.97242	E142.75327	2169 m
BAA 1 H1	H1-6	SE	S5.97245	E142.75325	2171 m
BAA 1 H1	H1-7	SE	S5.97253	E142.75325	2172 m
BAA 1 H1	H1-8	SE	S5.97266	E142.75317	2173 m
BAA 1 H1	H1-9	SE	S5.97277	E142.75311	2170 m
BAA 1 H1	H1-10	SE	S5.97288	E142.75295	2171 m
BAA 1 H1	H1-11	LE	S5.97305	E142.75297	2174 m
BAA 1 H1	H1-12	SE	S5.97304	E142.75295	2176 m
BAA 1 H1	H1-13	SE	S5.97314	E142.75291	2176 m
BAA 1 H1	H1-14	SE	S5.97326	E142.75276	2171 m
BAA 1 H1	H1-15	SE	S5.97329	E142.75278	2170 m
BAA 1 H1	H1-16	SE	S5.97339	E142.75281	2171 m
BAA 1 H1	H1-17	SE	S5.97366	E142.75256	2168 m
BAA 1 H1	H1-18	SE	S5.97368	E142.75253	2169 m
BAA 1 H1	H1-19	SE	S5.97370	E142.75250	2166 m
BAA 1 H1	H1-20	SE	S5.97370	E142.75249	2166 m
BAA 1 H1	H1-21	LE	S5.97370	E142.75249	2163 m
BAA 1 H1	H1-22	SE	S5.97370	E142.75248	2162 m
BAA 1 H1	H1-23	SE	S5.97370	E142.75248	2162 m
BAA 1 H1	H1-24	SE	S5.97370	E142.75247	2160 m
BAA 1 H1	H1-25	SE	S5.97381	E142.75232	2159 m
BAA 1 H1	H1-26	SE	S5.97376	E142.75236	2158 m
BAA 1 H1	H1-27	SE	S5.97375	E142.75254	2155 m
BAA 1 H1	H1-28	SE	S5.97381	E142.75222	2155 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 1 H1	H1-29	SE	S5.97389	E142.75227	2155 m
BAA 1 H1	H1-30	SE	S5.97390	E142.75224	2157 m
BAA 1 H1	H1-31	LE	S5.97396	E142.75224	2157 m
BAA 1 H1	H1-32	SE	S5.97405	E142.75216	2156 m
BAA 1 H1	H1-33	SE	S5.97406	E142.75217	2154 m
BAA 1 H1	H1-34	SE	S5.97407	E142.75207	2155 m
BAA 1 H1	H1-35	SE	S5.97405	E142.75216	2155 m
BAA 1 H2	H2-0	Start Point	S5.96907	E142.75124	2169 m
BAA 1 H2	H2-1	LE	S5.96915	E142.75110	2175 m
BAA 1 H2	H2-2	SE	S5.96914	E142.75109	2177 m
BAA 1 H2	H2-2.1	SE	S5.96916	E142.75109	2177 m
BAA 1 H2	H2-2.2	SE	S5.96918	E142.75109	2176 m
BAA 1 H2	H2-2.3	SE	S5.96920	E142.75109	2175 m
BAA 1 H2	H2-2.4	SE	S5.96913	E142.75109	2177 m
BAA 1 H2	H2-2.5	SE	S5.96911	E142.75109	2177 m
BAA 1 H2	H2-2.6	SE	S5.96910	E142.75109	2178 m
BAA 1 H2	H2-3	SE	S5.96917	E142.75102	2178 m
BAA 1 H2	H2-4	SE	S5.96918	E142.75100	2181 m
BAA 1 H2	H2-5	SE	S5.96914	E142.75095	2183 m
BAA 1 H2	H2-6	SE	S5.96916	E142.75079	2186 m
BAA 1 H2	H2-7	SE	S5.96918	E142.75074	2186 m
BAA 1 H2	H2-8	SE	S5.96913	E142.75057	2189 m
BAA 1 H2	H2-9	SE	S5.96913	E142.75056	2192 m
BAA 1 H2	H2-10	SE	S5.96912	E142.75054	2196 m
BAA 1 H2	H2-11	LE	S5.96912	E142.75052	2199 m
BAA 1 H2	H2-12	SE	S5.96911	E142.75045	2203 m
BAA 1 H2	H2-13	SE	S5.96915	E142.75037	2207 m
BAA 1 H2	H2-14	SE	S5.96917	E142.75032	2207 m
BAA 1 H2	H2-15	SE	S5.96923	E142.75025	2209 m
BAA 1 H2	H2-16	SE	S5.96926	E142.75020	2209 m
BAA 1 H2	H2-17	SE	S5.96930	E142.75017	2210 m
BAA 1 H2	H2-18	SE	S5.96926	E142.75002	2212 m
BAA 1 H2	H2-19	SE	S5.96922	E142.74994	2217 m
BAA 1 H2	H2-20	SE	S5.96919	E142.74991	2221 m
BAA 1 H2	H2-21	LE	S5.96915	E142.74987	2221 m
BAA 1 H2	H2-22	SE	S5.96912	E142.74977	2223 m
BAA 1 H2	H2-23	SE	S5.96910	E142.74975	2225 m
BAA 1 H2	H2-24	SE	S5.96908	E142.74970	2227 m
BAA 1 H2	H2-25	SE	S5.96905	E142.74967	2229 m
BAA 1 H2	H2-26	SE	S5.96906	E142.74957	2231 m
BAA 1 H2	H2-27	SE	S5.96906	E142.74953	2232 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 1 H2	H2-28	SE	S5.96908	E142.74946	2233 m
BAA 1 H2	H2-29	SE	S5.96909	E142.74941	2233 m
BAA 1 H2	H2-30	SE	S5.96909	E142.74932	2233 m
BAA 1 H2	H2-31	LE	S5.96911	E142.74927	2232 m
BAA 1 H2	H2-32	SE	S5.96913	E142.74920	2234 m
BAA 1 H2	H2-33	SE	S5.96914	E142.74917	2235 m
BAA 1 H2	H2-34	SE	S5.96913	E142.74912	2236 m
BAA 1 H2	H2-35	SE	S5.96914	E142.74914	2235 m
BAA 1 H3	H3-0	Start Point	S5.94376	E142.74178	2297 m
BAA 1 H3	H3-1	LE	S5.94376	E142.74178	2297 m
BAA 1 H3	H3-2	SE	S5.94374	E142.74176	2298 m
BAA 1 H3	H3-2.1	SE	S5.94383	E142.74186	2288 m
BAA 1 H3	H3-2.2	SE	S5.94382	E142.74188	2288 m
BAA 1 H3	H3-2.3	SE	S5.94381	E142.74193	2287 m
BAA 1 H3	H3-2.4	SE	S5.94385	E142.74170	2290 m
BAA 1 H3	H3-2.5	SE	S5.94397	E142.74163	2288 m
BAA 1 H3	H3-2.6	SE	S5.94389	E142.74152	2291 m
BAA 1 H3	H3-3	SE	S5.94379	E142.74176	2299 m
BAA 1 H3	H3-4	SE	S5.94388	E142.74177	2302 m
BAA 1 H3	H3-5	SE	S5.94391	E142.74177	2302 m
BAA 1 H3	H3-6	SE	S5.94394	E142.74178	2300 m
BAA 1 H3	H3-7	SE	S5.94402	E142.74177	2301 m
BAA 1 H3	H3-8	SE	S5.94409	E142.74178	2301 m
BAA 1 H3	H3-9	SE	S5.94419	E142.74180	2301 m
BAA 1 H3	H3-10	SE	S5.94429	E142.74179	2301 m
BAA 1 H3	H3-11	LE	S5.94436	E142.74178	2300 m
BAA 1 H3	H3-12	SE	S5.94440	E142.74180	2298 m
BAA 1 H3	H3-13	SE	S5.94446	E142.74182	2296 m
BAA 1 H3	H3-14	SE	S5.94450	E142.74184	2294 m
BAA 1 H3	H3-15	SE	S5.94456	E142.74186	2294 m
BAA 1 H3	H3-16	SE	S5.94464	E142.74194	2295 m
BAA 1 H3	H3-17	SE	S5.94476	E142.74189	2297 m
BAA 1 H3	H3-18	SE	S5.94483	E142.74190	2299 m
BAA 1 H3	H3-19	SE	S5.94485	E142.74190	2302 m
BAA 1 H3	H3-20	SE	S5.94490	E142.74189	2305 m
BAA 1 H3	H3-21	LE	S5.94506	E142.74187	2307 m
BAA 1 H3	H3-22	SE	S5.94508	E142.74185	2310 m
BAA 1 H3	H3-23	SE	S5.94513	E142.74182	2313 m
BAA 1 H3	H3-24	SE	S5.94519	E142.74165	2315 m
BAA 1 H3	H3-25	SE	S5.94525	E142.74163	2315 m
BAA 1 H3	H3-26	SE	S5.94530	E142.74163	2317 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 1 H3	H3-27	SE	S5.94537	E142.74159	2318 m
BAA 1 H3	H3-28	SE	S5.94544	E142.74155	2320 m
BAA 1 H3	H3-29	SE	S5.94547	E142.74153	2322 m
BAA 1 H3	H3-30	SE	S5.94550	E142.74148	2322 m
BAA 1 H3	H3-31	LE	S5.94562	E142.74137	2324 m
BAA 1 H3	H3-32	SE	S5.94568	E142.74134	2326 m
BAA 1 H3	H3-33	SE	S5.94569	E142.74134	2327 m
BAA 1 H3	H3-34	SE	S5.94572	E142.74133	2329 m
BAA 1 H3	H3-35	SE	S5.94574	E142.74133	2334 m
BAA 1 H4	H4-0	Start Point	S5.91835	E142.69533	2700 m
BAA 1 H4	H4-01	LE	S5.91842	E142.69532	2700 m
BAA 1 H4	H4-02	SE	S5.91846	E142.69533	2701 m
BAA 1 H4	H4-2-1	SE	S5.91845	E142.69532	2700 m
BAA 1 H4	H4-2-2	SE	S5.91850	E142.69536	2699 m
BAA 1 H4	H4-2-3	SE	S5.91850	E142.69538	2697 m
BAA 1 H4	H4-2-4	SE	S5.91847	E142.69531	2702 m
BAA 1 H4	H4-2-5	SE	S5.91844	E142.69527	2700 m
BAA 1 H4	H4-2-6	SE	S5.91844	E142.69521	2700 m
BAA 1 H4	H4-03	SE	S5.91854	E142.69529	2700 m
BAA 1 H4	H4-04	SE	S5.91860	E142.69521	2700 m
BAA 1 H4	H4-05	SE	S5.91873	E142.69509	2697 m
BAA 1 H4	H4-06	SE	S5.91874	E142.69508	2695 m
BAA 1 H4	H4-07	SE	S5.91873	E142.69509	2693 m
BAA 1 H4	H4-08	SE	S5.91881	E142.69506	2694 m
BAA 1 H4	H4-09	SE	S5.91890	E142.69501	2695 m
BAA 1 H4	H4-10	SE	S5.91894	E142.69500	2695 m
BAA 1 H4	H4-11	LE	S5.91900	E142.69497	2694 m
BAA 1 H4	H4-12	SE	S5.91903	E142.69496	2694 m
BAA 1 H4	H4-13	SE	S5.91910	E142.69497	2697 m
BAA 1 H4	H4-14	SE	S5.91918	E142.69494	2698 m
BAA 1 H4	H4-15	SE	S5.91924	E142.69492	2699 m
BAA 1 H4	H4-16	SE	S5.91930	E142.69495	2699 m
BAA 1 H4	H4-17	SE	S5.91934	E142.69498	2698 m
BAA 1 H4	H4-18	SE	S5.91938	E142.69502	2697 m
BAA 1 H4	H4-19	SE	S5.91945	E142.69507	2694 m
BAA 1 H4	H4-20	SE	S5.91951	E142.69512	2694 m
BAA 1 H4	H4-21	LE	S5.91957	E142.69512	2693 m
BAA 1 H4	H4-22	SE	S5.91960	E142.69512	2694 m
BAA 1 H4	H4-23	SE	S5.91964	E142.69511	2693 m
BAA 1 H4	H4-24	SE	S5.91968	E142.69502	2704 m
BAA 1 H4	H4-25	SE	S5.91977	E142.69498	2696 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 1 H4	H4-26	SE	S5.91975	E142.69487	2700 m
BAA 1 H4	H4-27	SE	S5.92002	E142.69492	2690 m
BAA 1 H4	H4-28	SE	S5.92010	E142.69497	2685 m
BAA 1 H4	H4-29	SE	S5.92007	E142.69467	2682 m
BAA 1 H4	H4-30	SE	S5.92019	E142.69480	2682 m
BAA 1 H4	H4-31	LE	S5.92028	E142.69482	2687 m
BAA 1 H4	H4-32	SE	S5.92026	E142.69466	2687 m
BAA 1 H4	H4-33	SE	S5.92024	E142.69458	2690 m
BAA 1 H4	H4-34	SE	S5.92026	E142.69456	2692 m
BAA 1 H4	H4-35	SE	S5.92029	E142.69456	2694 m
BAA 1 H5	H5-0	Start Point	S5.91623	E142.69285	2764 m
BAA 1 H5	H5-1	LE	S5.91630	E142.69281	2766 m
BAA 1 H5	H5-2	SE	S5.91629	E142.69281	2763 m
BAA 1 H5	H5-2.1	SE	S5.91631	E142.69281	2756 m
BAA 1 H5	H5-2.2	SE	S5.91632	E142.69283	2753 m
BAA 1 H5	H5-2.3	SE	S5.91635	E142.69288	2753 m
BAA 1 H5	H5-2.4	SE	S5.91627	E142.69280	2758 m
BAA 1 H5	H5-2.5	SE	S5.91626	E142.69273	2756 m
BAA 1 H5	H5-2.6	SE	S5.91627	E142.69269	2755 m
BAA 1 H5	H5-3	SE	S5.91632	E142.69280	2762 m
BAA 1 H5	H5-4	SE	S5.91634	E142.69278	2760 m
BAA 1 H5	H5-5	SE	S5.91636	E142.69275	2758 m
BAA 1 H5	H5-6	SE	S5.91641	E142.69271	2756 m
BAA 1 H5	H5-7	SE	S5.91651	E142.69259	2755 m
BAA 1 H5	H5-8	SE	S5.91648	E142.69256	2754 m
BAA 1 H5	H5-9	SE	S5.91647	E142.69239	2753 m
BAA 1 H5	H5-10	SE	S5.91645	E142.69245	2755 m
BAA 1 H5	H5-11	LE	S5.91649	E142.69236	2752 m
BAA 1 H5	H5-12	SE	S5.91649	E142.69228	2753 m
BAA 1 H5	H5-13	SE	S5.91651	E142.69222	2753 m
BAA 1 H5	H5-14	SE	S5.91658	E142.69214	2755 m
BAA 1 H5	H5-15	SE	S5.91659	E142.69212	2754 m
BAA 1 H5	H5-16	SE	S5.91653	E142.69207	2753 m
BAA 1 H5	H5-17	SE	S5.91653	E142.69199	2752 m
BAA 1 H5	H5-18	SE	S5.91656	E142.69192	2751 m
BAA 1 H5	H5-19	SE	S5.91654	E142.69184	2750 m
BAA 1 H5	H5-20	SE	S5.91652	E142.69181	2750 m
BAA 1 H5	H5-21	LE	S5.91648	E142.69167	2748 m
BAA 1 H5	H5-22	SE	S5.91647	E142.69162	2745 m
BAA 1 H5	H5-23	SE	S5.91664	E142.69146	2744 m
BAA 1 H5	H5-24	SE	S5.91671	E142.69140	2742 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 1 H5	H5-25	SE	S5.91673	E142.69137	2741 m
BAA 1 H5	H5-26	SE	S5.91675	E142.69132	2741 m
BAA 1 H5	H5-27	SE	S5.91682	E142.69126	2739 m
BAA 1 H5	H5-28	SE	S5.91687	E142.69119	2738 m
BAA 1 H5	H5-29	SE	S5.91691	E142.69117	2737 m
BAA 1 H5	H5-30	SE	S5.91698	E142.69115	2731 m
BAA 1 H5	H5-31	LE	S5.91701	E142.69109	2736 m
BAA 1 H5	H5-32	SE	S5.91699	E142.69100	2735 m
BAA 1 H5	H5-33	SE	S5.91699	E142.69098	2731 m
BAA 1 H5	H5-34	SE	S5.91700	E142.69096	2729 m
BAA 1 H5	H5-35	SE	S5.91699	E142.69098	2726 m
BAA 1 H6	H6-0	Start Point	S5.91389	E142.69018	2714 m
BAA 1 H6	H6-1	LE	S5.91380	E142.69020	2735 m
BAA 1 H6	H6-2	SE	S5.91377	E142.69011	2739 m
BAA 1 H6	H6-2.1	SE	S5.91379	E142.69010	2737 m
BAA 1 H6	H6-2.2	SE	S5.91379	E142.69012	2736 m
BAA 1 H6	H6-2.3	SE	S5.91382	E142.69012	2736 m
BAA 1 H6	H6-2.4	SE	S5.91376	E142.69017	2737 m
BAA 1 H6	H6-2.5	SE	S5.91374	e142.69019	2740 m
BAA 1 H6	H6-2.6	SE	S5.91368	E142.69021	2741 m
BAA 1 H6	H6-3	SE	S5.91375	E142.68999	2740 m
BAA 1 H6	H6-4	SE	S5.91375	E142.68997	2740 m
BAA 1 H6	H6-5	SE	S5.91376	E142.68992	2740 m
BAA 1 H6	H6-6	SE	S5.91381	E142.68985	2742 m
BAA 1 H6	H6-7	SE	S5.91386	E142.68986	2740 m
BAA 1 H6	H6-8	SE	S5.91389	E142.68985	2743 m
BAA 1 H6	H6-9	SE	S5.91397	E142.68980	2742 m
BAA 1 H6	H6-10	SE	S5.91401	E142.68976	2742 m
BAA 1 H6	H6-11	LE	S5.91404	E142.68972	2743 m
BAA 1 H6	H6-12	SE	S5.91414	E142.68966	2741 m
BAA 1 H6	H6-13	SE	S5.91419	E142.68963	2739 m
BAA 1 H6	H6-14	SE	S5.91427	E142.68956	2739 m
BAA 1 H6	H6-15	SE	S5.91432	E142.68956	2737 m
BAA 1 H6	H6-16	SE	S5.91435	E142.68946	2738 m
BAA 1 H6	H6-17	SE	S5.91445	E142.68940	2738 m
BAA 1 H6	H6-18	SE	S5.91451	E142.68938	2738 m
BAA 1 H6	H6-19	SE	S5.91462	E142.68932	2735 m
BAA 1 H6	H6-20	SE	S5.91464	E142.68930	2734 m
BAA 1 H6	H6-21	LE	S5.91463	E142.68923	2732 m
BAA 1 H6	H6-22	SE	S5.91465	E142.68918	2732 m
BAA 1 H6	H6-23	SE	S5.91466	E142.68917	2731 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 1 H6	H6-24	SE	S5.91472	E142.68915	2730 m
BAA 1 H6	H6-25	SE	S5.91480	E142.68907	2730 m
BAA 1 H6	H6-26	SE	S5.91487	E142.68898	2726 m
BAA 1 H6	H6-27	SE	S5.91492	E142.68898	2729 m
BAA 1 H6	H6-28	SE	S5.91502	E142.68888	2730 m
BAA 1 H6	H6-29	SE	S5.91515	E142.68892	2727 m
BAA 1 H6	H6-30	SE	S5.91525	E142.68891	2728 m
BAA 1 H6	H6-31	LE	S5.91538	E142.68892	2730 m
BAA 1 H6	H6-32	SE	S5.91544	E142.68892	2727 m
BAA 1 H6	H6-33	SE	S5.91549	E142.68889	2727 m
BAA 1 H6	H6-34	SE	S5.91550	E142.68878	2727 m
BAA 1 H6	H6-35	SE	S5.91549	E142.68884	2724 m
BAA 2 M1	M1-0	Start Point	S6.44016	E143.22424	1400 m
BAA 2 M1	M1-1	LE	S6.44016	E143.22421	1397 m
BAA 2 M1	M1-2	SE	S6.44018	E143.22415	1395 m
BAA 2 M1	M1-2.1	SE	S6.44021	E143.22416	1394 m
BAA 2 M1	M1-2.2	SE	S6.44024	E143.22417	1396 m
BAA 2 M1	M1-2.3	SE	S6.44027	E143.22417	1394 m
BAA 2 M1	M1-2.4	SE	S6.44014	E143.22414	1395 m
BAA 2 M1	M1-2.5	SE	S6.44010	E143.22414	1393 m
BAA 2 M1	M1-2.6	SE	S6.44006	E143.22413	1394 m
BAA 2 M1	M1-3	SE	S6.44019	E143.22409	1401 m
BAA 2 M1	M1-4	SE	S6.44022	E143.22404	1398 m
BAA 2 M1	M1-5	SE	S6.44023	E143.22396	1395 m
BAA 2 M1	M1-6	SE	S6.44023	E143.22389	1393 m
BAA 2 M1	M1-7	SE	S6.44021	E143.22379	1390 m
BAA 2 M1	M1-8	SE	S6.44020	E143.22371	1394 m
BAA 2 M1	M1-9	SE	S6.44018	E143.22363	1396 m
BAA 2 M1	M1-10	SE	S6.44016	E143.22355	1400 m
BAA 2 M1	M1-11	LE	S6.44016	E143.22346	1401 m
BAA 2 M1	M1-12	SE	S6.44016	E143.22338	1396 m
BAA 2 M1	M1-13	SE	S6.44016	E143.22332	1397 m
BAA 2 M1	M1-14	SE	S6.44016	E143.22326	1394 m
BAA 2 M1	M1-15	SE	S6.44017	E143.22320	1390 m
BAA 2 M1	M1-16	SE	S6.44018	E143.22313	1395 m
BAA 2 M1	M1-17	SE	S6.44018	E143.22305	1399 m
BAA 2 M1	M1-18	SE	S6.44017	E143.22297	1398 m
BAA 2 M1	M1-19	SE	S6.44017	E143.22289	1395 m
BAA 2 M1	M1-20	SE	S6.44017	E143.22281	1397 m
BAA 2 M1	M1-21	LE	S6.44016	E143.22273	1401 m
BAA 2 M1	M1-22	SE	S6.44014	E143.22267	1403 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 2 M1	M1-23	SE	S6.44013	E143.22262	1402 m
BAA 2 M1	M1-24	SE	S6.44011	E143.22257	1402 m
BAA 2 M1	M1-25	SE	S6.44006	E143.22253	1406 m
BAA 2 M1	M1-26	SE	S6.44004	E143.22248	1404 m
BAA 2 M1	M1-27	SE	S6.43998	E143.22248	1400 m
BAA 2 M1	M1-28	SE	S6.43991	E143.22249	1401 m
BAA 2 M1	M1-29	SE	S6.43985	E143.22250	1404 m
BAA 2 M1	M1-30	SE	S6.43979	E143.22251	1399 m
BAA 2 M1	M1-31	LE	S6.43973	E143.22248	1401 m
BAA 2 M1	M1-32	SE	S6.43970	E143.22244	1403 m
BAA 2 M1	M1-33	SE	S6.43965	E143.22242	1404 m
BAA 2 M1	M1-34	SE	S6.43959	E143.22245	1408 m
BAA 2 M1	M1-35	SE	S6.43954	E143.22244	1404 m
BAA 2 M2	M2-0	Start Point	S6.44052	E143.22558	1390 m
BAA 2 M2	M2-1	LE	S6.44060	E143.22554	1385 m
BAA 2 M2	M2-2	SE	S6.44069	E143.22554	1380 m
BAA 2 M2	M2-2.1	SE	S6.44069	E143.22561	1384 m
BAA 2 M2	M2-2.2	SE	S6.44068	E143.22567	1382 m
BAA 2 M2	M2-2.3	SE	S6.44067	E143.22575	1379 m
BAA 2 M2	M2-2.4	SE	S6.44067	E143.22546	1384 m
BAA 2 M2	M2-2.5	SE	S6.44066	E143.22539	1385 m
BAA 2 M2	M2-2.6	SE	S6.44064	E143.22533	1382 m
BAA 2 M2	M2-3	SE	S6.44075	E143.22552	1378 m
BAA 2 M2	M2-4	SE	S6.44084	E143.22553	1378 m
BAA 2 M2	M2-5	SE	S6.44091	E143.22556	1384 m
BAA 2 M2	M2-6	SE	S6.44099	E143.22559	1379 m
BAA 2 M2	M2-7	SE	S6.44106	E143.22558	1385 m
BAA 2 M2	M2-8	SE	S6.44113	E143.22555	1389 m
BAA 2 M2	M2-9	SE	S6.44117	E143.22551	1384 m
BAA 2 M2	M2-10	SE	S6.44124	E143.22545	1380 m
BAA 2 M2	M2-11	LE	S6.44128	E143.22541	1378 m
BAA 2 M2	M2-12	SE	S6.44134	E143.22538	1365 m
BAA 2 M2	M2-13	SE	S6.44139	E143.22532	1353 m
BAA 2 M2	M2-14	SE	S6.44141	E143.22526	1344 m
BAA 2 M2	M2-15	SE	S6.44142	E143.22520	1346 m
BAA 2 M2	M2-16	SE	S6.44145	E143.22516	1332 m
BAA 2 M2	M2-17	SE	S6.44149	E143.22512	1324 m
BAA 2 M2	M2-18	SE	S6.44154	E143.22506	1315 m
BAA 2 M2	M2-19	SE	S6.44158	E143.22502	1332 m
BAA 2 M2	M2-20	SE	S6.44164	E143.22500	1348 m
BAA 2 M2	M2-21	LE	S6.44169	E143.22502	1352 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 2 M2	M2-22	SE	S6.44174	E143.22502	1370 m
BAA 2 M2	M2-23	SE	S6.44179	E143.22503	1375 m
BAA 2 M2	M2-24	SE	S6.44184	E143.22504	1384 m
BAA 2 M2	M2-25	SE	S6.44191	E143.22505	1391 m
BAA 2 M2	M2-26	SE	S6.44197	E143.22503	1395 m
BAA 2 M2	M2-27	SE	S6.44202	E143.22500	1388 m
BAA 2 M2	M2-28	SE	S6.44208	E143.22493	1395 m
BAA 2 M2	M2-29	SE	S6.44211	E143.22486	1392 m
BAA 2 M2	M2-30	SE	S6.44218	E143.22479	1389 m
BAA 2 M2	M2-31	LE	S6.44221	E143.22474	1392 m
BAA 2 M2	M2-32	SE	S6.44225	E143.22473	1396 m
BAA 2 M2	M2-33	SE	S6.44230	E143.22472	1398 m
BAA 2 M2	M2-34	SE	S6.44235	E143.22468	1399 m
BAA 2 M2	M2-35	SE	S6.44240	E143.22463	1394 m
BAA 2 M3	M3-0	Start Point	S6.44170	E143.22722	1385 m
BAA 2 M3	M3-1	LE	S6.44172	E143.22717	1377 m
BAA 2 M3	M3-2	SE	S6.44178	E143.22710	1380 m
BAA 2 M3	M3-2.1	SE	S6.44179	E143.22714	1382 m
BAA 2 M3	M3-2.2	SE	S6.44183	E143.22718	1378 m
BAA 2 M3	M3-2.3	SE	S6.44186	E143.22721	1382 m
BAA 2 M3	M3-2.4	SE	S6.44174	E143.22707	1385 m
BAA 2 M3	M3-2.5	SE	S6.44170	E143.22704	1378 m
BAA 2 M3	M3-2.6	SE	S6.44166	E143.22701	1383 m
BAA 2 M3	M3-3	SE	S6.44184	E143.22708	1369 m
BAA 2 M3	M3-4	SE	S6.44187	E143.22703	1373 m
BAA 2 M3	M3-5	SE	S6.44191	E143.22699	1369 m
BAA 2 M3	M3-6	SE	S6.44195	E143.22693	1367 m
BAA 2 M3	M3-7	SE	S6.44198	E143.22688	1376 m
BAA 2 M3	M3-8	SE	S6.44202	E143.22683	1375 m
BAA 2 M3	M3-9	SE	S6.44207	E143.22677	1378 m
BAA 2 M3	M3-10	SE	S6.44213	E143.22669	1374 m
BAA 2 M3	M3-11	LE	S6.44218	E143.22663	1372 m
BAA 2 M3	M3-12	SE	S6.44224	E143.22660	1376 m
BAA 2 M3	M3-13	SE	S6.44231	E143.22657	1369 m
BAA 2 M3	M3-14	SE	S6.44239	E143.22651	1375 m
BAA 2 M3	M3-15	SE	S6.44246	E143.22648	1378 m
BAA 2 M3	M3-16	SE	S6.44252	E143.22643	1381 m
BAA 2 M3	M3-17	SE	S6.44259	E143.22637	1378 m
BAA 2 M3	M3-18	SE	S6.44266	E143.22631	1380 m
BAA 2 M3	M3-19	SE	S6.44229	E143.22630	1384 m
BAA 2 M3	M3-20	SE	S6.44271	E143.22630	1388 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 2 M3	M3-21	LE	S6.44277	E143.22629	1381 m
BAA 2 M3	M3-22	SE	S6.44283	E143.22628	1384 m
BAA 2 M3	M3-23	SE	S6.44291	E143.22627	1388 m
BAA 2 M3	M3-24	SE	S6.44298	E143.22626	1391 m
BAA 2 M3	M3-25	SE	S6.44306	E143.22626	1392 m
BAA 2 M3	M3-26	SE	S6.44314	E143.22626	1388 m
BAA 2 M3	M3-27	SE	S6.44319	E143.22625	1385 m
BAA 2 M3	M3-28	SE	S6.44325	E143.22622	1389 m
BAA 2 M3	M3-29	SE	S6.44329	E143.22621	1393 m
BAA 2 M3	M3-30	SE	S6.44334	E143.22618	1390 m
BAA 2 M3	M3-31	LE	S6.44338	E143.22616	1389 m
BAA 2 M3	M3-32	SE	S6.44345	E143.22611	1387 m
BAA 2 M3	M3-33	SE	S6.44349	E143.22605	1390 m
BAA 2 M3	M3-34	SE	S6.44352	E143.22602	1386 m
BAA 2 M3	M3-35	SE	S6.44355	E143.22597	1387 m
BAA 2 M4	M4-0	Start Point	S6.46204	E143.25665	996 m
BAA 2 M4	M4-1	LE	S6.46201	E143.25662	998 m
BAA 2 M4	M4-2	SE	S6.46200	E143.25657	1005 m
BAA 2 M4	M4-2.1	SE	S6.46203	E143.25656	1004 m
BAA 2 M4	M4-2.2	SE	S6.46205	E143.25654	1003 m
BAA 2 M4	M4-2.3	SE	S6.46208	E143.25651	1005 m
BAA 2 M4	M4-2.4	SE	S6.46195	E143.25657	1006 m
BAA 2 M4	M4-2.5	SE	S6.46190	E143.25658	1009 m
BAA 2 M4	M4-2.6	SE	S6.46186	E143.25657	1010 m
BAA 2 M4	M4-3	SE	S6.46199	E143.25651	1018 m
BAA 2 M4	M4-4	SE	S6.46199	E143.25645	1015 m
BAA 2 M4	M4-5	SE	S6.46199	E143.25637	1020 m
BAA 2 M4	M4-6	SE	S6.46198	E143.25627	1025 m
BAA 2 M4	M4-7	SE	S6.46197	E143.25619	1030 m
BAA 2 M4	M4-8	SE	S6.46197	E143.25612	1035 m
BAA 2 M4	M4-9	SE	S6.46194	E143.25603	1032 m
BAA 2 M4	M4-10	SE	S6.46190	E143.25597	1037 m
BAA 2 M4	M4-11	LE	S6.46187	E143.25591	1041 m
BAA 2 M4	M4-12	SE	S6.46185	E143.25584	1039 m
BAA 2 M4	M4-13	SE	S6.46180	E143.25580	1037 m
BAA 2 M4	M4-14	SE	S6.46177	E143.25574	1035 m
BAA 2 M4	M4-15	SE	S6.46174	E143.25569	1037 m
BAA 2 M4	M4-16	SE	S6.46171	E143.25561	1034 m
BAA 2 M4	M4-17	SE	S6.46171	E143.25554	1030 m
BAA 2 M4	M4-18	SE	S6.46172	E143.25548	1035 m
BAA 2 M4	M4-19	SE	S6.46172	E143.25543	1033 m

BAA No and Transect Line	Trap No	Trap type	Latitude	Longitude	Elevation (asl)
BAA 2 M4	M4-20	SE	S6.46171	E143.25537	1031 m
BAA 2 M4	M4-21	LE	S6.46169	E143.25530	1033 m
BAA 2 M4	M4-22	SE	S6.46169	E143.25524	1036 m
BAA 2 M4	M4-23	SE	S6.46169	E143.25517	1040 m
BAA 2 M4	M4-24	SE	S6.46169	E143.25507	1037 m
BAA 2 M4	M4-25	SE	S6.46166	E143.25499	1041 m
BAA 2 M4	M4-26	SE	S6.46163	E143.25494	1037 m
BAA 2 M4	M4-27	SE	S6.46161	E143.25489	1036 m
BAA 2 M4	M4-28	SE	S6.46161	E143.25482	1041 m
BAA 2 M4	M4-29	SE	S6.46159	E143.25474	1037 m
BAA 2 M4	M4-30	SE	S6.46156	E143.25467	1039 m
BAA 2 M4	M4-31	LE	S6.46154	E143.25461	1042 m
BAA 2 M4	M4-32	SE	S6.46154	E143.25453	1040 m
BAA 2 M4	M4-33	SE	S6.46153	E143.25443	1041 m
BAA 2 M4	M4-34	SE	S6.46155	E143.25434	1037 m
BAA 2 M4	M4-35	SE	S6.46156	E143.25427	1035 m
BAA 2 M4	M4-36	SE	S6.46158	E143.25421	1038 m
BAA 2 M4	M4-37	SE	S6.46157	E143.25416	1040 m
BAA 2 M4	M4-38	SE	S6.46155	E143.25410	1043 m
BAA 2 M4	M4-39	SE	S6.46155	E143.25404	1041 m
BAA 2 M4	M4-40	SE	S6.46154	E143.25398	1043 m
BAA 2 M4	M4-41	LE	S6.46153	E143.25393	1039 m
BAA 2 M4	M4-42	SE	S6.46152	E143.25388	1038 m
BAA 2 M4	M4-43	SE	S6.46153	E143.25383	1035 m
BAA 2 M4	M4-44	SE	S6.46150	E143.25378	1038 m
BAA 2 M4	M4-45	SE	S6.46148	E143.25372	1042 m
BAA 2 M4	M4-46	SE	S6.46149	E143.25367	1038 m
BAA 2 M4	M4-47	SE	S6.46151	E143.25362	1038 m
BAA 2 M4	M4-48	SE	S6.46153	E143.25358	1036 m
BAA 2 M4	M4-49	SE	S6.46154	E143.25352	1032 m
BAA 2 M4	M4-50	SE	S6.46155	E143.25346	1038 m
BAA 2 M4	M4-51	LE	S6.46157	E143.25342	1043 m
BAA 2 M4	M4-52	SE	S6.46159	E143.25338	1041 m
BAA 2 M4	M4-53	SE	S6.46161	E143.25333	1038 m
BAA 2 M4	M4-54	SE	S6.46162	E143.25327	1036 m
BAA 2 M4	M4-55	SE	S6.46163	E143.25323	1041 m
BAA 2 M4	M4-56	SE	S6.46162	E143.25316	1039 m
BAA 2 M4	M4-57	SE	S6.46159	E143.25310	1036 m
BAA 2 M4	M4-58	SE	S6.46157	E143.25303	1040 m
BAA 2 M4	M4-59	SE	S6.46154	E143.25296	1037 m
BAA 2 M4	M4-60	SE	S6.46153	E143.25289	1042 m

Appendix 5.2. Trap-line schedules and time budgets

The 2015 trapping schedule for BAA 1 and BAA 2 is shown in Table A5.2.1.

Time spent on establishment and daily operation of the various transects is shown in Tables A5.2.2 and A5.2.3. The times are based on a two-person team who worked together during the setup process but divided their efforts during the operations phase – one person started checking and rebaiting at the first trap position, while the other went straight to the last trap position and worked back along the line. Both people worked together to record captures.

With the additional time needed to move between transect lines it proved possible to operate only four trap-lines simultaneously within each of the BAAs. At BAA 1 two trap-lines were operated at each of the different elevations (H1–2, H5–6) but trap-line H1 and H2 were closed early due to excessive disturbance by people and wild dogs, respectively. Trap-line H3 was operated briefly at the end of the survey period in BAA 1. Trap-line H4 was established (i.e. positions tagged) but was not operated due to time constraints. At BAA 2 the four trap-lines were operated simultaneously.

Table A5.2.1. Trapping effort and trapping schedule for the BAA 1 and BAA 2 survey areas. Cell values are the number of traps set. For BAA 1 the number disturbed by dogs is also shown in brackets.

BAA 1	18-Jun	19-Jun	20-Jun	21-Jun	22-Jun	23-Jun	24-Jun	25-Jun	26-Jun	27-Jun	Total trapping days
H6	46	46	46	46	46(3)	46	46 (2)				7
H5	44	46	46	46	46(2)	46 (9)	46 (3)				7
H4											
H3							46	44			2
H2		46	45	46 (25)	46	46 (32)					5
H1	46	46	46	46	46 (5)						5
BAA 2	29-Jun	30-Jun	01-Jul	02-Jul	03-Jul	04-Jul	05-Jul	06-Jul	07-Jul	08-Jul	Total trapping days
M1			46	46	46	46	46	46	46		7
M2	46	46	46	46	46	46	46	46	46		9
M3				46	46	46	46	46	46	46	7
M4			60	60	60	60	60	60	60		7

Table A5.2.2. Time spent (in minutes) in operation of each of the trap-lines in BAA 1. (S = setup day; b = traps baited; c+b = traps checked and rebaited; c + p = traps checked and collected).

Transect	17-Jun	18-Jun	19-Jun	20-Jun	21-Jun	22-Jun	23-Jun	24-Jun	25-Jun
H6	S	65 (b)	70 (c+b)	80 (c+b)	70 (c+p)	65 (c+b)	43 (c+b)	55 (c+p)	
H5	S	80 (b)	69 (c+b)	50 (c+b)	60 (c+p)	55 (c+b)	65 (c+b)	34 (c+p)	
H4									
H3						S	65 (b)	70(c+b)	75(c+p)
H2	S	70 (b)	75 (c+b)	65 (c+b)	75 (c+b)	70 (c+b)	40 (c+p)		
H1	S	75 (b)	84 (c+b)	65 (c+b)	68 (c+b)	75 (c+p)			

Table A5.2.3. Time spent (in minutes) in operation of each of the trap-lines in BAA 2.

Transect	29-Jun	30-Jun	01-Jul	02-Jul	03-Jul	04-Jul	05-Jul	06-Jul	07-Jul	08-Jul
M1		S	68 (c+b)	75 (c+b)	65 (c+b)	70 (c+b)	63 (c+b)	76 (c+b)	70 (c+p)	
M2	S	75 (c+b)	70 (c+b)	68 (c+b)	65 (c+b)	70 (c+b)	62 (c+b)	69 (c+b)	65 (c+p)	
M3			S	72 (c+b)	70 (c+b)	62 (c+b)	68 (c+b)	65 (c+b)	72 (c+b)	70 (c+p)
M4		S	82 (c+b)	88 (c+b)	85 (c+b)	78 (c+b)	80 (c+b)	83 (c+b)	90 (c+p)	

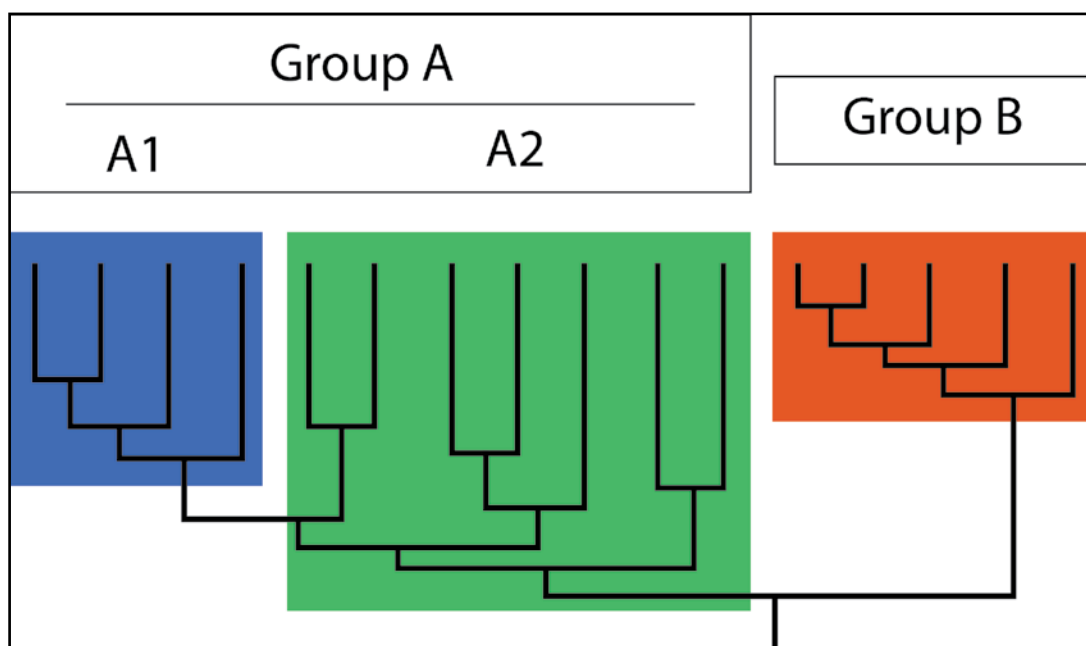
Appendix 5.3. Results of genetic analyses and other taxonomic notes

INTRODUCTION

The genetic work undertaken for this report falls under a general category of methods that is commonly termed 'DNA barcoding', or 'mtDNA barcoding' when it is based on a portion of the mitochondrial genome (see Chapter 7 for a general introduction to concepts and terms). mtDNA barcoding as a global initiative has focused on one particular gene called *cytochrome c oxidase subunit I (COI)*, but any part of the mtDNA genome can be used in the same way. For two reasons we chose to use a different gene—*cytochrome b (cyt b)*. Firstly, there is a larger reference library of *cyt b* sequences already available for New Guinean rodents; and secondly, *cyt b* typically evolves at a higher rate than COI and thus shows more sequence variation within and between species.

As explained more fully in Chapter 7, mtDNA barcoding usually works because most species in nature contain discrete subsets of the total sequence variation observed within a particular gene. For species that have been evolving separately for a long time the subsets of variation will usually show what is called reciprocal monophyly (see Figure A5.3.1 for an explanation). However, where species have only recently diverged, they may either show discrete subsets of variation but without reciprocal monophyly (i.e. as shown by groups A1 and A2 in Figure A5.3.1) or partially overlapping subsets. mtDNA barcoding obviously works best as an identification tool where all species under consideration are well-differentiated and display reciprocal monophyly, and less well where there are closely related species with partially overlapping patterns of variation.

Figure A5.3.1. Explanation of terms used to refer to genetically defined lineages. Groups A and B show reciprocal monophyly (i.e. separate histories of descent from discrete ancestors), as do Groups A1 and B. However, Groups A1 and A2 do not, as Group A1 is more closely related to some members of Group A2 than to others.



mtDNA barcoding can also produce confusing results where hybridization between species has resulted in the transfer (either 'introgression' or 'capture') of mtDNA from one species into another (see Chapter 7 for more detailed explanation). In this case, the barcoding will give an incorrect result for the identity of the species even though it is correct for its mtDNA.

Because of these infrequent problems it is important that mtDNA results are treated with caution, particularly during the initial phase of a project that intends to use barcoding for species identification. In this study, all captured non-volant mammals were examined and provisionally identified in the field by Ken Aplin who has considerable prior experience with small mammals of the general region. In addition, a small number of voucher specimens were retained in order to carry out more detailed morphological studies in the event that genetic results did not tally with field-based determinations.

MATERIALS AND METHODS

We aimed to generate mtDNA barcode sequences for all of the non-volant mammals captured in 2015 to provide a solid foundation for future sampling periods and the greatest chance of detecting cryptic species that might warrant further investigation. Laboratory methods and analytical procedures are described in Chapter 7. A list of the PMA3 survey samples submitted for sequencing is provided in Table A5.3.1.

In addition, we generated sequences from 134 samples selected from existing tissue holdings of the Australian Biological Tissue Collection (ABTC) at the South Australian Museum. Our purpose was to provide a genetic 'context' for the PMA3 samples and the selection was made according to two criteria: 1) to test whether the species trapped in 2015 in the two BAAs are also represented outside of the Upstream Project Area; and 2) to represent species that might be captured during future surveys in the BAAs. A full list of this 'context' sampling is provided in Table A5.3.2.

The *cytb* gene failed to amplify in seven samples. Six of these were examples of *Paramelomys* cf. *rubex* from Agogo Range. Failure to amplify is usually due to a substitution in the DNA region targeted by one or other of the primers. The *cytb* sequencing also failed for one sample of the marsupial *Neophascogale* cf. *lorentzii*. Because it was particularly important to gain some molecular data for this sample, we sequenced an alternative portion of mtDNA (Control Region - CR) for this sample. CR is less suitable for barcoding because it sometimes contains nucleotide insertions and deletions that can make it difficult to align sequences across multiple taxa.

RESULTS

We obtained partial *cytochrome b* sequences from 122 non-volant mammals from the two BAAs and a further 134 from 'context' samples. Phylogenetic trees were produced using a Neighbor-Joining Method as explained in Chapter 7.

The majority of captures in 2015 belonged to one of two genera of murid rodents – *Rattus* and *Paramelomys*. Members of the two genera are readily distinguished in the hand by the appearance of the tail but determination to species level is notoriously difficult in both genera. In part this is simply because the species do not differ greatly from each other in appearance. However, it is also widely acknowledged that some of the difficulty relates to an imprecise taxonomy with either too many or too few species currently distinguished (e.g. Robins et al. 2014 for *Rattus*).

The results of the genetic analysis are illustrated in Figures A5.3.2 to A5.3.5.

Genus *Rattus*

Field identifications distinguished four nominal species of *Rattus*. Only one taxon was identified among captures at BAA 1 – a small-bodied, soft and dark furred species tentatively identified as *Rattus* cf. *niobe*. By contrast, three species were identified among captures at BAA 2, namely:

1. a soft furred species also tentatively identified as *Rattus* cf. *niobe* but differing from the BAA 1 population in being slightly larger and with slightly paler fur;
2. a small, spiny-furred species identified as the Pacific Rat, *Rattus exulans*, an exotic invasive species that originated on Flores Island in eastern Indonesia but which now occurs widely through Asia and the Pacific;
3. a larger spiny-furred species captured only at the Arakubi Quarry site that could not be referred to any of the species recognized in current taxonomic listings (e.g. Musser and Carleton 2005) but which appears to be similar to a population sampled in 2014 on the flanks of the P'nyang Range in Western Province of Papua New Guinea and to populations in the Kikori catchment reported by Leary and Seri (1997: Mt Kemenagi) and by Leary (2004: Darai Plateau).

One additional species was sampled only at the HGCP site where a freshly dead carcass was discovered, most likely a result of poisoning as part of rodent control measures. This species was identified as a form of Black Rat, a member of the *Rattus rattus* Complex that probably includes several species of Asian origin (Aplin et al. 2011).

The genetic analysis of *Rattus* samples from BAA 1 and BAA 2 shows individuals clustered in six lineages (Figure A5.3.2). Each of the lineages was also detected in samples drawn from sites in the wider region.

The two populations of *Rattus cf. niobe*, from BAA 1 and BAA 2 respectively, are almost certainly different species and, judging from the mtDNA sequence data, they may not even be each other's closest relatives (Figure A5.3.2). *Rattus cf. niobe* B from Hides Ridge is genetically intermingled with populations from the nearby Mananda Ridge and from Apia River on the northeast side of Mt Sisa, and also closely related to *R. cf. niobe* A from high elevation habitats on the Muller Range. *Rattus cf. niobe* D from the Agogo Range is genetically intermingled with a population confined to the highest elevation forests on the P'nyang Range, and is most closely related to a population from Sol River in West Sepik Province referred to *R. verecundus*. These populations are together most closely related to *R. giluwensis* and to *R. cf. niobe* C, a form currently known only from mid-elevational forest habitat on Mt Karimui in Chimbu Province.

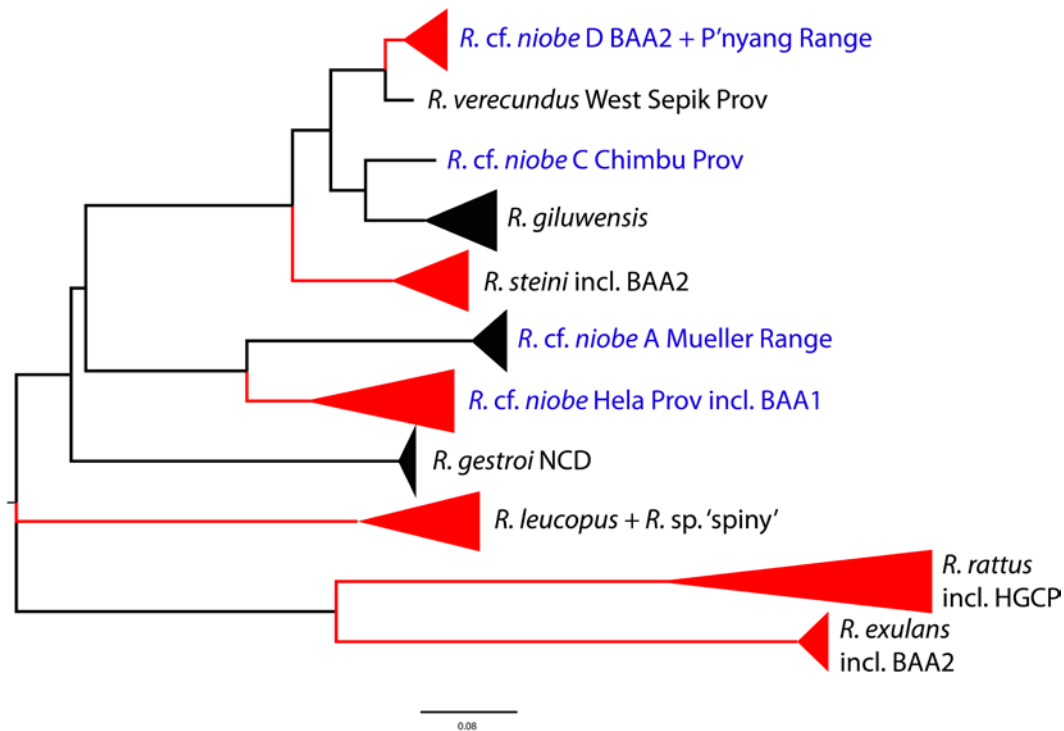


Figure A5.3.2. Phylogenetic relationships among mtDNA sequences for representatives of the genus *Rattus*. Species recorded from BAA 1 or BAA 2 are indicated by red branches and triangles. The four discrete clusters of *R. cf. niobe* are labeled in blue. The 'depth' of the triangle represents the amount of genetic variation observed among members of that lineage (e.g. more in *R. rattus* than in *R. exulans*).

Although these results support and extend the earlier conclusion of Robins et al. (2014) that there is more than one small-bodied, soft furred species living in the montane forests of New Guinea, it is not clear which of the various forms represents the 'true' *niobe* (which was named from specimens from mid-elevations in the Owen Stanley Range) and which others might already have other available scientific names. A more extensive genetic assessment of the small, soft-furred montane *Rattus* of New Guinea is urgently needed to resolve the taxonomy and nomenclature of this group.

The spiny-furred rat captured on the Arakubi Quarry trap-line along transect M4 falls into a genetic group that includes the morphologically similar P'nyang population, some smaller-bodied but similarly spiny-furred animals previously identified as *R. verecundus* (e.g. Flannery 1995) from sites in Chimbu Province (e.g. Noru Village on the western margin of the Karimui Plateau) and Southern Highlands Province (Namasado and Bobole Villages on the southwestern flanks of Mt Sisa), and various populations of a much larger spiny-furred lowland rat called *R. leucopus* (Figure A5.3.3). This group is morphologically heterogenous and clearly includes more than one species, despite the close relationship of their mtDNAs.

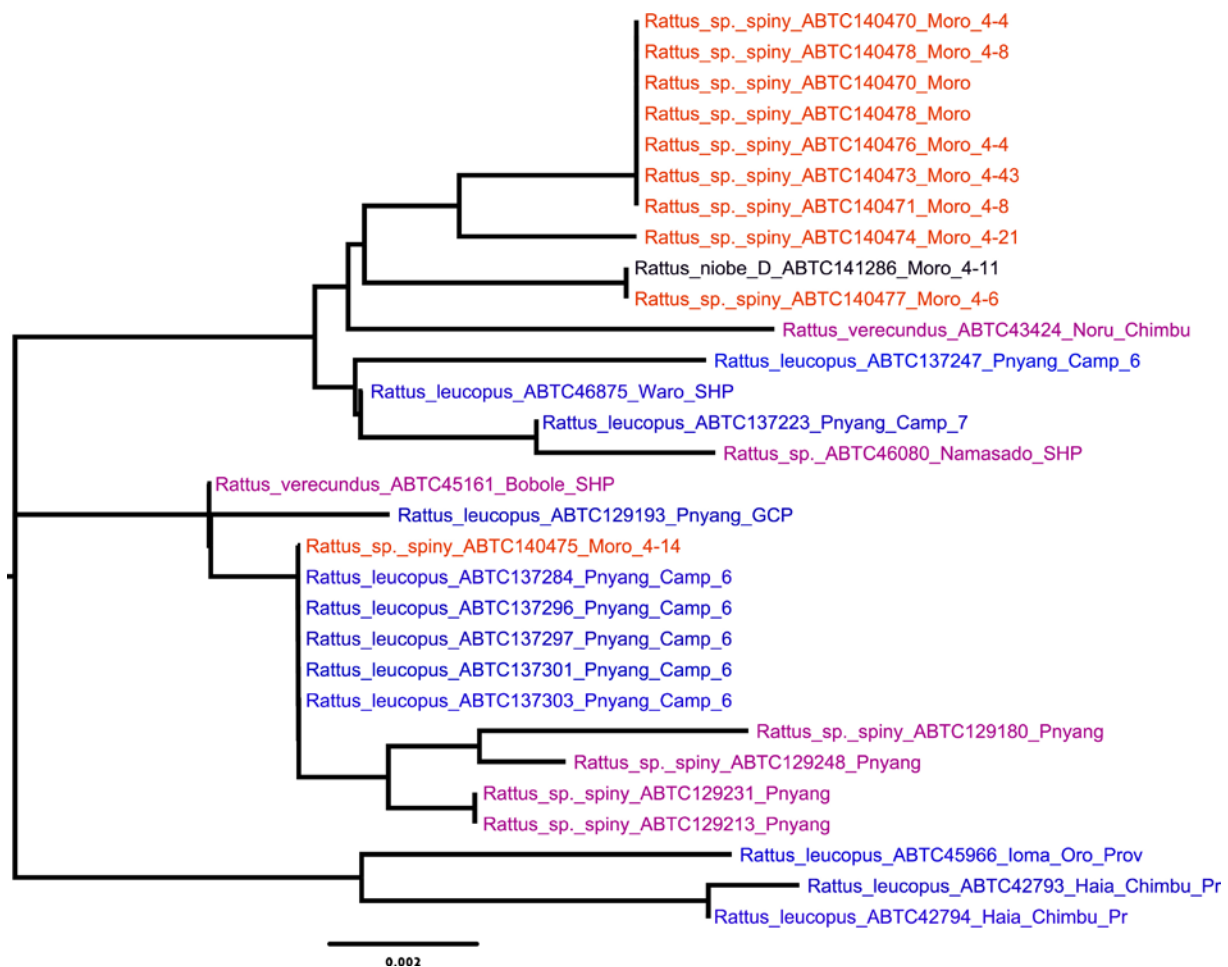


Figure A5.3.3. Phylogenetic relationships among mtDNA sequences for *R. leucopus* (labels in blue) and *R. sp.* 'spiny' (labels in red), and some specimens identified previously as a form of *R. verecundus* (labels in purple). The sample labeled in black was captured at KP107 in BAA 2 and identified on morphological grounds as *R. cf. niobe* but its mtDNA is identical with an individual of *R. sp.* spiny from the same locality. In this figure 'Moro' refers to the Agogo Range.

Robins et al. (2014) reported the close mtDNA relationship between Chimbu and Southern Highlands Province populations of *R. 'verecundus'* and *R. leucopus* and provided various possible interpretations of this anomaly, several of which posited past hybridization events between *R. leucopus* and an as yet undetermined second species of *Rattus*. Importantly, *R. leucopus* itself does not occur at any of the sites that produced the spiny-furred form of *R. 'verecundus'*, though it does occur at lower elevations on the P'nyang Range.

The Arakubi and P'nyang Range populations are larger than the spiny-furred form of *R. 'verecundus'* from Mt Karimui and Mt Sisa but substantially smaller than typical lowland populations of *R. leucopus*. On the P'nyang Range *R. leucopus* occurs only in the surrounding foothills while the smaller species is found in the karst upland. The nearest records of *R. leucopus* to BAA 2 are from Mt Kemenagi and Waro where they occur at elevations of 900 m asl and c. 450 m asl, respectively. To determine the relationship among the various populations of the small spiny-furred *Rattus* it will be necessary to do a more extensive genetic analysis that includes broad coverage of their nuclear genomes.

Two individuals identified in the field as *R. cf. niobe* from the Agogo Range produced anomalous mtDNA sequences:

- a subadult female *Rattus cf. 'niobe'* from trap-line M4 at Arakubi Quarry produced a mtDNA haplotype referable to the *Rattus sp.* 'spiny' genetic group.
- an adult male *Rattus* (body weight 80.7 g) identified in the field as *R. cf. niobe* from trap-line M2 on the Agogo Range produced a mtDNA sequence that falls into a discrete cluster of *R. steini* drawn from across Papua New Guinea.

These examples of 'mismatch' between morphological assessment and the mtDNA identity are most likely the product of occasional interbreeding between different species of *Rattus*, leading to mtDNA introgression. If this interpretation is correct for the individual from Agogo Range triline M2 it would imply that *R. steini* occurs locally. This may well be the case, as there are regional records of *R. steini* from 1,100-1,500 m a.s.l. on Mt Sisa (Dwyer 1984) and 700 m a.s.l. on Mt Bosavi (Taylor et al. 1982; Leary and Seri 1997).

The genetic results confirmed the field identification of *Rattus exulans* from BAA 2 and of *Rattus rattus* from the HGCP (Figure A5.3.2). These are two invasive non-native species.

Two different mtDNA haplotypes of *R. exulans* were obtained from the Agogo Range samples. Both are identical to haplotypes found elsewhere in Papua New Guinea.

The *R. rattus* sample collected at HGCP produced a mtDNA haplotype that belongs to Lineage II of Aplin et al. (2011). This mtDNA lineage originated in East Asia but has spread from there to various parts of the world including Australia, South Africa and the U.S.A. There was just one previous record of Lineage II of the Black Rat from Papua New Guinea, from Sideia Island in the Louisiade Archipelago, Milne Bay Province (Robins et al. 2014). However we also sequenced four Black Rat samples collected in 2005 at Bobia near Lae, Madang Province, and two collected at Moitaka near Port Moresby in 1984. The Bobia samples produced an identical Lineage II mtDNA haplotype to that from Sideia Island but all of these differ from the HGCP haplotype which points to at least two independent introductions of Lineage II Black Rats to Papua New Guinea. The Moitaka samples, by contrast, produced a haplotype of Lineage I which is typical of Black Rats of European derivation (with an origin in southern India; Aplin et al. 2011). Further work on the samples including assessment of their nuclear genomes will be carried out as part of a broader investigation of global Black Rat diversity. This work will shed further light on the origin of the Papua New Guinea populations which in turn will cast light on their likely mode of transportation to the sites where they occur. Such information is likely to be extremely useful in developing effective control strategies.

In summary, the first survey period has produced evidence for the regional occurrence of six species of *Rattus*, four of which were recognized on morphological criteria. Five of the six species were confirmed by captures while the sixth is inferred on the basis of a potentially introgressed mitochondrial genome (i.e. an individual of *R. cf. niobe* D that carries the mtDNA of *R. steini* as a result of hybridization).

Rattus sp. 'spiny' is known from two or more other localities in the Kikori and Fly River catchments. This species lacks a scientific name and it could be described from any one of the known populations on the basis of data currently in hand. However, to demonstrate that each of the morphologically similar populations represents the same newly-described species it will be necessary to undertake more extensive genetic studies to eliminate the possibility that each of the regional populations has originated independently through unrelated hybridization events.

The two small soft-furred *Rattus* (*R. cf. niobe* B and *R. cf. niobe* D) may also lack existing scientific names. However, to name either or both of these forms it will be necessary to determine their relationship to various named populations that are usually regarded as regional variants of *R. niobe*. The first step will be to expand the 'context' work to include more of the currently available samples (the ABTC alone holds 220 samples). This will clarify the geographic extent of each species—information which will also help to determine their conservation status and sensitivities. The next step will be to assess the type specimens of the previously proposed names for *R. niobe* and other *niobe*-like species. This assessment will need to include a morphological component but it might also require genetic analysis. In any event, resolving the taxonomic names for *R. cf. niobe* B and *R. cf. niobe* D will require a significant research effort.

Genus *Paramelomys*

Field identifications distinguished three nominal species of *Paramelomys*. Two taxa were identified among captures at BAA 1—one small-bodied species and one larger-bodied species; and three at BAA 2—one small species and two larger species.

All of the small-bodied *Paramelomys* were tentatively identified as *Paramelomys cf. rubex*, which is substantially smaller than all other species of *Paramelomys* and is thought to have a wide elevational range and a broad distribution throughout the mountains of New Guinea (Menzies 1990; Flannery 1995; Musser and Carleton 2005).

The larger species were initially identified as examples of *P. mollis* in BAA 1, and *P. mollis* and *P. platyops* in BAA 2. On more detailed examination, the population of '*P. mollis*' from BAA 2 was reassessed as *P. lorentzii* (primarily on the presence of 3 rather than 1 tiny hairs behind each tail scale; see Menzies 1996). All of these putative species have been recorded previously at similar elevations in the Kikori catchment and elsewhere in southern Papua New Guinea (Flannery 1995; Leary and Seri 1997; Musser and Carleton 2005).

The genetic analysis of *Paramelomys* samples from BAA 1 and BAA 2 shows individuals clustered in six lineages (Figure A5.3.4).

The individual identified as *P. platyops* from BAA 2 clusters tightly with samples of this species from multiple sites across southern Papua New Guinea.

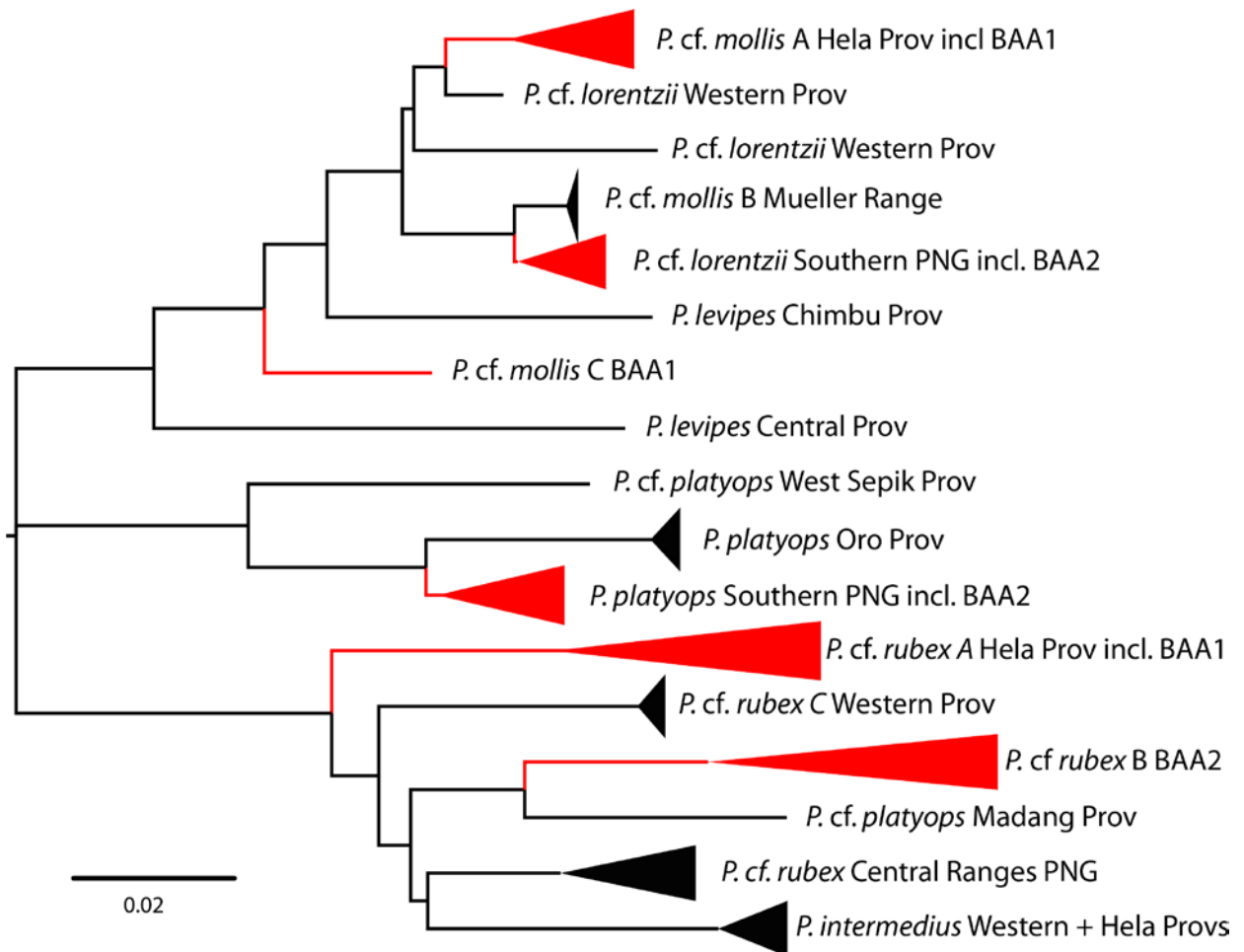


Figure A5.3.4. Phylogenetic relationships among mtDNA sequences for *Paramelomys*. Lineages that are represented among samples from BAA 1 and BAA 2 are indicated by red triangles and branches.

Samples identified as *P. 'rubex'* fall into four discrete clusters, two of which are represented in the samples collected in 2015. *Paramelomys* cf. '*rubex*' A includes all samples from BAA 1 as well as a sample from Mananda Ridge. *Paramelomys* cf. '*rubex*' B includes numerous samples from BAA 2; the majority come from transects at KP107 but one sample was obtained at Arakubi Quarry. This mtDNA lineage is not otherwise represented among the 'context' samples tested to date. Thus far the closest relative of *P. cf. 'rubex'* B is a sample identified as *P. platyops* from Bundi at c.800 m a.s.l. in Madang Province. Other 'context' samples yielded two additional lineages of *P. cf. rubex*. *Paramelomys* cf. *rubex* C is represented exclusively among samples from the P'nyang Range in the upper Fly River catchment, while *Paramelomys* cf. *rubex* D is represented by samples from four widely dispersed localities in Central, Morobe and Enga Provinces. A fifth member of what might be thought of as a '*Paramelomys rubex* group' is *P. intermedius*, a larger-bodied species of lowland and hill forest habitats in southwest New Guinea. This species is usually included within *P. platyops* (Flannery 1995; Musser and Carleton 2005), though it is sometimes distinguished as a subspecies (e.g. Menzies 1996).

The mtDNA data indicate much unrecognized species diversity within the *P. rubex* group. At least in the upper Kikori catchment, this diversity appears to have an elevational component, with *P. cf. rubex* A found at higher elevations than *P. cf. rubex* B. The original description of *Paramelomys rubex* was of specimens from Doormanpad-Bivak at 1,410 m asl in the central range of Indonesian Papua Province. Since then nine other names have been proposed for small montane *Paramelomys*; hence, it is likely that the two small *Paramelomys* from BAA 1 and BAA 2 will already have scientific names. However, to identify the correct names for each species it will be necessary to extend the present study in several ways. The first step will be to expand the 'context' work to include more of the currently available samples (the ABTC alone holds 152 samples). This will clarify the geographic extent of each species which will be useful for assessment of their conservation status and sensitivity. The next step will be to assess the type specimens of the previously proposed names for members of this group. This assessment will need to include a morphological component but it might also require genetic analysis, probably including analysis of nuclear genes. In any event, resolving the taxonomic names for *P. cf. rubex* A and *P. cf. rubex* B will require a significant effort.

The larger *Paramelomys*

The larger-bodied *Paramelomys* from BAA 1 and BAA 2 belong to a diverse assemblage of lineages that includes samples variously identified on morphological criteria as *P. platyops*, *P. mollis*, *P. levipes* and *P. lorentzii*. Two distinct mtDNA lineages were found among the larger-bodied *Paramelomys* from BAA 1 and two different lineages among those from BAA 2.

One animal captured on the Arakubi Quarry trapline (M4) produced a sequence that falls squarely into a selection of 'context' samples of *P. platyops* drawn from low elevations sites across southern Papua New Guinea and in Oro Province in the southeast. This very likely represents true *P. platyops* which was described from the hinterland of Port Moresby.

All but one of the larger-bodied *Paramelomys* captured on Hides Ridge fall into a lineage labeled as *P. cf. mollis* A; this lineage also includes intermingled samples identified as *P. mollis* from Mananda Ridge. A second group of specimens identified as *P. mollis* from the Muller Range (Aplin and Kale 2011) represents a separate lineage (labelled *P. cf. mollis* 'B' on Fig. A5.3.4). Although *P. cf. mollis* A and *P. cf. mollis* B are not strongly differentiated by comparison with other major species lineages within *Paramelomys*, several considerations favour them being representative of separate species, namely: 1) the fact they display reciprocal monophyly, despite the relatively short distance and continuity of habitat between them; 2) the elevational contrast between *P. 'mollis'* A (>2,200 m asl) and *P. 'mollis'* B (<1,800 m asl); and 3) the interposition between the two groups of 'mollis' of several clusters of sequences from another nominal species—*P. lorentzii* of the southern lowlands and hill forests of New Guinea.

One individual from Hides Ridge (trap-line H3) produced a more highly divergent sequence that does not closely match any of the 'context' sequences. This is labeled *P. cf. 'mollis'* C on Fig. A5.3.4. This unique capture was not vouchered which suggests a lack of any pronounced morphological distinction between this animal and examples of *P. cf. mollis* A captured on Hides Ridge.

All of the individuals of *P. cf. lorentzii* captured on trap-lines M1–3 at KP107 shared a single mtDNA haplotype that groups with 'context' samples of *P. lorentzii* from the foothills of Mts Bosavi and Sisa. All of these populations share a distinctive morphological feature—the presence of three hairs growing from below each tail scale – which gives the tail a slightly hairier appearance. By contrast, in all populations referred to *P. mollis*, *P. platyops* and *P. rubex* there is a single hair per tail scale.

As noted above, the suite of *P. 'lorentzii'* sequences are not clearly separated from those of *P. mollis*. Indeed, mtDNA of *P. cf. lorentzii* from KP107 and Mts Bosavi and Sisa is most closely related to that of *P. cf. mollis* B from 1,500–1,600 m in the Muller Range, whereas two other 'context' samples of *P. lorentzii* (from the Upper Strickland and Upper Fly catchments) do not group with the KP107/Bosavi/Sisa *lorentzii* but are instead more closely related to the Hides Ridge *P. cf. 'mollis'* A. This mosaic pattern of samples identified as either *P. 'mollis'* or *P. 'lorentzii'* suggests either that the number of hairs per tail scale is not a good indicator of relatedness among species of *Paramelomys* or that there the phylogenetic pattern is complicated by instances of mtDNA introgression between *P. mollis* and *P. lorentzii*. Given the general constancy of scale hair counts observed across other species of *Paramelomys* and related genera (Menzies 1996), we suspect that the latter interpretation is more likely correct.

Both *P. mollis* and *P. lorentzii* were described from specimens collected on the southern side of present day Indonesian Papua—*P. mollis* from c. 1,680 m asl in the upper Utakwa River catchment and *P. lorentzii* from 900 m asl on the Lorentz River. The applicability of these names to any populations in Papua New Guinea remains untested. Menzies (1996) referred additional material from the Mimika and Fly Rivers, and from Mt Bosavi, to *P. lorentzii*; his concept of *mollis* included material from throughout the mountains of New Guinea, from the Bird's Head to the southeast peninsula, and including six named forms. Further work is needed to determine the species identity and appropriate names of each of *P. cf. mollis* A, B and C.

Other DNA-based comparisons

Speckled Dasyure *Neophascogale cf. lorentzii*

The Speckled Dasyure (*Neophascogale lorentzii*) is a spectacularly beautiful but rarely encountered carnivorous marsupial. The few records from Papua New Guinea come mainly from high elevations on the ranges of the central cordillera and there are no prior records from anywhere in Hela Province (Leary and Seri 1997). During the 2015 fieldwork on Hides Ridge one individual was captured in a mist net set for birds at 2,600 m asl and several others were observed moving on the trunks of *Nothofagus* trees during the day in the same area. In Papua New Guinea there are recent records from the Kaijende Highlands of Enga Province (Helgen and Opiang 2011) and the Muller Range of Southern Highlands Province (Aplin and Kale 2011) but at these localities the species does not seem to be as abundant as on Hides Ridge. The species *lorentzii* was described from Indonesian Papua Province and the application of this name to Papuan New Guinean populations is untested.

We generated a partial control region sequence of mitochondrial DNA and compared this with a Genbank sequence for an individual from the vicinity of Porgera in Enga Province. The comparison found 2% sequence divergence which implies recent genetic interchange between populations on Hides Ridge and the mountains of Enga Province.

White-eared Giant Rat *Hyomys* sp.

An adult female White-eared Giant Rat, a species of *Hyomys*, was picked up from the road on the evening of the 2nd July 2015, presumably after a road casualty.

The taxonomy of this genus is not yet well-studied, although recent works tend to recognize two species—*H. goliath* in the east and *H. dammermani* in the west (Flannery 1995; Musser and Carleton 2005). The morphological and genetic distinction between them remains undocumented and the geographic contact is ill-defined.

We tested the population affinities of the Hides Ridge *Hyomys* by comparing its cytochrome b sequence with those from samples from Mt Sisa in Southern Highlands Province and Okefamin in West Sepik Province. According to the distribution maps in Flannery (1995) these samples should represent *H. goliath* and *H. dammermani*, respectively. All of the sequences proved to be very similar, with 1.1% nucleotide divergence between the individuals from Hides Ridge and Mt Sisa, and 1.7–2.3% between these and the two samples from Ofekamin. Due to the possibility of mtDNA introgression across a boundary between *H. goliath* and *H. dammermani*, this result does not refute the current taxonomic arrangement. However, it does imply some degree of interpopulational continuity that extends all the way from Hides Ridge to the mountains of West Sepik Province.

Giant White-tailed Rat *Uromys cf. caudimaculatus*

Our single capture of *Uromys cf. caudimaculatus* from KP107 was compared with three 'context' samples from Central, Chimbu and West Sepik Provinces. It was found to be minimally divergent for *cytb* from the sample from Mt Karimui in Chimbu Province. However, together these were deeply divergent from the other samples which also differed greatly from each other.

Other genetic and morphological studies in progress suggest that there are multiple species of the *Uromys caudimaculatus* group in New Guinea. However, at this stage it is not certain how many species are present, nor is it clear which of the 14 available names might apply to any of them.

Other taxonomic notes

A spiny bandicoot *Echymipera cf. kalubu*

This species was identified from camera trap images obtained at Arakubi Quarry. The form depicted appears to be an unnamed montane species that is otherwise known only from populations near Mt Hagen in Western Highlands Province and Mt Elimabari in Eastern Highlands Province (K. Aplin, unpublished data). These populations differ in important cranial and dental features from typical *E. kalubu* of lowland to mid-elevation habitats and they also have one distinctive external trait—conspicuous white ‘gloves’ on the forelimbs, a feature that is visible on the camera trap images. This identification needs to be confirmed by capture and DNA-sampling of an individual at Arakubi Quarry.

A small forest wallaby *Dorcopsulus cf. vanheurni*

The small forest wallabies are currently under taxonomic investigation and early results indicate that populations in the eastern part of the central cordillera of New Guinea are distinct from *Dorcopsulus vanheurni* which was named from a locality within Indonesian Papua Province. The eastern populations do not seem to have a prior scientific name. Because *D. vanheurni* has been rated by IUCN as Near Threatened, the undescribed species is provisionally accorded the same rank.

A species of Leptomys *Leptomys sp.*

A member of this distinctive genus of rats was imaged on camera traps at KP107. Three species of the genus are recorded regionally—*L. ernstmayeri* at 1,750–2,200 m asl on Mt Karimui in Chimbu Province; *L. signatus* on the Darai Plateau at 380 m asl and Mt Bosavi at 1,400 m asl; and the Papuan Plateau and lower Kikori catchment between 490 and 1,500 m asl (Musser et al. 2008). Capture of one or more individuals is required to determine which of these species (potentially more than one) is present in BAA 2.

A species of Woolly Rat *Mallomys sp.*

A member of this distinctive genus was imaged on a camera trap at KP107. This is an unusually low elevation record for this genus, which is more typically encountered in montane forest habitats above 1,500 m asl (Flannery 1995). Two species of the genus are recorded regionally—*M. aroaensis* and *M. rothschildi*.

Externally the main difference between them is the intensity of coat colour which can be difficult to discern on camera traps images. Capture of one or more individuals is required to determine which of these species (potentially more than one) is represented in BAA 2. Occurrence of one or more species of *Mallomys* in BAA 1 is also anticipated.

REFERENCES

- Aplin, K. P. & Kale, E. 2011. Non-volant mammals of the Muller Range, Papua New Guinea. Pp. 210-221 in Richards, S. J. & Gamui, B. G. (eds) *Rapid Biological Assessments of the Nakanai Mountains and the upper Strickland Basin: surveying the biodiversity of Papua New Guinea's sublime karst environments*. RAP Bulletin of Biological Assessment 60. Conservation International, Arlington, VA, USA.
- Aplin K.P., Suzuki H., Chinen, A. A., Chesser, R. T., ten Have, J., Donnellan, S. C., Austin, J., Frost, A., Gonzalez, J.-P.,Herbreteau, V., Catzeflis, F., Soubrier, J., Fang, Y.-P., Robins, J., Matisoo-Smith, E., Bastos, A. D. S., Maryanto, I., Sinaga, M. H., Denys, C., Yap, G., Van Den Bussche, R. A., Conroy, C., Rowe, K. & Cooper, A. 2011. Multiple geographic origins of commensalism and complex dispersal history of black rats. *PLoS One* 6: e26357.
- Dwyer, P. D. 1984. From garden to forest: small rodents and plant succession in Papua New Guinea. *Australian Mammalogy* 7: 29-36.
- Flannery, T. F. 1995. *The Mammals of New Guinea*. Revised Edition. Reed Books, Chatswood, NSW.
- Helgen, K. M. & Opiang, M. D. 2011. Notes on the high elevation mammal fauna of the Kaijende Highlands, Enga Province, Papua New Guinea. Pp. 235-245 in Richards, S. J. & Gamui, B. G. (eds) *Rapid Biological Assessments of the Nakanai Mountains and the upper Strickland Basin: surveying the biodiversity of Papua New Guinea's sublime karst environments*. RAP Bulletin of Biological Assessment 60. Conservation International, Arlington, VA, USA.
- Leary T. 2004. *Mammal Survey of Darai Plateau, Gulf Province, and Libano Sok, Southern Highlands Province, July - August, 2003*. WWF KICDP area Report, 2004.
- Leary, T. & Seri, L. 1997. An annotated checklist of mammals recorded in the Kikori River Basin, Papua New Guinea. *Science in New Guinea* 23: 79-100.
- Musser, G. G. & Carleton, M. D. 2005. Family Muridae. Pp. 894–1531 in Wilson, D. E. & Reeder, D. M. (eds) *Mammal species of the world: a taxonomic and geographic reference*. Third edition. Johns Hopkins University Press, Baltimore, Maryland.
- Musser, G. G., Helgen, K. M. & Lunde, D. P. 2008. Systematic review of New Guinea *Leptomys* (Muridae, Murinae) with descriptions of two new species. *American Museum Novitates* 3624, 60 pp.
- Robins, J. H., Tintinger, V., Aplin, K. P., Hingston, M., Matisoo-Smith, E., Penny, D. & Lavery, S. D. 2014. Phylogenetic species identification in *Rattus* highlights rapid radiation and morphological similarity of New Guinean species. *PLoS one* 9: e98002.

Appendix 5.4. Trap-line capture data

A list of captures on all trap-lines is presented in Table A5.4.1. Other observations on non-volant mammals made during the course of the 2015 fieldwork are shown in Table A5.4.2.

Table A5.4.1 List of mammals captured on trap-lines in both BAAs. Captures are either novel (N) or a recapture (R).

BAA	Transect-Trap No	Field No.	Field ID	Genetic ID	Sex	Capture
BAA 1	H6-1	1	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N
BAA 1	H5-2.3	2	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H1-4	3	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H1-2.1	4	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H1.1	5	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N
BAA 1	H1-34	6	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H1-19	7	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H1-8	8	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H2-4	9	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N
BAA 1	H1-2.6	10	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H2-28	11	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H2-32	12	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N
BAA 1	H6-28	13	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H6-3	14	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H6-2	15	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N
BAA 1	H5-27	16	<i>Rattus cf. niobe</i>	<i>v Rattus cf. niobe</i> B	M	N
BAA 1	H5-18	17	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H5-16	18	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H5-6	19	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N
BAA 1	H1-35	20	<i>Microperoryctes ornata</i>		F	N
BAA 1	H6-34	21	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex</i> A	M	N
BAA 1	H6-31	22	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex</i> A	F	N
BAA 1	H6-28	23	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N
BAA 1	H6-25	24	<i>Paramelomys mollis</i>	<i>Paramelomys cf. mollis</i> A	M	N
BAA 1	H2-31	25	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H2-28	26	<i>Rattus cf. niobe</i>		M	R
BAA 1	H2-11	27	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H2-3	28	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	M	N
BAA 1	H1-19	29	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex</i> A	F	N
BAA 1	H6-18	30	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N
BAA 1	H6-11	31	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe</i> B	F	N

BAA	Transect-Trap No	Field No.	Field ID	Genetic ID	Sex	Capture
BAA 1	H6-6	32	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	F	N
BAA 1	H6-3	33	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>		N
BAA 1	H1-34	34	<i>Paramelomys cf. rubex</i>		F	N
BAA 1	H1-2.5	35	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	F	N
BAA 1	H1-2.6	36	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>		N
BAA 1	H6-33	38	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex A</i>	F	N
BAA 1	H6-28	39	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex A</i>	F	N
BAA 1	H2-28	40	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex A</i>	F	N
BAA 1	H2-3	41	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	F	N
BAA 1	H1-2.1	42	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	M	N
BAA 1	H1-2.4	43	<i>Paramelomys cf. rubex</i>		M	N
BAA 1	H1-19	44	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	M	N
BAA 1	H1-8	45	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	F	N
BAA 1	H1-4	46	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	M	N
BAA 1	H1-13	47	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	F	N
BAA 1	H6-28	48	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	M	N
BAA 1	H6-29	49	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	M	N
BAA 1	H6-28	50	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex A</i>	M	N
BAA 1	H6-6	51	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex A</i>	F	N
BAA 1	H5-40	52	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	M	N
BAA 1	H3-25	53	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex A</i>	F	N
BAA 1	H3-21	54	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe B</i>	F	N
BAA 1	H3-19	55	<i>Paramelomys mollis</i>	<i>Paramelomys cf. mollis A</i>	M	N
BAA 1	H3-3	56	<i>Paramelomys mollis</i>	<i>Paramelomys cf. mollis A</i>	M	N
BAA 1	H3-19	57	<i>Paramelomys mollis</i>	<i>Paramelomys cf. mollis A</i>	F	N
BAA 1	H3-14	58	<i>Dasyurus albopunctatus</i>			N
BAA 1	H3-26	61	<i>Paramelomys mollis</i>	<i>Paramelomys cf. mollis C</i>	F	N
BAA 1	H3-18	62	<i>Rattus cf. niobe</i>			N
BAA 1	H3-3	63	<i>Rattus cf. niobe</i>		F	N
BAA 1	H2-4	64	<i>Paramelomys mollis</i>	<i>Paramelomys cf. mollis A</i>	F	N
BAA 1	H2-2	65	<i>Rattus cf. niobe</i>		M	N
BAA 2	M2-5	66	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M2-6	67	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M2-7	68	<i>Paramelomys lorentzii</i>	<i>Paramelomys cf. lorentzii</i>	M	N
BAA 2	M2-22	69	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N

BAA	Transect-Trap No	Field No.	Field ID	Genetic ID	Sex	Capture
BAA 2	M4-3	70	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	M	N
BAA 2	M4-4	71	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	F	N
BAA 2	M4-8	72	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	F	N
BAA 2	M2-2.1	73	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M2-2.2	74	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M2-12	75	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M2-13	76	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M2-19	77	<i>Rattus cf. niobe</i>			N
BAA 2	M2-32	78	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D with R. steini mtDNA</i>	M	N
BAA 2	M1-31	79	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M1-2.1	80	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M3-22	82	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M3-17	83	<i>Paramelomys lorentzii</i>	<i>Paramelomys cf. lorentzii</i>	F	N
BAA 2	M2-32	84	<i>Paramelomys lorentzii</i>	<i>Paramelomys cf. lorentzii</i>	M	N
BAA 2	M2-22	85	<i>Rattus cf. niobe</i>		F	R
BAA 2	M2-17	86	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M2-2.1	87	<i>Rattus cf. niobe</i>		F	R
BAA 2	M1-29	88	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M1-31	94	<i>Paramelomys lorentzii</i>	<i>Paramelomys cf. lorentzii</i>	?	N
BAA 2	M1-15	95	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M1-16	96	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M1-2.3	97	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M2-7	98	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-32	99	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M3-12	100	<i>Rattus cf. niobe</i>		F	N
BAA 2	M3-5	101	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex B</i>	M	N
BAA 2	M4-43	102	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	F	N
BAA 2	M4-21	103	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	M	N
BAA 2	M4-14	104	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	M	N
BAA 2	M4-4	108	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	F	N
BAA 2	M4-11	109	<i>Rattus cf. niobe</i>	<i>Rattus sp. 'spiny'</i>	F	N
BAA 2	M4-5	110	<i>Rattus sp. 'spiny'</i>		F	R
BAA 2	M3-22	111	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex B</i>	F	N
BAA 2	M3-17	112	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex B</i>	M	N
BAA 2	M3-8	113	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N

BAA	Transect-Trap No	Field No.	Field ID	Genetic ID	Sex	Capture
BAA 2	M3-9	114	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M3-5	115	<i>Rattus cf. niobe</i>		F	R
BAA 2	M3-6	116	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M2-32	117	<i>Paramelomys cf. rubex</i>		F	N
BAA 2	M2-28	118	<i>Paramelomys lorentzii</i>		M	R
BAA 2	M2-13	119	<i>Rattus cf. niobe</i>		M	R
BAA 2	M1-26	120	<i>Rattus cf. niobe</i>		F	R
BAA 2	M1-25	121	<i>Rattus cf. niobe</i>		M	R
BAA 2	M1-18	122	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M1-2.3	123	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M4-6	129	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	M	N
BAA 2	M4-8	130	<i>Rattus sp. 'spiny'</i>	<i>Rattus sp. 'spiny'</i>	M	N
BAA 2	M2-10	131	<i>Uromys cf. caudimaculatus</i>	<i>Uromys cf. caudimaculatus</i>		N
BAA 2	M2-34	132	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M2-32	133	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex B</i>	M	N
BAA 2	M2-13	134	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M2-9	135	<i>Paramelomys lorentzii</i>	<i>Paramelomys cf. lorentzii</i>		N
BAA 2	M2-11	136	<i>Rattus cf. niobe</i>		M	R
BAA 2	M2-8	137	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M2-5	138	<i>Rattus exulans</i>	<i>Rattus exulans</i>	F	N
BAA 2	M1-31	139	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M1-29	140	<i>Rattus cf. niobe</i>		M	R
BAA 2	M1-25	141	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M1-2.2	142	<i>Rattus exulans</i>	<i>Rattus exulans</i>	F	N
BAA 2	M3.33	143	<i>Rattus cf. niobe</i>	<i>Rattus niobe D</i>	M	N
BAA 2	M3-32	144	<i>Rattus cf. niobe</i>	<i>Rattus niobe D</i>	M	N
BAA 2	M3-21	145	<i>Rattus cf. niobe</i>	<i>Rattus niobe D</i>	F	N
BAA 2	M3-6	146	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex B</i>	F	N
BAA 2	M3-5	147	<i>Rattus cf. niobe</i>	<i>Rattus niobe D</i>	M	N
BAA 2	M4-39	149	<i>Paramelomys cf. rubex</i>		F	N
BAA 2	M4-39	150	<i>Paramelomys platyops</i>	<i>Paramelomys platyops</i>	F	N
BAA 2	M4-21	151	<i>Dasyurus albopunctatus</i>			N
BAA 2	M4-5	152	<i>Rattus sp. 'spiny'</i>		F	R
BAA 2	M1-33	154	<i>Paramelomys cf. rubex</i>		M	N
BAA 2	M1-31	155	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N

BAA	Transect-Trap No	Field No.	Field ID	Genetic ID	Sex	Capture
BAA 2	M1-30	156	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M1-18	157	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M1-22	158	<i>Rattus cf. niobe</i>		F	R
BAA 2	M1-2.3	159	<i>Rattus exulans</i>	<i>Rattus exulans</i>	M	N
BAA 2	M2-35	160	<i>Rattus cf. niobe</i>		F	R
BAA 2	M2-32	161	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex B</i>	F	N
BAA 2	M2-13	162	<i>Rattus cf. niobe</i>		F	R
BAA 2	M2-8	163	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-23	164	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M3-22	165	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex B</i>	M	N
BAA 2	M3-12	166	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M3-9	167	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-6	168	<i>Rattus cf. niobe</i>		F	R
BAA 2	M3-5	169	<i>Rattus cf. niobe</i>		M	R
BAA 2	M4-5	170	<i>Rattus sp. 'spiny'</i>		M	R
BAA 2	M1-30	171	<i>Rattus cf. niobe</i>		M	R
BAA 2	M1-33	172	<i>Rattus cf. niobe</i>		F	R
BAA 2	M1-16	173	<i>Rattus cf. niobe</i>		M	R
BAA 2	M1-2.3	174	<i>Rattus exulans</i>	<i>Rattus exulans</i>	M	N
BAA 2	M2-32	175	<i>Rattus cf. niobe</i>		M	R
BAA 2	M2-28	176	<i>Paramelomys lorentzii</i>		M	R
BAA 2	M2-13	177	<i>Rattus cf. niobe</i>		F	R
BAA 2	M2-9	178	<i>Paramelomys cf. rubex</i>		M	N
BAA 2	M3-15	179	<i>Paramelomys cf. rubex</i>	<i>Paramelomys cf. rubex B</i>	M	N
BAA 2	M3-12	180	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-5	181	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-4	182	<i>Paramelomys cf. rubex</i>		M	N
BAA 2	M3-2.2	183	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	F	N
BAA 2	M3-2.4	184	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-2.5	185	<i>Rattus cf. niobe</i>	<i>Rattus cf. niobe D</i>	M	N
BAA 2	M3-17	186	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-22	187	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-23	188	<i>Rattus cf. niobe</i>		M	R
BAA 2	M3-28	189	<i>Paramelomys cf. rubex</i>		F	N
BAA 2	M3-31	190	<i>Paramelomys cf. rubex</i>		M	R

BAA	Transect-Trap No	Field No.	Field ID	Genetic ID	Sex	Capture
BAA 2	M3-2.5	191	<i>Rattus cf. niobe</i>		F	R
BAA 2	M3-2.3	192	<i>Rattus exulans</i>		M	N
BAA 2	M3-4	193	<i>Rattus cf. niobe</i>		F	R
BAA 2	M3-5	194	<i>Rattus cf. niobe</i>		F	R

Table A5.4.2. List of all other observations on non-volant mammals made during the course of the 2015 fieldwork.

Location	Taxon	Observ. Type	Observ. Date	Field No
BAA 1 H5	<i>Neophascogale cf. lorentzil</i>	sighting	19-06-15	
BAA 1 near H6	<i>Dorcopsulus cf. vanheurni</i>	dog faeces	20-06-15	
BAA 1 near H3	<i>Neophascogale cf. lorentzil</i>	mist-net capture	21-06-15	37
Hides GCP	<i>Rattus rattus</i>	baiting casualty	02-07-15	92
BAA 1 near H1	<i>Hyomys sp.</i>	road-kill casualty	02-07-15	93

Appendix 5.5. The Hides Ridge owl roost assemblage

INTRODUCTION AND METHODS

Origin and properties of the sample

In August 2011 Mr Steve Hamilton of Common Scents Wildlife Tracking Pty Ltd collected a sample of bones from below an owl roost in a cave at c. 2,065 m asl on Hides Ridge during a preclearance survey. The sample was examined by Ken Aplin on 19–21 December 2012.

The sample consists of five partial 'owl pellets' (bones and hair regurgitated by a roosting owl following digestion of soft tissues) along with a quantity of bones derived from disaggregated pellets. The total sample consists of 115 partial crania, 55 isolated maxillae, 263 dentaries, and a quantity of postcranial bones. It includes the remains of 25 species of mammal and one species of bird. The mammals include nine species of marsupials, 13 species of rodents, two species of small fruit bats and one species of insectivorous bat. No remains of large cave-roosting fruit bats (genera *Aproteles* and *Dobsonia*) were found in the sample.

Analytical methods

Crania, jaws and teeth were sorted into taxa and then by anatomical elements (e.g. left lower jaw, right lower jaw). The most numerous anatomical element for each taxon represents the 'minimum number of individuals' (MNI) required to account for the remains. MNI is used here for comparisons of relative abundance.

RESULTS AND DISCUSSION

Source and age of the remains

The physical condition of the sample provides information on its disposition within the cave, its age, and its likely origin. The absence of adherent cave earth on the bones indicates that they were exposed on a cave floor or on perched rocks, as reported by Hamilton (pers. communication, 2015). The presence of numerous partially intact skulls indicates a lack of water transport or other major disturbance, while presence of characteristic signs of microbial degradation, including surface pitting on some of the bones, indicates a humid environment. Given these observations, it is significant that several of the partial pellets contain mammal hair. Hair is unlikely to survive for more than a few months in a humid cave environment due to rapid fungal attack, and unless the bones and teeth are protected by burial in sediment, they too may be destroyed within a few years through a combination of biological activity and demineralization. The physical condition of the sample thus indicates a contemporary age for the remains. The absence in the Hides Ridge sample of any large mammal bone and any burnt remains of any species indicates that the site was rarely if ever used by human hunters.

The presence of five partial pellets establishes the sample as the prey remains of a raptorial bird. Raptors ingest their prey whole or in large chunks and regurgitate the bones, hair and other indigestible remains in a pellet while resting at a roost site. The raptor most likely responsible for the Hides Ridge sample is the Sooty Owl (*Tyto tenebricosa*). This species is known to use caves for roosts across its range in Melanesia and Australia, is known to feed on prey items up to size of small possums and bandicoots, and is one of only two large owl species reported to occur at 2,000 m asl in New Guinea (Beeler et al. 1986). The other large-bodied owl in montane New Guinea is the Eastern Grass Owl, *Tyto longimembris*, which typically occurs in montane grasslands in New Guinea and tends to roost on the ground in tussock grassland (Beeler et al. 1986).

Owl roost assemblages are used worldwide as indicators of past ecological communities (e.g. Andrews 1990), though interpretation requires consideration of various factors including patterns of predation across a local landscape and potential differences in vulnerability of potential prey items. In degraded forest habitats in Australia Sooty Owls may hunt up to a few kilometers from a regular roost site (Bilney et al. 2011). In the context of a pristine New Guinean montane forest, where prey is likely to be both more abundant and evenly distributed, it is likely that most of the prey items found below a roost are derived from within a smaller foraging radius. Even so, this might provide access to forest across quite a wide elevational range.

Composition of the owl roost assemblage

Individual element counts and MNIs for the non-volant mammals of the assemblage are shown in Table A5.5.1.

Table A5.5.1. Skeletal element counts for the owl pellet assemblage collected in 2011 at c. 2,065 m asl on Hides Ridge. Cell values are counts of each individual element by symmetry. The MNI values represent the minimum number of individuals (MNI) required to account for the identified remains of each species. *Melomys* and *Protochromys* spp. could not be reliably distinguished from fragmentary dentaries and these are listed as *Melomys* or *Protochromys*. The general lifestyle or 'habitus' of each species is shown in the last column, coded as A = arboreal; S = scansorial; T = terrestrial.

Taxon	Crania	L Maxilla	R Maxilla	L Dentary	R Dentary	MNI	Habitus
DASYURIDAE							
<i>Murexia naso</i>		2	2	1		2	S
<i>Murexia melanurus</i>	1	1	1	2	3	3	S
<i>Murexia cf. habbema</i>		2	2	1		2	S
Peramelidae							
<i>Microperoryctes ornata</i>				1	1	1	T
ACROBATIDAE							
<i>Distoechurus cf. pennatus</i>	4	2	1	2		4	A
BURRAMYIDAE							
<i>Cercartetus cf. caudatus</i>	2	7	6	7	7	7	A
PETAURIDAE							
<i>Petaurus cf. breviceps</i>	2	3	2	2	2	3	A
PSEUDOCHEIRIDAE							
<i>Pseudochirulus larvatus</i>	8	11	11	12	10	12	A
<i>Pseudochirulus mayeri</i>	1	5	4	4	4	5	A
MURIDAE							
<i>Abeomelomys sevia</i>	13	14	14	7	3	14	A
<i>Chiruromys vates</i>	2	3	3	5	1	5	A
<i>Lorentzimys cf. nouhuysi</i>		1	2	4	4	4	A
<i>Melomys cf. dollmani</i>	8	11	12	1	2	12	S
<i>Melomys cf. rufescens</i>	9	9	9			9	S
<i>Protochromys cf. fellowsi</i>	2	2	2	1	2	2	T
<i>Melomys</i> or <i>Protochromys</i>				26	28	28	S/T
<i>Paramelomys cf. mollis</i>	12	12	12	7	8	12	T
<i>Paramelomys cf. rubex</i>	5	6	5			6	T
<i>Pogonomys cf. macrourus</i>	9	10	9	7	8	10	A
<i>Pogonomys cf. loriae</i>	22	26	24	22	28	28	A
<i>Rattus cf. niobe</i>	6	8	9	10	12	12	T
<i>Rattus steini</i>	2	2	2	1	1	2	T
<i>Rattus cf. verecundus</i>	1	2	2	3	2	3	T
Total all taxa	109	139	134	126	126	187	

Two species detected in the owl pellet sample – *Protochromys* cf. *fellowsi* and *Murexia* cf. *habbema*– were not included in any of the previously compiled lists for Southern Highlands (incl. what is now Hela) Province (Leary and Seri 1997; Mamu 2005). Each of these represents a significant geographic range extension. For one species (*Chiruromys vates*) the remains are the highest elevational record.

The broad ecological niche or 'habitus' is classed as arboreal for ten species, as scansorial (mainly ground dwelling but also capable of climbing) for five, and as terrestrial for seven. Arboreal species make up 55% of the individual animals in the sample, followed by terrestrial species at 23%, and scansorial species at 17%. Although the hunting effort was probably biased to some extent toward arboreal species, the owls clearly hunted mammals living at all strata within the montane forest community, including the forest floor.

The sample clearly identifies a number of species as being locally abundant and others as being substantially less so. Among the rodents active at night in the canopy and understory, *Pogonomys* cf. *loriae* was clearly the species most frequently predated, followed more or less equally by *Abeomelomys* cf. *sevia*, *Pogonomys* cf. *macrourus* and *Melomys* cf. *dollmani*. Arboreal rodents of the genera *Chiruromys* and *Lorentizmys* were evidently much less commonly predated. Among the small to medium-sized possums, *Pseudochirulus larvatus* was presumably very abundant, especially considering the fact that adults are not being taken by the owls, while the smaller *Pseudochirulus mayeri* and much smaller *Cercartetus* cf. *caudatus* were less frequently predated and small possums of the genera *Distoechurus* and *Petaurus* were even less frequently predated again. The small insectivorous to carnivorous *Murexia* spp. were all relatively uncommonly taken, as anticipated from their trophic level. Among the terrestrial species, the rodents *Rattus* cf. *niobe* and *Paramelomys* cf. *mollis* were quite frequently predated, while *Paramelomys* cf. *rubex* and *Rattus* cf. *verecundus* group were less often taken and *Protochromys* cf. *fellowsi* and *Rattus steini* were rarely so. *Rattus* cf. *steini* can be common in disturbed habitats up to quite high elevations, but like other lowland to mid-montane *Rattus* spp., it appears to be naturally rare in undisturbed montane forests.

The mammal community recorded by the Hides Ridge sample is an interesting mix of elements typical of hill forests to lower elevation montane forests (e.g. *Chiruromys vates*; *Pogonomys* cf. *macrourus*; *Melomys* spp.) and of higher elevation montane forests (e.g. *Protochromys* cf. *fellowsi*; *Pseudochirulus mayeri*). This mix of species is consistent with the elevation of the site (c. 2,000 m asl), near to the usual upper limits of Lower Montane Forest in New Guinea (c. 2,500 m asl), and the fact that isolated ranges and ridges in New Guinea often support plants and animal species more typically found at higher elevations, due to local climatic effects including depression of persistent cloud cover (the 'Massenerhebung' Effect; Grubb 1971). The species associations produced in such situations may be locally distinctive and differ from range to range, even over short distances.

REFERENCES

- Andrews, P. 1990. Owls, Caves and Fossils. Natural History Museum Publications, London.
- Beehler, B. M., Pratt, T. K. & Zimmerman, D. A. 1986. Birds of New Guinea. Princeton University Press.
- Bilney, R. J., White, J. G., L'Hotellier, F. A. & Cooke, R. 2011. Spatial ecology of Sooty Owls in south-eastern Australian coastal forests: implications for forest management and reserve design. *Emu* 111: 92–99.
- Grubb, P. J. 1971. Interpretation of the 'Massenerhebung' effect on tropical mountains. *Nature* 229: 44–45.
- Leary, T. & Seri, L. 1997. An annotated checklist of mammals recorded in the Kikori River Basin, Papua New Guinea. *Science in New Guinea* 23: 79-100.
- Mamu, T., Gebia, O., Enoch, I., Kuduk, M. & Ona, A. 2005. Report for an assessment survey of terrestrial mammals for PNG Gas Project, Papua New Guinea. Annex 3 in: Crome, F. H. J. et al. 2008. Terrestrial biodiversity analysis of the Upstream Project Area. Papua New Guinea Liquefied Natural Gas Project. Appendix 1 in: The PNG LNG Project Environmental Impact Statement. Prepared by Coffey Natural Systems for Esso Highlands Limited.

Appendix 5.6. Statistical analyses of trapping data.

This appendix provides a detailed description of the statistical approaches to data analysis that are summarised in Chapter 5. Statistical analyses were performed using scripts written in [R] language (R Core Team 2016).

The input data matrix consists of a single line entry for each individual trap event, and included the following variables:

- Site (BAA 1, BAA 2)
- Elevational zone (1 = M4; 2 = M1–3; 3 = H1–3; 4 = H5–6)
- Transect (e.g. H1, H2 etc; M1, M2 etc)
- Trap number (1–40 or 60; latter for M4 which had more traps); this value is converted to Distance (from road/ ROW) by multiplication by trap spacing (6 m).
- Trapping Date (dates in June-July converted to sequential date 1–38).
- Trapping Day (1, 2, 3 etc)
- Capture (0 = no; 1 = yes)
- Recapture (0 = no; 1 = yes)
- One column for each of the species, each scored as capture (0 = no; 1 = yes).

After future surveys the variable 'Sampling Episode' will be added (2015 = 1; 2017 = 2 etc).

Analysis 1: Exploring the differences in capture rates between transect lines.

This analysis asks whether the likelihood of any novel capture (i.e. excluding recaptures) on the transect in question (e.g. H2) is different from that on an arbitrarily selected transect (in this case H1). The statistical approach is a Generalized Linear Mixed Model fit by maximum likelihood (Laplace Approximation). For this analysis the R script is:

```
model1<-glmer(capture~Transect+(1|Replicate)+(1|Trapping_Date), family="binomial", data=PMA3_Year_1)
```

Statistical output

AIC	BIC	logLik	deviance	df.resid
1078.3	1143.1	-528.2	1056.3	2660

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.3498	-0.2661	-0.2215	-0.1722	7.2196

Random effects:

Groups	Name	Variance	Std.Dev.
Trapping_Date	(Intercept)	6.145e-02	2.479e-01
Site	(Intercept)	6.827e-10	2.613e-05

Number of observations = 2671; groups=Trapping_Day 17, Site = 2.
 Fixed effects (significant contrasts are in bold type).

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-2.463362	0.267925	-9.194	< 2e-16***
TransectH2	-0.909923	0.435048	-2.092	0.03648*
TransectH3	0.322071	0.457063	0.705	0.48103
TransectH5	-1.530857	0.478837	-3.197	0.00139**
TransectH6	-0.451792	0.349695	-1.292	0.19637
TransectM1	-0.453438	0.374482	-1.211	0.22596
TransectM2	-0.329246	0.354049	-0.930	0.35240
TransectM3	-0.005528	0.352231	-0.016	0.98748
TransectM4	-1.033429	0.389384	-2.654	0.00795**

Each of transects H2, H5 and M4 had a significantly lower likelihood of capture than transect H1. The only transect which had a higher likelihood of capture than H1 was H3 but this contrast was not statistically significant.

These contrasting likelihood values are illustrated graphically in Figure A5.6.1

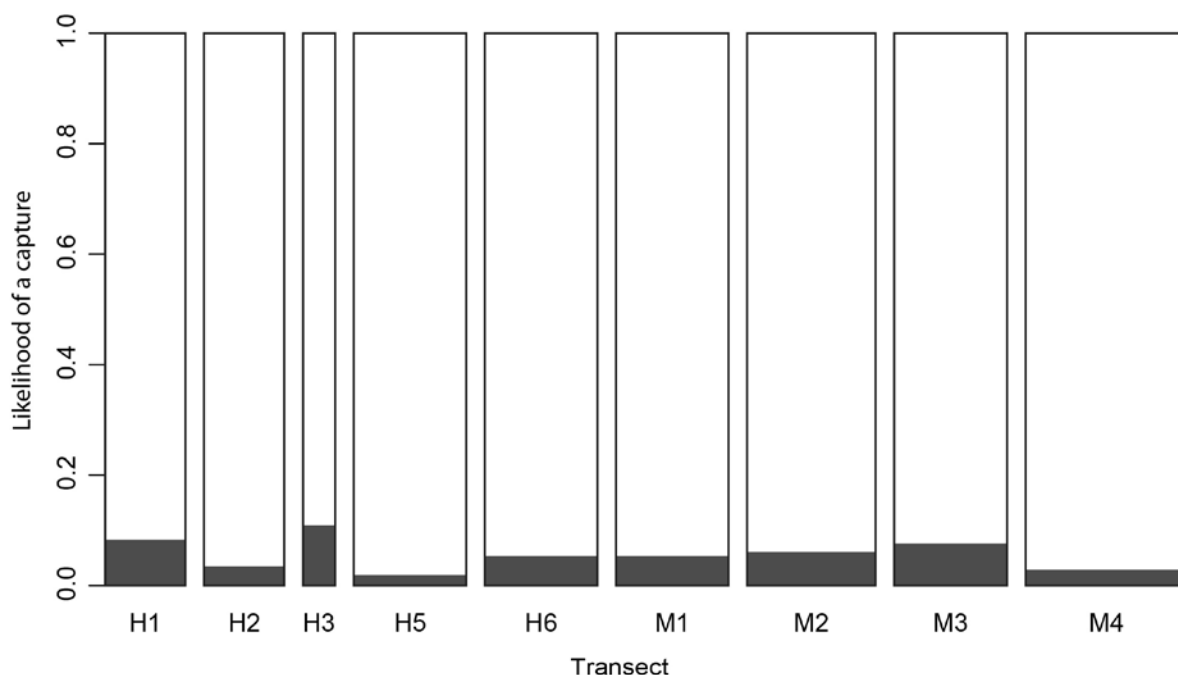


Figure A5.6.1. Likelihood of a capture (excluding recaptures) on each transect, based on GLMM analysis that takes into account other fixed and random effects. The relative width of each column is proportional to the number of trap nights on each transect ((i.e. sampling effort).

Analysis 2: Exploring the impacts of proximity to the road/ROW.

This analysis asks whether the likelihood of a new capture (i.e. excluding recaptures) at any point along a particular transect is influenced by the fixed effect Distance (from ROW). The statistical approach is a Generalized Linear Mixed Model fit by maximum likelihood (Laplace Approximation). For this analysis the R script is:

```
model2<-glmer(captureY/N~Replicate+Trapping.day+Elevation_Zone+Trapping_Date+sqrt(Distance)+(1|Transect),
family="binomial", data=PMA3_Year_1)
```

Statistical output

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) [‘glmerMod’]

AIC	BIC	logLik	Deviance	df.resid
925.5	965.8	-455.8	911.5	2334

Scaled residuals:

Min	1Q	Median	3Q	Max
-0.4562	-0.2521	-0.2116	-0.1786	6.4316

Random effects:

Groups

Name	Variance	Std.Dev
Transect (Intercept)	0.04566	0.2137

Number of observations = 2341; groups = Transects 9.

Fixed effects (significant contrasts in bold type):.

	Estimate Std.	Error	Z value	Pr(> z)
(Intercept)	-4.86326	2.08714	-2.330	0.019800*
Replicate	-1.02290	0.98269	1.041	0.297912
Trapping_day	-0.22278	0.08955	-2.488	0.012857*
Elevation_Zone	0.19348	0.28094	0.689	0.491024
Trapping_Date	0.13234	0.08280	1.598	0.109992
sqrt(Distance)	-0.08269	0.02330	-3.549	0.000386***

Correlation of Fixed Effects:

	Intercept	Site	Trapping Day	Elevation Zone	Trapping Day
Site	0.535	-			
Trapping_Day	0.733	0.653	-		
Elevation_Zn	-0.699	0.169	-0.340	-	
Trapping_Date	-0.884	-0.849	-0.835	0.321	-
sqrt(Distance)	-0.168	0.004	-0.020	0.075	0.022

This analysis revealed a small but statistically significant tendency for captures to occur closer to the ROW. It also revealed that capture of new individuals occurred more often earlier in the trapping period. For BAA 2 where recapture rates were high, this is probably indicative of trapping saturation (i.e. captures of a high proportion of the total resident population). In BAA 1, trap avoidance following capture seems a more likely explanation. The two factors are not correlated. The results are summarized graphically in Figure A5.6.2.

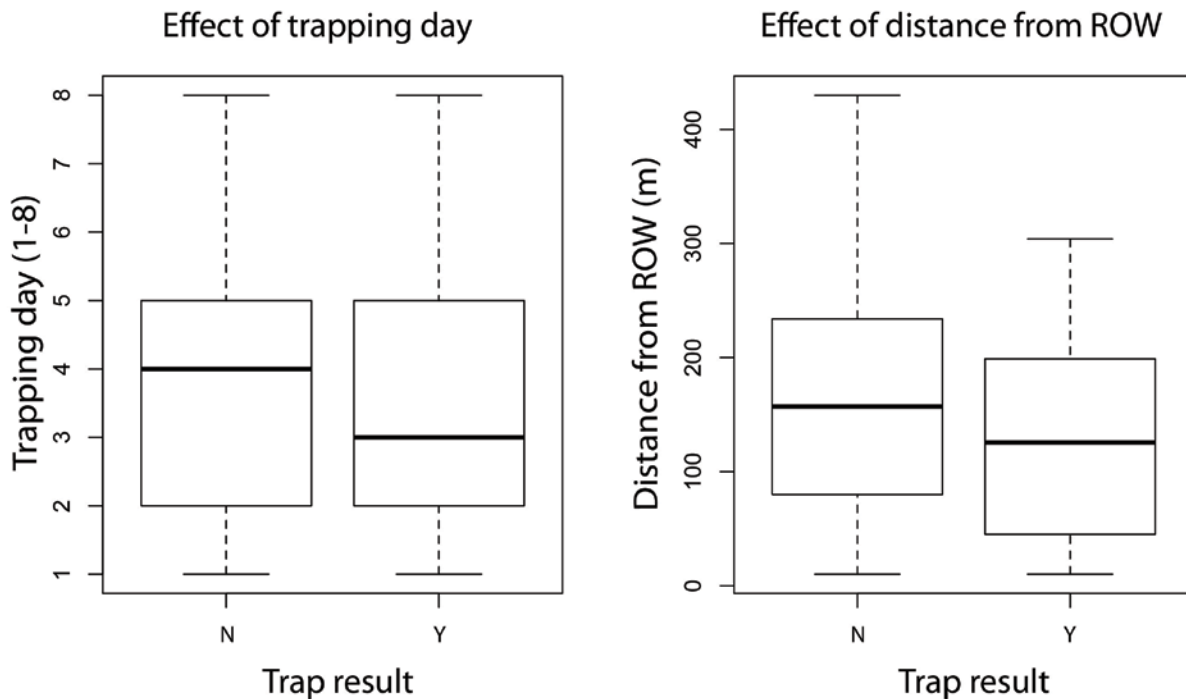


Figure A5.6.2. Results of GLMM analysis of trap captures, all species combined. In each figure the left hand box and whisker entry are non-captures, the right are captures. The left hand figure shows the fixed effect of the day of trapping (Day 1, Day 2 etc); the right hand figure shows the fixed effect of distance from the road/ROW. Each figure contrasts the likelihood of not making a capture (N) with the likelihood of making a capture (Y). The central bar is the maximum likelihood estimate of the most likely position on the transect to either make a capture or not make a capture, while the box and whisker represent one and two standard errors, respectively.

Analysis 3: Differences in influence of road/ROW proximity between genera

This analysis explored whether there was any difference in capture likelihood in relation to distance from the road/ROW between members of the various groups of captured mammals.

The first analysis was of the most commonly captured group—the various species of *Rattus*. This analysis asks whether or not the likelihood of capturing *Rattus* spp. is influenced by proximity to the road/ROW. It used only novel captures of *Rattus* (i.e. excluded recaptures). This analysis showed no relationship between distance from ROW and the likelihood of a novel capture of a *Rattus* species [$\sqrt{\text{Distance}}$ est= 0.08367, std.error=0.10518, z= 0.796, p=0.42631]. This pattern is also apparent from Figure A5.6.3 that summarizes the likelihood of new captures of *Rattus* spp. with the capture data from all transects grouped in 50 m intervals at increasing distances from the road/ROW.

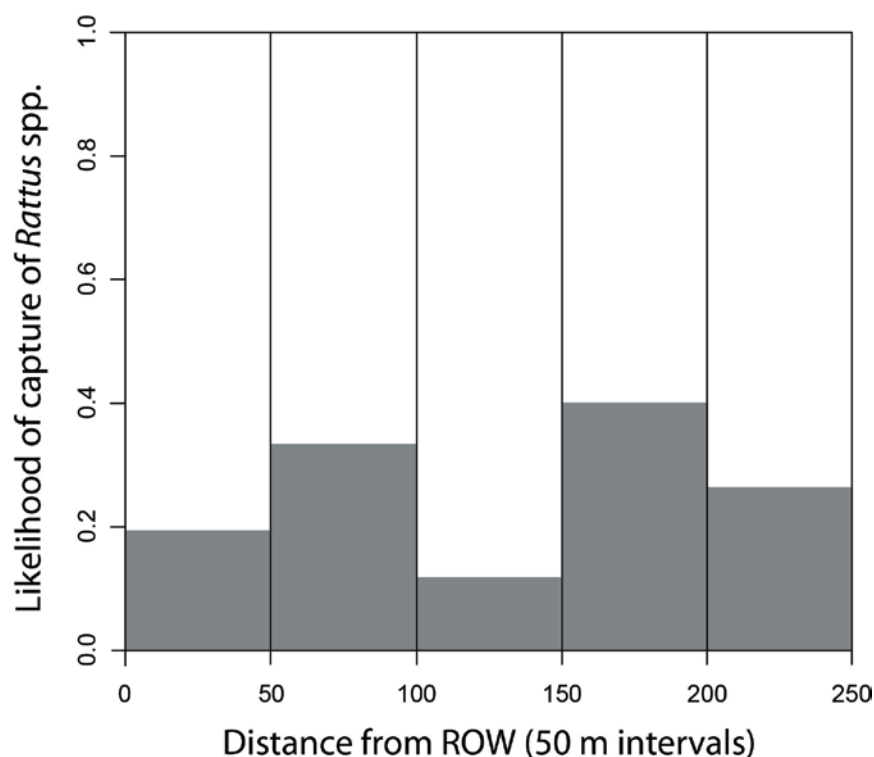


Figure A5.6.3. Likelihood of capture of *Rattus* spp. (excluding recaptures) at various distances (in 50 m intervals) from the ROW, based on GLMM of data from all transects and taking into account all other fixed and random effects.

For the remaining less commonly captured taxa, the potentially most informative analysis asks whether the likelihood of capture differs from that of *Rattus* spp. at varying distance from the road/ROW. Data from two other groups of mammals were analysed in this way—*Paramelomys* spp. and marsupials (species of *Dasyurus* and *Microperoryctes*).

The statistical approach is a Linear Mixed Model fit by maximum likelihood (Laplace Approximation). For this analysis the R script is: `model3<lmer(Distance~Replicate+Elevation_Zone+taxon+(1|Transect)+(1|Trapping.day)+(1|Trapping_Date), data=PMA3_Year_1)`

Statistical output

REML criterion at convergence: 1647.2

Scaled residuals:

Min	1Q	Median	3Q	Max
-1.6999	-0.7991	-0.1112	0.7457	2.8964

Random effects:

Groups	Name	Variance	Std.Dev.
Trapping Date	(Intercept)	80.91	8.995
Transect	(Intercept)	905.95	30.099
Trapping Day	(Intercept)	0.00	0.000
Residual		4921.54	70.154

Number of observations = 148, groups = Trapping_Date 17; Transect, 9; Trapping.day, 8
 Fixed effects:

	Estimate	Std. Error	t-value	p-value*
(Intercept)	69.93	91.55	0.764	
Site	28.55	49.52	0.577	
Elevation Zone	10.72	26.39	0.406	
taxon marsupials	42.14	36.70	1.148	0.27
taxon <i>Paramelomys</i>	56.92	13.87	4.105	<0.0001

* p-values derived from t-value lookup table.

This analysis confirms the impression that the likelihood of capturing *Paramelomys* spp. was more strongly influenced by distance from the road/ROW than were captures of *Rattus* spp. (see also Figure A5.6.4). The fact that a response was detected indicates that the impact may be least partially restricted to the zone sampled by the transects, i.e. within c. 150–250 m of the ROW. Whether the impact is entirely contained within this zone or extends further into flanking forests cannot be answered from the present data.

Too few captures of marsupials were made to derive a meaningful comparison.

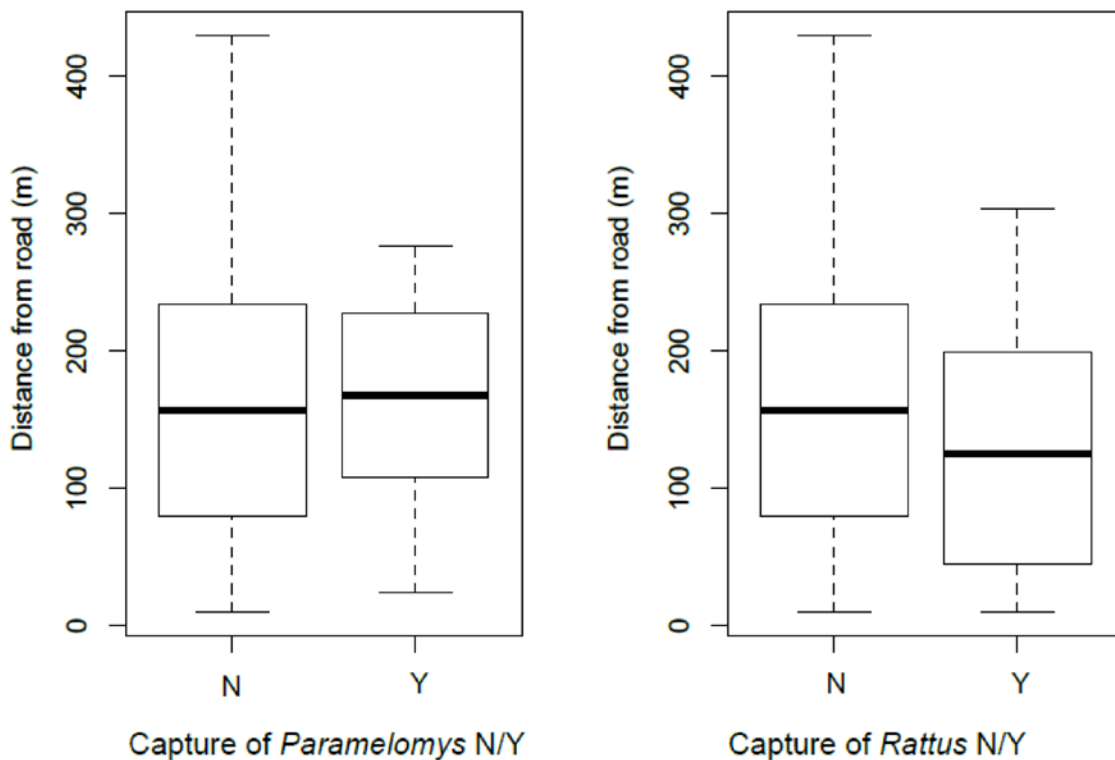


Figure A5.6.4. Results of GLMM analysis of trap captures, comparing the fixed effect of distance from road/ROW on captures of *Paramelomys* spp. (left) and *Rattus* spp. (right). Each figure contrasts the likelihood of not making a capture (N) with the likelihood of making a capture (Y). The central bar is the maximum likelihood estimate of the most likely position on the transect to either make a capture or not make a capture, while the box and whisker represent one and two standard errors, respectively.

CHAPTER 6 – BATS

Kyle Armstrong



An insectivorous bat, *Rhinolophus megaphyllus*, that was captured in Biodiversity Assessment Area 2 near Moro

SUMMARY

Background and aims

Bats were included in the PMA3 long term monitoring study because it is relatively simple to survey a high proportion of bat species present by recording signature ultrasonic echolocation calls in a well-replicated study using acoustic recorders (or 'bat detectors'). These data can be used to detect changes to the diversity of bat communities that reflect ecologically relevant changes in forest habitats adjacent to the ROW.

The primary goals of the 2015 survey were to obtain baseline data on the species of echolocating bats in two Biodiversity Assessment Areas (BAAs) in the Upstream Project Area, and to establish a network of permanent acoustic recording sites that can detect quantitative changes in the diversity and composition of the bat community over the life of the study.

Major results

A total of 19 species was detected in the acoustic recordings. Another two species of non-echolocating blossom bat (*Syconycteris* spp.) were amongst the captures, bringing the total number of bat species detected to 21. This represents 43% of all mammal species recorded on the 2015 survey.

Two measures of bat diversity—Species Richness and Phylogenetic Diversity—were significantly higher in bat communities at 1,000 m asl adjacent to Arakubi Quarry and the ROW in BAA 2, compared to higher elevations. However, there was no significant difference in bat diversity between the open space at the forest edge and at distances further from the clearing disturbance in either BAA. Although not statistically significant there was a trend at 1,000 m asl, but not at other sites, for both diversity measures to be higher at or close to the open spaces. These results suggest that, to date, bat communities have not been negatively impacted by construction of the ROW linear infrastructure.

Although overall patterns of species diversity did not vary with increasing distance from the ROW, inspection of the Relative Abundance values of each species at increasing distances from the forest edge indicated that several might be useful as Indicator Species because of their specific habitat requirements. Statistical power will increase with data from successive years, and help to provide more information on subtle community responses to the ROW infrastructure.

Conclusions

Data collected on the 2015 survey suggest that the forest adjacent to the ROW has so far retained its key environmental values for bats. This study detected no significant differences in any of several measures of bat diversity calculated for increasing distances from the ROW, and the main measurable difference amongst bat communities was that diversity was higher at lower elevations. The identification of several candidate Indicator Species that either prefer closed forest (*Murina* sp. cf. *florium*, *Nyctophilus* sp.) or that take advantage of open areas for foraging (*Emballonura* spp., *Philetor brachypterus*, *Pipistrellus* spp.) might help in the detection of subtle environmental changes in future surveys.

A potentially new species of bat with a characteristically high echolocation call (172 kHz) was recorded on transect M5 in BAA 2. Capture of this species is a high priority for the next survey in order to support its formal taxonomic description. It would also be valuable to incorporate baseline information on bats from the period before ROW and access road construction. Relevant data is available from the work of Richards (2005, 2008), but reanalysis of the raw data will be necessary to ensure consistency in identifications.

Investigation of potential control sites remote from project infrastructure (including the ROWs) might be appropriate. A control site would improve the ability to detect larger scale changes that might be occurring in the forest at distances greater than 220 m from the ROW, and to help decide whether these are caused by project influences or by external factors such as climate change. Previously surveyed sites in the nearby Muller Range would be ideal, as baseline data for bats have already been collected using comparable methods, showing that the region supports many of the same bat species (Armstrong and Aplin 2011). A change in the genetic methods to incorporate the use of next-generation DNA sequencing markers is also recommended. This will provide taxonomic certainty across all groups of bats found in the BAAs.

INTRODUCTION

Bats (Chiroptera) generally comprise somewhere between a quarter to a half of all mammals present in a particular habitat, though this can be as much as 90% as in the case of Timor-Leste (Armstrong 2007). There are 94 species of bats currently recognised in Papua New Guinea (PNG) (Bonaccorso 1998; Simmons 2005), and at least 37 are known or expected to occur in the PMA3 study area based on data compiled from the IUCN Red List. In any given forest habitat in PNG, the diversity of bat species reflects the many different ecological niches that they can occupy, and the diversity of morphological and behavioural features that allow them to partition the available resources. This study considers both the short- and long-term effects of linear infrastructure corridors on closed forest ecosystems in PNG, as seen through the responses of bat communities, and as measured by the number and types of species present, by their evolutionary and ecological diversity, and by the responses of individual species.

Effects of linear infrastructure corridors on bats

The effects of linear infrastructure corridors such as roads on the structure, dynamics and components of ecosystems is well documented. Road networks are associated with edge effects that reduce habitat quality and biodiversity beyond actual carriageways (Trombulak and Frissel 2000; Spellerberg 2002; Coffin 2007; Fahrig and Rytwinski 2009). Roads increase connectivity for people but can reduce it dramatically for the populations of animals remaining in dissected landscapes.

In addition to the initial direct impacts associated with removal of habitat for new roads, there can be continuing direct and indirect effects on bats in adjacent natural habitats. Road construction creates open habitats, exposing bats to a greater level of perceived or real threat from 'predators' (including vehicles), reduces habitat connectivity, and can introduce high levels of artificial illumination, noise from traffic and wind intrusion into habitats (Kuijper et al. 2008; Schaub et al. 2008; Stone et al. 2009, 2012; Zurcher et al. 2010). Bat species that forage in dense vegetation cover within forest habitats and rely on passive listening for prey capture tend to be affected to a greater extent by roads, but even bats that forage in the open and are attracted by insect accumulations at lights have decreased levels of activity closer to roads (Blake et al. 1994; Kerth and Melber 2009; Berthinussen and Altringham 2011).

Little is known of the extent to which forest adjacent to linear infrastructure corridors might become less suitable for bats over time, and how far into the forest any edge effects might intrude. There are few long-term studies of bat communities occupying forest edge habitats, and most short-term studies derive from Europe where landscapes have been subject to modification for hundreds of years. The response of bat communities to linear gaps in broad areas of pristine forest has not been studied in PNG. The PMA3 study presents a unique opportunity to learn about bat assemblages in PNG and how they respond to linear infrastructure corridors in relatively intact tropical ecosystems.

Monitoring bat biodiversity

The study of bats was once challenging and logistically demanding—until hardware became available that allowed bat species to be identified from recordings of their echolocation calls. The use of acoustic recorders to detect and monitor bats is now commonplace, with an ever-expanding array of recording hardware available (Parsons and Szewczak 2009). They find application in a variety of projects designed to document the composition of bat assemblages or the presence of just one target species; to conduct surveys of almost entirely unknown bat assemblages (e.g. Armstrong and Aplin 2011; Armstrong et al. 2015a; Aplin et al. 2015); to detect changes in either diversity or activity; and to detect bats during emergence from roost entrances or while foraging. In contrast, estimating changes in bat populations using capture/recapture to estimate abundance requires substantially greater investment in field studies, and often requires significantly longer timeframes (>20 years) to detect effects unless gross changes are obvious (Bernard and Fenton 2007; Meyer et al. 2010).

Long-term studies that span at least 10 years and target entire bat assemblages via acoustic recordings are rare, and essentially absent from the publicly available literature. This is partly because completely-automated ultrasonic recording systems ('bat detectors') that can sample uninterrupted over a full night have only been available since around 2002 (Armstrong and Ford 2002). The application of bat detectors in PNG is also relatively new. The first comprehensive acoustic survey of bats in PNG was undertaken as part of baseline studies for the PNG LNG project

by Richards (2005, 2008), which was a commendable effort despite being limited severely by the almost complete absence of information on the different types of echolocation produced by PNG bats. Since that study, several projects conducted by universities, environmental organisations and development proponents have characterised the calls of many PNG bat species (Armstrong and Aplin 2011, 2014a,b; Leary and Pennay 2011; Robson et al. 2012; Armstrong et al. 2015a,b; K.N. Armstrong and K.P. Aplin unpublished data). It is now possible to confidently identify many more species from their calls, and while taxonomic issues continue to confound the identification of some bats, there is now sufficient knowledge of PNG bat calls to support a long-term acoustic monitoring study.

Bats perform important ecological roles in forest ecosystems, including reducing insect abundance and levels of herbivory (Williams-Guillén et al. 2008; Kalka et al. 2008), and most notably performing keystone roles of pollination and seed dispersal (Fujita and Tuttle 1991; McConkey and Drake 2006; Lobova et al. 2009). They can be a good indicator group for long-term monitoring of biodiversity values and habitat quality (Jones et al. 2009), for numerous practical reasons, as summarised below:

1. Bats typically comprise at least a third of any mammal assemblage in forested areas, so there is sufficient potential to observe changes in species composition and richness.
2. Each insectivorous bat species can be recognised by its unique echolocation call, so given adequate coverage, acoustic recordings provide the means to document all echolocating bat species in a study area.
3. Acoustic surveys can provide information on insectivorous bat diversity with less effort and with a greater encounter rate than through trapping.
4. Some bat species are very sensitive to changes in the structure of forest habitats—with some disappearing and others becoming more common when habitats are opened up (Kalko 1998; Jones et al. 2003).
5. Bat species can be grouped into 'call types' based on the structure of their echolocation calls, and these call types reflect how and where bats utilise their habitats to feed (Denzinger and Schnitzler 2013). Thus, the relative representation of bat feeding groups, as indicated by echolocation call type, has the potential to change, reflecting broader structural changes to their habitat.
6. Recording hardware can be deployed by non-specialists, and analysis of the large datasets that accumulate is expedited by recent advances in customised semi-automated analysis approaches (Armstrong and Aplin 2014c; Armstrong et al. 2016).

Aims of the PMA3 bat study

This study addresses the overarching question: "Is there an ongoing level of habitat change following linear infrastructure construction that is reflected in changes to bat communities?".

In this first field phase, acoustic recording sites were established to allow long-term monitoring of bat species, with the following aims:

1. Document the diversity of bats along the ROW in the PMA3 project area as a baseline for future comparisons over the life of the monitoring study;
2. Determine whether or not bat communities have responded significantly to the construction of the ROW by assessing whether two measures of bat diversity, Species Richness and Phylogenetic Diversity, vary with increasing distance from the linear infrastructure corridor;
3. Quantify bat diversity through several other measures that provide additional perspectives on the differences of bat communities at different elevations, distances from the ROW and the potential responses over time.

METHODS

Sampling design

The success of this long-term monitoring study depends on standardisation of effort, equipment type and site placements. A total of 66 permanent acoustic recording sites was distributed along the 11 transects established in BAA 1 (transects H1–H6) and BAA 2 (transects M1–M5) (Figures 2–6 in Executive Summary). The transects were located within two narrow elevational bands in each BAA: at approximately 2,200 m asl and 2,700 m asl in BAA 1 on Hides Ridge; and approximately 1,000 m asl (Arakubi Quarry) and 1,400 m asl (KP107) in BAA 2 on the Agogo Range near Moro.

Bat detectors were spaced along each transect at 50 m intervals so that an individual bat could only be detected by a single recorder at any given moment. The first detector on each transect was oriented to receive signals from the open area over the ROW (distance '0 m'). The remaining bat detectors (distances of 20–220 m) represented treatments of potentially decreasing edge effect. Thus, each transect had six placements, giving a total of 36 recording nights over a 9-night survey period for BAA 1, and 30 recording nights over a 7-night survey period for BAA 2 in June–July 2015 (Table 6.1). A full night of recording was made at each site from sunset to sunrise. Descriptions of the vegetation at each elevation are provided in the Executive Summary.

Recordings were made in high quality full spectrum format with Pettersson Elektronik D500X bat detectors, which were protected in a plastic box and a waterproof bag. Microphones on a 3 m extension cable were placed in a funnel made from a drink bottle to keep out rain, and set 2.5 m above the ground (Figure 6.1).

Table 6.1. Summary of the experimental design and bat recording site placements. Factors include 'elevation' (4 treatments, total 11 replicates) and 'distance from the ROW' (6 treatments, total 66 replicates). GPS coordinates are listed in Appendix 6.1.

Area	Elevation (m asl)	Replicate (m asl)	Distance from ROW (m)						Total
			0	20	70	120	170	220	
BAA 1	'2,700 m'	H4—2,700 m (2,681–2,696 m)	1	1	1	1	1	1	
		H5—2,750 m (2,726–2,756 m)	1	1	1	1	1	1	
		H6—2,730 m (2,725–2,736 m)	1	1	1	1	1	1	
	'2,200 m'	H1—2,150 m (2,148–2,163 m)	1	1	1	1	1	1	
		H2—2,200 m (2,171–2,229 m)	1	1	1	1	1	1	
		H3—2,300 m (2,296–2,327 m)	1	1	1	1	1	1	36
BAA 2	'1,400 m'	M1—1,400 m (1,397–1,405 m)	1	1	1	1	1	1	
		M2—1,380 m (1,315–1,397 m)	1	1	1	1	1	1	
		M3—1,380 m (1,369–1,389 m)	1	1	1	1	1	1	
	'1,000 m'	M4—1,030 m (995–1,041 m)	1	1	1	1	1	1	
		M5—1,050 m (1,051–1,073 m)	1	1	1	1	1	1	30



Figure 6.1. Set up of the D500X bat detectors. The microphone is placed in a funnel and tied to a pole 2.5 m from the ground, and the detector is placed inside a waterproof bag.

Captures

Despite recent progress in documenting the calls of echolocating bats in PNG (Armstrong and Aplin 2011, 2014a,b; Leary and Pennay 2011; Robson et al. 2012; Armstrong et al. 2015a,b; K.N. Armstrong and K.P. Aplin unpublished data), the calls of some species are unknown, or remain difficult to identify because of their similarity to those of other species, or because they show geographic variation in call characteristics. There is also the possibility that new and unnamed species will be detected. Therefore, to provide a confident association of 'anonymous' (i.e. recorded without seeing the animal) echolocation calls detected during the survey, bats were trapped, identified and had their calls recorded at several sites.

Trapping equipment, deployed when weather and logistics permitted, included a multi-layered vertical mist net arrangement ('canopy net') that was hung from a rope frame between two tall trees (Figure 6.2). This was operated over two nights for three hours each adjacent to transect H3 in BAA 1. A v-shaped arrangement of mist nets was also erected on poles nearby. Four harp traps (a 3 m high rectangular frame with a triple-offset arrangement of vertical fishing line strings suspended over a catch bag; Figure 6.3) were also positioned along drainage features and tracks over multiple nights throughout both BAAs. Captures were identified based on their external features and descriptions in Bonaccorso (1998), and a tissue biopsy was taken for DNA barcoding to assist further with identifications. Recordings of echolocation calls were made with a Titley Scientific Walkabout bat detector.

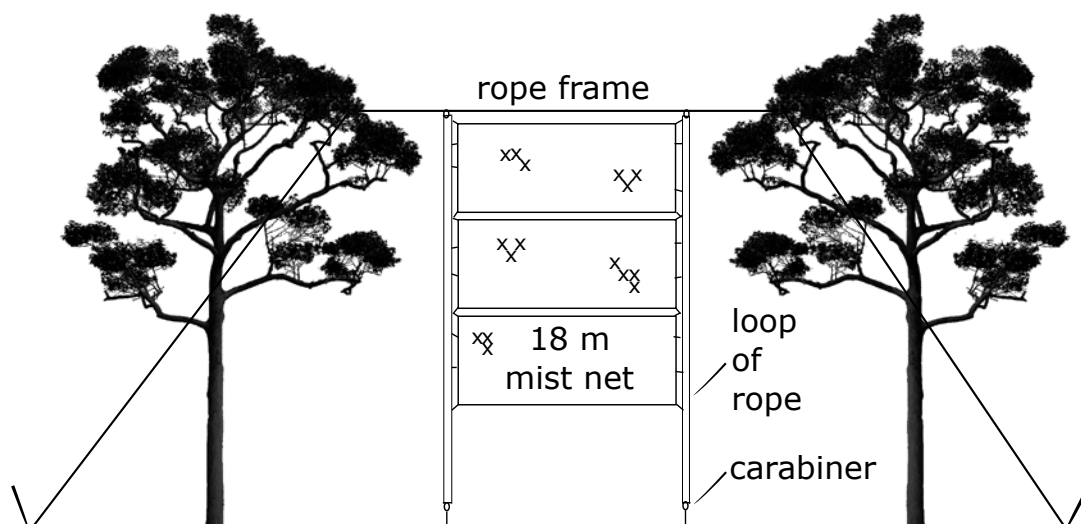


Figure 6.2. Schematic diagram of the rope-mounted 'canopy' mist net apparatus.



Figure 6.3. Triple-bank harp trap placed in a drainage feature close to the access road on Hides Ridge.

Processing of acoustic signals

A customised, multi-step acoustic processing procedure that can filter large bat echolocation recording datasets from Papua New Guinea (Armstrong and Aplin 2014c; Armstrong et al. 2016) was applied to the recordings made on the survey (further details in Appendix 6.2). Processing first involved the recognition of bat echolocation 'call types', followed by a separate step of allocating a species identification to each of these. The 'call types' are defined based on a standardised naming scheme that has been used in many published and unpublished surveys across Papua New Guinea and Wallacea in recent years (Armstrong and Aplin 2011, 2014a,b; Armstrong et al. 2015a,b; K.N. Armstrong and K.P. Aplin unpublished confidential reports; Appendix 6.3). This two-step approach, along with the provision of illustrated examples of identified call types, provides a greater level of transparency that allows for future verification of call identifications, retrospective correction of the species name on the basis of updated information, and a comparison of diversity across sites and studies that is independent of taxonomic allocations.

Data analysis

A brief overview of the data analysis is presented here, and further details are provided in Appendix 6.4. Note that the term 'diversity' is used in this chapter in a general sense rather than as a specific measure. The simplest measure of diversity is a tally of the number of species at a site, for which the term 'Species Richness' is used here. Other commonly used measures of diversity incorporate estimates of abundance in addition to the number of species. Because it was not possible to estimate the abundance of each bat species within the scope of this project, several other measures of diversity ('Phylogenetic Diversity', 'Functional Diversity' and 'Relative Abundance'; see below) are calculated instead. Thus, mention of 'diversity' in this chapter can encompass the number of species in combination with their identity ('composition' of bat communities), as well as the breadth of their evolutionary relationships and ecological roles. Specific measurements used in analyses to compare or illustrate diversity among sites are capitalised.

All analyses were conducted using a custom written [R] language script, which can be modified and rerun for subsequent surveys.

Data analysis

Two measures of bat diversity ('Species Richness' and 'Phylogenetic Diversity') were employed for the statistical comparisons between sites, and for analysis of potential impacts and edge effects associated with construction of the ROW.

'**Species Richness**' is the number of echolocating bat species detected, as measured for each recording site.

'**Phylogenetic Diversity**' (*sensu* Faith 1992) is an overall measure of evolutionary diversity among the species present at a site, and takes into account both the number of species, as well as the degree of genetic distance among them. It is calculated by summing the branch lengths in phylogenetic trees amongst species. As an example, a community with five species of bat from more than one bat family will have a higher Phylogenetic Diversity, and thus higher value in terms of genetic diversity, than another community containing five bat species from the same family. To calculate this metric, a genetic distance matrix and phylogenetic tree was first produced by sequencing a DNA barcode of each representative species present in the acoustic recordings (further details in Appendix 6.4, and in Chapter 7). Tissue samples used for DNA barcoding were those collected from captures, as well as other samples from the Australian Biological Tissue Collection (South Australian Museum).

These two measures were compared across elevations and distances from the ROW by fitting a Generalised Linear Mixed Model by Maximum Likelihood (Laplace Approximation) to the data.

Further analyses were conducted to provide a greater depth of understanding of the patterns of bat diversity in the BAAs and the potential responses of bats to the ROW. These were:

'**Relative Abundance**'. The calculation of Relative Abundance across sampling sites provides an indication of 'commonness' or 'rarity' of bat species. The Relative Abundance of each species/call type was calculated as a proportional representation using presence/absence data from replicate transects for defined distances from the ROW and at each elevation. For example, for a given distance from the ROW (e.g. 0 m), a species would have a Relative Abundance of 0.45 if it was present in 5 of 11 transects (i.e. across all four elevations combined) at a distance of 0 m. Likewise, a species would have a Relative Abundance of 0.5 if it was present in 9 of 18 recording sites across all three transects and all distances from the ROW at one particular elevation. We might anticipate that a common and widely distributed species will be detected in a high proportion of all recording sessions, whereas a rare or localised species (or to confound the situation, one that is difficult to detect) will be detected only occasionally. Relative Abundance was used to calculate Functional Diversity (see below), and also to summarise patterns for individual species as a means of identifying candidate Indicator Species.

'**Species composition**'. The combination of species found at each recording site, also called species composition, can be compared among sites. It is not a discrete metric, but a simple way to summarise the difference in species composition by ordination that groups recording sites in two-dimensional space on the basis of the similarity of their component species. This involves calculating Bray-Curtis Dissimilarity, and then performing Non-metric Multidimensional

Scaling (NMDS). Species composition was also summarised after grouping species according to the similarity of their echolocation call structure, which reflects where they fly (their 'flight space') when foraging (in the 'Open', at the 'Edge' of vegetation boundaries, or in the forest interior 'Clutter'). Analyses performed on such groupings provide information on whether certain broad ecological groups of bats might be under-represented or dominant. See Appendix 6.4 for further explanation of the groupings.

'Functional Diversity' The calculation of the measure 'Functional Diversity' (*sensu* Petchey and Gaston 2002a) allows further consideration of the diversity of bat communities in the BAAs. It is a measure of diversity that incorporates information on the range of 'functional types' (groups of species with similar ecological niches) present within bat communities, with more complex ecosystems typically showing both a greater range of functional types and a greater level of redundancy (i.e. they have more species performing similar ecological roles so loss of a species may have less impact on ecosystem function). Functional Diversity is calculated from estimates of Relative Abundance as well as a categorisation of several aspects of the biology of each species (their 'ecological traits').

RESULTS

Bat detector deployments

A total of 66 full-night recordings was collected from the six sites (at distances of 0, 20, 70, 120, 170, and 220 m) on each of the 11 transects (approximate elevations of 1,000, 1,400, 2,200, and 2,700 m asl). Of these, 36 nightly recordings were made over 9 nights at BAA 1, and 30 nightly recordings over 7 nights at BAA 2 (Table 6.1). GPS locations for each recording site are presented in Appendix 6.1.

Captures

A total of 21 individuals from six bat species was captured (Figures 6.4–6.6; Appendix 6.5). Tissue biopsy samples were taken from each of these, and deposited in the Australian Biological Tissue Collection at the South Australian Museum. Two of the species are small blossom bats that are common in PNG, but do not produce vocalisations for echolocation, and are not part of the analyses. The remaining four species were all represented on the acoustic recordings.

Acoustic detections

A total of 19 echolocation call types was recognised from the recordings, which probably represents one species in each case (Figure 6.7). Appendix 6.6 contains a brief justification for assigning individual call types to particular bat species.

A tabulation of species/call type presence at each of the nightly recording sites reveals some differences in composition between the bat communities of the two BAAs (Table 6.2; raw data in Appendix 6.7). Overall, there were five bat families represented but in BAA 1 most of the detections were attributable to members of the Miniopteridae and Vespertilionidae, with just a few detections from the Emballonuridae and Rhinolophidae, and none from the Hipposideridae. In BAA 2, there was a relatively even representation of all bat families across the recording sites, though with possibly fewer detections of the Vespertilionidae than in BAA 1.

One of the more remarkable observations was call type *172sCF* at 1,000 m asl near Arakubi Quarry (20 m on transect M5), which is closest in characteristic frequency to the Dusky Leaf-nosed Bat *Hipposideros ater*. Other individuals of this species in Papua New Guinea have been recorded between 140–150 kHz (K.N. Armstrong and K.P. Aplin, unpublished data). Such a difference of at least 25 kHz is typical of species-level differences, and therefore it is very likely that this call type derives from a species that is completely new to science, but related to *H. ater*.

In addition to the species identified from echolocation calls, the detection of social (non-echolocation) calls that appeared to be derived from insectivorous bats (rather than small fruit bat species such as *Nyctimene* and *Syconycteris*) was noted. These could not be attributed to species, but their identification may be possible after future surveys. Social calls are often much louder than echolocation calls, especially those produced by flute-nosed bats *Murina* spp., which were recorded commonly at the higher elevation sites.



Figure 6.4. Bat captures at BAA 1 on Hides Ridge:

Top: Undescribed blossom bat *Syconycteris* sp. 1 'montane' (Pteropodidae); **Bottom:** Unidentified bent-winged bat *Miniopterus* sp. 1 'large' (Miniopteridae), echolocation call type 38 *st.cfm*.

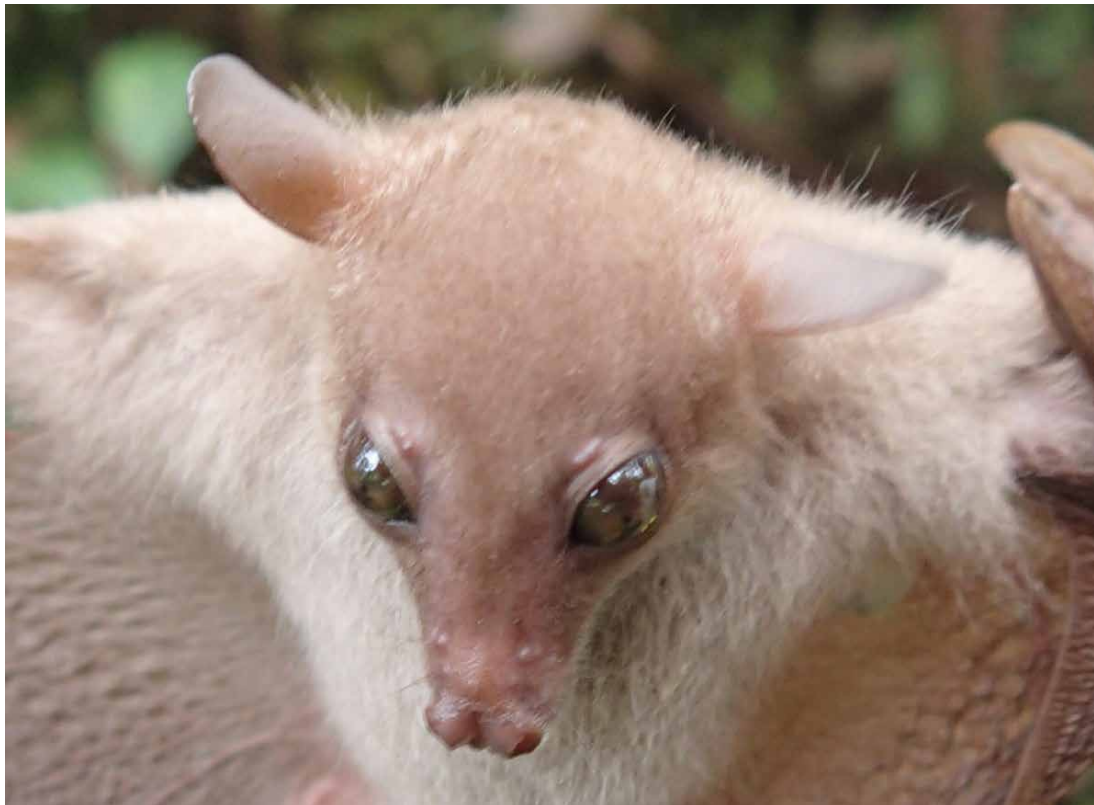


Figure 6.5. Bat captures in BAA 2 at Arakubi Quarry on the Agogo Range near Moro: **Top:** Undescribed blossom bat *Syconycteris* sp. cf. *australis* (Pteropodidae); **Bottom:** Eastern Horseshoe Bat *Rhinolophus megaphyllus* (Rhinolophidae), echolocation call type 70 ICF.

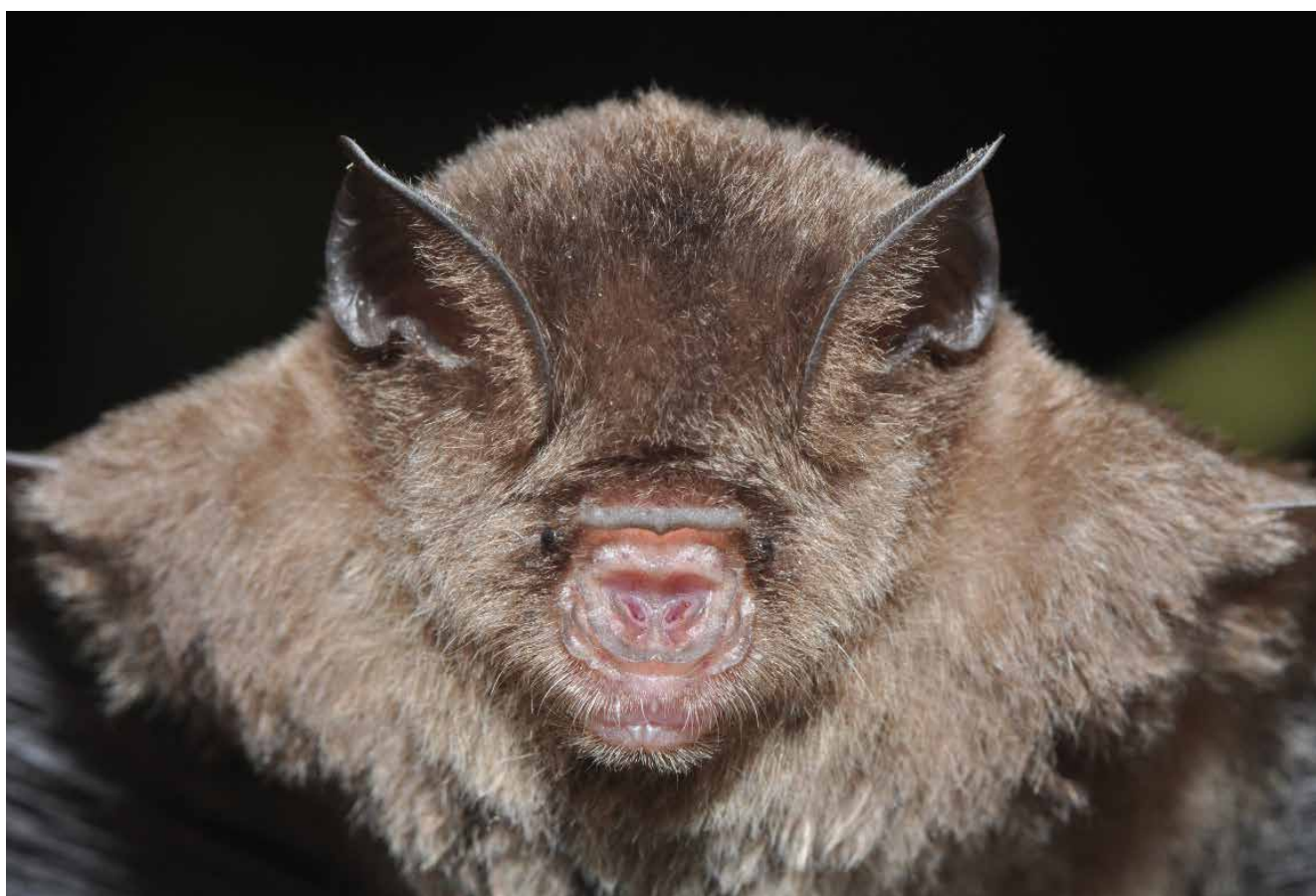
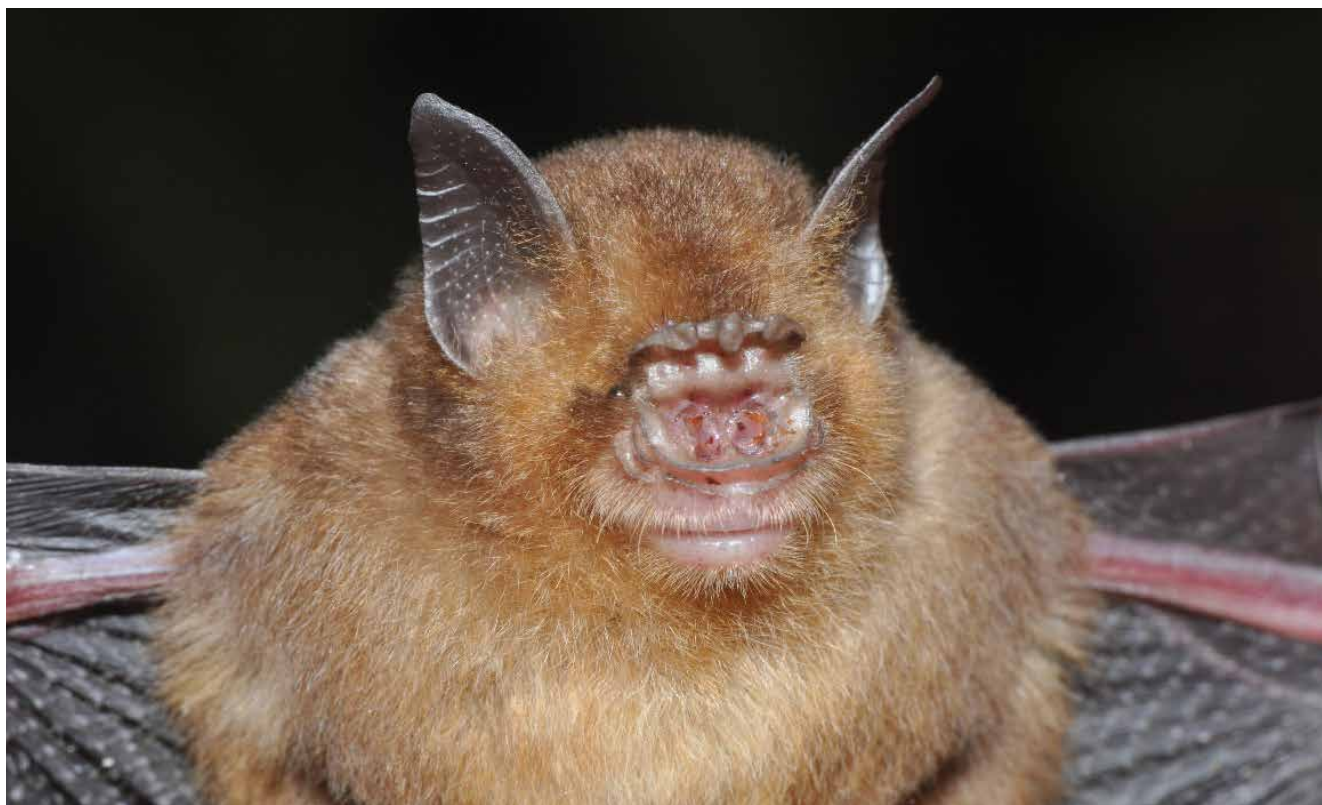
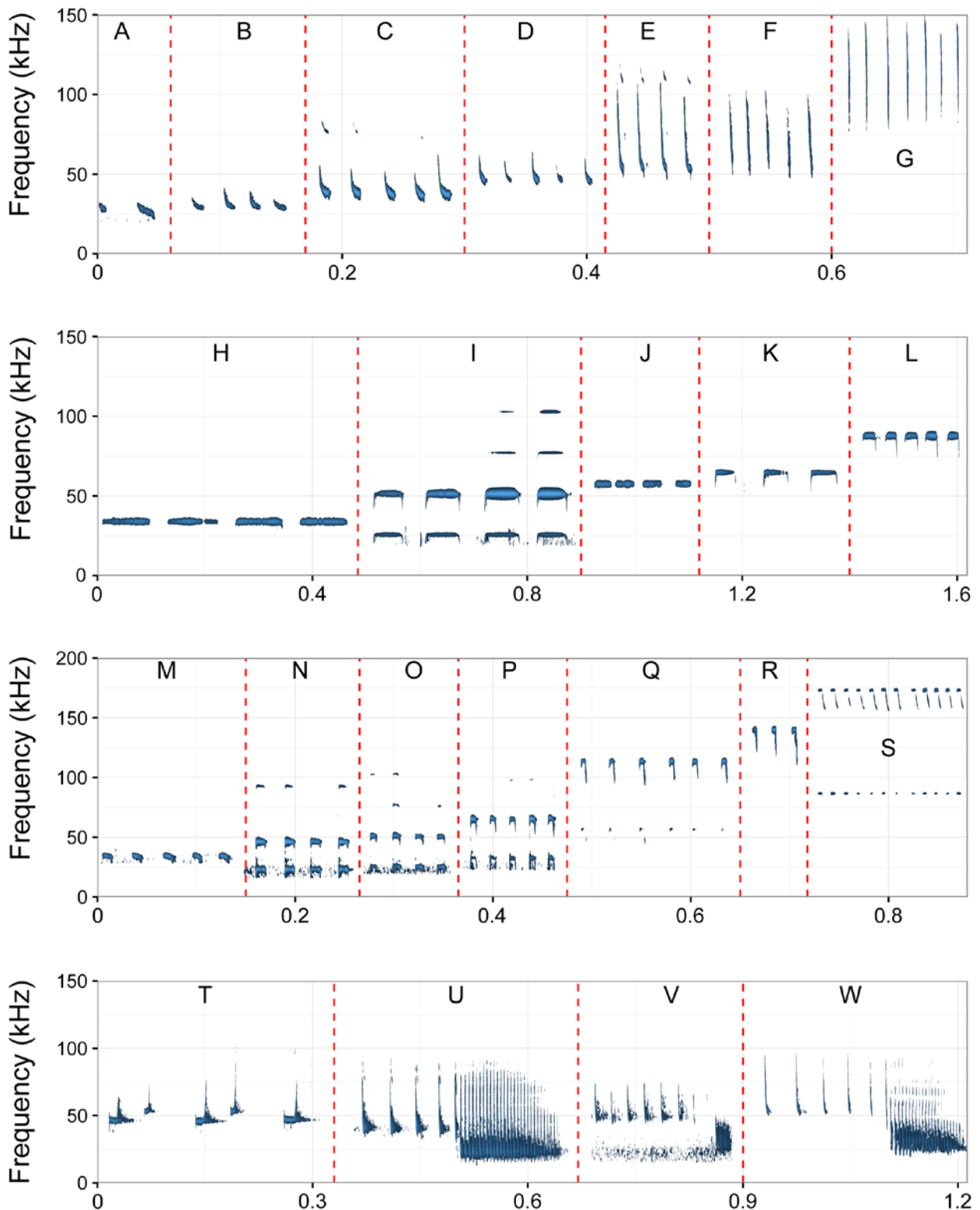


Figure 6.6. Bat captures at Arakubi Quarry:

Top: Trident Leaf-nosed Bat *Aselliscus tricuspis* (Hipposideridae), echolocation call type 120 sCF;

Bottom: Fawn Leaf-nosed Bat *Hipposideros cervinus* (Hipposideridae), echolocation call type 140 sCF.



A: 25 sFM *Saccolaimus saccolaimus*; **B:** 30 cFM *Philetor brachypterus*; **C:** 38 st.cFM *Miniopterus* sp. 1 'large'; **D:** 45 st.cFM *Miniopterus* sp. 2 'medium'; **E:** 53 st.cFM *Miniopterus* sp. 3 'small'; **F:** 50 bFM *Nyctophilus* sp.; **G:** 80 bFM *Murina* sp. cf. *florium*; **H:** 33 ICF *Rhinolophus* sp. cf. *robertsi*; **I:** 52 ICF *Rhinolophus euryotis*; **J:** 58 mCF *Hipposideros diadema*; **K:** 70 ICF *Rhinolophus megaphyllus*; **L:** 88 mCF *Hipposideros wollastoni*; **M:** 35 i.fFM.d *Emballonura diana*; **N:** 45 i.fFM.d *Emballonura raffrayana*; **O:** 52 i.fFM.d *Emballonura furax*; **P:** 65 i.fFM.d *Mosia nigrescens*; **Q:** 120 sCF *Aselliscus tricuspis*; **R:** 140 sCF *Hipposideros cervinus*; **S:** 172 sCF *Hipposideros* sp. cf. *ater*; **T:** unidentified social calls; **U:** feeding buzz of 38 st.cFM *Miniopterus* sp. 1 'large'; **V:** feeding buzz of 45 st.cFM *Miniopterus* sp. 2 'medium'; **W:** feeding buzz of 53 st.cFM *Miniopterus* sp. 3 'small'.

Figure 6.7. Representative sequence portions of the call types recognised from the acoustic recordings, grouped by main body type of the call (time between pulses is compressed; scale of x and y axes vary; comments on identifications are presented in Appendix 6.6).

Data analysis

Species Richness at different distances from the ROW (*dist*) and at different elevations (*elev*) was compared statistically. The tests showed significant differences in both factors *dist* and *elev*, though pairwise tests revealed that it was the greater Species Richness at 1,000 m asl that produced the strongest pattern of difference. There was no significant interaction between distance from the ROW and elevation, highlighting that distance from the ROW has no significant effect on the number of bat species using the forest at any elevation (Tables 6.3 and 6.4).

The analysis was repeated using Phylogenetic Diversity as a dependent variable, with a similar outcome (Tables 6.3 and 6.4).

Table 6.3. Summary of the tests of the Generalised Linear Mixed Model and post hoc pairwise comparisons (only significant pairs shown; values are elevations in metres above sea level; Significance codes: '*' <0.05; '**' <0.01; '***' <0.001). See Appendix 6.4 for more information on the statistical models.

Species Richness	Chi-square	df	P	Pairwise
Distance	13.8	5	0.016*	—
Elevation	17.2	3	<0.001***	1,000 > 1,400** 1,000 > 2,200*** 1,000 > 2,700***
Distance*Elevation	14.2	15	0.51	—
Phylogenetic Diversity				
Distance	14.9	5	0.011*	0 > 120*
Elevation	21.1	3	<0.001***	1,000 > 1,400** 1,000 > 2,200** 1,000 > 2,700***

Note: no interaction term is available for the test of Phylogenetic Diversity because the model did not converge.

Table 6.4. Summary of means \pm standard deviation for the two dependent variables (Species Richness and Phylogenetic Diversity) at each distance from the ROW (*dist*) and elevation (*elev*), plus the metric of Petchey and Gaston's (2002a) Functional Diversity. Values in bold are significantly and consistently higher than the others (see Table 6.3).

	Species Richness	Phylogenetic Diversity	Functional Diversity
Distance (m)			
0	4.00 \pm 3.16	0.41 \pm 0.33	1.21
20	2.09 \pm 2.91	0.26 \pm 0.32	0.97
70	2.36 \pm 1.75	0.34 \pm 0.19	1.01
120	1.64 \pm 1.12	0.22 \pm 0.14	0.91
170	1.64 \pm 1.29	0.18 \pm 0.13	0.81
220	2.27 \pm 1.95	0.37 \pm 0.22	0.98
Elevation (m)			
1,000	5.17 \pm 3.10	0.56 \pm 0.27	1.42
1,400	2.28 \pm 1.93	0.27 \pm 0.21	0.95
2,200	1.50 \pm 1.10	0.20 \pm 0.15	0.72
2,700	1.33 \pm 0.69	0.16 \pm 0.11	0.59

Patterns in Species Richness and Phylogenetic Diversity

To further understand the outcomes of the statistical tests, boxplots of Species Richness and Phylogenetic Diversity were plotted against distance from the ROW and elevation. It is clear that there is no overall relationship of either variable with increasing distance from the ROW (Figure 6.8), reflecting the results of pairwise tests that were not significant. However, there was a conspicuous increase in both variables at distances of 0 m and 20 m at the lowest elevation of 1,000 m asl. Increased degrees of freedom available for analyses in future years might provide a greater level of statistical power to detect some of the subtler patterns in the dataset, especially in the interaction terms.

When Species Richness and Phylogenetic Diversity were plotted against elevation, it was clear that these variables had higher values at 1,000 m asl compared to all other elevations (Figure 6.9), which is reflected in the significance of pairwise tests (Tables 6.3 and 6.4).

Patterns in species composition

Non-metric Multidimensional Scaling ordination plots constructed from a Bray-Curtis Dissimilarity matrix revealed similar patterns to the boxplots. In terms of both their species tallies and after being grouped into the major call categories (see summary in Table 6.5), clustering patterns in the distribution of points and the partial separation of confidence ellipses indicates a marked contrast in species composition in the two lower elevations compared to sites above 2,000 m asl (Figure 6.10). By contrast, there is no clear difference in species or call type composition at different distances from the ROW (Figure 6.10; confidence ellipses are not shown, since they all overlap considerably without obvious separations). It should be noted however that there is a suggestion that the call category composition at distance 0 m differs from that at all positions within the forest.

Patterns in the Relative Abundance of species

A compilation of species presence is enhanced by the calculation of Relative Abundance, or how common each species is. Inspection of patterns of Relative Abundance for each species, and their 'flight space' group according to distance from the ROW and increasing elevation (summarised in the miniature 'sparkline' plots in Table 6.5), reveals some clear patterns. For example two bent-winged bats *Miniopterus* sp. 1 'large' (call type 38 st.cFM) and *Miniopterus* sp. 3 'small' (call type 53 st.cFM), had higher Relative Abundance at higher elevations, and were detected mainly at the forest boundary. Their elevated Relative Abundance at distance 0 m suggests they prefer the more open habitats where they forage against vegetation.

The low Species Richness and Relative Abundance of 'Clutter' species above 2,000 m asl was a consequence of the absence or near-absence of forest-interior bats in the families Hipposideridae and Rhinolophidae. However not all groups of forest-interior bats were absent from higher elevations, with species such as *Murina* sp. cf. *florium*, (call type 80 bFM), and *Nyctophilus* sp., (call type 50 bFM) equally if not more common at higher elevations compared to lower sites.

In general, Relative Abundance of species according to their 'flight space' grouping (see summaries at the bottom of Table 6.5; Figure 6.11) showed that 'Edge' species were more common at distance 0 m, as might be expected, and that this relative proportion increased with increasing elevation. By contrast, 'Clutter' species were more common at lower elevations but occurred at uniformly low Relative Abundances across all distances from the open habitat (Figure 6.11).

Patterns in Functional Diversity

Functional Diversity—a measure of ecological 'breadth' in the bat community—was clearly higher at 1,000 m asl elevation and right at the forest edge. (Table 6.4; Figure 6.12). This corresponds with patterns observed in Species Richness and Phylogenetic Diversity. Collectively, these reflect the relatively higher number and variety of species in the open areas at the lowest study elevation.

There was also a reasonably good correspondence between genetic (=phylogenetic) relatedness and the ecology of species. Species in the same family tended to have similar ecological traits overall (Figure 6.13), though there was slight overlap in Functional Diversity between closely related families (Miniopteridae–Vespertilionidae; Hipposideridae–Rhinolophidae). The relevance of correspondence between genetic and ecological traits is that the appearance or disappearance of a particular family will be accompanied by changes in the representation of a significant proportion of unique ecological niches. Thus, any differences in or changes to the membership of communities at particular elevations or distances from a disturbance can reflect not only species richness and evolutionary diversity, but ecological diversity and resilience as well.

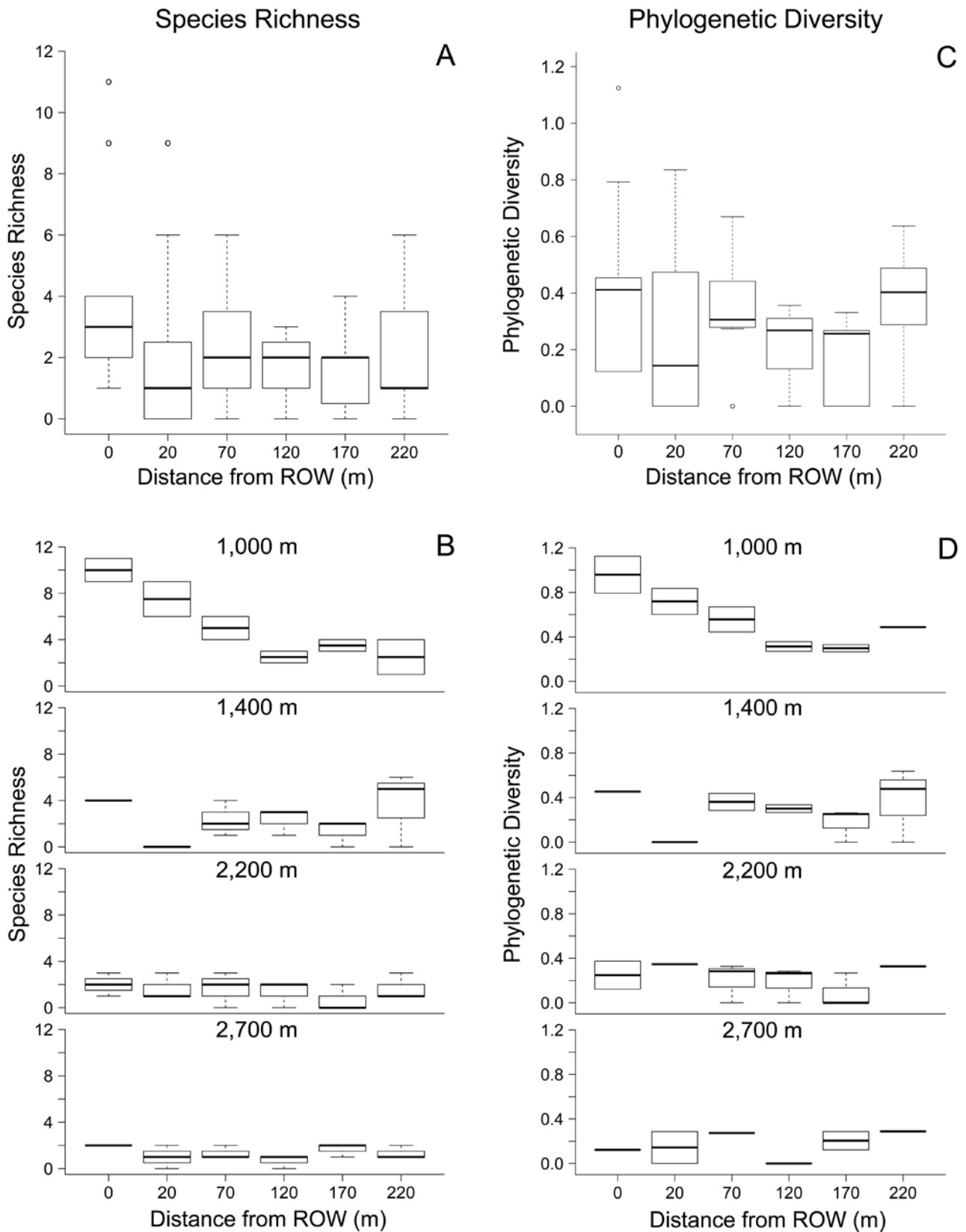


Figure 6.8. Summary of Species Richness (**A**—all elevations combined, **B**—shown separately for each elevation) and Phylogenetic Diversity (**C**—all elevations combined, **D**—shown separately for each elevation) at different distances from the ROW. [Boxplot components: central bar—median; boxes—inter-quartile range, with second quartile group below median, third quartile group above median; bars—minimum and maximum values; circles—outliers]

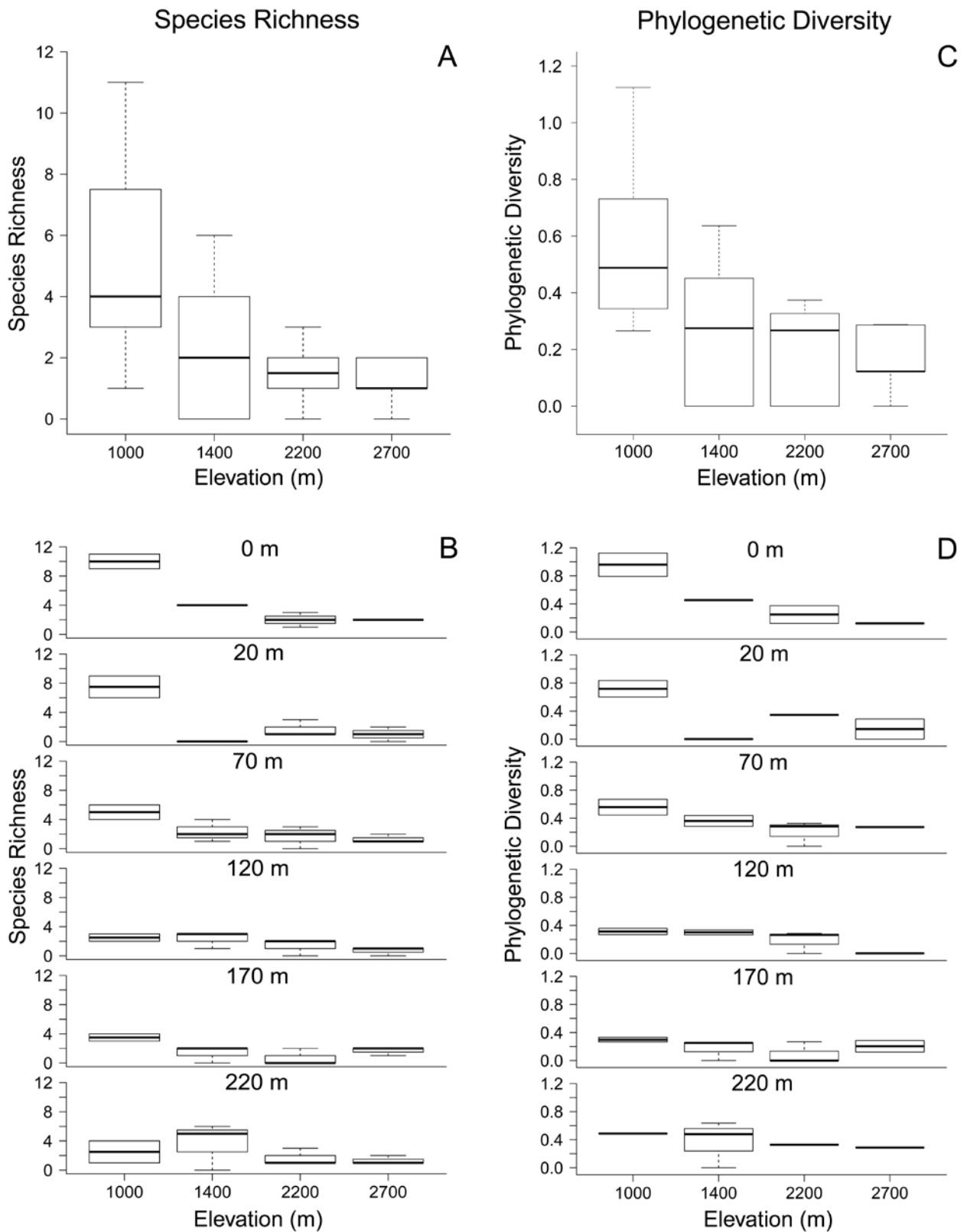
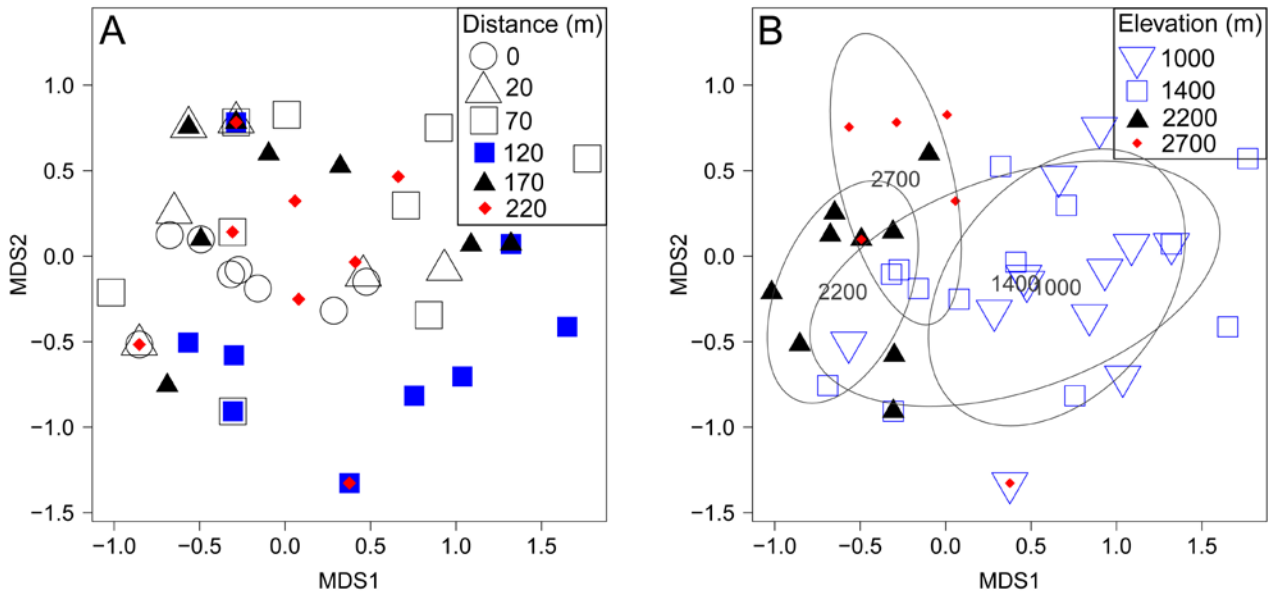


Figure 6.9. Summary of Species Richness (A—all distances from ROW combined, B—shown separately for each distance from the ROW) and Phylogenetic Diversity (C—all distances from ROW combined, D—shown separately for each distance from the ROW) at different elevations.

Species composition



Call type category composition

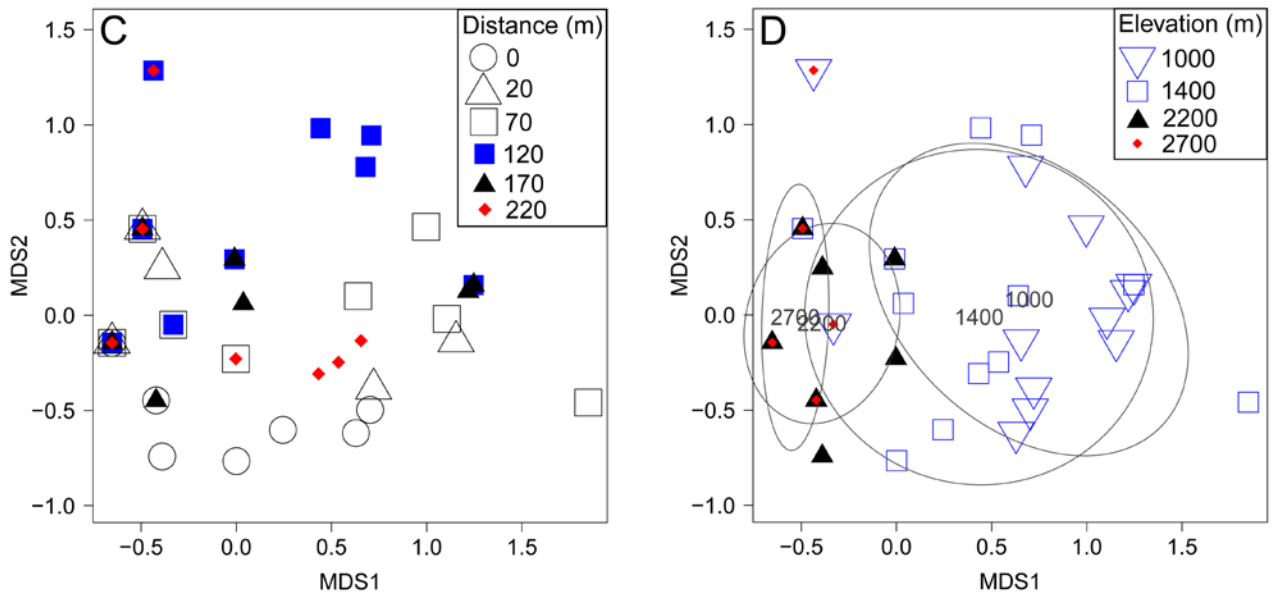


Figure 6.10. Multidimensional Scaling (NMDS) ordinations summarising patterns of species composition and call type category composition at different distances from the ROW (**A, C**) and elevations (**B, D**) (confidence ellipses are one standard deviation, and are shown if there is a clear separation among factor levels, in this case elevations).

Table 6.5. Summary of phylogenetic and ecological traits against Relative Abundance values (blue heat-scale) and trend for increasing distances from the ROW and elevation. ('Call cat.': echolocation call category).

Species	Call type	Call cat.	Flight space	Roost	0	20	70	120	170	220	Trend 0 ⇨ 220m	1,000	1,400	2,200	2,700	Trend 1,000 ⇨ 2,700m
EMBALLONURIDAE																
<i>Mosia nigrescens</i>	65 i.fFM.d	iffM.d	Edge	Veg	0.2	0.2	0.3	0.1	0	0.1	0.7	0	0	0	0.1	
<i>Emballonura raffrayana</i>	45 i.fFM.d	iffM.d	Edge	Cave	0.5	0.1	0.1	0	0	0.1	0.3	0.2	0	0	0	
<i>Emballonura furax</i>	52 i.fFM.d	iffM.d	Edge	Cave	0.2	0	0	0	0	0	0.1	0.1	0	0	0	
<i>Emballonura diana</i>	35 i.fFM.d	iffM.d	Edge	Cave	0.2	0	0	0	0	0	0.1	0.1	0	0	0	
<i>Saccolaimus saccolaimus</i>	25 sFM	loFM	Open	Veg	0.1	0	0	0	0	0	0.1	0	0	0	0	
VESPERTILIONIDAE																
<i>Nyctophilus</i> sp.	50 bFM	bFM	Clutter	Veg	0	0.2	0.1	0	0.1	0	0	0	0	0.1	0.1	
<i>Philetor brachypterus</i>	30 cFM	cFM	Edge	Veg	0.1	0	0	0	0	0	0	0	0	0.1	0	
<i>Murina</i> sp. cf. <i>florium</i>	80 bFM	bFM	Clutter	Veg	0	0	0.2	0.4	0	0.2	0.3	0.1	0.1	0.1	0.1	
MINIOPTERIDAE																
<i>Miniopterus</i> sp. 2 'medium'	45 st.cFM	cFM	Edge	Cave	0.1	0	0	0	0	0	0.1	0	0	0	0	
<i>Miniopterus</i> sp. 1 'large'	38 st.cFM	cFM	Edge	Cave	1.0	0.4	0.3	0.3	0.2	0.5	0.3	0.4	0.7	0.2	0.2	
<i>Miniopterus</i> sp. 3 'small'	53 st.cFM	cFM	Edge	Cave	0.9	0.4	0.5	0.1	0.5	0.6	0.3	0.4	0.3	0.8	0.8	
HIPPOSIDERIDAE																
<i>Hipposideros</i> sp. cf. <i>ater</i>	172 sCF	sCF	Clutter	Both	0	0.1	0	0	0	0	0.1	0	0	0	0	
<i>Hipposideros cervinus</i>	140 sCF	sCF	Clutter	Cave	0.2	0.1	0.1	0	0.1	0.1	0.3	0.2	0	0	0	
<i>Hipposideros diadema</i>	58 mCF	mCF	Edge	Cave	0	0	0.1	0	0	0	0.1	0	0	0	0	
<i>Hipposideros wollastoni</i>	88 mCF	mCF	Clutter	Both	0.2	0.2	0.2	0.2	0.2	0.2	0.8	0.2	0	0	0	
<i>Aselliscus tricuspidatus</i>	120 sCF	sCF	Clutter	Cave	0.1	0.2	0.4	0.1	0.2	0.2	0.7	0.2	0	0	0	
RHINOLOPHIDAE																
<i>Rhinolophus megaphyllus</i>	70 ICF	ICF	Clutter	Cave	0.2	0.2	0.2	0.2	0.2	0.1	0.5	0.1	0.2	0	0	
<i>Rhinolophus</i> sp. cf. <i>robertsi</i>	33 ICF	ICF	Clutter	Cave	0.1	0	0	0	0	0.1	0.1	0.1	0	0	0	
<i>Rhinolophus euryotis</i>	52 ICF	ICF	Clutter	Cave	0.1	0.2	0.1	0.4	0.3	0.2	0.5	0.4	0	0	0	
			Open		0.1	0	0	0	0	0	0.1	0	0	0	0	
			Edge		0.4	0.1	0.1	0.1	0.1	0.2	0.2	0.1	0.1	0.1	0.1	
			Clutter		0.1	0.1	0.1	0.1	0.1	0.1	0.3	0.1	0	0	0	

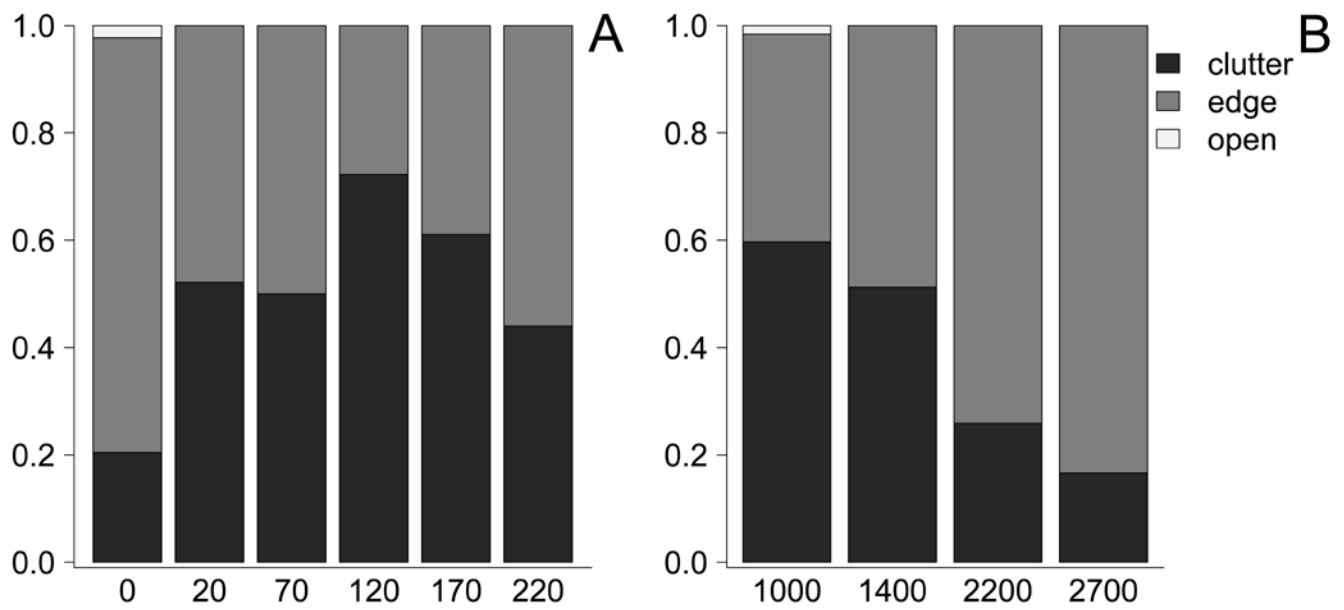


Figure 6.11. Summary plots of the proportion of bats occupying three different flight spaces at increasing distance from the ROW (A) and at increasing elevation (B).

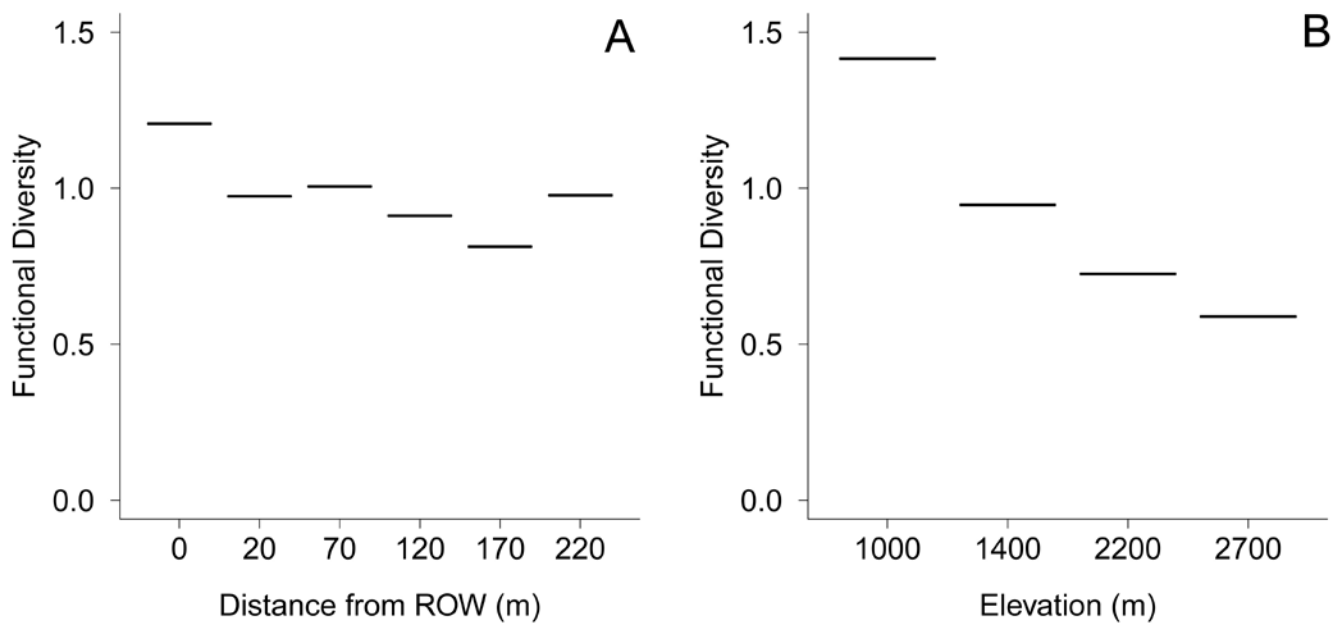


Figure 6.12. Summary plots of Functional Diversity at increasing distance from the ROW (A) and at increasing elevation (B).

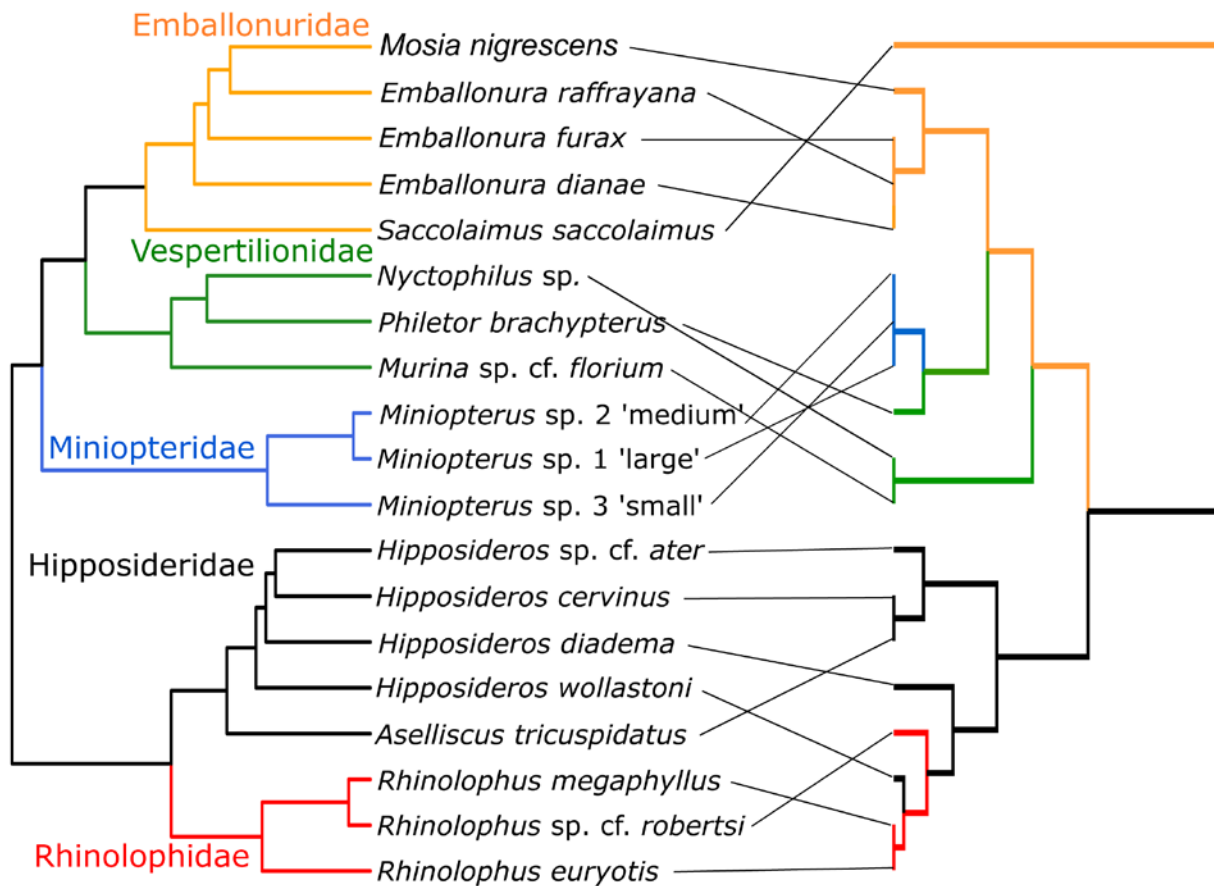


Figure 6.13. Correspondence between similarity dendrograms calculated from mitochondrial DNA sequence data (left) and ecological traits (right).

DISCUSSION

Bat communities at different elevations

There were clear differences between the bat communities at different elevations. Species Richness and Phylogenetic Diversity were both highest at 1,000 m asl and declined with increasing elevation. The greater Species Richness and Phylogenetic Diversity at lower elevations correlates with the higher values of Functional Diversity there because the additional species at lower altitudes occupied a broader range of niche types. Furthermore, a summary of flight space usage showed that at 1,000 m asl a higher number of bat species foraged within vegetation produced echolocation calls designed to detect and capture prey in the structurally complex forest interior.

One factor that might contribute to the richness of the bat community at 1,000 m asl was the presence near Arakubi Quarry of limestone outcropping that contained caves suitable for cave-roosting species, including members of the families Hipposideridae and Rhinolophidae. These species emit tonal calls through their nostrils rather than chirps through the mouth, which is a specialisation for detecting the fluttering wings of insect prey against a close background of vegetation clutter. Their relatively short, broad wings also allow them to manoeuvre in narrow spaces. These species often forage at the boundary between vegetation and open areas, which would explain why measures of diversity at distances of 0 m and 20 m were relatively high on the two transects at Arakubi Quarry. These patterns suggest that areas of rocky outcrop may be responsible for relatively high but potentially localised bat diversity. These results also demonstrate that, for the purpose of assessing the risk of new infrastructure on bat communities, avoiding significant impacts on patchy but critical resources such as bat caves that are outside the immediate infrastructure footprints may be important.

The trend for reduced bat diversity at higher elevations probably reflects reduced food resources and eco-physiological constraints due to lower temperatures, perhaps combined with a lack of nearby cave roosts. Most species at the higher elevations were of two main groups: bent-winged bats *Miniopterus* spp. that forage in edge habitats, can fly relatively long distances during their nightly foraging excursions, and therefore may roost far from where they were recorded; and species such as long-eared bats *Nyctophilus* sp. and the Flute-nosed Bat *Murina* sp. cf. *florium* that are characterised by small home ranges, and have a wing morphology and call types that allow them to detect and capture prey close to background vegetation clutter. These species also have the ability to enter torpor to conserve energy resources in habitats that are relatively unproductive.

Miniopterus spp. probably roost some distance from the study area but take advantage of the open space of the ROW to access forest habitat for large distances. *Miniopterus* in the southern part of Australia roost in cool caves and enter torpor to conserve fat reserves when food resources are low in winter (Churchill 2008) and higher elevation populations of *Miniopterus* spp. in PNG may exhibit similar behaviour. The absence of other cave-roosting species above 2,000 m asl (except for a few records of *Rhinolophus megaphyllus*) probably reflects a combination of the limited availability of suitable caves, the thermal physiology of the species, and limits to their nightly foraging ranges.

Bat communities at different distances from the ROW

The analyses showed no significant influence of increasing distance from the ROW on any measure of bat diversity. There was a trend for higher Species Richness and Phylogenetic Diversity at distances of 0 m and 20 m at 1,000 m asl in BAA 2, but this was not statistically significant.

Although no significant associations between bat diversity and distance from the ROW were detected during this survey, the impacts of edge effects develop over time and they might present on future surveys. Over time opening of the forest to create a linear corridor increases the penetration of light, heat and wind at the vegetation boundary and these factors have the potential to cause drying and loss of key plant species, promote the growth of smothering climbers, and increase the risk of wind damage from strong gusts channelled by roads. Given the global trend of climate change, it is also prudent to consider the possibility that habitats will become warmer and drier in the coming decades, with the potential to exacerbate the effects of light, heat and wind. So far these factors do not appear to have had a significant effect on the bat community or its habitat (assuming the habitat at 220 m is representative of the baseline condition), but the consequences might take some time to become measurable, and changing use of the road in the future might hasten any processes. Future data analysis should retain the approaches initiated here, and incorporate additional analyses to detect subtler patterns that might start to emerge with the addition of data from subsequent surveys.

The baseline work of Richards (2005, 2008) conducted as part of the original environmental impact assessment for the PNG LNG project represented the first comprehensive acoustic survey for bats in PNG. Some of his sampling sites are near the permanent transects established for PMA3, and they captured information about the bat community well before road and pipeline construction. Given the lack of any preconstruction baseline data for the present study, it would be valuable to reprocess these historical data. The study of Richards (2005, 2008) was based on recordings made with AnaBat bat detectors, which have different microphone characteristics to the D500X and a different process for saving acoustic recordings. Reanalysis of the recordings from the earlier study is also necessary because there has been a considerable advance in understanding of the echolocation calls of PNG bats since that time.

Consideration of individual species

Indicator Species

In addition to the various analyses of bat diversity, it will be useful to identify Indicator Species that are particularly sensitive to changes in their habitat.

For example attention might be given to examining whether there is a significant increase in abundance over time of uncommon species that forage in the open against vegetation, such as the small Emballonuridae (*Emballonura* spp., *Mosia nigrescens*) and *Philetor brachypterus*. These species were detected mainly at lower elevations (1,000 m asl and 1,400 m asl) and it is possible that they may begin to move along the ROW to use higher elevation habitats.

Another suite of species that might be useful as Indicator Species are those that were detected only deeper in the forest. These include *Nyctophilus* sp. and *Murina* sp. cf. *florium*. There exists the potential for these species to decline without a gross change in forest structure and they are flagged here as candidate Indicator Species for future analyses.

Species of conservation significance

The New Guinea Sheath-tailed Bat *Emballonura furax* is listed as Data Deficient by the IUCN (Bonaccorso and Leary 2008). It was detected at both elevations in BAA 2 but was not common. This species is distributed broadly across southern New Guinea and there have been numerous new records in the past five years (K.P. Aplin and K.N. Armstrong unpublished data) so it is possibly more common and widespread than previously thought.

Putative new species

The most significant bat detected on the survey may be a putative new species in the family Hipposideridae. A single call consisting of a high quality sequence of pulses with a characteristic frequency of around 172 kHz at the second harmonic was recorded near Arakubi Quarry. The species with the most similar call is *Hipposideros ater* but it has a characteristic call frequency of c. 140–150 kHz in PNG (K.P. Aplin and K.N. Armstrong unpublished data) and commonly 150–155 kHz in Australia (K.N. Armstrong unpublished data). The magnitude of the difference is sufficient to suggest the presence of a species that has never been encountered previously. No other PNG bat species emits a frequency as high as 172 kHz at the second harmonic. Capture of this animal might be possible in the areas of rocky outcrop near transect M5.

Other species of uncertain identity

The taxonomy of bent-winged bats (*Miniopterus* spp.) in New Guinea is completely unresolved. Applying names based on morphological descriptions (e.g. as from Bonaccorso 1998; Simmons 2005) is fraught with the possibility of misidentification, and some names used for PNG populations are probably not applicable. It is therefore possible that one or more *Miniopterus* species encountered on the survey are unnamed. The taxonomy of this group in PNG is currently under review (K.N. Armstrong and K.P. Aplin research in progress).

Three other species detected during the survey are also only tentatively allocated to named forms. The Large-eared Horseshoe Bat, listed here as *Rhinolophus* sp. cf. *robertsi*, belongs to a group that is often lumped together as *Rhinolophus philippinensis*. (Cooper et al. 1998; K.N. Armstrong unpublished data). There are at least two forms of '*R. philippinensis*' in PNG based on echolocation call types, and the form recorded in BAA 2 that emits calls at around 33 kHz does not seem to have been collected anywhere. It would be extremely valuable to capture this *Rhinolophus* on a future survey to determine whether it represents a new species.

The Flute-nosed Bat *Murina florium* is thought to be distributed widely on the island of Flores in Indonesia, parts of Wallacea, the islands of New Guinea and New Britain, and Cape York Peninsula in Queensland, Australia (Hutson et al. 2008a). If this taxon is similar to other *Murina* in having small home ranges, there is a very good chance that *Murina florium* comprises more than one species. In PNG, it is known only from several widely separated sites.

A relatively small number of calls typical of those produced by long-eared bats *Nyctophilus* spp. were detected at higher elevation sites in BAA 1. They might be attributable to the Papuan Long-eared Bat *Nyctophilus microtis*, which has a similar call type (K.P. Aplin and K.N. Armstrong, unpublished data) or to the Small-toothed Long-eared Bat *Nyctophilus microdon* for which the call type is undocumented. The IUCN distribution map does not place *N. microtis* in the region of the PMA3 study area (Hutson et al. 2008b), but it is the most likely candidate. Capture and follow-up genetic comparisons would help to clarify the identity of this species.

Missing species

It is useful to anticipate additional species that should have been found in 2015, and might be encountered on future surveys. Given information provided by the IUCN and the authoritative guides of Flannery (1995) and Bonaccorso (1998), at least another five insectivorous species might be expected to occur. These may not have been detected on the 2015 survey because of the relatively limited spatial extent of the survey, and because some species have ecological requirements not present within the two BAAs. For example, the Large-footed Myotis *Myotis moluccarum* is closely associated with river systems, which are lacking in the karst habitats on Hides Ridge and the Agogo Range. Failure to

detect any species of *Pipistrellus* is more unusual, but it might be explained by the similarity of their calls to those of two species of bent-winged bats (*Miniopterus* sp. B 'medium' (call type 45 st.cFM), and *Miniopterus* sp. C 'small' (call type 53 st.cFM)). If *Pipistrellus* spp. are captured on future surveys and their call types documented, it may become possible to distinguish them from *Miniopterus* in future. If so, the acoustic recordings made in 2015 could be reprocessed and the analyses rerun.

The absence of the Arcuate Horseshoe Bat *Rhinolophus arcuatus* is somewhat baffling as it is usually captured and recorded on surveys within its known range. It would have been expected at the lower elevations of the study area, but instead the Eastern Horseshoe Bat *R. megaphyllus* was captured. This latter species has an echolocation call with a frequency very similar to that of *R. arcuatus*, and it is possible that calls in acoustic recordings have been misidentified. It would be valuable to capture *Rhinolophus* at the 2,200 m asl transects in BAA 2 because the calls of this type recorded there may prove to be from *R. arcuatus*. Additional capture effort at the elevations of 1,000 m asl and 1,400 m asl would be useful to determine whether the two species occur in sympatry there. However these two species occupy very similar ecological niches, and any influence of the ROW is likely to be similar for both species.

Only one species that forages in open spaces well above the tree canopy was detected on the 2015 survey, Bare-rumped Sheath-tailed Bat *Saccolaimus saccolaimus*. Open space foragers seem to be relatively uncommon in PNG at elevations above 1,000 m asl so their absence from the study area is not surprising.

CONCLUSIONS

1. The combined results from this survey suggest that the forest adjacent to the ROW has so far retained its value as a habitat for bats.
2. The main measurable difference amongst bat communities on the 2015 survey was that diversity declined significantly with increasing elevation. This pattern is consistent with other locations in PNG (Bonaccorso 1998; K.P. Aplin and K.N. Armstrong unpublished data).
3. There was no statistically significant difference in bat diversity at increasing distances from the ROW into the forest using two measures of bat diversity. Analysis of other indicators of bat community composition and functional diversity also did not reveal any strong influence of the ROW other than a slight increase at the forest edge (0 m) in the Relative Abundance of some species that forage in open spaces.
4. The lack of available baseline data from the area prior to the study limited the opportunity to assess broader changes in the bat community that might have occurred during or subsequent to ROW construction. This can be rectified to some extent through reanalysis of data collected on Hides Ridge in 2005 and 2008, and at some other regional localities for the PNG LNG EIS.
5. Several candidate Indicator Species were identified that either prefer closed forest (*Murina* sp. cf. *florium*, *Nyctophilus* sp.) or that take advantage of open areas for foraging (*Emballonura* spp., *Philetor brachypterus*, *Pipistrellus* spp.). More detailed monitoring and assessment of these species on future surveys might help in the detection of subtle environmental changes.
6. The results from the 2015 survey provide strong grounds for continuation of an acoustic monitoring study for bats into the future, and for further trapping efforts to capture several enigmatic and potentially new species of bats that were detected only in acoustic recordings.

REFERENCES

- Aplin K. P, Novera J. & Armstrong K. N. 2015. Mammals of Manus and Mussau islands. pp. 50–68 in *A Rapid Biodiversity Survey of Papua New Guinea's Manus and Mussau Islands*. (N. Whitmore, ed.). Wildlife Conservation Society Papua New Guinea Program. Goroka, Papua New Guinea.
- Armstrong, K. N. 2007. *Survey for bats on the proposed Ira Lalaro hydropower scheme, Timor-Leste. Field survey and impact assessment*. Unpublished report by Molhar Pty Ltd for EPANZ Services Pty Ltd (New Zealand) and the Norwegian Water Resources and Energy Directorate, 19 June 2007.
- Armstrong, K. & Ford, G. 2002. Notes from the Microbat Forum and Panel discussion held on 6 April 2002 after the 10th ABS conference. *The Australasian Bat Society Newsletter* 18: 43–48.
- Armstrong, K. N. & Aplin, K. P. 2011. Bats of the Muller Range, Papua New Guinea. Chapter 19, pp. 222–234 in *Rapid Biological Assessments of the Nakanai Mountains and the upper Strickland Basin: surveying the biodiversity of Papua New Guinea's sublime karst environments* (S. J. Richards and B. G. Gamui, eds.). RAP Bulletin of Biological Assessment 60. Conservation International, Arlington, USA.
- Armstrong, K. N. & Aplin, K. P. 2014a. Chapter 7. A survey of bats (Chiroptera) in the Baiyer River Wildlife Sanctuary, Western Highlands Province, Papua New Guinea. pp. 111–133 in *A rapid biodiversity assessment of the Baiyer River region, Western Highlands Province, Papua New Guinea* (S. J. Richards, ed.). A report to the Mul Baiyer Lumusa District Administration, Papua New Guinea.
- Armstrong, K. N., Novera, J. & Aplin K. P. 2014b. Survey for bats in the P'nyang Range, Western Province, Papua New Guinea. Field survey and acoustic analysis. PNG LNG Expansion Project. Unpublished report by Specialised Zoological, Ken Aplin Fauna Studies Pty Ltd and the Papua New Guinea Institute for Biological Research for Coffey Environments Pty Ltd and ExxonMobil, 21 April 2014.
- Armstrong, K. N. & Aplin, K. P. 2014c. Identifying bats in an unknown acoustic realm using a semi-automated approach to the analysis of large full spectrum datasets. Oral presentation at the 16th Australasian Bat Society Conference 22–25 April 2014, Townsville, Queensland. *The Australasian Bat Society Newsletter* 42: 35–36.
- Armstrong K. N., Novera J. & Aplin K. P. 2015a. Acoustic survey of the echolocating bats of Manus Island and Mussau Island, Papua New Guinea. pp. 69–85 in *A Rapid Biodiversity Survey of Papua New Guinea's Manus and Mussau Islands* (N. Whitmore, ed.) Wildlife Conservation Society Papua New Guinea Program. Goroka, Papua New Guinea.
- Armstrong, K. N., Aplin K. P. & Lamaris J. S. 2015b. Chapter 10. Bats. pp. 166–180 in *A rapid biodiversity assessment of Papua New Guinea's Hindenburg Wall region* (S.J. Richards and N. Whitmore, eds.). Wildlife Conservation Society Papua New Guinea Program. Goroka, Papua New Guinea.
- Armstrong, K. N., Aplin, K. P., & Crotty, S. 2016. A pipeline and app for massive filtering and assisted inspection of enormous acoustic datasets. Poster presentation at the 17th Australasian Bat Society Conference, Hobart, Tasmania, Australia 29 March–1 April 2016. *The Australasian Bat Society Newsletter* 46: 51.
- Bernard, E. & Fenton, M. B. 2007. Bats in a fragmented landscape: Species composition, diversity and habitat interactions in savannas of Santarém, Central Amazonia, Brazil. *Biological Conservation* 134: 332–343.
- Berthinussen, A. & Altringham, J. 2012. The effect of a major road on bat activity and diversity. *Journal of Applied Ecology* 49: 82–89.
- Blake, D., Hutson, A. M., Racey, P. A., Rydell, J., & Speakman, J.R. 1994. Use of lamplit roads by foraging bats in southern England. *Journal of Zoology* 234: 453–462.

- Bonaccorso F. J. 1998. *Bats of Papua New Guinea*. Conservation International Tropical Field Guide Series. Conservation International, Washington, D.C.
- Bonaccorso, F. & Leary, T. 2008. *Emballonura furax*. The IUCN Red List of Threatened Species 2008: e.T7667A12841369. <http://dx.doi.org/10.2305/IUCN.UK.2008.RLTS.T7667A12841369.en>.
- Cadotte, M. W., Carscadden, K. & Mirotchnick, N. 2011. Beyond species: functional diversity and the maintenance of ecological processes and services. *Journal of Applied Ecology* 48: 1079–1087.
- Churchill, S. K. 2008. Australian bats. 2nd edition, Allen and Unwin, Crows Nest, NSW.
- Coffin, A. W. 2007. From roadkill to road ecology: A review of the ecological effects of roads. *Journal of Transport Geography* 15: 396–406.
- Collins, R. A. & Cruikshank, R. H. 2012. The seven deadly sins of DNA barcoding. *Molecular Ecology Resources* 13: 969–975.
- Cooper, S. J. B., Reardon, T. B. & Skilins, J. 1998. Molecular systematics of Australian rhinolophid bats (Chiroptera: Rhinolophidae). *Australian Journal of Zoology* 46: 203–220.
- Corben, C. & O'Farrell, M. J. 1999. *AnaBat system user's guide*. *AnaBat system manual*, 2nd ed. Published by the authors, 1999.
- de Oliveira, M. C. & Schulz, M. 1997. Echolocation and roost selection in Semon's leaf-nosed bat *Hipposideros semoni*. *Memoirs of the Queensland Museum* 42: 158.
- de Oliveira, M. C. 1998a. Towards standardized descriptions of the echolocation calls of microchiropteran bats: pulse design terminology for seventeen species from Queensland. *Australian Zoologist* 30: 405–411.
- de Oliveira, M. C. 1998b. *Anabat system practical guide*. Queensland Department of Natural Resources.
- Denzinger, A. & Schnitzler, H.-U. 2013. Bat guilds, a concept to classify the highly diverse foraging and echolocation behaviors of microchiropteran bats. *Frontiers in Physiology* 4 (Article 164): 1–15.
- Fahrig, L. & Rytwinski, T. 2009. Effects of roads on animal abundance: an empirical review and synthesis. *Ecology and Society* 14: <http://www.ecologyandsociety.org/vol14/iss1/art21/>
- Faith, D. P. 1992. Conservation evaluation and phylogenetic diversity. *Biological Conservation* 61: 1–10.
- Flannery, T. F. 1995. *Mammals of New Guinea*. Revised edition. Reed Books, Chatswood, NSW.
- Fujita, M. S. & Tuttle, M. D. 1991. Flying foxes (Chiroptera: Pteropodidae): Threatened animals of key ecological and economic importance. *Conservation Biology* 5: 455–463.
- Gannon, W. L., O'Farrell, M. J., Corben, C. & Bedrick, E. J. 2004. Call character lexicon and analysis of field recorded bat echolocation calls. pp. 478–484 in *Echolocation in Bats and Dolphins* (J. A. Thomas, C. F. Moss and M. Vater, eds.). University of Chicago Press, Chicago.
- Hall, T. A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.
- Hutson, T., Schlitter, D., Csorba, G., Bonaccorso, F. & Hall, L. 2008a. *Murina florium*. The IUCN Red List of Threatened Species 2008: e.T13939A4367794. <http://dx.doi.org/10.2305/IUCN.UK.2008.RLTS.T13939A4367794.en>.
- Hutson, T., Schlitter, D., Csorba, G., Bonaccorso, F. & Parnaby, H. 2008b. *Nyctophilus microtis*. The IUCN Red List of Threatened Species 2008: e.T15008A4486704. <http://dx.doi.org/10.2305/IUCN.UK.2008.RLTS.T15008A4486704.en>.

- Jones, K. E., Purvis, A. & Gittleman, J. L. 2003. Biological correlates of extinction risk in bats. *The American Naturalist* 161: 601–614.
- Jones, G., Jacobs, D. S., Kunz, T. H., Willig, M. R. & Racey, P. A. 2009. Carpe noctem: the importance of bats as bioindicators. *Endangered Species Research* 8: 93–115.
- Kalka, M. B., Smith, A. R. & Kalko, E. K. V. 2008. Bats limit arthropods and herbivory in a tropical forest. *Science* 320: 71.
- Kalko, E. K. V. 1998. Organization and diversity of tropical bat communities through space and time. *Zoology: Analysis of Complex Systems* 101: 281–297.
- Kerth, G. & Melber, M. 2009. Species-specific barrier effects of a motorway on the habitat use of two threatened forest-living bat species. *Biological Conservation* 142: 270–279.
- Kuijper, D. P. J., Schut, J., van Dullemen, D., Toorman, H., Goossens, N., Ouweland, J. & Limpens, H. J. G. A. 2008. Experimental evidence of light disturbance along the commuting routes of pond bats (*Myotis dasycneme*). *Lutra* 51: 37–49.
- Leary, T. & Pennay, M. 2011. Echolocation calls of eight microchiroptera from Papua New Guinea. pp. 106–127 in *The biology and conservation of Australasian bats*, (B. Law, P. Eby, D. Lunney and L. Lumsden, eds.). Royal Zoological Society of New South Wales.
- Lobova, T. A., Geiselman, C. K. & Mori, S. A. 2009. Seed dispersal by bats in the Neotropics. New York Botanical Garden Press, New York.
- McConkey K. R. & Drake D. R. 2006. Flying foxes cease to function as seed dispersers long before they become rare. *Ecology* 87: 271–276.
- Meyer, C. F. J. et al. 2010. Long-term monitoring of tropical bats for anthropogenic impact assessment: Gauging the statistical power to detect population change. *Biological Conservation* 143: 2797–2807.
- Milne, D. J. 2002. *Key to the bat calls of the Top End of the Northern Territory*. Parks and Wildlife Commission of the Northern Territory, Technical Report No. 71.
- Milne, D. J., Jackling, F. C., Sidhu, M., & Appleton, B. R. 2009. Shedding new light on old species identifications: morphological and genetic evidence suggest a need for conservation status review of the critically endangered bat, *Saccolaimus saccolaimus*. *Wildlife Research* 36: 496–508.
- Parsons, S. & Szewczak, J. M. 2009. Detecting, recording, and analysing the vocalizations of bats. pp. 91–111 in *Ecological and behavioral methods for the study of bats*, 2nd Edition (T. H. Kunz and S. Parsons, eds.). Johns Hopkins University Press, Baltimore.
- Petchey, O. L. & Gaston, K. J. 2002a. Functional diversity (FD), species richness and community composition. *Ecology Letters* 5: 402–411.
- Petchey, O. L. & Gaston, K. J. 2002b. Extinction and the loss of functional diversity. *Proceedings of the Royal Society B* 269: 1721–1727.
- Petchey, O. L. & Gaston, K. J. 2006. Functional diversity: back to basics and looking forward. *Ecology Letters* 9: 741–758.
- R Core Team 2016. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL: <https://www.R-project.org/>

- Richards, G. C. 2005. The PNG gas project: a study of bat faunal biodiversity and an assessment of potential impacts. Prepared by Greg Richards and Associates Pty Ltd for Enesar Consulting Pty Ltd, July 2005. Included as *Annex 05. Biodiversity survey results: Bats at Hides, Nogoli and Benaria in 2005* in the PNG LNG Project Environmental Impact Statement Part II. Existing Environment, prepared by Coffey Natural Systems Pty Ltd for Esso Highlands Ltd, January 2005.
- Richards, G. C. 2009. The PNG liquefied natural gas project: a study of bat faunal biodiversity and an assessment of potential impacts. Prepared by Greg Richards and Associates Pty Ltd for Coffey Natural Systems Pty Ltd, July 2008. Included as *Annex 06. Biodiversity survey results: Bats at Juha North, Juha South, Baia River, South Karius and Deviation Camp in 2008* in the PNG LNG Project Environmental Impact Statement Part II. Existing Environment, prepared by Coffey Natural Systems Pty Ltd for Esso Highlands Ltd, January 2009.
- Robson, S. K. A., Inkster, T. E. & Krockenberger, A. K. 2012. *Bats of the YUS Conservation Area, Papua New Guinea*. Result 5. Task 3.1. Centre for Tropical Biodiversity and Climate Change, and Centre for Tropical Environmental and Sustainability Science, School of Marine and Tropical Biology, James Cook University, Australia.
- Safi, K., Cianciaruso, M. V., Loyola, R. D., Brito, D., Armour-Marshall, K. & Diniz-Filho, J. A. F. 2011. Understanding global patterns of mammalian functional and phylogenetic diversity. *Philosophical Transactions of the Royal Society of London B Biological Sciences* 366: 2536–2544.
- Schaub, A., Ostwald, J. & Siemers, B. J. 2008. Foraging bats avoid noise. *Journal of Experimental Biology* 211: 3174–3180.
- Simmons, N. B. 2005. Order Chiroptera. pp. 312–529 in *Mammal species of the world: a taxonomic and geographic reference*, 3rd edition, (D. E. Wilson and D. M. Reeder, eds.). Johns Hopkins University Press, Baltimore.
- Spellerberg, I. 2002. Ecological effects of roads and traffic: a literature review. *Global Ecology and Biogeography* 7: 317–333.
- Stone, E. L., Jones, G. & Harris, S. 2009. Street lighting disturbs commuting bats. *Current Biology* 19: 1123–1127.
- Stone, E. L., Jones, G. & Harris, S. 2012. Conserving energy at a cost to biodiversity? Impacts of LED lighting on bats. *Global Change Biology* 18: 2458–2465.
- Trombulak, S. C. & Frissell, C. A. 2000. Review of ecological effects of roads on terrestrial and aquatic communities. *Conservation Biology* 14: 18–30.
- Underwood, A. J. 1991. Beyond BACI: the detection of environmental impacts on populations in the real, but variable, world. *Journal of Experimental Marine Biology and Ecology* 161: 145–178.
- Williams-Guillén, K., Perfecto, I. & Vandermeer, J. 2008. Bats limit insects in a Neotropical agroforestry system. *Science* 320: 70.
- Zurcher, A. A., Sparks, D. W. & Bennett, V. J. 2010. Why the bat did not cross the road? *Acta Chiropterologica* 12: 337–340.

APPENDICES

Appendix 6.1. Bat recording site locations in BAA 1 and BAA 2. Coordinates in WGS84 datum.

Elevation category	Transect	Site	Latitude	Longitude	Elevation (m asl)
2,200	H1	H1_0	S5.972360	E142.753298	2,163
2,200	H1	H1_020	S5.972497	E142.753298	2,150
2,200	H1	H1_070	S5.972957	E142.753051	2,155
2,200	H1	H1_120	S5.973372	E142.752755	2,159
2,200	H1	H1_170	S5.973687	E142.752518	2,157
2,200	H1	H1_220	S5.973912	E142.752120	2,148
2,200	H2	H2_0	S5.969293	E142.751274	2,172
2,200	H2	H2_020	S5.969139	E142.751088	2,173
2,200	H2	H2_070	S5.969094	E142.750609	2,188
2,200	H2	H2_120	S5.969277	E142.750173	2,202
2,200	H2	H2_170	S5.969125	E142.749803	2,217
2,200	H2	H2_220	S5.969091	E142.749293	2,230
2,200	H3	H3_0	S5.943749	E142.741850	2,303
2,200	H3	H3_020	S5.943883	E142.741758	2,301
2,200	H3	H3_070	S5.944320	E142.741780	2,297
2,200	H3	H3_120	S5.944858	E142.741989	2,305
2,200	H3	H3_170	S5.945233	E142.741622	2,322
2,200	H3	H3_220	S5.945649	E142.741343	2,328
2,700	H4	H4_0	S5.918348	E142.695273	2,693
2,700	H4	H4_020	S5.918538	E142.695284	2,694
2,700	H4	H4_070	S5.919073	E142.694984	2,695
2,700	H4	H4_120	S5.919384	E142.695017	2,697
2,700	H4	H4_170	S5.919837	E142.694977	2,693
2,700	H4	H4_220	S5.920187	E142.694850	2,681
2,700	H5	H5_0	S5.916239	E142.692811	2,757
2,700	H5	H5_020	S5.916357	E142.692759	2,752
2,700	H5	H5_070	S5.916466	E142.692307	2,749
2,700	H5	H5_120	S5.916473	E142.691844	2,745
2,700	H5	H5_170	S5.916812	E142.691275	2,732
2,700	H5	H5_220	S5.916997	E142.690949	2,726
2,700	H6	H6_0	S5.913852	E142.690190	2,731


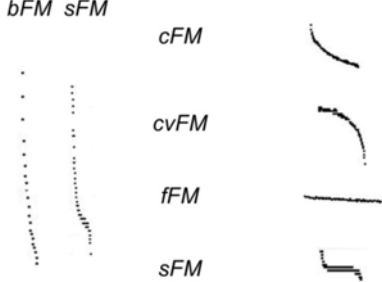
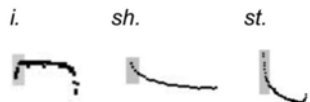

Elevation category	Transect	Site	Latitude	Longitude	Elevation (m asl)
2,700	H6	H6_020	S5.913800	E142.689950	2,726
2,700	H6	H6_070	S5.914234	E142.689675	2,737
2,700	H6	H6_120	S5.914501	E142.689400	2,734
2,700	H6	H6_170	S5.914857	E142.689007	2,727
2,700	H6	H6_220	S5.915382	E142.688917	2,729
1,400	M1	M1_0	S6.440162	E143.224209	1,400
1,400	M1	M1_020	S6.440274	E143.224016	1,401
1,400	M1	M1_070	S6.440128	E143.223569	1,399
1,400	M1	M1_120	S6.440168	E143.223003	1,398
1,400	M1	M1_170	S6.440065	E143.222567	1,406
1,400	M1	M1_220	S6.439821	E143.222548	1,398
1,400	M2	M2_0	S6.440552	E143.225534	1,390
1,400	M2	M2_020	S6.440850	E143.225515	1,378
1,400	M2	M2_070	S6.441427	E143.225470	1,378
1,400	M2	M2_120	S6.441541	E143.225238	1,315
1,400	M2	M2_170	S6.442067	E143.224994	1,391
1,400	M2	M2_220	S6.442281	E143.224750	1,398
1,400	M3	M3_0	S6.441697	E143.227190	1,385
1,400	M3	M3_020	S6.441857	E143.227087	1,369
1,400	M3	M3_070	S6.442226	E143.226594	1,380
1,400	M3	M3_120	S6.442637	E143.226361	1,382
1,400	M3	M3_170	S6.443096	E143.226258	1,392
1,400	M3	M3_220	S6.443447	E143.226106	1,390
1,000	M4	M4_0	S6.462027	E143.256626	996
1,000	M4	M4_020	S6.461973	E143.256496	1,021
1,000	M4	M4_070	S6.461926	E143.256018	1,030
1,000	M4	M4_120	S6.461675	E143.255574	1,031
1,000	M4	M4_170	S6.461714	E143.255003	1,041
1,000	M4	M4_220	S6.461505	E143.254388	1,041
1,000	M5	M5_0	S6.461952	E143.250070	1,051
1,000	M5	M5_020	S6.462011	E143.250174	1,054
1,000	M5	M5_070	S6.462146	E143.250623	1,054
1,000	M5	M5_120	S6.462055	E143.251072	1,060
1,000	M5	M5_170	S6.461496	E143.251829	1,073
1,000	M5	M5_220	S6.461260	E143.252340	1,068

Appendix 6.2. Further description of processing procedures for acoustic recordings.

A multi-step acoustic analysis procedure developed to handle large echolocation recording datasets from insectivorous bats in Papua New Guinea (Armstrong and Aplin 2014c; Armstrong et al. 2016) was applied to the recordings made on the survey. Recordings on the D500X Compact Flash memory cards were first downloaded using Pettersson Elektronik D500X Utility version 1.5 software, which renames each WAV format sound file in a standardised format “unitserial_date_time_Mnumber.wav”.

The WAV files were then scanned for bat echolocation calls using several parameter sets optimised for the main call types (defined in Appendix 6.3) in the software SCAN'R version 1.7.7 (Binary Acoustic Technology), which also provides measurements (in “SonoBat™ compatible output”) from each putative bat pulse. The output was used to determine if putative bat pulses measured in SCAN'R could be identified to species. This was done using a custom-written script in [R] language (R Core Team 2016) that performed three tasks: 1. undertook a Discriminant Function Analysis on training data comprising reference calls and representative anonymous call types of Papua New Guinean bats (Armstrong and Aplin 2014a,b; Armstrong et al. 2015b; K.N. Armstrong and K.P. Aplin unpublished data); 2. from the measurements of each putative bat pulse from SCAN'R, calculated values for the first two Discriminant Functions derived from the training data that could separate the echolocation call types, and plotted these resulting coordinates over confidence regions for the defined call types; and 3. facilitated an inspection in a spectrogram of multiple examples of each call type for each recording night by opening the original WAV files containing pulses of interest in Adobe Audition CS6 version 5.0.2. Species were then identified from the scored call types based on information in Armstrong and Aplin (2011, 2014a,b), Leary and Pennay (2011), Robson et al. (2012), Armstrong et al. (2015b), and K.N. Armstrong and K.P. Aplin (unpublished data).

Appendix 6.3. Echolocation call categories based on the morphology of the dominant type of search-phase pulses in high quality sequences.

Code	Description	Example
CF sCf mCF ICF	Constant Frequency main Body Sub Type (BST) Short duration (>15Ms) Medium duration (15–30 ms) Long duration (>30 ms)	
FM bFM cFM cvFM fFM sFM	Frequency Modulated Main Body Sub Type (BST) Broadband, slightest degree of curvature only, no significant development of serpentine component (sFM) Curved, simple or curvilinear trace Convex curved, essentially cFM rotated 180° Flat or with a very slight curve, narrowband, not CF Serpentine, generally S-shaped	
<i>i.</i> <i>sh.</i> <i>st.</i>	Initial Frequency Sweep (IFS) Inclined, a narrowband increasing frequency sweep Short, shallow or narrowband frequency sweep Steeply decreasing, broadband frequency sweep	
<i>.d</i> <i>.h</i>	Terminating Frequency Sweep (TFS) Drooped, decreasing frequency sweep following the characteristic frequency in the main body of the call Hooked, increasing in frequency	

Notes: Adapted from de Oliveira (1998a,b); Corben and O’Farrell (1999); Gannon et al. (2004); Armstrong and Aplin (2011); examples are from a Zero Crossings Analysis output and are not scaled equally. Pulses generally consist of three main sections: an initial frequency sweep (IFS), followed by the main body (BST: Body Sub Type), and ending in a terminating frequency sweep (TFS). The shape of the pulse is represented by the codes in the form ‘IFS.BST.TFS’, prefixed by a value representing the mean characteristic frequency in kHz. All CF pulses have initial and terminating frequency sweeps, so the IFS and TFS descriptors are not used.

Appendix 6.4 Further explanation of the data analysis conducted for the 2015 bat monitoring study.

Experimental design and overview of data analysis.

The experimental design comprises 11 transects spread over four elevations, with bat detector recording sites placed at six points of increasing distance from the road along each transect (Table A6.4.1), surveyed every two years over a 3-week period in the middle of the year. Each elevation represents a particular vegetation community and, while each site was relatively homogeneous in terms of vegetation structure, replicate transects within each elevation account for slight variations that might be present based on micro-topographic relief. The experimental design was developed within the constraints of the available study landscape, and uses the same transects as the other vertebrate groups. Bat diversity at each recording site is compared at standardised distances from the ROW route because the habitat will potentially be subject to edge effects originating at the pipeline ROW or access road.

Generally, monitoring programmes rely on being able to compare the relative amount of change at 'impact' sites over time with that at the same sites prior to the disturbance activity (baseline condition), and at control sites sufficiently removed in space from the 'impact' sites. A common experimental design is therefore the 'Beyond BACI' ('Before/After and Control/Impact', with multiple controls; Underwood 1991). In the current programme, there were constraints on data collection from sites prior ('Before') or distant ('Control') to road infrastructure construction. The difficulty of accessing the terrain more than 250 metres from the road limited the addition of control sites, and the timing of the programme prevented the collection of baseline data. A period of two or more years has elapsed between Year 0 (when road construction was begun) and Year 1 (the first monitoring study in 2015), and while not ideal, an assumption is made that the habitat condition and therefore the composition of the bat community at a distance of 220 metres from the road edge in 2015 is closest to the original condition prior to Year 0.

The output from the analysis of acoustic recordings is a simple data matrix of recording site by recognised species/echolocation call types. To detect differences caused by environmental factors and over time, the data matrix can be analysed in two main ways:

1. Using statistics to detect possible significant differences in Species Richness (number of species identified, plus number of unidentified call types) and an overall measure of evolutionary diversity (Phylogenetic Diversity; Faith 1992) in different years, elevations and distances from the road;
2. Together with additional ecological and genetic information, exploring patterns in the data among study site elevations and distances from the ROW, and possible changes over time. This includes consideration of other measures of bat diversity:
 - a. Relative Abundance, which summarises the patterns in individual species;
 - b. Species composition, in terms of both species and representation of echolocation call group categories;
 - c. Functional Diversity as calculated from the Relative Abundance of each species/call type, plus categorisations of various ecological traits that are related to how each bat species functions in its habitat.

Note that definitions of various measures of bat diversity are further discussed in the Methods section.

Data analysis

Analysis of impacts on Species Diversity and Phylogenetic Diversity

This analysis examined whether bat diversity, as measured by Species Richness and Phylogenetic Diversity, varied according to distance from the ROW, based solely on the transect results from 2015.

The statistical approach fit a Generalised Linear Mixed Model by Maximum Likelihood (Laplace Approximation) to the data. The experimental unit is any single whole-night acoustic recording at a particular elevation and distance from the road/ROW. Replicate experimental units were located on the 2–3 replicate transects at each elevation. The power of the tests (dependent on the degrees of freedom) will increase with successive surveys. The various components of the statistical model include:

- Year (fixed effect *year*; total ten years beginning at Year 1 in 2015);
- Distance from the road (fixed effect *dist*; levels—0, 20, 70, 120, 170, 220 metres);
- Elevation (fixed effect *elev*; levels—1,000, 1,400, 2,200, 2,700 metres asl);
- Transect (random effect *transect*; two or three transects per elevation);
- Bat Species Richness (dependent variable *total_richness*; bat species per nightly recording, as non-negative count data);
- Bat Phylogenetic Diversity (dependent variable *PD*; as a continuous non-negative index value).

All statistical analyses were performed using a custom script written in [R] language (R Core Team 2016). The analysis will be expanded upon in subsequent sampling periods to incorporate the fixed effect year. The statistical models were coded in the analysis as follows:

For Species Richness:

```
glmer(total_richness.t ~ dist + elev + dist*elev + (1 | transect), family=poisson(), data = y) #Species Richness values transformed prior to analysis by adding 1 in each case.
```

For Phylogenetic Diversity:

```
glmer(PD.t ~ dist + elev + (1 | transect), family=Gamma(link='log'), data = comm.pd) #note: model with interaction term failed to converge; PD values transformed prior to analysis by adding 1 in each case.
```

Further understanding of the outcome from statistical tests calculated using Species Richness and Phylogenetic Diversity was derived from boxplots.

A third dependent variable summarising the total amount of bat activity, as indicated by the total number of call sequences or individual pulses detected, was considered initially for inclusion in statistical analyses. The current ability of the automated process for recognising echolocation pulses is not at a level that can adequately reduce the proportion of false detections (signals that derive from sources other than bats), so the rate of error is too high for robust statistical analysis. Progress in automated identification systems is ongoing, raising the possibility of including this variable in future analyses, which would include datasets from all preceding years.

Relative Abundance of species

Populations of animals are generally monitored by observing changes in their abundance over time. Unfortunately, the absolute abundance of echolocating bat species at a site cannot be estimated from bat detector recordings because it is not possible to distinguish the calls from each individual. Thus, a relatively large number of recorded pulses could equally be derived from either a few or many individuals. This limitation can be circumvented to some extent by taking advantage of a well-replicated sampling design. An appreciation of 'commonness' versus 'rarity' can be gained by calculating Relative Abundance across sampling sites. We might anticipate that a common and widely distributed species will be detected in a high proportion of all recording sessions, whereas a rare or localised species (or to confound the situation, one that is difficult to detect) will be detected only occasionally. The Relative Abundance of each species/call type was calculated as a proportional representation using presence/absence data from replicate transects for defined distances from the road and at each elevation. In addition to tabular summaries of this information, trends were used to identify candidate Indicator Species, and these values were used to calculate a measure of Functional Diversity.

Species composition


In addition to Species Richness, it can also be informative to look at the effect of the same environmental factors on the composition of the bat community. Two communities may have equivalent in Species Richness, but differ in terms of the identity of species. Comparisons of species composition amongst treatment sites is generally summarised from site-by-species tables using multivariate statistics. The Bray-Curtis dissimilarity statistic was used to quantify compositional dissimilarity amongst sites and Non-metric Multidimensional Scaling (NMDS) was then used to represent the resulting relationships in two dimensions. Analyses were applied to both a site-species matrix and one that collapsed species into major echolocation call categories (see section below for further information).

Ecological groupings and Functional Diversity

An additional perspective on bat diversity is the representation of different species in groupings that reflect their ecological role and how they use the available habitat. Management of biodiversity commonly relies on measures of the presence and abundance of species, but diversity can also be quantified in ways that consider the ecological functions performed by guilds of species with similar niches or roles. Loss of the diversity of ecological traits is important because it represents a simplification of ecosystems and a potential erosion of their resilience (Petchey and Gaston 2002a,b, 2006; Cadotte et al. 2011; Safi et al. 2011). Insectivorous bats are easily characterised into groups that represent functional feeding guilds based on their flight morphology and ability, the spaces they fly in the available habitat, how they detect and capture their prey, and where they roost. A summary of these features can be used to calculate Functional Diversity, with one of the simpler metrics chosen for the 2015 survey (Petchey and Gaston 2002a), using calculations of Relative Abundance as input. Further information on how bats were grouped into feeding guilds according to their echolocation call design is explained below.








Bats occupy two biotopes that are generally separated in space—their roosting and foraging habitats. The foraging habitat can be thought of in terms of the broad structure of the vegetation community (e.g. a 'closed-canopy forest'), and also the flight spaces contained within particular vegetation communities. Flight spaces are structural components of the vegetation community, and are defined by how far the bats fly from vegetation—e.g. spaces within it, closely above and beside it, and located far from it. These spatial components are relevant because bat species vary in their ability to distinguish acoustic echoes of prey items from those derived from background 'clutter' (typically vegetation, but sometimes water; Denzinger and Schnitzler 2013). Echolocation pulse shape reflects the distance at which bats forage from vegetation clutter, and particular call types are generally correlated with certain types of flight space (summary schematic in Table 6.6). Three categories of flight space were distinguished in the present study:

- **Open:** uncluttered space, where clutter echoes are undetectable or clearly distinct from prey echoes. Such flight spaces include open clearings and air space well above the forest canopy or rivers.
- **Edge:** background cluttered space, where prey echoes follow closely but do not overlap with clutter echoes. Such flight spaces include the edges of forest, large gaps within forest, open spaces between different vegetation layers (e.g. canopy, subcanopy or understory), and open space immediately above water and the forest canopy.
- **Clutter** ("narrow" in Denzinger and Schnitzler 2013): highly cluttered space, where prey echoes are intermingled with those from background clutter. Such flight spaces include dense understory or canopy vegetation, and low over the ground.

Bats with similar echolocation call structures were grouped into 'feeding guilds' whose members have a similar foraging strategy, and which use a particular flight space. As an example, one echolocation call category would include all species that produce high frequency calls with a dominant short constant frequency tonal component (call type category *sCF*; for example: ; Appendix 6.2), with each species differing in the characteristic frequency of the tonal component. Each of these call categories allows the bat species to exploit resources in its environment in a particular way—for example, *sCF*-type calls allow the bat to detect fluttering insect wings at short range within cluttered vegetation habitats, or in the open but against a close background of vegetation clutter. Other bat species also feed in this narrow acoustic space, but their call types differ in structure, and therefore how they function to allow the bat to detect its prey and surroundings. The 'clutter' feeding guild therefore comprises all species producing call types that allow bats to forage at short range against a background of vegetation—in this case, species that use *bFM*-, *ICF*- and *sCF*-type calls, and some that produce *mCF*-type calls (Table 6.6).

The trait matrix required for the calculation of Functional Diversity was developed based on information in the literature (Bonaccorso 1998). It included echolocation call types and category (Table 6.6), flight space (open, edge, clutter), roost type (cave, vegetation), prey capture method (intercept, hawk, flutter, glean), agility (low, medium, high), flight speed (low, medium, high), characteristic call frequency category (low <30 kHz, medium 30<x<100 kHz, high >100 kHz), and mode of echolocation emission (mouth, nares).

Table A6.4.1. Schematic representation of functional feeding guilds of echolocating bat species within defined flight spaces in each vegetation community (see also Appendix 6.2).

Vegetation habitat type 1 (at elevation level 1)						
Flight space/feeding guild						
Clutter			Edge		Open	
Call categories						
<i>ICF</i>	<i>mCF</i>	<i>sCF</i>	<i>bFM</i>	<i>cFM</i>	<i>i.fFM.d</i>	<i>loFM</i>
						
Call types of different species						
33 <i>ICF</i> etc	88 <i>mCF</i> etc	120 <i>sCF</i> etc	50 <i>bFM</i> etc	38 <i>st.cFM</i> etc	35 <i>i.fFM.d</i> etc	25 <i>sFM</i> etc
Vegetation habitat type 'n' (at elevation level 'n') etc.						

DNA barcoding

A genetic framework based on mitochondrial DNA barcodes was generated for two reasons. Firstly, DNA barcoding helped to confirm the identities of some captured bats ('specimen identification'; see Chapter 7) and thus the origin of various echolocation calls. All tissues collected on the 2015 survey were sequenced, but confidence in the field identification of captures based on external morphology was generally high. A larger effort was not devoted to DNA barcoding of comparative material, since single-gene frameworks are not able to overcome outstanding issues of taxonomy in PNG bats. The development of a genomic-scale comparative framework based on next-generation DNA sequencing and broader taxon-level and geographic-level representation currently in progress outside of the PMA3 study (K.N. Armstrong and K.P. Aplin research in progress) will likely provide the opportunity in the future to remove ambiguities around species identifications.

Secondly, the DNA sequences allow calculations of Phylogenetic Diversity (Faith 1992) at each nightly recording site. Underlying the calculations of Faith's PD was a phylogenetic tree constructed from DNA barcodes. Barcode sequence representing the complete mitochondrial cytochrome-b gene was derived from tissue samples collected from captured bats on the 2015 survey and preserved in either 95% ethanol or dried on silica beads, as well as several tissues available in the Australian Biological Tissue Collection at the South Australian Museum, and sequences already deposited in Genbank (<http://www.ncbi.nlm.nih.gov/genbank/>). Laboratory protocols are described in detail in Chapter 7.

Survey considerations

The results of the present survey for bats should be considered in the context of the following concepts.

Taxonomic uncertainty

Several of the echolocation types recorded during the survey could not be identified to species. This partly reflects the current state of taxonomic knowledge of New Guinean bats, which for some genera does not yet allow for confident allocation of a captured or recorded bat to a formally described species. Much of the existing taxonomy of Papua New Guinean bats is based on quite basic morphological comparisons, done without the benefit of information from morphometric or genetic analyses. Thus, one broadly distributed species as currently recognised can contain two or more actual species with narrower distributions and contrasting ecological niches. Experience to date is that genetic investigations of any widely distributed bat 'species' in the Melanesian region is likely to reveal the presence of additional species 'hidden' within the current arrangement (K.N. Armstrong and K.P. Aplin unpublished research in progress). The most relevant example in the present study is the set of call types allocated to three species of

bent-winged bat *Miniopterus* spp. There are clearly three species represented in the acoustic recordings, and call characteristics suggest they derive from *Miniopterus*, but because of the significant taxonomic problems within this group, it is not possible to allocate species-level names to these call types.

Species identification of echolocation signals

In the past decade, there has been a considerable advance in knowledge of the calls that are produced by Papua New Guinean bats (Armstrong and Aplin 2011, 2014a,b; Leary and Pennay 2011; Robson et al. 2012; Armstrong et al. 2015a,b; K.N. Armstrong and K.P. Aplin, unpublished data). However, the compilation of echolocation call types is not complete, and it is not yet possible to identify some species. For some groups, acoustic recordings may never be able to provide an unambiguous identification because call characteristics overlap too much between two or more species. For example, the long-eared bats *Nyctophilus* spp. are widely regarded as 'difficult' to distinguish acoustically in Australia, and a similar situation may exist amongst PNG forms of *Nyctophilus* and their close relative Thomas's Big-eared Bat, *Pharotis imogene*. As a second example, the calls of species of *Miniopterus* and *Pipistrellus* that produce *cFM* calls with a characteristic frequency between 35 and 55 kHz are also difficult to distinguish unambiguously at this time. An unambiguous identification of some bat species will come only after capture and possibly additional morphological and genetic comparisons.

Equating call types with species richness

The number of call types recognised may not equate to the same number of bat species, for three reasons: 1) two or more closely related bat species may produce calls that are so similar that they cannot be distinguished reliably using the available methods (e.g. Reinhold et al. 2001; Milne 2002); 2) the males and females of a few bat species are reported to produce calls with a slightly different mean characteristic frequency, albeit of comparable type (e.g. Semon's Leaf-nosed Bat *Hipposideros semoni* in Australia; de Oliveira and Schulz 1997; K.N. Armstrong unpublished data); and 3) a single bat species may produce more than one call type (e.g. clutter calls, search phase calls, approach phase calls), some of which may resemble the calls of other species. With sufficient experience of related species, it is generally possible to control for the last of these factors, and to limit the analysis to the typically more diagnostic search phase calls. Considering the call types encountered on the present survey, species richness might be slightly under-represented for call types *st.cFM* because of the first reason.

Relative detectability—signal characteristics

Detection rate is clearly a product not only of local abundance but also of the acoustic detectability amongst species. Detectability varies amongst species based on echolocation call characteristics, particularly the characteristic frequency and amplitude of emitted signals. Some bats produce signals of very low power (for example species of Long-eared Bats *Nyctophilus*) and others produce very high frequency signals that attenuate quickly (for example the Dusky Leaf-nosed Bat *Hipposideros ater*). Calls in either category are possible to detect only when the bat is close to the microphone.

Relative detectability—equipment and analysis considerations

The recording equipment chosen in the survey maximised the possibility that species with ultra-high frequency calls over 100 kHz would be recorded because the type of microphone present in the D500X hardware is high quality and reliable in humid atmospheres. In addition, the post-recording semi-automated data processing technique is designed to massively filter the many gigabytes of data that are recorded in a way that minimises the potential for loss of signals, especially ultra-high frequency calls. However, some types might still be slightly under-represented in the identifications; for example, the calls of species with a characteristic frequency below 30 kHz (call types *cFM*, *sFM*) were often buried in background environmental noise making it difficult for the call detection software to recognise them. Also, infrequently encountered low amplitude short duration broadband signals (call type *bFM*) were possibly combined with clutter calls of other species (for example some *st.cFM* calls). Replication of recording sessions across transects maximised the chance of detection of all echolocating species.

Appendix 6.5 Summary of bat captures from which tissue was taken for DNA barcoding, and echolocation recordings made (except the non-echolocating *Syconycteris* spp.).

Species	Trap type	Location	Lat	Long	Field No.	Tissue types	ABTC No.
<i>Syconycteris</i> sp. 1 'montane'	Canopy mist net	Pipeline ROW H3	S5.94477	E142.7443	59	W.P.S, L.Et	ABTC141240
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S1	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S2	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S3	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S4	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S5	W.P.Et	ABTC141271
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S6	W.P.S	ABTC141332
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S7	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S8	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S9	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S10	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S11	W.P.S	—
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	S12	L.Et	ABTC141295
<i>Syconycteris</i> sp. cf. <i>australis</i>	Harp trap	Arakubi Quarry M4	S6.46197	E143.2565	S13	W.P.S	—
<i>Aselliscus tricuspидatus</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	90	W.P.S, L.Et	ABTC141270
<i>Aselliscus tricuspидatus</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	153	L.Et	ABTC141315
<i>Hipposideros cervinus</i>	Harp trap	Arakubi Quarry M4	S6.46197	E143.2565	107	L.Et	ABTC141284
<i>Hipposideros cervinus</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	148	L.Et	ABTC141313
<i>Rhinolophus megaphyllus</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	81	W.P.S	ABTC141263
<i>Rhinolophus megaphyllus</i>	Harp trap	Arakubi Quarry M4	S6.46186	E143.256	89	W.P.S, L.Et	ABTC141269
<i>Miniopterus</i> sp. (call type 38 cFM)	Canopy mist net	Pipeline ROW H3	S5.94477	E142.7443	60	W.P.S, L.Et	ABTC141241

Tissue type codes: **L.Et**: liver sample in 95% ethanol; **W.P.Et**: 4mm wing punch biopsy in 95% ethanol; **W.P.S**: 4mm wing punch biopsy in silica beads.

Appendix 6.6 Notes on the species identifications of echolocation types.

EMBALLONURIDAE
<p>Large-eared Sheath-tailed Bat <i>Emballonura diana</i> Call type 38 i.fFM.d Call shape typical of <i>Emballonura</i>, and identification based on the recording of reference calls made elsewhere (K.P. Aplin and K.N. Armstrong unpublished data).</p>
<p>New Guinea Sheath-tailed Bat <i>Emballonura furax</i> Call type 52 i.fFM.d Call shape typical of <i>Emballonura</i>, and identification based on the recording of reference calls made elsewhere (K.P. Aplin and K.N. Armstrong unpublished data).</p>
<p>Raffray's Sheath-tailed Bat <i>Emballonura raffrayana</i> Call type 45 i.fFM.d Call shape typical of <i>Emballonura</i>, and identification based on the recording of reference calls made elsewhere (K.P. Aplin and K.N. Armstrong unpublished data).</p>
<p>Lesser Sheath-tailed Bat <i>Mosia nigrescens</i> Call type 65 i.fFM.d Attributable based on reference calls collected elsewhere in Papua New Guinea (Leary and Pennay 2011; K.P. Aplin and K.N. Armstrong unpublished data). The characteristic frequency of <i>M. nigrescens</i> overlaps with that of Beccari's Sheath-tailed Bat <i>Emballonura beccarii</i> and this may conceal its presence. The study area does not fall inside the known geographic range of <i>E. beccarii</i>, but the distribution of this species is not fully understood.</p>
<p>Bare-rumped Sheath-tailed Bat <i>Saccolaimus saccolaimus</i> Call type 25 sFM Most likely attributable to <i>Saccolaimus saccolaimus</i> based on characteristic frequency, the 'serpentine' pulse shape and the harmonic profile (most energy in the second harmonic, harmonics around 12 kHz apart), though characteristic frequency was higher than has been recorded for this species in Australia (Milne 2002; Milne et al. 2009; K.N. Armstrong unpublished data). Unlikely to be a molossid such as <i>Otomops</i> sp. because the harmonic profile is typical of the Emballonuridae rather than Molossidae.</p>
HIPPOSIDERIDAE
<p>Trident Leaf-nosed Bat <i>Aselliscus tricuspidatus novaguinea</i> Call type 120 sCF Attributable to this species based on information in Leary and Pennay (2011), and also on reference calls recorded on the survey and elsewhere (K.P. Aplin and K.N. Armstrong unpublished data).</p>
<p>Unnamed Leaf-nosed Bat <i>Hipposideros</i> sp. cf. <i>ater</i> Call type 172 sCF A single high quality sequence of pulses with a characteristic frequency of around 172 kHz at the second harmonic was recorded near Arakubi Quarry. The closest match is <i>Hipposideros ater</i> that has a characteristic call frequency of c. 150 kHz in PNG (K.P. Aplin and K.N. Armstrong unpublished data) and generally around 150–155 kHz in Australia (K.N. Armstrong unpublished data). The magnitude of the difference is sufficient to suggest the presence of a species that has never been encountered previously. No other bat species emits a frequency as high at 172 kHz at the second harmonic. The unambiguous presence of the fundamental component of calls at around 86 kHz rules out the detection of the third harmonic of <i>Aselliscus tricuspidatus</i>. The taxonomy of <i>H. ater</i> is currently being reviewed by several authors and nomenclature may change soon.</p>

Fawn-coloured Leaf-nosed Bat *Hipposideros cervinus***Call type 140 sCF**

Attributable to this species based on information in Leary and Pennay (2011), and also on reference calls recorded on the survey and elsewhere (K.P. Aplin and K.N. Armstrong unpublished data).

Diadem Leaf-nosed Bat *Hipposideros diadema griseus***Call type 58 mCF**

Attributable to this species based on information in Leary and Pennay (2011), and reference calls recorded elsewhere (K.P. Aplin and K.N. Armstrong unpublished data).

Wollaston's Leaf-nosed Bat *Hipposideros wollastoni parnabyi***Call type 88 mCF**

Attributed based on reference calls recorded elsewhere (K.P. Aplin and K.N. Armstrong unpublished data).

RHINOLOPHIDAE**New Guinea Horseshoe Bat *Rhinolophus euryotis*****Call type 52 ICF**

Attributable based on reference calls recorded elsewhere in Papua New Guinea (K.P. Aplin and K.N. Armstrong unpublished data), and also Leary and Pennay (2011).

Eastern Horseshoe Bat *Rhinolophus megaphyllus***Call type 70 ICF**

Attributable based on reference calls collected on the survey, elsewhere in Papua New Guinea (K.P. Aplin and K.N. Armstrong unpublished data), and also Robson et al. (2012). It is very similar to the call of *Rhinolophus arcuatus*, and the two species might not be distinguishable on the basis of their echolocation calls, unless it is known that their habitats do not overlap, and identifications can be confirmed with a capture, as was the case on the current survey.

Large-eared Horseshoe Bat *Rhinolophus sp. cf. robertsi***Call type 33 ICF**

Attributable with high confidence to a member of the *Rhinolophus philippinensis* complex, of which several forms occur in each of Australia and New Guinea, potentially with some sharing of species. The characteristic frequency (of the second harmonic) is most similar to that of the large form ('*robertsi*') in northern Australia and it may represent the same species (K.N. Armstrong unpublished data). This form may never have been captured in PNG.

MINIOPTERIDAE**Unidentified Bent-winged Bat *Miniopterus sp. 1 'large'*****Call type 38 st.cFM**

Attributable to one of several medium-large candidate species of *Miniopterus* (all except *M. australis*), or an undescribed species of *Miniopterus*. Feeding buzzes that dropped significantly in frequency below search phase pulses were present—these are thought to be typical of *Miniopterus*.

Unidentified Bent-winged Bat *Miniopterus sp. 2 'medium'***Call type 45 st.cFM**

One of several candidate species in the Miniopteridae, but a species of *Pipistrellus* is also possible, since the calls of several Papua New Guinean *Pipistrellus* (Vespertilionidae) and medium-sized *Miniopterus* overlap in characteristic frequency. Feeding buzzes that dropped significantly in frequency below search phase pulses were present—these are thought to be typical of *Miniopterus*.

Unidentified Bent-winged Bat *Miniopterus* sp. 3 'small'

Call type 53 st.cFM

Most likely the small-bodied *Miniopterus australis* or an allied undescribed taxon, but a species of *Pipistrellus* is also possible, since the calls of several Papua New Guinean *Pipistrellus* (Vespertilionidae) overlap in characteristic frequency. Feeding buzzes that dropped significantly in frequency below search phase pulses were present—these are thought to be typical of *Miniopterus*.

VESPERTILIONIDAE

Flute-nosed Bat *Murina* sp. cf. *florium*

Call type 80 st.bFM

Attributable to *Murina* sp. cf. *florium* based on reference calls recorded elsewhere (K.P. Aplin and K.N. Armstrong unpublished data). This call type is also very similar to those of both *Kerivoula* sp. cf. *muscina* and *Phoniscus papuensis* so the identification is not unambiguous. The distribution of all three species is incompletely known.

Unidentified Long-eared Bat *Nyctophilus* sp.

Call type 55 st.bFM

Possibly attributable to the Papuan Long-eared Bat *Nyctophilus microtis* or an affiliated undescribed taxon based on reference calls recorded elsewhere (K.P. Aplin and K.N. Armstrong unpublished data). Calls of this type may also be attributable to those of other species of *Nyctophilus* (e.g. the Small-toothed Long-eared Bat *Nyctophilus microdon*), or *Pharotis imogene* whose calls have not yet been characterised. The IUCN distribution map does not place *N. microtis* in the region of the PMA3 study area (Hutson et al. 2008b), but this species or *N. microdon* are the most likely candidates.

Short-winged Pipistrelle *Philetor brachypterus*

Call type 30 cFM

This call type is attributed to *P. brachypterus* based on reference calls collected elsewhere (Armstrong et al. 2014a). There is a possibility that the name encompasses two distinct forms at higher and lower elevations, but this has yet to be tested.

Appendix 6.7 Summary of species detections at each nightly recording site in 2015 (to allow future verification).

BAA_transect_elevation (m asl)	Distance from road (m)	Recording unit serial	Recording night																				
				35 i.fFM.d	45 i.fFM.d	52 i.fFM.d	65 i.fFM.d	25 sFM	120 sCF	172 sCF	140 sCF	58 mCF	88 mCF	52 ICF	70 ICF	33 ICF	38 st.cFM	45 st.cFM	53 st.cFM	80 bFM	50 bFM	30 cFM	social
BAA 1_H1_2,200	0	953	23/06/2015													X							
	20	957	16/06/2015													X							
	70	956	16/06/2015											X	X		X						
	120	955	16/06/2015											X	X								
	170	955	23/06/2015											X				X					
	220	956	23/06/2015												X	X		X					
BAA 1_H2_2,200	0	957	23/06/2015													X	X						
	20	957	17/06/2015													X	X		X				
	70	956	17/06/2015																	X			
	120	955	17/06/2015																				
	170	954	17/06/2015																				
	220	953	17/06/2015													X							
BAA 1_H3_2,200	0	954	18/06/2015													X	X				X		
	20	955	18/06/2015													X							
	70	956	18/06/2015													X				X			
	120	957	18/06/2015													X		X					
	170	955	24/06/2015																				
	220	953	18/06/2015													X							
BAA 1_H4_2,700	0	954	21/06/2015													X	X						
	20	955	22/06/2015																				
	70	956	22/06/2015															X				X	
	120	957	22/06/2015															X					
	170	957	21/06/2015															X					
	220	956	21/06/2015															X					

CHAPTER 7 – ENHANCING BIOLOGICAL MONITORING WITH GENETIC INFORMATION

Kyle Armstrong and Ken Aplin



A Giant White-tailed Rat (*Uromys cf. caudimaculatus*) from KP107 in BAA 2 - genetic evidence links this population to others at similar elevations in Hela and Chimbu Provinces

SUMMARY

Background and aims

Monitoring studies depend on the ability to make reliable and consistent identifications of the study species across surveys. There are two aspects to identification—placing the correct species name on a capture (where species are described), and placing the same name or identifier consistently on the same taxon across surveys, and also across sampling sites in different habitats or elevations. Species identification is often difficult in PNG because of a high prevalence of cryptic species (morphologically similar but genetically distinct) and a lack of good published identification resources for many groups. The use of genetic markers can substantially enhance our ability to identify species, even if they are not yet formally described by taxonomists.

We applied a DNA barcoding approach to three groups on the 2015 PMA3 survey—frogs, non-volant mammals (marsupials and rodents) and bats. For each of these groups, a particular mitochondrial gene was chosen based either on its published ability to provide good resolution of relationships amongst species, and/or the availability of published sequences for comparison. For mammals and frogs, a series of comparative sequences were generated from tissues in the Australian Biological Tissue Collection at the South Australian Museum.

Major results

Some of the more important outcomes of applying DNA barcoding in the study included:

1. Identification of additional and/or potentially new species of frogs and rodents

- A number of potentially new species were either identified or confirmed by the DNA barcoding results: Three cryptic species were recognised among the rodents, all belonging to the frequently captured genera *Rattus* and *Paramelomys*.
- For frogs, the genetic markers provided confirmation of a putatively new species of frog, and also revealed a level of separation that is suggestive of an entirely new genus.
- Frog species initially identified as *Liophryne schlaginhaufeni* and *Sphenophryne cornuta* from their morphology and calls were found to be genetically quite distinct from other barcoded populations of these species, suggesting that they may represent distinct species.

2. Identification of related populations from localities outside the study area

DNA from rodents and marsupials captured during the PMA3 surveys was compared to 'context' samples from outside the study area to identify any links with other populations. In all but a few cases, this resulted in the identification of closely related populations. In each of these cases, recent gene flow between populations in the BAAs and in surrounding regions is indicated. However two of the 'cryptic' species identified from among those captured in the PMA3 surveys did not genetically match any other sampled population:

- *Paramelomys* cf. *rubex* B from all trapping transects in the Agogo Range.
- *Paramelomys* cf. *mollis* C from transect H1 on Hides Ridge.

3. Identification of several instances of interbreeding between species

Interbreeding can lead to anomalous genetic results in which the DNA barcoding does not accurately reflect the true species identity of the individual. Several instances were detected during this study:

- Two individuals of *Rattus* cf. '*niobe*' D produced anomalous DNA barcode sequences, one referable to the *Rattus* sp. 'spiny' genetic group, and the other with affinity to *Rattus steini*, a species that was not collected during the survey but which is known to occur in the Kikori catchment.

- The morphologically distinctive species *Rattus* sp. 'spiny' produced DNA barcode sequences referable to *R. leucopus*. (This is interpreted as an instance of ancient hybridization leading to DNA capture).

4. Generation of a phylogenetic (evolutionary) framework for comparing genetic diversity and ecologically informative functional groups in bats.

Phylogenetic Diversity (PD) is a measure of biodiversity that incorporates the amount of evolutionary difference amongst species (Faith 1992). PD is higher for a community made up of distantly related species than one with a few groups of closely related species. High PD is often indicative of high ecological diversity. The development of the PD metric will improve our understanding of how changes in bat community structure might also affect the ecological functions that they provide over the life of the study.

Conclusions

The DNA barcoding effort produced a much clearer picture of species diversity and identities, especially among the rodents where the method was used most extensively. Some complications were identified among the rodents, probably related in each case to rare or ancient hybridization events. Because of the high prevalence of cryptic species, future surveys of non-volant mammals will need to incorporate some kind of genetic analysis to guarantee reliable and consistent identifications. For the other groups, a number of potential benefits are identified that justify continuation of genetic approaches, though perhaps for more targeted groups.

For future PMA3 surveys we also recommend the use of 'Restriction site associated DNA sequencing' (RADseq) rather than the single gene DNA barcoding method used in 2015. This powerful and diverse method can be implemented at little if any additional cost and with diverse benefits.

INTRODUCTION

Genetic analysis was used in the 2015 PMA3 study to add value to the studies of amphibians, non-volant mammals and bats. This chapter provides much of the background and detail on the contribution of the genetic studies and has four objectives:

1. to explain the rationale for including genetic analyses in the 2015 PMA3 monitoring activities;
2. to describe the genetic methods used for samples collected in 2015, including their advantages and limitations;
3. to illustrate the various advantages gained by including genetic analyses in monitoring programs, using examples from mammals and amphibians;
4. to explore the potential future contribution of genetic approaches for meeting the objectives of PMA3 over coming decades.

Genetic analysis in the context of PMA3 2015

The scientific validity of any ecological monitoring study rests heavily on two foundations. The first is the use of standardised methods for data collection (e.g. trapping designs, timing of surveys) that ensure data is gathered in the same way across consecutive sampling periods. The second is consistency in the identification of the biological units (individual species to communities) that are being monitored. Worldwide, more attention is typically given to the first of these foundations and less to the second. Indeed, the process of identifying biological units is often taken for granted.

In many parts of the world this assumption is justifiable—identification of plants or animals to species is comparatively easily because species diversity is low, all of the major groups are well-known both taxonomically and ecologically, and comprehensive field guides and other identification tools are available. Furthermore, there is often detailed information available on species distributions and ecology that form a solid basis for interpreting monitoring results. None of these

conditions are met for Papua New Guinea, which is a global 'hot-spot' for biodiversity (Myers et al. 2000), where the process of species inventory is still far from complete for almost all groups of plants and animals (Allison and Tallwin 2015; Aplin 2015; Gideon 2015; birds may be the only exception), and where few ecological studies of individual species or communities have been undertaken (Novotny and Toko 2015).

Given this context, several questions need to be considered prior to implementation of any monitoring study. Firstly, does it matter if all of the species in a target group are not discriminated? Secondly, does it matter whether or not identifications are reliable and consistent both within and between sampling periods? And thirdly, does it matter whether they have a formal scientific name? Each of these issues is discussed below.

Note that the process described below is concerned with the identification of specimens and their allocation to described or undescribed species units. It is separate from taxonomic study that involves the description of new species and the resolution of species boundaries and correct nomenclature.

Species discrimination

Species discrimination is the process of deciding how many species exist within any particular group. While this may sound straightforward, in areas of high biodiversity it is often complicated by the presence of so-called 'cryptic' species—pairs or groups of species that are morphologically very alike but genetically distinct (Bickford et al. 2007; Pfenninger and Schwenk 2007; Oliver et al. 2009). In some cases, a specialist may be alerted to cryptic species by subtle differences in appearance or behaviour but in other cases they go unsuspected until genetic analysis is performed.

Species discrimination can be done at a global level (i.e. determining how many species exist across the entire geographic range of the group) or at a local or regional level (i.e. determining how many species are present at a particular locality or within a given region). An important point here is that, in the modern age of genetic-based taxonomy, species discrimination is no longer a function of competing 'species concepts' but is a matter of evidence. Species are by definition genetically discrete entities and it follows that, with an appropriate level of genetic analysis, any group of samples can be resolved into the true number of species (Baker and Bradley 2006; De Queiroz 2007). Importantly, this even applies in a situation where there is some genetic admixture through interspecific hybridisation.

Full species discrimination is clearly ideal in any study monitoring focal groups of species, as this will produce the most detailed baseline characterisation and the best chance of detecting any subsequent changes in composition. If this ideal is not met, and two or more species in a particular group are not distinguished, the result is a potential loss of monitoring sensitivity. Whether or not this matters depends on the goal of the monitoring.

If the goal of a monitoring study is to detect changes in biodiversity then underestimation of true species diversity is clearly undesirable. Local extinction of one species might go undetected because a similar species persists; if the survivor also increases in abundance there may be no lasting evidence of the event. Simplification of an animal or plant community through 'drop-out' extinction of members of ecologically similar groups of species is a well-known phenomenon on islands and in artificially fragmented habitats (e.g. Leck 1979; Karr 1990), and it might also occur in response to project-related impacts.

If, on the other hand, the goal is to monitor trends in ecosystem functionality, the local extinction of ecologically very similar species may have little net impact and thus be of limited concern. However, even in such circumstances, simplification of communities arguably might impact on key ecological properties such as resilience which is determined in part by species diversity (i.e. multiple options for response to change) (Elmqvist et al. 2003).

Given these considerations, we suggest that full species discrimination (whether or not they are formally named) should be the objective for all taxonomic groups targeted for monitoring under PMA3. Meeting this objective is more difficult for some of the target groups than others, as indicated below:

Birds—as mentioned above, an inventory of the birds of New Guinea is probably close to complete. Birds not only attract more attention than any other group but they also use plumage and calls to tell each other apart, hence the differences are usually obvious also to people. Nevertheless, there are groups where species boundaries remain unclear and where genetic analysis may be necessary to resolve uncertainty (e.g. Deiner et al. 2011).

Frogs—in most frog species the males use calls to inform females and rival males of their whereabouts. Different species usually possess recognisably distinct call types that permit discrimination among them. Taxonomic allocation of females is sometimes problematic and it can also be difficult to allocate other life stages (eggs and tadpoles) to species on morphological criteria alone (see below under 2.2 Specimen Identification).

Mammals—various groups of mammals display high local species diversity coupled with conservative body forms. For non-flying mammals scents may be more important than vision in communication within and between species, which means that there may be no obvious and consistent differences in external body features by which to identify them. Closely related bat species may also be very similar in terms of external body form, though they often have contrasting echolocation calls that can be used to identify them. However, geographic variation in call characteristics within species can mask differences between bat species.

Specimen identification

The term 'specimen identification' is used here to mean the allocation of an individual plant or animal to one among the range of discriminated species units. These units may include a species with an acknowledged scientific name, a clearly undescribed taxon, or a member of a taxonomically unresolved group. Species that may lack a formal scientific name can be given an informal name for the purpose of the study.

The importance of accurate and consistent identifications in a monitoring study cannot be overstated. Inconsistent identifications among sites and across survey years will reduce the integrity of comparisons and evaluations. At best, the monitoring outcomes will be blurred and imprecise; at worst, they might be the basis for erroneous interpretations.

Determination of species names

Once the true species units have been discriminated, it is appropriate to ask whether or not they have previously proposed (or 'available') scientific names. In most cases this step is straightforward and the answer will be obvious (often 'yes' for mammals; commonly 'no' for frogs). However, for groups that contain both higher diversity and cryptic species, the connection between species units and available species names may not be so readily made. For example, if two very similar frog species occur at a study site and there is one available name for a similar kind of frog from elsewhere, how can we tell which one should bear that name and which one is without a scientific name?

To make these connections between species units and available names, it is necessary to investigate the relationships among the various populations. This might be done by using morphological criteria alone, or a combination of morphology and call characteristics in the case of frogs and bats. In some cases, where critical data are missing (e.g. no description of the call is given in the original description), genetic methods might be required to determine the degree of relatedness among the various populations.

Where it is not possible to decide whether or not a species has an available name, it is usual practice to designate species units in the following way: *Rattus cf. niobe* A, *Rattus cf. niobe* B, etcetera

This example signifies two different species of rat, both of which are most similar to *Rattus niobe* (cf. means 'compare') but neither of which is definitely referable to this species.

Use of letter- or number-coded species names in this format is perfectly adequate within a single project. However, it does not provide an ambiguous means of communication between projects, as there is no certainty that *Rattus cf. niobe* A from one project area is the same as *Rattus cf. niobe* A from another project area. Avoiding this kind of confusion is one good reason to quickly determine the applicability of available names and to propose new species names if these are needed. Another reason is that formal description of a species initiates other processes such as consideration of conservation status by the IUCN and by the Government of PNG. As an interim measure, inclusion of the primary genetic information in a report will allow the necessary comparisons to be made between projects.

GENETIC METHODS USED FOR PMA3 PHASE 1

Objectives and potential applications

The objectives of PMA3 suggested a number of relevant applications of genetic methods:

1. Effective discrimination of species units;
2. Reliable identification of specimens;
3. Determination of whether populations in the study area belong to more widely distributed species or potentially occur only in the study area;
4. Generation of a phylogenetic (evolutionary) framework for use in community-level analyses that account for genetic diversity and ecologically informative functional groups.

Each of these applications ideally might use a different set of genetic tools. However, given the availability of methods and budget constraints within Phase 1, the decision was made to select one tool that could satisfy all of the requirements to some extent. The selected tool is an approach commonly known as 'DNA barcoding'.

DNA barcoding—advantages and limitations

DNA barcoding has been the most popular genetics-based approach for tackling problems of species discrimination and specimen identification (both as defined above). It rests on the premise that short nucleotide sequences (a 'barcode') from a single, 'universal' genetic marker common to all animals or all plants (but different from each other) would allow for discrimination of every species from all others. For animals the chosen genetic marker is mitochondrial cytochrome c oxidase1 (COI); for plants it was necessary to choose two chloroplast genes. The accumulation of DNA barcodes from representatives of all species on Earth became a global enterprise involving several consortia of scientists focused on particular groups and supported by a global database (<http://www.ibol.org>; <http://www.barcodeoflife.org/>).

Although there was much initial enthusiasm that DNA barcoding could circumvent the traditional taxonomic process and accelerate the discovery and description of biological diversity, this has been tempered by the realisation that sequences from a single gene might not always be sufficient for either species discrimination or specimen identification (see reviews in Collins and Cruikshank 2012; Taylor and Harris 2012). In reality, there are several circumstances in which DNA barcoding will produce incorrect results, namely:

Failure to distinguish species when they exist in nature—This can occur where interspecific cross-breeding results in the transfer of mitochondrial DNA between species, causing two different species to share the same 'barcode' (this is called 'mitochondrial capture'). It can also occur where species have diverged only recently, giving insufficient time for the mitochondrial sequences to diverge to a sufficient level to be regarded as 'different' (this is called 'incomplete lineage assortment').

Discrimination of species where they do not exist in nature—This can occur where mitochondrial capture has occurred in only some populations of a species, or where the mitochondrial genomes have undergone rapid divergence either due to strong selection or population bottlenecking (population expansion from only a few founder individuals), such that the level of mtDNA divergence is not representative of the wider genome.

Incorrect identification of a species—This can occur where occasional interbreeding between species generates individuals which carry mitochondrial DNA that does not match their primary genetic identity (this is called mitochondrial introgression). It could also occur if the initial DNA barcoding has not sufficiently sampled the variation within the various species and their mitochondrial DNA is not as well-differentiated as thought (i.e. lineage assortment is actually incomplete).

Despite its various shortcomings, DNA barcoding nevertheless has potential to deliver information relevant to each of the four desirable applications (see *Objectives and potential applications*). This broad applicability, coupled with the relative ease and low cost of obtaining suitable portions of mitochondrial DNA, made DNA barcoding a valuable addition to Phase 1 of PMA3.

Specific goals for the DNA barcoding

The four potential applications of genetic markers for this project were tested on three of the five focal groups—frogs, bats, and non-volant mammals (rodents, marsupials) and the relative importance of each application varied among these groups.

1. Effective discrimination of species units—frogs, marsupials, rodents

This addresses the fundamental question of how many distinct species units are present within each of these groups in the BAAs, regardless of what they might be called. By adding a genetic perspective to identifications based on external morphology and calls, we aimed to produce a more robust and comprehensive species inventory that would detect a significant proportion of any cryptic species present.

Analyses started with the generation of a phylogenetic tree for each major group. Consideration was given to whether observed genetic clusters corresponded with morphological or call types identified in the field. In addition, examination of 'branch lengths' (showing the extent of genetic divergence) and statistical analyses of 'barcode gaps' provided further means for discrimination of potential species units.

Because the genetic barcode clusters might not correspond perfectly to biological species units, care was taken to compare the genetic results with information from morphology and calls where these were available. As an additional measure, a broader 'genetic framework' was generated by combining barcode sequences obtained during the 2015 survey with sequences from potentially related populations and species, referred to here as 'context' sequences. Some of these context sequences were obtained from public databases (Genbank: (<http://www.ncbi.nlm.nih.gov/genbank/>)) but others were newly generated for this study using samples held in the Australian Biological Tissue Collection (ABTC) of the South Australian Museum. The context sequences were selected to give relevant taxon-level and geographic-level sampling across PNG.

2. Reliable species and specimen identifications—frogs, bats, marsupials, rodents

The genetic framework provided a means of comparing species present in the BAAs with populations found elsewhere in PNG, including those considered to be typical of various named forms. Where a close genetic match was observed and this did not clash with the evidence from morphology or calls, an established species name was applied with confidence to the BAA population. However, where higher levels of genetic differentiation were observed, doubt was cast over whether the name should be applied or whether the BAA population might represent a distinct and potentially undescribed species. In several cases among the frogs, the genetic evidence supported earlier conclusions based on morphology and calls as to the presence of undescribed and novel species. In the case of the mammals, suspicions as to the presence of cryptic species were greatly strengthened by the genetic results. Where appropriate species names could not be decided upon through these measures, a system of informal nomenclature was developed to serve as an interim standard across survey years.

The DNA barcoding framework established during the first phase of PMA3 offers the ability to allocate any future captures to previously discriminated species based on their barcodes alone, irrespective of the level of confidence of a morphological determination. Importantly, this can include life stages or forms that might not be readily identified in the field from their external appearance or calls. For frogs, this includes non-calling females and males, eggs and tadpoles. For mammals, it could assist with the identification of juveniles that can appear quite different from adults, and might even resemble the adults of another smaller species.

Capture of a previously unsampled species during a future survey should be obvious from barcoding because its DNA sequence is likely to fall outside of all previously discriminated BAA clusters. Furthermore, provided there is sufficient taxonomic coverage among 'context' samples, the general identity of a newly sampled taxon should be apparent

from its placement on the phylogenetic tree, even if identity is not evident from its morphology. This is because the sequence of clustering on the phylogenetic tree reflects the degree of evolutionary relatedness of the species—groups of closely-related species form tight clusters, while species with no close relatives will be positioned on isolated branches of the tree. As a rule, the more comprehensive the ‘context’ sampling the greater the likelihood that a previously undetected species from one of the BAAs will cluster with a previously known species from another locality.

Although the barcoding framework thus offers many advantages for specimen identification, the possibility of mitochondrial capture or introgression (as discussed in *DNA barcoding—advantages and limitations*) cautions against a total reliance on this approach. Ideally, a morphological or call based identification should also be available for every capture to allow for the detection of genetic mismatches of this kind.

3. Determination of degree of relatedness of BAA populations to other regional populations—marsupials, rodents

For undescribed species that are identified within the BAAs, it is important to determine whether they have been collected elsewhere, or are only known from the study area.

This application was most relevant to non-volant mammals because morphological criteria provide a relatively poor estimate of relatedness between populations. Accordingly, more effort was made to generate a relatively extensive genetic framework from ‘context’ samples, including material from nearby localities that might be expected to contain closely related populations. For frogs, the genetic framework was compiled from published sources, but this only contained described species and none of the many putative new taxa that have been collected over recent years from field surveys in many areas of PNG. A new genetic framework might need to be developed in the future for frogs in order to better understand the distribution and taxonomic affinities of some specimens from PMA3.

4. Generation of a phylogenetic (evolutionary) framework for comparing genetic diversity and ecologically informative functional groups in bats

The simplest measure of biodiversity is the total number of species at a site (this is often termed ‘Species Richness’). More complex analyses usually include data on species composition based on presence/absence or measures of relative or absolute abundance to determine how common each species might be at each site. An additional perspective considers the genetic diversity present within communities. Phylogenetic Diversity (PD) is a measure of biodiversity that incorporates the amount of evolutionary difference among species (Faith 1992). It is calculated from phylogenetic trees by summing the branch lengths amongst species. As an example, a site or community with five species each from a different family will have a higher PD, and thus higher value in terms of genetic diversity, than another site or community that contains five species from the same family.

It was particularly informative to calculate a measure of genetic diversity for bat communities because they can be further categorised into feeding guilds based on their echolocation call design and flight capability, as well as other groups that reflect where they roost. Given that species in the same family tend to have similar ecological traits, a change in PD can indicate a change in the presence of ecological or functional groups, which might indicate ecological simplification and the erosion of ecological resilience as a response to changes in habitats. While Phylogenetic Diversity generally increases linearly with increasing Species Richness, a large difference in PD could indicate differences in representation at the family level, which would invite interpretation around the ability of the habitat to support certain groups.

Field and laboratory methods

Sample collection

Tissue biopsy samples were collected from frogs, rodents, marsupials and bats using methods that are consistent with global ethical standards and routine practices for conducting research on wild mammals (Sikes et al. 2011). Samples were submitted to the Australian Biological Tissue Collection (ABTC) at the South Australian Museum and are currently embargoed against their use outside the scope of the present study. Samples were also requested from the ABTC to provide comparative ‘context’ for individuals collected from the study area.

DNA extraction and marker sequencing

Rather than the standard barcoding gene (COI), two other mitochondrial regions were chosen for investigation of frogs (12S ribosomal RNA; 12S) and mammals (cytochrome**b**; *cyt-b*). These were selected over COI because of the ease with which many species can be barcoded using a single set of universal primers, the availability of published comparative sequences from other related species, and previous published experience demonstrating the utility of the marker for resolving evolutionary relationships.

Laboratory work was conducted at the South Australian Regional Facility for Molecular Ecology and Evolution, with all post-PCR work conducted downstream of DNA extraction and PCR preparation. DNA was extracted using a salting-out precipitation method with a Gentra Puregene DNA isolation kit. A full list of samples and their provenance is listed in Chapters 2, 5 and 6. Up to two pairs of primers were used to amplify mitochondrial DNA markers in the case of each group (**Table 7.1**). Amplification of markers by PCR was conducted in 20 μ L reaction volumes and included: 2 μ L of 10x buffer, 1.6 μ L of 25 nMMgCl, 2 μ L of dNTP each at 25 mM and 0.1 μ L of Invitrogen Amplitaq Gold[®] DNA Polymerase. Thermocycling conditions were: an initial denaturation at 94 °C for 10 mins, followed by 35 cycles of 94°C for 30 sec, 50°C for 30 sec and 72°C for 2 mins, and ending with a final step of 72°C for 10 mins. Products were visualised on agarose gels, purified with a Millipore Multiscreen[®]384 PCR plate on a vacuum manifold and sequenced in both directions on an Applied Biosystems capillary DNA sequencer using Applied Biosystems Big Dye Terminator version 3.1 chemistry at the Australian Genome Research Facility (AGRF).

Table 7.1 Summary of primers used for DNA barcodes in the different vertebrate groups.

Group	Region	Primer name	DNA sequence (5'→ 3')
Frog	12S rRNA	M001	TGACTGCAGAGGGTGACGGGCGGTGTGT
Frog	12S rRNA	M002	AAAAAGCTTCAAACCTGGGATTAGATACCCCACTAT
Frog	12S rRNA	M973	AAACTGGGATTAGATACCCCACTAT
Frog	12S rRNA	M974	GCTAGACCATKATGCAAAAAGGTA
Bat	Cytochrome- <i>b</i>	M1706	ATGATATGAAAAACCATCGTTG
Bat	Cytochrome- <i>b</i>	M1707	TTCCNTTCTGGTTTACAAGAC
Marsupial	Cytochrome- <i>b</i>	M989	ACCATCAACACCCAAAGCTGA
Marsupial	Cytochrome- <i>b</i>	M990	CCTGAAGTAGCAACCACTAG
Rodent	Cytochrome- <i>b</i>	M296	TCTTCATTTTTGGTTTACAAGACCA
Rodent	Cytochrome- <i>b</i>	M444	CATGAAAAATCATCGTTGTAA

Analysis of DNA barcode sequence alignments

The resulting barcode sequences were edited and aligned manually in BioEdit version 7.2.5 software (Hall 1999), with ends trimmed or replaced with an ambiguity code to equalise the alignment. The alignments of mammal sequences included those generated from tissues collected in the PMA3 study areas, as well as 'context' sequences drawn from published sources and produced from samples selected from the ABTC to provide appropriate taxonomic and geographic coverage. For frogs, the comparative genetic framework comprised sequenced from the studies of Köhler and Günther (2008) and Rittmeyer et al. (2012). All published sequences are available on Genbank (<http://www.ncbi.nlm.nih.gov/genbank/>).

Distance matrices, Neighbour Joining phylograms and dendrograms were constructed using a custom-written [R] language script. For non-volant mammals, the interpretation and designation of species units was made from the Neighbour Joining phylogram.

To highlight potential species boundaries amongst frog sequences, the position of the DNA barcoded vouchers was first inspected in the phylogenetic tree. Following that, these vouchers were assigned to hypothetical species based on their 'barcode gap' using the Automatic Barcode Gap Discovery (ABGD) tool of Puillandre et al. (2011) (parameters: Pmin 0.001; Pmax 0.1; steps 50; X 1; Nb bins 50; simple distance). The barcode gap can be observed whenever the divergence among samples from the same species is smaller than divergence among samples from different species. A fasta-format file of the entire sequence alignment was used in ABGD.

SELECTED RESULTS FROM THE GENETIC ANALYSIS

The results of the genetic work are presented and interpreted in each of the relevant taxon chapters. Here we present some selected results that highlight firstly how the inclusion of a genetic component in PMA3 was key to meeting its objectives, and secondly how the 'barcoding' approach might produce misleading results if used as the sole basis for species discrimination and/or specimen identification.

The detection of cryptic species

The barcoding results for PMA3 rodents highlighted the likely occurrence in the BAAs of cryptic species in two genera—*Rattus* and *Paramelomys*—with three extra species represented in the genetic results compared with the initial list based solely on morphological criteria. These cryptic species were only detected using the DNA barcodes—there was no prior indication that they were present, beyond a slight difference in one case in maximum body weights. A reliance on traditional morphological approaches would have significantly underestimated the species level diversity in the survey areas and potentially reduced the usefulness of monitoring results for the detection of changes in community composition.

Within *Rattus*, each of the two main sampling areas (BAA1 on Hides Ridge and BAA2 on the Agogo Range near Moro) supports a genetically distinct population of *Rattus* cf. *niobe* (Chapter 5). The genetic clusters show the usual signs of a distinct species—they display reciprocal monophyly (complete and exclusive separation into different branches of the gene tree) and they are widely separated on the tree with other accepted species of *Rattus* placed in intervening positions.

Within *Paramelomys* an identical result was obtained for *Paramelomys* cf. *rubex*—genetically distinct groups occur in each of BAA1 and BAA2, with no especially close relationship between the two groups (Chapter 5). For *Paramelomys* cf. *mollis* the result was slightly different insofar as the two genetic groups within *P.* cf. *mollis* both occur within BAA1, with examples of each coming from transect H3.

The two species of *R.* cf. *niobe* and two of *P.* cf. *rubex* are examples of elevational replacement—morphologically similar forms occurring in different zones along an altitudinal gradient, presumably because of differences in their physiologies that confer selective advantages under contrasting climatic conditions. In both cases it is likely that populations of each pair of 'species' either abut or intermingle somewhere between the elevation of KP107 and transects H1–H3 on Hides Ridge. Tracking the elevation of these 'contact zones' through time could be a valuable tool for monitoring climate change impacts in Papua New Guinea.

One of the more remarkable results of the frog genetic analysis was the demonstration of an entirely novel species of frog probably belonging to an entirely new genus most closely related to *Pseudocallulops*. In this case, field observations of external features identified the species as potentially new and undescribed but it was unclear what the putative new frog might be related to.

Species name confirmation (or not) in local populations

Two of the project components compared the barcode sequences obtained from samples collected in the BAAs with available or newly generated 'context' sequences.

In the case of frogs, the sequences came from public databases (Genbank; Köhler and Günther 2008; Rittmeyer et al. 2012), and they were selected because of their status as 'verified' sequences of the various species. As shown in Chapter 5, some of the BAA samples yielded sequences that were reasonably close to the available reference barcode sequences (e.g. *Liophryne schlaginhaufeni* and *Sphenophryne cornuta*; though in each case the PMA3 animals may be distinct at the species level), while others proved to be much less similar (e.g. *Cophixalus* sp. 2 'tiny A', *Cophixalus* sp. 3 'tiny B', *Oreophryne* sp. 2 'ratchet call' and *Oreophryne* sp. 4 'yellow spots' are all very distinct genetically). These results serve to highlight several taxa that show unexpectedly large or small levels of divergence and thus stand out as obvious targets for further taxonomic investigation.

The frog phylogenetic tree also reflects some of the limitations of using the 12S mitochondrial genetic marker used for DNA barcoding. One issue is the poor resolution of higher level relationships amongst some genera, which may be responsible for potentially erroneous relationships. For example, one species appeared in an unexpected position in the tree (*Austrochaperina* sp. 1 'short call' between *Oreophryne* sp. 2 'ratchet call' and *Oreophryne* sp. 4 'yellow spots'), and there is an unexpectedly low level of genetic divergence between two morphologically and acoustically very different frog forms named as *Choerophryne* sp. 3 'buzz call' and *Choerophryne* sp. 4 'montane clicker'. Some of these unexpected patterns may be the result of sample processing errors (despite diligent efforts to avoid these) but equally they might be a consequence of the difficulty of aligning the 12S sequence across stretches characterised by abundant insertions and deletions, or of another natural genetic process. Regardless of their origin, these patterns can be validated in future years by sequencing additional individuals of the same morphological types, with the same and, ideally, with other different genetic markers.

For small mammals, the few publicly available barcode sequences were supplemented by sequencing of a considerable number of 'context' samples drawn from the tissue holdings of the ABTC. These were selected according to two criteria: the ability to provide links to various described species; and to facilitate the identification of potentially related regional populations (see *The assessment of broad relationships with populations outside the study area*). Two observations of note include:

1. Sequences from populations in BAA1 and BAA2 that demonstrated a high level of similarity to all other available sequences of the same species, for example *Neophascogale* cf. *lorentzii*, *Hyomys* sp. and *Paramelomys* cf. *lorentzii*.
2. Sequences from populations in BAA1 and BAA2 that demonstrated a high level of similarity to some of the available sequences of the putative same species, but not to others, for example *Uromys* cf. *caudimaculatus*, *Paramelomys platyops* and *P. cf. mollis* A, and the various forms of *Rattus* cf. *niobe*, and *Paramelomys* cf. *rubex*. These probably all represent species complexes containing multiple cryptic species across parts of New Guinea and all are in need of comprehensive taxonomic revision.

The assessment of broad relationships with populations outside the study area

The inclusion of 'context' samples in the rodent DNA barcoding component was effective for identifying likely inter-population links for most of the species present in BAA1 and BAA2.

Rattus cf. *niobe* B from Hides Ridge is genetically intermingled with populations from other sites in Hela Province, and it is also closely related to *R. cf. niobe* A from high elevation habitats on the Muller Range. Similarly, *Rattus* cf. *niobe* D from the Agogo Range near Moro is genetically intermingled with a population from high elevation forests on the P'nyang Range in the Upper Fly River catchment.

Of the various genetic clusters detected within *Paramelomys* cf. *rubex*, A was detected at Hides Ridge and additionally in a sample from a similar elevation locality on Mananda Ridge in Hela Province. By contrast, *Paramelomys* cf. *rubex* B that occurs on all transects in BAA 2 is not otherwise represented among the regional samples tested to date. Further regional sampling is needed to determine whether or not this mtDNA lineage occurs anywhere outside of BAA 2. The genetic analysis also identified potentially related populations outside of the study area for each of *Rattus* sp. 'spiny', *Paramelomys platyops*, *P. cf. mollis* A and *P. cf. lorentzii*, but not for *P. cf. mollis* C that is currently known only from transect H1 on Hides Ridge.

The incorporation of a phylogenetic framework for analyses of ecological function

This approach was followed only for the analysis of the bat survey results and full details are available in Chapter 6. In summary, the differences in measures of Species Richness and species composition at different elevations were mirrored by differences in PD. There was a clear pattern of increased PD at lower elevations that was related to greater Species Richness there.

Instances of mitochondrial capture and introgression

Mitochondrial capture and introgression are two of the three main reasons why DNA barcoding approaches might lead to incorrect species identifications and therefore erroneous interpretations of species diversity. The results from the PMA3 rodent barcoding likely contain examples of both problems, and thus serve as a cogent reminder that morphological and acoustic assessments should accompany genetic analyses.

Mitochondrial capture is the most likely explanation for the observed relationships of the species listed as *Rattus* sp. 'spiny'. This taxon is morphologically very distinct on account of its relatively small body size, very spiny fur and long, narrow snout, but its mtDNA sequence suggests that it is closely related to populations of *R. leucopus* from southern PNG.

The pattern of genetic variation among the known populations of *R. sp. 'spiny'* (including the P'nyang Range; see Chapter 5 for details) suggests the possibility of multiple origins of this species from within adjacent lowland populations of *R. leucopus*, either through a process of 'budding' speciation or through interspecific hybridisation with an as yet unidentified second species. Understanding the relationships among the various populations of this small, spiny-furred *Rattus* will require more than simple DNA barcoding—analysis of genetic markers from across the genome is required, as well as wider taxon sampling to identify possible parental species.

Two individuals identified in the field as *R. cf. niobe* from the Agogo Range in BAA 2 produced anomalous mitochondrial DNA sequences. One of these produced a mtDNA haplotype referable to the *Rattus* sp. 'spiny' genetic group and the other produced a haplotype that is closest to some 'context' sequences of regional samples of *R. steini*, a larger-bodied spiny rat that was not captured in BAA 2 but is known to occur at low to mid-elevations in the Kikori catchment.

These examples of a mismatch between the morphological assessment and mitochondrial DNA identity are most likely the product of occasional interbreeding between different species of *Rattus*, leading to mitochondrial DNA introgression. If this interpretation is correct, it would imply that *R. steini* occurs locally but has not yet been encountered in the BAAs.

Interspecific interbreeding is sometimes thought to be a marker of environmental stress and dysfunction. If this were the case, a mismatch between mitochondrial DNA and morphology could represent another way of measuring habitat condition in the study sites. However, at present there is no benchmark from undisturbed PNG forests against which to compare rates of genetic admixture in the PMA3 BAAs.

A VISION FOR THE FUTURE OF GENETIC ANALYSIS IN PMA3

A vision for the future is essential because the time frame of the project coincides with a period of exceptionally rapid growth in molecular technology and anticipated improvements in both analytical and interpretative capacity. The 2015 data has demonstrated the utility of DNA barcoding for increasing the robustness of identifications and comparisons amongst sites and enhanced the understanding of evolutionary and ecological diversity at sampling sites, but it has also exposed some issues that limit identifications and interpretations. We argue below for a realignment of the approach to taxon sampling and genetic marker choice.

For non-volant mammals, the cytochrome-*b* gene provided a relatively clear picture of evolutionary relationships, but it did not have the power to demonstrate species boundaries in some cases because of the possible existence of natural genetic processes that confound such a pattern. In such cases use of multiple genetic markers (Petit and Excoffier 2009) is preferred. In our view a technique called Restriction site Associated DNA sequencing (RADseq; Peterson et al. 2012; Narum et al. 2013), that produces many thousands of markers from across the genome is best placed to answer these questions. RADseq is an extremely powerful technique capable of resolving species boundaries between very closely-related taxa, given sufficient geographic representation. Given that the non-volant mammal component of the survey involves numerous morphologically similar species, there is a strong case to be made for early investment in the development of a new genetic framework based on a system such as RADseq that can overcome the issues identified.

For bats, there was less reliance on DNA barcoding for species identifications because this component relies on the categorisation of acoustic call types and there were fewer captures to provide genetic samples. However, some call types were possibly from more than one species, in groups that are often difficult to identify from external morphology. This includes *Pipistrellus* spp., which might be important as Indicator Species, and *Miniopterus* spp. that are in need of a complete taxonomic revision in Australasia. Interpretations after future surveys will benefit from confirming the identity of some call types, and this will require trapping of bats and the use of RADseq to better identify species and allocate names to them. Adopting the RADseq system currently used by the authors (http://www.hermonslade.org.au/projects/HSF_15_14/hsf_15_14.html), would minimise costs and take advantage of a genetic framework that spans Papua New Guinea and includes a significant proportion of archived museum tissues.

For frogs, an approach based on RADseq would also be ideal, and could be standardised in terms of both tissue collection and laboratory analysis protocols.

In summary, we put forward the following reasons for early replacement of a single-gene DNA barcoding system with RADseq:

1. The process itself does not require development, and can be applied to any species;
2. Current overall costs per sample are equivalent to those for DNA barcoding and are likely to decrease in the near future;
3. In common with a single-gene approach, tissue samples can be taken by non-specialists and placed directly into plates that are then sent to a commercial sequencing service;
4. The RADseq marker systems (there are several options for restriction enzymes and their associated sequencing adapters) can be standardised across a wide range of taxa, so that a single tissue plate can be filled with multiple taxa and sent for bulk sequencing;
5. Much of the context tissue needed for comparative analysis, and the laboratory protocols and analysis capability are currently available through the South Australian Museum;
6. Significant progress in the development of a RADseq-based identification system could be made after the next 2017 round of surveys.

Data analysis would still need to be undertaken or supervised by a specialist with relevant experience of both the taxa and molecular systematics. However, RADseq datasets also have much broader scope for analyses than do single-gene datasets, spanning issues of species discrimination and levels of genetic introgression, as well as levels of gene flow between contemporary and past populations, and aspects of demographic history. Like conventional DNA barcodes, RADseq markers are cumulative and will serve as an ever more powerful resource for identifications and for conservation planning and management across the entirety of the PNG LNG operations.

CONCLUSIONS

1. The DNA barcoding effort made a substantial and valuable contribution to the determination of species diversity and species relationships, especially among the rodents where the method was put to greatest use. Some complications were identified, probably related in each case to rare or ancient hybridisation events among the rodents, but these were detected by the use of morphological observations to verify the genetic results. The use of 'context' sampling of populations from localities outside of the study area was effective at identifying related populations for most of the marsupial and rodent species.
2. For frogs, the use of DNA methods helped to rapidly identify the generic identities of some species, including the presence of an entirely new genus of frog represented by a new species.
3. For bats, the incorporation of DNA data provided a useful perspective through the metric of 'Phylogenetic Diversity' that takes into account evolutionary distinctiveness among species.

REFERENCES

- Allison, A. & Tallouin, O. 2015. Chapter 5. Occurrence and status of Papua New Guinea vertebrates. Pp. 87–101 in Bryan, J. E. & Shearman, P. L. (eds) *The state of the forests of Papua New Guinea 2014: Measuring change over the period 2002–2014*. University of Papua New Guinea, Port Moresby.
- Aplin, K. 2015. Chapter 8. Ongoing discovery of mammal diversity in New Guinea. Pp. 137–142 in Bryan, J. E. & Shearman, P. L. (eds) *The state of the forests of Papua New Guinea 2014: Measuring change over the period 2002–2014*. University of Papua New Guinea, Port Moresby.
- Baker, R. J. & Bradley, R. D. 2006. Speciation in mammals and the genetic species concept. *Journal of Mammalogy* 87: 643–662.
- Bickford, D., Lohman, D. J., Sodhi, N. S., Ng, P. K., Meier, R., Winker, K., & Das, I. 2007. Cryptic species as a window on diversity and conservation. *Trends in Ecology and Evolution* 22: 148–155.
- Collins, R. A. & Cruikshank, R. H. 2012. The seven deadly sins of DNA barcoding. *Molecular Ecology Resources* doi:10.1111/1755-0998.12046
- De Queiroz, K. 2007. Species concepts and species delimitation. *Systematic Biology* 56: 879–886.
- Deiner, K., Lemmon, A. R., Mack, A. L., Fleischer, R. C. & Dumbacher, J. P. 2011. A passerine bird's evolution corroborates the geologic history of the island of New Guinea. *PLoS ONE* 6: e19479. doi:10.1371/journal.pone.0019479
- Elmqvist, T., Folke, C., Nyström, M., Peterson, G., Bengtsson, J., Walker, B. & Norberg, J. 2003. Response diversity, ecosystem change, and resilience. *Frontiers in Ecology and the Environment* 1: 488–494.
- Faith, D. P. 1992. Conservation evaluation and phylogenetic diversity. *Biological Conservation* 61: 1–10.
- Faure, P. A., Re, D. E. & Clare, E. L. 2009. Wound healing in the flight membranes of Big Brown Bats. *Journal of Mammalogy* 90: 1148–1156.
- Gideon, O. 2015. Chapter 7. The flora of New Guinea: its origins, affinities and patterns of diversity and endemism. Pp. 115–136 in Bryan, J. E. & Shearman, P. L. (eds) *The state of the forests of Papua New Guinea 2014: Measuring change over the period 2002–2014*. University of Papua New Guinea, Port Moresby.
- Hall, T.A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.
- Karr, J. R. 1990. Avian survival rates and the extinction process on Barro Colorado Island, Panama. *Conservation Biology* 4: 391–397.

- Köhler, F. & Günther, R. 2008. The radiation of microhylid frogs (Amphibia: Anura) on New Guinea: A mitochondrial phylogeny reveals parallel evolution of morphological and life history traits and disproves the current morphology-based classification. *Molecular Phylogenetics and Evolution* 47: 353–365.
- Leck, C. F. 1979. Avian extinctions in an isolated tropical wet-forest preserve, Ecuador. *The Auk* 96: 343–352.
- Myers, N., Mittermeier, R. A., Mittermeier, C. G., Da Fonseca, G. A. & Kent, J. 2000. Biodiversity hotspots for conservation priorities. *Nature* 403 (6772): 853–858.
- Narum, S. R., Buerkle, C. A., Davey, J. W., Miller, M. R. & Hohenlohe, P. A. 2013. Genotyping-by-sequencing in ecological and conservation genomics. *Molecular Ecology* 22: 2841–2847.
- Novotny, V. & Toko, P. 2015. Chapter 4. Ecological research in Papuan New Guinean rainforests: insects, plants and people. Pp. 71–85 in Bryan, J. E. and Shearman, P. L. (eds) *The state of the forests of Papua New Guinea 2014: Measuring change over the period 2002–2014*. University of Papua New Guinea, Port Moresby.
- Oliver, P. M., Adams, M., Lee, M. S., Hutchinson, M. N., & Doughty, P. 2009. Cryptic diversity in vertebrates: molecular data double estimates of species diversity in a radiation of Australian lizards (*Diplodactylus*, Gekkota). *Proceedings of the Royal Society of London B: Biological Sciences*, rspb-2008.
- Peterson, B. K., Weber, J. N., Kay, E. H., Fisher, H. S. & Hoekstra, H. E. 2012. Double digest RADseq: an inexpensive method for de novo SNP discovery and genotyping in model and non-model species. *PloSOne* 7: e37135.
- Petit, R. J. & Excoffier, L. 2009. Gene flow and species delimitation. *Trends in Ecology and Evolution* 24: 386–393.
- Pfenninger, M. & Schwenk, K. 2007. Cryptic animal species are homogeneously distributed among taxa and biogeographical regions. *BMC Evolutionary Biology* 7: 121.
- Puillandre, N., Lambert, A., Brouillet, S. & Achaz, G. 2011. ABGD, Automatic Barcode Gap Discovery for primary species delimitation. *Molecular Ecology* 21: 1864–1877. URL: <http://www.wabi.snv.jussieu.fr/public/abgd/abgdweb.html>
<http://www.wabi.snv.jussieu.fr/public/abgd/>
- Rittmeyer, E.N., Allison, A., Gründler, M.C., Thompson, D.K. & Austin, C.C. 2012. Ecological guild evolution and the discovery of the world's smallest vertebrate. *PLOS One* <http://dx.doi.org/10.1371/journal.pone.0029797>
- Sikes, R. S., Gannon, W. L. and the Animal Care and Use Committee of the American Society of Mammalogists 2011. Guidelines of the American Society of Mammalogists for the use of wild mammals in research. *Journal of Mammalogy* 92:235–253.
- Taylor, H. R. & Harris, W. E. 2012. An emergent science on the brink of irrelevance: a review of the past 8 years of DNA barcoding. *Molecular Ecology Resources* doi: 10.1111/j.1755-0998.2012.03119.x
- Worthington Wilmer J. & Barratt E. 1996. A non-lethal method of tissue sampling for genetic studies of chiropterans. *Bat Research News* 37: 1–3.

