Threatened Species Recovery Hub

National Environmental Science Programme

Interim report

Project 8.3.3: Genetic assessment of bushfire-impacted vertebrate species

October 2020

Australian National University

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Kangaroo Island dunnart. Image: Jody Gates

1. Introduction

The 2019-20 bushfires had severe impacts on many animal species. Some of these species were considered threatened prior to the fires, and as a consequence of the fires may have lost a substantial proportion of their remaining population and habitat. For other species, not previously considered threatened, substantial reductions in population size and habitat may lead to their reassessment as threatened. As a result of the fires, the Department of Agriculture, Water and the Environment rapidly developed a draft framework to evaluate and prioritise emergency action for all vertebrate species whose distributions were substantially fire-affected (Legge *et al*., 2020). The published draft framework ranks species for priority action utilising a combination of data: the overlap of the species with fire, pre-fire threat status, traits that influence during- and post-fire mortality, and the likelihood of species' recovery. This detailed prioritisation was carried out on threatened or migratory taxa with more than 10% of their known and likely distribution in fire-affected areas, and unlisted taxa where more than 30% of the distribution was fire affected. Both species and subspecies were assessed for birds.

The draft framework provides an important and consistent method for prioritising taxa for management interventions. However, ongoing genetic assessments of vertebrate species identify that the species and subspecies definitions on which the initial fire-affected distributions were calculated may in some cases be misleading. These genetic data reveal a number of issues that may lead to mis-prioritisation of species, or highly impacted species not being assessed. Genetic assessments of fire-affected species have revealed that:

- Some species are incorrectly defined using traditional (mostly morphological) taxonomy.
    - A significant number of "species", particularly in morphologically uniform groups such as frogs and reptiles, are species complexes with one or more currently undescribed species.
    - Subspecies often do not form unique genetic clades and can have less genetic divergence than geographic populations within subspecies.
- Species are not genetically uniform across geography. Well-defined species have multiple independently evolving segments, potentially recognisable as "important populations" under the Environment Protection and Biodiversity Conservation Act 1999 (EPBC Act), that are not typically represented by taxonomy (e.g. defined as subspecies).
- The description of subspecies is not consistent across taxonomic groups, despite equivalent levels of genetic and/or morphological diversity (i.e. subspecies are more commonly formally described in birds than other taxonomic groups).

Correct identification of both taxonomic and genetic diversity has significant implications for the long-term recovery and persistence of fire-impacted species (Coates, Byrne and Moritz, 2018). Unrecognised cryptic diversity can lead to the unintentional loss of unknown species following catastrophic events. The maintenance of high levels of genetic diversity in and between populations helps species recover and avoid inbreeding depression. These issues are especially prevalent in low-dispersal species along the east coast of Australia where there are current and historical barriers to dispersal that contribute to the evolution of diversity between isolated populations. Consideration of this diversity is essential if we are to avoid "cryptic" extinction and so lose large components of the genetic diversity within species.

Over-splitting of taxonomic units, when this could deter managed admixture between threatened and declining populations, can also have detrimental effects for long term persistence. Declining populations are subject to the combined effects of inbreeding depression and genetic drift, which reduce the probability of survival. Management efforts such as genetic rescue endeavour to increase background genetic diversity within populations while maintaining adaptive differences through targeted translocations (Kriesner *et al*., unpublished). Genetic rescue has been shown to increase the genetic diversity and abundance of threatened populations through increased offspring fitness, helping reduce the risk of extinction (Weeks *et al*., 2017).

Understanding genetic diversity across species and populations therefore allows a more complete prioritisation and management of threatened species. It prevents the accidental loss of currently undescribed species or "important populations" within species by recognising highly distinct genetic units (Moritz, 1994) . Acknowledging and understanding patterns of genetic diversity can also allow managers to make calculated decisions about admixture between specified taxonomic units in order to genetically rescue declining populations.

For many species, the ability to assess patterns of genetic diversity is limited by poor sampling of tissues. Most genetic studies rely on tissues stored in our history collections. However, the amount and geographic distribution of samples for many species is relatively low or patchily distributed. These gaps in sampling, or complete lack of sampling, can prevent the inclusion of valuable information about genetic diversity in conservation assessment.

2. Purpose of assessment

Genetic diversity is hugely important in recovery and long-term persistence of bushfire-affected species, and this assessment seeks to provide that information to relevant state and government agencies. This assessment focuses on species where genetic data, often so far unpublished, provides information that is relevant to prioritisation and management. These data include:

- Information on highly genetically divergence lineages that likely represent undescribed species;
- Identification of subspecies with little genetic support, where separate management should be reassessed;
- Detailed data on genetic diversity and genetic structure that is relevant to conservation management.

This initial report focuses on species that have pre-existing genetic data, and this genetic data identifies structure or endemism relevant to the prioritisation and management of fire-affected species. This assessment also provides links to relevant experts for each species, who may be contacted by management agencies for further detailed information. Through these data and links, we hope to promote the incorporation of new genetic and taxonomic knowledge in the conservation and recovery of bushfire-affected vertebrate species.

For many fire-impacted species, assessment of population genetic structure is not possible due to insufficient genetic samples available through state museum collections. Genetic samples (e.g., blood, toe clips, tail clips) are not taken when opportunities arise, and this reduces the ability of researchers to provide information relevant to conservation. For birds in particular, opportunistic sampling during monitoring is essential to genetic assessments as captures are rare. These sampling gaps are a significant barrier to genetic-informed conservation management. Therefore, each species assessment provides information on where additional sampling is necessary to improve our understanding of the population genetics of the species.

For species not in the initial assessment due to sampling limitations, we provide information on areas and species that require additional sampling, as well as geographically organised information on the areas where sampling is needed for further genetic assessment. We provide two types of data: first, identification of areas where few genetic samples exist across species and are therefore areas where we know little about the genetic value – and therefore conservation value - of the region; and second, a list by protected area of the species for which samples are needed. The purpose of this information is to enable targeted sampling of conservation-concern species by field teams assessing impacts of fires on wildlife in areas where the value of new genetic information is the greatest.

Following this report, additional sequencing of priority species requiring additional genetic data – those with sufficient existing samples or new samples from field surveys, and also considered to likely have significant genetic structure – is being undertaken over the next 6-10 months. This will include a targeted project on fire-affected species on Kangaroo Island (SA), comparing island vs nearby mainland populations, and further work on eastern forest species thought to have strong population structure. Additionally, we will target a small number of species for high resolution analysis of within-population diversity to inform genetic risk analyses. These species' assessments will be included in the final report. The final report will also focus on identifying areas with high levels of genetic diversity across all taxa. These hotspots of unique diversity should be considered for priority targeting of habitat restoration and future fire management.

3. Assessment process

In April 2020, the Centre for Biodiversity Analysis organised an online fire genetics workshop in response to the bushfire emergency. Experts on the taxonomy and genetic diversity of mammals, birds, fish, frogs, and reptiles were identified across Australia and invited to attend (Appendix 1). Attendees were provided the premise that the extensive fires have likely impacted cryptic species and evolutionarily significant units within species, which were invisible to the federal assessment team. By mapping these, we could provide useful guidance to short-term assessment and medium-long term restoration efforts.

Prior to the workshop, experts were requested to:

1. Review the priority assessment list (Legge *et al*., 2020) and identify species for which there was relevant existing published or unpublished landscape genetic data,
2. Identify species that were not highly ranked and/or assessed, but existing genetic data identified potentially fire-impacted undescribed species, or species with high levels of genetic structure where unique genetic units were potentially fire-impacted,
3. Identify fire-impacted short-range endemic species with potential for genetic risk analysis, and
4. Identify fire-impacted species with no existing genetic data that were highly likely, due to their biology, to have significant genetic structure.

This assessment considered 202 species identified by state and federal agencies and experts for review at the workshop (Appendix 2). During the workshop, experts were divided by taxonomic group and asked to review the list of species relative to a specific workflow (Appendix 3). In short, this workflow requested experts assess if existing population genetic data was sufficient to understand the population structure, and if so, whether there were significant units of genetic data that were potentially fire-affected. If no or insufficient genetic data exists, the expert panel was asked to assess whether high levels of population genetic structure were likely based on the biology of the species. They were then asked to prioritise all genetic-data-deficient species for additional sequencing. Prioritisation for additional sequencing was based on a combination of species' conservation status, likely fire impact, likelihood of population genetic structure, and availability of existing tissue samples for sequencing.

Of the 202 species on the list for review, 23.2% had no existing population genetic data to inform genetic structure (Table 1). Fifty-two percent of species had either just mitochondrial data, or a combination of nuclear and mitochondrial data. Single nucleotide polymorphism (SNP) data was available for 24% of species. SNP data has the most utility for conservation genetic assessments as it provides more robust fine-scale information on population structure, admixture between populations, and levels of genetic diversity and inbreeding within populations. Birds represented the most poorly sampled taxonomic group, with no population genetic data for 58% of reviewed species.

Table 1. Summary of population genetic data available by taxonomic group (number of species), including those with no data, only mitochondrial data (mtDNA), mitochondrial plus nuclear data (nDNA) and single nucleotide polymorphism data (SNP). SNPs are considered the highest-grade population genetic data.

	No data	mtDNA	mtDNA+nDNA	SNP
Frogs (44)	4	14	9	17
Reptiles (55)	8	19	13	15
Mammals (40)	6	9	14	11
Birds (43)	25	7	7	4
Fish (20)	4	0	14	2

Short-range endemic species (SRE) located within fire zones were also reviewed by the relevant expert group. For these species, experts were asked to assess whether existing genetic data was able to be used for the assessment of the genetic risk to the persistence of the species. If not, the experts were asked to rank SREs for additional sequencing on the basis of current conservation status, possible fire-impact, and existing tissue samples. The purpose of reviewing these species, which are less likely to have significant genetic divergence among populations, is to provide information on genetic diversity within populations and the level of inbreeding depression. These data are particularly relevant to genetic rescue of small populations that have been isolated or decimated by fires.

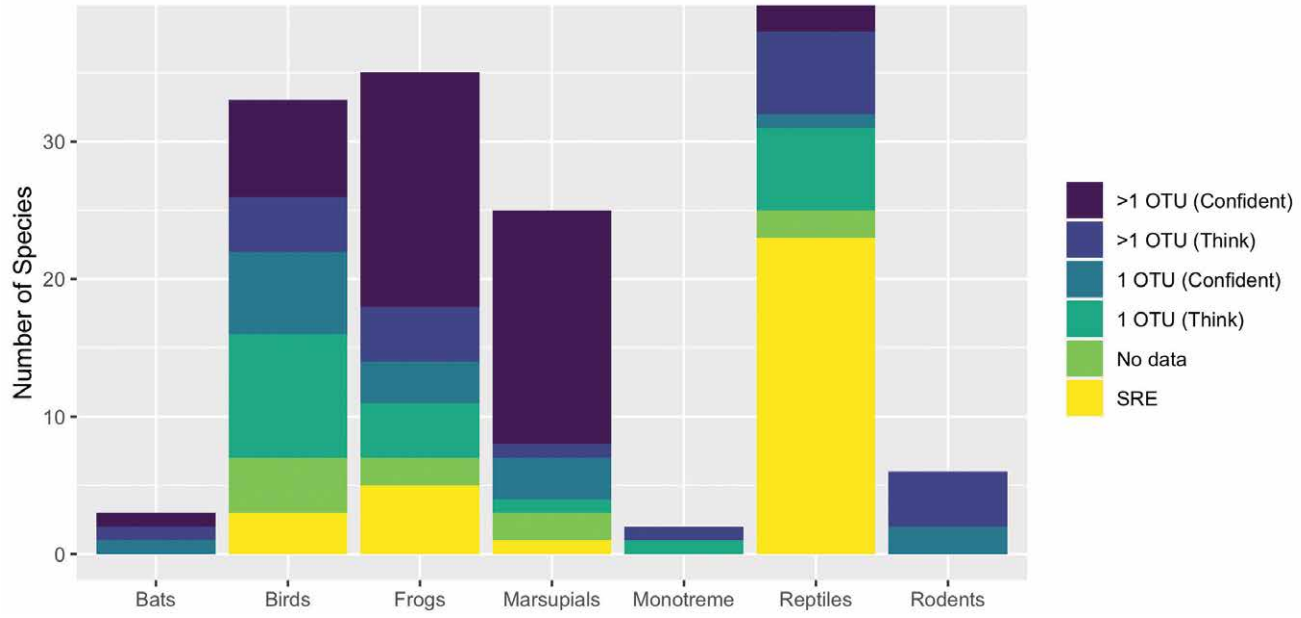


Figure 1. Assessed species in fire-affected areas by taxonomic group, and expert opinion on genetic structure within them. Operational taxonomic units (OTU), including management units, evolutionarily significant units, subspecies, and undescribed species, indicate whether experts know (Confident) or believe (Think) there to be substantial genetic structure within the species.

This interim report provides, in a confidential appendix, detailed assessments of genetic structure and mapping of conservation units (Box 1) for 59 species (listed in Appendix 5 on page 23), and information on high-value genetic populations where this is available. These are species for which existing genetic data provide relevant information for conservation management and monitoring priorities in bushfire-affected areas. Across these 59 assessments, as well as many of the other high priority species, samples are not available in all areas of the species' distribution. This report categorises these areas where genetic data is missing, first by summarising the areas with the poorest sampling across taxa, and also providing lists, by protected area, of species that require sampling.

Box 1. Definition and relevance of conservation units used in this report:

"Management units (MUs)" – Metapopulations with significant divergence at nuclear or mitochondrial loci.

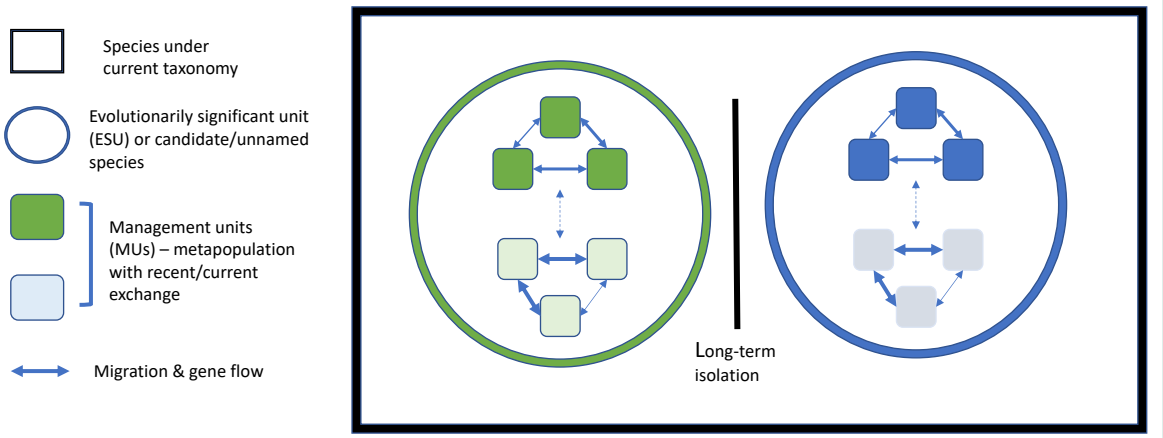
"Evolutionarily Significant Units (ESUs)" – Historically isolated set of populations that are reciprocally monophyletic and show significant divergence.

"Subspecies" – Distinct populations within a species that are usually diagnosable using morphological or genetic characters.

"Candidate species" – A taxon considered by the expert to potentially meet the criteria for full species status, but further information is required for further taxonomic revision.

"Phrase named/undescribed species" – A taxon that is considered by the expert to meet the criteria for full species status but has never received a formal species description.

"Short range endemic (SRE)" – A taxon with a range size of <10,000 km^2, approximately 100 x 100 km.



Relevance to EPBC Act: "Important populations"

An 'important population' is a population that is necessary for a species' long-term survival and recovery. This may include populations identified as such in recovery plans, and/or that are:

- key source populations either for breeding or dispersal [**i.e., source populations for viability of management units**]
- populations that are necessary for maintaining genetic diversity, [**ESUs**] and/or
- populations that are near the limit of the species range [**ESUs if important to overall adaptive diversity**]

4. Information contained in assessment for each group and species

Each assessment (see Box 2) is structured to provide expert delineation of conservation units (Box 1), based on genetic data, within each individual species. Conservation units with high levels of known or potential fire impact are explicitly identified. Where available, information on high genetic-value populations, for example those with high diversity, is given. Uncertainties in the distribution of conservation units or the taxonomic status within or between species, and areas where more sampling is needed are also noted. Summary recommendations on conservation units and fire impact are provided for each assessment.

Box 2: Example species assessment

Alpine Water-skink *Eulamprus kosciuskoi* and Blue Mountains Swamp-skink *Eulamprus leuraensis*

Expert: Prof. Scott Keogh

Taxonomic and genetic diversity assessment

The Alpine Water-skink (*E. kosciuskoi*) is found throughout south-eastern Australia in several geographically isolated regions of the Great Dividing Range, from VIC to northern NSW. Despite multiple disjunct populations, it is currently regarded as a single species. The Blue Mountains Swamp-skink (*E. leuraensis*) is a closely related species restricted to high altitude swamps in the Blue Mountains. *Eulamprus leuraensis* is listed as Endangered in NSW under the Biodiversity Conservation Act and under the federal EPBC Act. *Eulamprus kosciuskoi* is listed as Critically Endangered in VIC under the Flora and Fauna Guarantee Act.

Recent genetic analyses do not support the current taxonomy of *E. kosciuskoi.* Pepper et al. (2018) sequenced mitochondrial DNA and hundreds of nuclear genes to analyse the phylogeographic structure of the *Eulamprus* genus. They found that *E. kosciuskoi* is paraphyletic. One lineage, *E. kosciuskoi* South, is more closely related to *E. leuraensis*. *Eulamprus kosciuskoi* South and *E. kosciuskoi* North are separated by the Hunter Valley (Pepper *et al*., 2018). Therefore, the *E. kosciuskoi/leuraensis* species complex includes three separate candidate species.

The Blue Mountains Swamp-skink displays strong genetic structuring across its range, with separate lineages on the Newnes Plateau and in the Blue Mountains. Individual populations of this species have low genetic diversity but are genetically distinct from nearby populations and should be considered MUs (Dubey & Shine, 2010; Dubey *et al.*, 2010).

Fire impact on conservation units

The *E. kosciuskoi* South candidate species is distributed in fire-affected areas in Kosciuszko National Park and Namadgi National Park, along with a smaller burnt area in the southern end of its range in Alpine National Park, Victoria. *Eulamprus kosciuskoi* North has had large sections of the eastern half of its range burnt by fires in the Barrington Tops, Werrikimbe, Washpool, Guy Fawkes River and Nymboida National Parks, and throughout the New England Tableland region. The Blue Mountains Swamp-skink *E. leuraensis* has had the majority of its small range burnt by fires in the Blue Mountains and Kanangra-Boyd National Parks. Several genetically distinct populations may have been badly impacted or destroyed.

Uncertainties, and priorities for sample collection and field assessment

The northern candidate species of the Alpine Water-skink, *E. kosciuskoi* North, likely represents an undescribed species with high conservation value. Field sampling of populations in this clade is recommended to assess fire impact; in particular, the Barrington Tops National Park is a priority area for population-monitoring due to the extensive fire impacts on this area. Likewise, post-fire sampling of the southern candidate species, *E. kosciuskoi* South, would be valuable, as this clade has had its range severely burnt. Estimates of genetic diversity in the Alpine Water-skink are limited, and additional sample collection for populations on some mountains may be valuable.

The Blue Mountains Swamp-skink is primarily distributed within fire-affected areas, and field sampling is recommended to assess the full impact of the fires on this species. Genetic and population assessments of the Newnes National Park populations using SNP data are a priority; samples for this are available and further collection is not necessary at this time.

Box 2, continued

Phylogeny and distribution maps

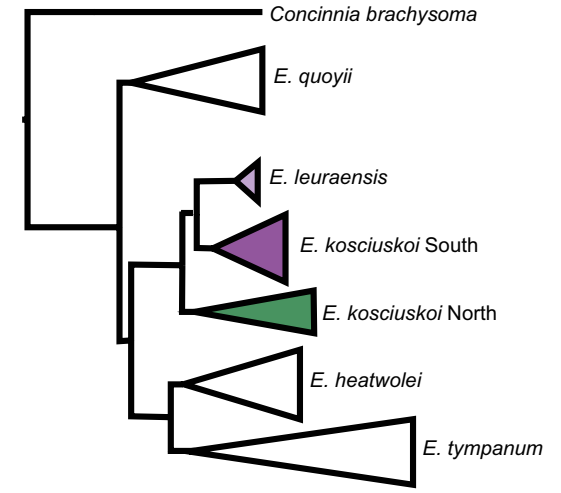
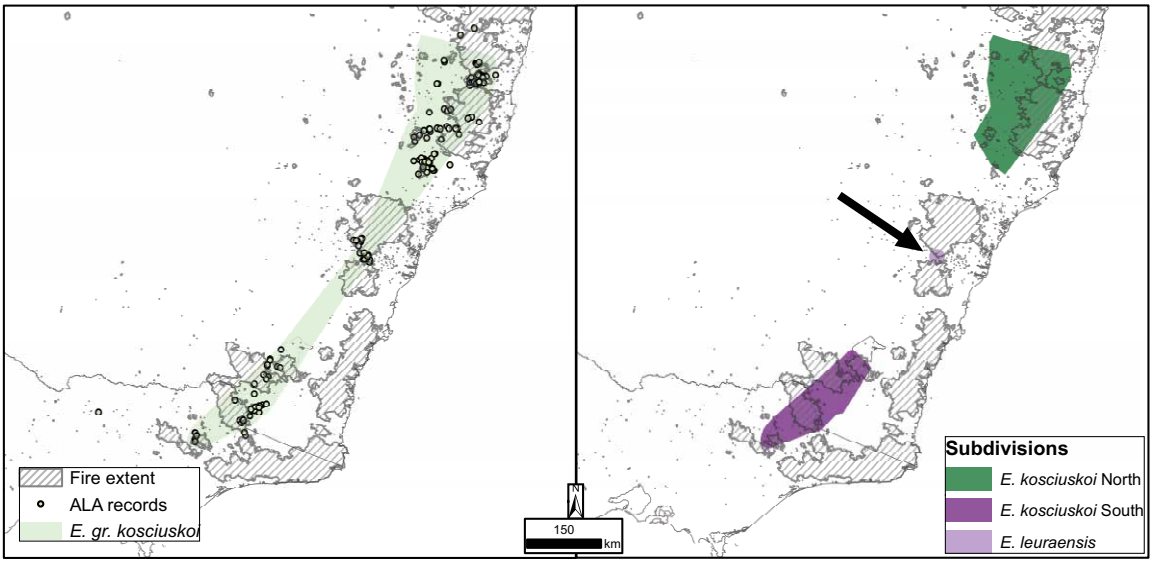


Figure 1. Phylogeny of the Eulamprus genus, showing candidate species within the E. kosciuskoi/E. leuraensis species complex (top left). Distribution of the three ESUs (bottom right). Currently described distribution (bottom left).



Summary recommendations

- Genetic analyses do not support the current taxonomy of the Alpine Water-skink. This species contains two distinct clades, of which the northern clade likely represents an undescribed species. Therefore, all three clades in this species complex should be managed and monitored independently as separate candidate species.
- Genetic and population assessments of the Blue Mountains Swamp-skink across its range would be valuable.

References

Dubey, S., & Shine, R. (2010). Restricted dispersal and genetic diversity in populations of an endangered montane lizard (Eulamprus leuraensis, Scincidae). *Molecular Ecology*, 19(5), 886-897. doi:10.1111/j.1365-294X.2010.04539.x

Dubey, S., Shine, R., & Birks, J. (2010). Plio-Pleistocene diversification and genetic population structure of an endangered lizard (the Blue Mountains water skink, Eulamprus leuraensis) in south-eastern Australia. *Journal of Biogeography*, 37(5), 902-914. doi:10.1111/j.1365-2699.2009.02266.x

Pepper, M., Sumner, J., Brennan, I. G., Hodges, K., Lemmon, A. R., Lemmon, E. M., . . . Keogh, J. S. (2018). Speciation in the mountains and dispersal by rivers: Molecular phylogeny of Eulamprus water skinks and the biogeography of Eastern Australia. *Journal of Biogeography*, 45(9), 2040-2052. doi:10.1111/jbi.13385

5. Summary by taxonomic group

Expert data on the genetic diversity of fire-affected vertebrate species reveals high levels of taxonomic instability (Table 2). This includes relatively high numbers of undescribed and candidate species, particularly in frogs, with fewer in mammals and reptiles. No undescribed species were identified in birds. Some subspecies designations were not supported by available genetic data, particularly in birds (designated by negative numbers in Table 2).

Substantial genetic structure was identified within species from all taxonomic groups (Figure 1, Table 2). Mammals and reptile species had particularly high prevalence of ESUs that should be taken into account when planning conservation of individual species. These data reflect the deep genetic structure that likely is a consequence of low dispersal in these taxa. This is also reflected in the high number of management units identified, which suggest that metapopulation genetic structure also exists within ESUs.

For birds with sufficient data, the evidence typically identified real but relatively shallow divergences in geographically separated populations (i.e. MUs). These data suggest many now fragmented bird populations were, until relatively recently, connected through occasional dispersal.

Table 2. Sum of conservation units identified by experts in the 59 species assessed, by taxonomic group (number of species assessed under current taxonomy). See definitions in Box 1.

	Undescribed species	Candidate Species	Subspecies	ESU	MU
Frogs (18)	8	10	-2	7	>10
Reptiles (14)	1	3	-2	19	>18
Mammals (22)	2	5	1	40	>22
Birds (5)	0	0	-7	0	6

Individual species were prioritised by the relevant expert panel for additional genetic sequencing to determine population structure (Table 3). Species ranked the highest priority were those that are likely to have significant genetic structure or are short-range endemic species. The expert group identified 15 taxa, including endemic subspecies, from Kangaroo Island that warrant further genomic analysis to determine levels of genetic diversity and difference from the adjacent SA mainland (Table 3). This discrete project will inform genetic risk analysis and options for demographic and genetic rescue of island populations should surveys to assess fire impacts point to this need.

Table 3. Species ranked by experts as a high priority for additional sequencing, or medium/high for Kangaroo Island. Species with some existing data and therefore included in initial assessments are marked with an asterisk. Kangaroo Island priorities are marked by a +.

	Genus	Species
Frogs	*Crinia*	*signifera**
	Litoria	*olongburensis**
	Mixophyes	*iteratus*
	Pseudophryne	*pengilleyi*
	Adelotus	*brevis*
	Crinia	*tinnula**
	Limnodynastes	*dumerilii*+*
	Litoria	*ewingii*+*
	Philoria	*kundagungan**
	Philoria	*loveridgei**
	Philoria	*pughi**
	Philoria	*richmondensis**
	Philoria	*sphagnicola**
	Litoria	*piperata*
	Pseudophryne	*bibroni*+*
	Pseudophryne	*corroboree*
	Pseudophryne	*dendyi*

	Genus	Species
Reptiles	*Anepischetosia*	*maccoyi*
	Eulamprus	*heatwolei**
	Eulamprus	*kosciuskoi**
	Eulamprus	*leuraensis**
	Eulamprus	*tympanum**
	Pseudemoia	*cryodroma**
	Pseudemoia	*pagenstecheri A*
	Saiphos	*equalis*
	Saltuarius	*kateae*
	Saltuarius	*moritzii**
	Saltuarius	*wyberba*
	Cyclodomorphus	*michaeli*
	Coeranoscincus	*reticulatus*
	Harrisoniascincus	*zia**
	Intellagama	*leseurii*
	Liopholis	*whitii*
	Phyllurus	*caudiannulatus*
	Phyllurus	*platurus*
	Pseudemoia	*rawlinsoni*
	Varanus	*rosenbergi*+*
Mammals	*Antechinus*	*argentus**
	Antechinus	*arktos**
	Cercartetus	*nanus*+*
	Cercartetus	*lepidus*+*
	Dasyurus	*maculatus*
	Petaurus	*breviceps**
	Petrogale	*penicillata**
	Pseudomys	*fumeus**
	Antechinus	*mimetes**
	Mastacomys	*fuscus*
	Potorous	*longipes*
	Potorous	*tridactylus**
	Rattus	*lutreolus*+*
	Sminthopsis	*fulignosus aitkeni*+*
	Vespadelus	*darlingtoni*+*
	Vespadelus	*regulus*+*
Birds	*Anthochaera*	*chrysoptera* +
	Calyptorhynchus	*lathami** +
	Hylacola	*cauta halmaturina*+*
	Psophodes	*nigrogularis lashmari**+
	Pezoporus	*wallicus**
	Stipiturus	*malachurus**+
	Zoothera	*lunulata halmaturina*+*

Many priority species have sufficient existing genetic samples in museum collections for sequencing, but the majority of species require either targeted sampling from particular areas, or have very few existing samples across the range of the species. For each species, sampling gaps for tissue/blood samples were determined and are provided in Appendix 4. Areas with high-levels of sampling gaps are shown in Fig. 2 and these areas should be prioritised for additional collection of genetic samples across taxonomic groups. This map highlights that there are fire-affected areas where genetic data to assess conservation units is lacking across a high number of vertebrate taxa. Indeed, most of the poorly documented areas are substantially fire affected, including Kangaroo Island, the Blue Mountains, Washpool National Park, Main Range and the Border Ranges.

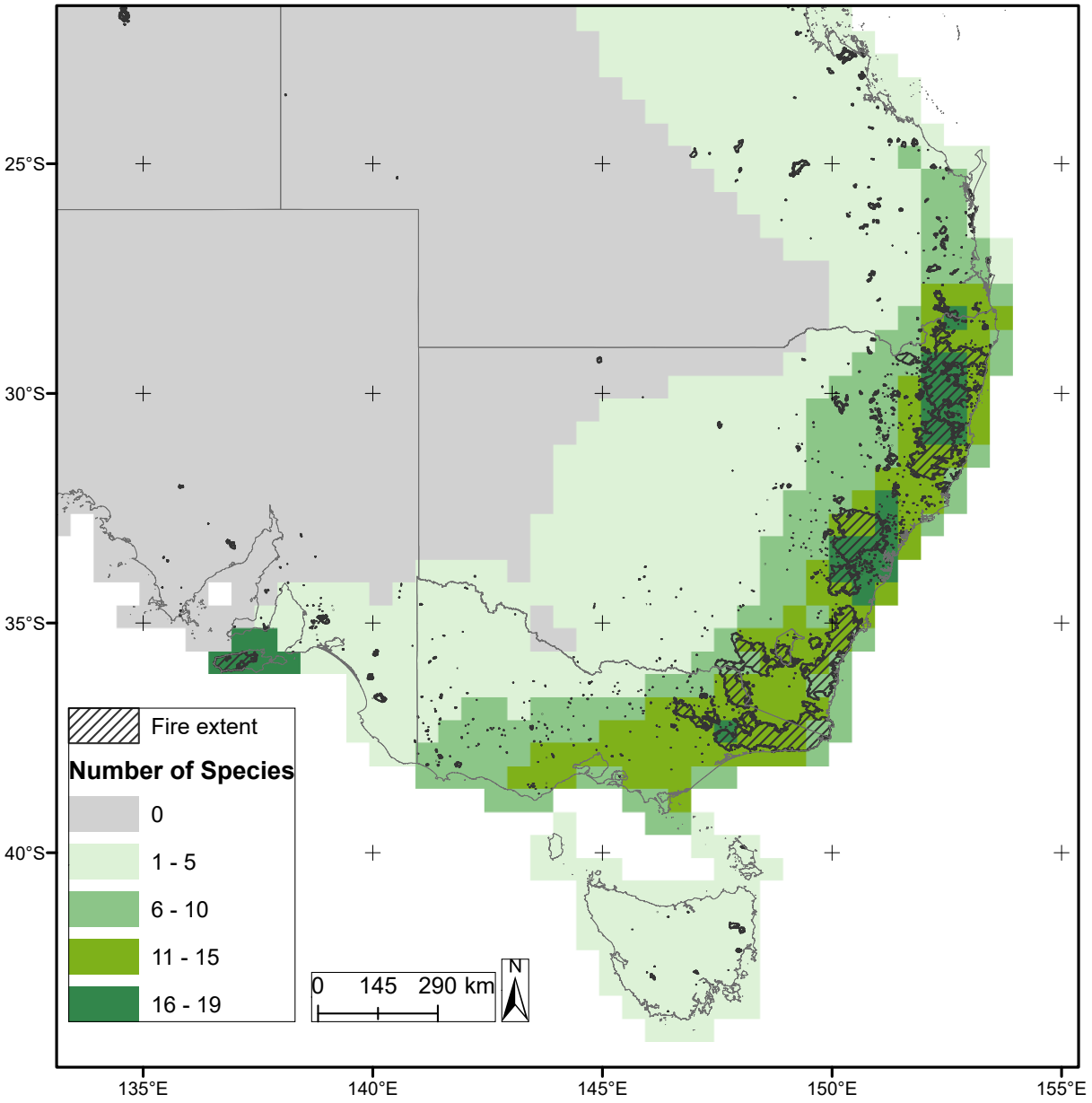


Figure 2. Map of sampling gaps, indicating the number of species needing genetic data collection in a grid cell. The value is the number of species needing tissue sampling out of a total of 67 species that have an assessment or are a high priority for assessment. A list of species needing collection by protected area is provided in Appendix 4, a searchable Excel file.

During the CBA expert panel assessment of species, many widespread (i.e non-SRE) species were identified as known (from genetic evidence) or very likely (based on species' biology) to be just one species and lacking multiple ESUs at least across the fire-affected areas (Table 4). These species should be assessed for fire impacts as a single entity. We note that for some, there is solid genetic evidence for multiple MUs reflecting limited dispersal among populations or recent isolation. For some taxa (e.g. *Isoodon obesulus*; Cooper *et al.*, 2020) there is evidence for substantial genetic structuring (i.e. multiple ESUs) in parts of the species range not affected by fire.

Table 4. Species considered by expert panel to have low genetic divergence across their range as a whole or the fire zones in particular. The expert panel's confidence of this assessment is noted, whether "Confident" or "Think".).

	Genus	Species	Expert Assessment
Frogs	*Litoria*	*aurea*	Think
	Litoria	*barringtonensis*	Think
	Litoria	*nudidigita*	Think
	Litoria	*subglandulosa*	Think
	Taudactylus	*pleione*	Confident
	Uperoleia	*martini*	Confident
Reptiles	*Acritoscincus*	*platynotus*	Think
	Ctenotus	*taeniolatus*	Think
	Egernia	*saxatilis*	Think
	Lissolepis	*coventryi*	Think
	Morelia	*spilota spilota*	Confident
Bat	*Pteropus*	*poliocephalus*	Confident
Marsupials	*Isoodon*	*obesulus obesulus*	Confident
	Petaurus	*norfolcensis*	Think
	Phascolarctos	*cinereus*	Confident
Monotreme	*Tachyglossus*	*aculeatus multiaculeatus*	Think
Rodent	*Pseudomys*	*oralis*	Confident
Birds	*Anthochaera*	*phrygia*	Confident
	Calyptorhynchus	*banksii banksii*	Confident
	Climacteris	*erythrops*	Think
	Falco	*hypoleucos*	Confident
	Glyciphila	*melanops*	Confident
	Lathamus	*discolor*	Think
	Malurus	*lamberti*	Think
	Menura	*alberti*	Confident
	Origma	*solitaria*	Confident
	Pandion	*haliaetus cristatus*	Think
	Parvipsitta	*pusilla*	Think
	Petroica	*phoenicea*	Think
	Tyto	*longimembris*	Think
	Tyto	*novaehollandiae*	Think
	Tyto	*tenebricosa*	Think

6. Summary recommendations

Assessments of fire impacts should rely on the corrected taxonomy as provided in this report, and consider likely fire-impacts on candidate species and/or ESUs within currently recognised taxa, these representing "important populations" as defined in the EPBC Act. Redefining the spatial overlap with fire for a number of re-defined taxa covered in this report will be required, which may result in their inclusion in the list of highly-ranked priority species. Where conservation units have extensive overlap with fire zones and are judged ecologically sensitive to fire, consideration should be given to formal status assessments under the Important Populations provision of the EPBC Act. This action may be particularly relevant to protecting conservation units with high genetic diversity, which are essential to the recovery and persistence of species.

Ongoing consideration of conservation status should be provided for high-priority taxa that experts consider likely to have significant genetic structure (Table 3), but do not have individual assessments in this report. Like the species included in this report, these species are likely to have additional conservation units, including candidate species and ESUs. These conservation units will require further priority assessment as genetic data becomes available.

High priority should be given to increasing available data on genetic diversity and distinctiveness for taxa (species, candidate species, ESUs) restricted to Kangaroo Island. Sampling from Kangaroo Island across priority species is relatively low (Fig. 2, Appendix 4), which currently prevents genetic assessment of conservation units. Further information on genetic diversity would also allow prioritisation of recovery actions, including determining which species require genetic rescue, and identifying the most appropriate mainland populations for augmenting Kangaroo Island populations. This is a particular priority for Kangaroo Island species of birds and some bats.

Bat species represent a significant gap in genetic assessments due to low numbers of samples available for genetic sequencing across the range of virtually all species that are potentially fire impacted. Where possible, genetic samples should be taken in order to enable similar assessments. This requires a conscious effort of field survey teams across the range of the fires in order to ensure genetic assessments are available in the future to help guide bat conservation. Bat species have not been included specifically in the list of samples needed by protected area (Appendix 4), as samples are generally needed for all bat species everywhere.

Field survey teams across the fire region should ensure monitoring occurs for small-range taxa (including both species and ESUs) that significantly overlap with fire zones. Targeted survey based on maps included in the individual species assessments will enable these regions to be prioritised. These assessments, while not publicly available due to the sensitivity of the data, can be accessed by relevant agencies by contacting the authors and providing information on the taxonomic groups and regions of interest.

Sampling of materials for genetic analysis in priority species and regions should target areas with substantial sampling gaps, especially where this involves multiple species (Fig. 2) and/or could strongly impact prioritisations. Samples may include, but are not limited to, toe, tail or ear clips, and blood samples. Samples of bird and bat species should be taken wherever possible due to the low existing sampling for most species. Engagement with taxon experts can help address the best method to take and preserve samples. Samples taken as part of monitoring should be given to the relevant state-based museum, as this will enable them to be preserved, databased, and therefore incorporated into broad-scale genetic analyses.

7. Future reporting

In the next stage of this project, high priority species with sufficient genetic samples will be sequenced in order to provide additional individual-species assessments in the final report. Target species will be from the high priority list (Table 3), and the individual species chosen will be based on a combination of stakeholder priority and availability of tissues samples. For target species identified with state and federal stakeholders, we will undertake to provide genetic risk assessments (Kriesner *et al*., unpublished). Genetic risk assessment allows genetic interventions, such as translocations or captive breeding, to be undertaken for the persistence of species. Using the genetic data included here and generated prior to the final report, we will identify hotspots of endemism to inform selection of areas for investment, including rehabilitation and protection from future fires.

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Antechinus argentus. Image: Gary Cranitch Qld Museum

Appendix 1: Expert panel

Name	Organisation/	Contribution
Leo Joseph	CSIRO	Expert panel - Birds
Andrew Baker	QUT	Expert panel - Mammals
Anna MacDonald	ANU/BPA	Expert panel - Mammals
Emily Roycroft	ANU	Expert panel - Mammals
Kevin Rowe	Museum Victoria	Expert panel - Mammals
Linda Neaves	ANU	Expert panel - Mammals
Mark Eldridge	Australian Museum	Expert panel - Mammals
Conrad Hoskin	James Cook University	Expert panel - Reptiles
Jane Melville	Museum Victoria	Expert panel - Reptiles
Joanna Sumner	Museum Victoria	Expert panel - Reptiles
Maggie Haines	Museum Victoria	Expert panel - Reptiles
Mitzy Pepper	ANU	Expert panel - Reptiles
Paul Oliver	Queensland Museum	Expert panel - Reptiles
Scott Keogh	ANU	Expert panel - Reptiles, Frogs
Jodi Rowley	Australian Museum	Expert panel - Frogs
Michael Mahony	Univ Newcastle	Expert panel - Frogs
Renee Catullo	ANU, CSIRO	Expert panel - Frogs
Steve Donnellan	Sth Australian Museum	Expert panel - Frogs
Peter Unmack	Univ Canberra	Expert panel - Fish
Jennifer Pierson	ACT Parks & Wildlife	Expert panel - Conservation Priorities
Sarah Legge	ANU/NESP	Expert panel - Conservation Priorities
Bernd Gruber	Univ Canberra	Expert panel - Spatial expertise
Jason Bragg	Royal Botanic Gardens	Expert panel - Spatial expertise
Sam Banks	CDU	Expert panel - Spatial expertise
Simon Ferrier	CSIRO	Expert panel - Spatial expertise
Katherine Farquharson	University of Sydney	BPA Threatened Species Advisor
Sophie Mazard	BPA	BPA Genomics Advisor

Appendix 2: Species reviewed by expert panel. Prioritiser is the state or federal lister, or whether the species was suggested for review by the expert panel.

Group	Prioritiser	Genus	Species	Common name
Frog	VDEWLP	*Litoria*	*aurea*	Green & golden bell frog
	VDEWLP, NSW	*Litoria*	*booroolongensis*	Booroolong frog
	NSW	*Litoria*	*brevipalmata*	Green-thighed frog
	Expert	*Litoria*	*caerulea*	Green tree frog
	Expert	*Litoria*	*chloris*	Red-eyed tree frog
	VDEWLP	*Litoria*	*citropa*	Blue Mountains tree frog
	QLD	*Litoria*	*cooloolensis*	Cooloola sedge frog
	DEWA, NSW	*Litoria*	*daviesae*	Davies' tree frog
	Expert	*Litoria*	*dentata*	Bleating tree frog
	Expert	*Litoria*	*ewingi*	Southern brown tree frog
	QLD	*Litoria*	*freycineti*	Wallum rocketfrog
	Expert	*Litoria*	*gracilenta*	Dainty green tree frog
	DEWA, VDEWLP	*Litoria*	*littlejohni*	Littlejohn's tree frog
	VDEWLP	*Litoria*	*nudidigita*	Leaf green tree frog
	QLD, NSW	*Litoria*	*olongburensis*	Olongburra frog
	QLD	*Litoria*	*pearsoniana*	Cascade tree frog
	Expert	*Litoria*	*peronii*	Peron's tree frog
	DEWA, NSW	*Litoria*	*piperata*	Peppered tree frog
	DEWA, NSW, VDEWLP	*Litoria*	*spenceri*	Spotted tree frog
	DEWA, NSW	*Litoria*	*subglandulosa*	New England treefrog
	VDEWLP	*Litoria*	*verreauxii*	Verreaux's tree frog
	Expert	*Litoria*	*barringtonensis*	Barrington Tops tree frog
	QLD, NSW	*Adelotus*	*brevis*	Tusked frog
	NSW	*Assa*	*darlingtoni*	Pouched frog
	Expert	*Crinia*	*signifera*	Eastern common froglet
	QLD, NSW	*Crinia*	*tinnula*	Wallum froglet
	DEWA, NSW, VDEWLP	*Heleioporus*	*australiacus*	Giant burrowing frog
	Expert	*Limnodynastes*	*dumerilii*	Banjo frog
	DEWA, NSW, VDEWLP	*Mixophyes*	*balbus*	Southern barred frog
	DEWA, QLD, NSW	*Mixophyes*	*fleayi*	Fleay's frog
	DEWA, NSW	*Mixophyes*	*iteratus*	Giant barred frog
	DEWA, QLD	*Philoria*	*kundagungan*	Mountain frog
	Expert	*Philoria*	*loveridgei*	Loveridge's frog
	DEWA, NSW	*Philoria*	*pughi*	Pugh's frog
	DEWA	*Philoria*	*richmondensis*	Richmond Range sphagnum frog
	DEWA, NSW	*Philoria*	*sphagnicola*	Sphagnum frog
	NSW	*Pseudophryne*	*australis*	Red-crowned toadlet
	Expert	*Pseudophryne*	*bibronii*	Bibron's toadlet
	DEWA, NSW	*Pseudophryne*	*corroboree*	Southern corroboree frog
	VDEWLP	*Pseudophryne*	*dendyi*	Dendy's toadlet
	DEWA	*Pseudophryne*	*pengilleyi*	Northern corroboree frog
	DEWA	*Taudactylus*	*pleione*	Kroombit tinker frog
	VDEWLP	*Uperoleia*	*martini*	Martin's toadlet

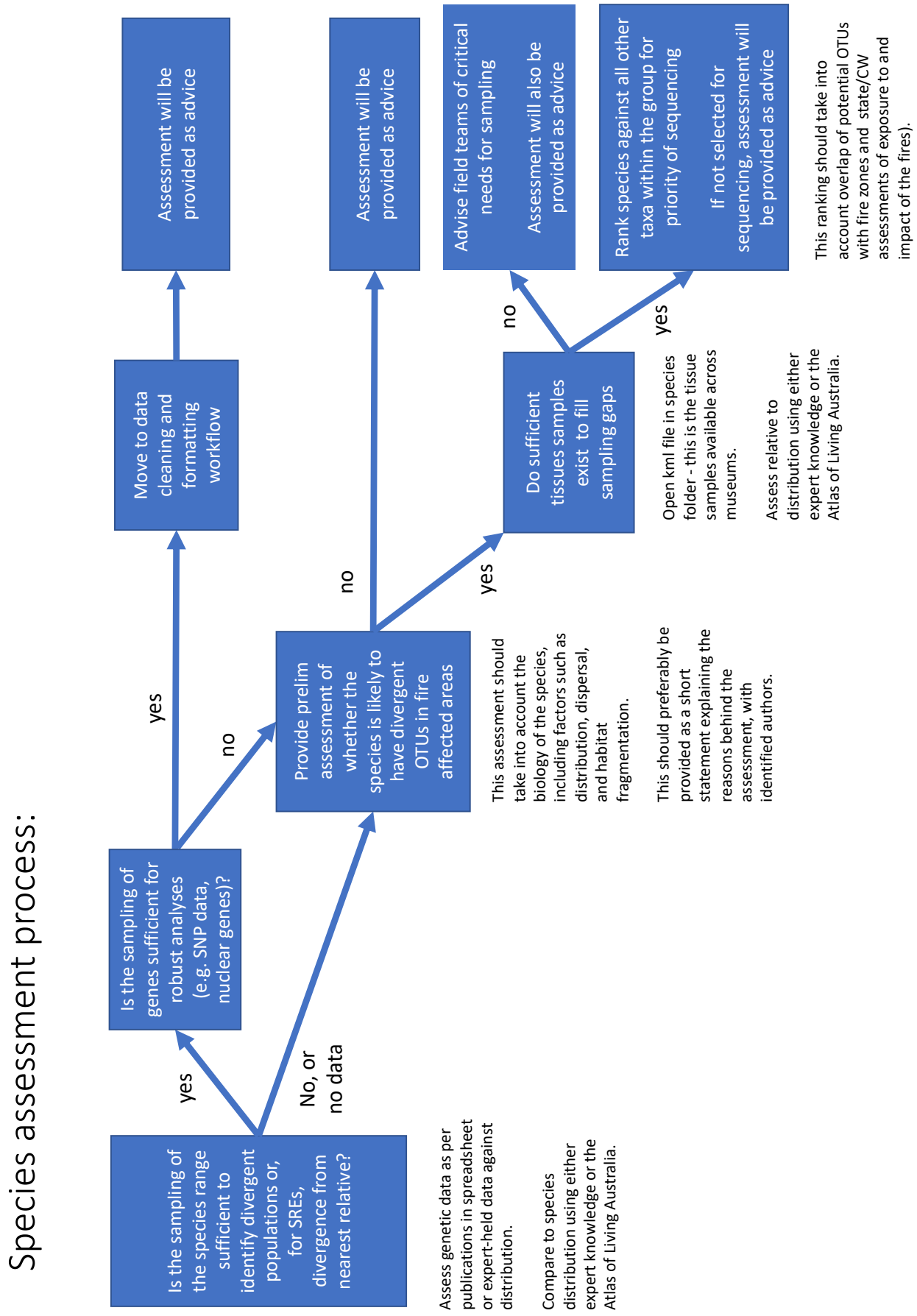
Group	Prioritiser	Genus	Species	Common name
Reptiles	Expert	*Acritoscincus*	*duperreyi*	Bold-striped cool skink
	VDEWLP	*Acritosincus*	*platynotus*	Red-throated skink
	Expert	*Anepischetosia*	*maccoyi*	Maccoy's skink
	Expert	*Calyptotis*	*lepidorostrum*	Cone-eared calyptotis
	DEWA Prov	*Calyptotis*	*ruficauda*	Red-tailed calyptotis
	Expert	*Calyptotis*	*scutirostrum*	Scute-snouted calyptotis
	Expert	*Calyptotis*	*temporalis*	Broad-templed calyptotis
	DEWA, QLD	*Coeranoscincus*	*reticulatus*	Three-toed snake-tooth skink
	Expert	*Concinnia*	*martini*	Dark barsided skink
	VDEWLP	*Ctenotus*	*taeniolatus*	Copper-tailed skink
	VDEWLP	*Cyclodomorphus*	*michaeli*	Eastern she-oak skink
	DEWA, VDEWLP	*Cyclodomorphus*	*praealtus*	Alpine she-oak skink
	DEWA Prov	*Drysdalia*	*rhodogaster*	Mustard-bellied snake
	Expert	*Egernia*	*cunninghami*	Cunningham's skink
	DEWA	*Egernia*	*roomi*	Kaputar rock skink
	Expert	*Egernia*	*saxatilis*	Black rock skink
	Expert	*Elseya*	*albagula*	Southern snapping turtle
	Expert	*Emydura*	*macquarii*	Macquarie turtle
	VDEWLP	*Eulamprus*	*heatwolei*	Yellow-bellied water skink
	VDEWLP	*Eulamprus*	*kosciuskoi*	Alpine water skink
	DEWA, NSW	*Eulamprus*	*leuraensis*	Blue Mountains water skink
	Expert	*Eulamprus*	*quoyii*	Eastern water skink
	DEWA Prov	*Eulamprus*	*tympanum*	Southern water-skink
	DEWA Prov	*Harrisoniascincus*	*zia*	Rainforest cool-skink
	DEWA	*Hoplocephalus*	*bungaroides*	Broad-headed snake
	NSW	*Hoplocephalus*	*stephensii*	Stephens' banded snake
	VDEWLP	*Intellagama*	*lesueurii howittii*	Gippsland water dragon
	DEWA	*Lampropholis*	*elongata*	Long sunskink
	Expert	*Lampropholis*	*guichenoti*	Pale-flecked garden sunskink
	DEWA, VDEWLP	*Liopholis*	*guthega*	Guthega skink
	Expert	*Liopholis*	*montana*	Mountain skink
	Expert	*Liopholis*	*whitii*	White's skink
	VDEWLP	*Lissolepis*	*coventryi*	Swamp skink
	VDEWLP	*Morelia*	*spilota spilota*	Diamond python
	Expert	*Myuchelys*	*bellii*	Western sawshell turtle
	NSW	*Myuchelys*	*georgesi*	Bellinger River snapping turtle
	DEWA, NSW	*Myuchelys*	*purvisi*	Manning River helmeted turtle
	DEWA, QLD	*Nangura*	*spinosa*	Nangur spiny skink
	Expert	*Oedura*	*tryoni*	Spotted velvet gecko
	Expert	*Ophioscincus*	*ophioscincus*	Yolk-bellied snake-skink
	DEWA, QLD	*Phyllurus*	*caudiannulatus*	Ringed thin-tail gecko
	DEWA, QLD	*Phyllurus*	*kabikabi*	Oakview leaf-tailed gecko
	DEWA Prov	*Phyllurus*	*platurus*	Broad-tailed gecko
	DEWA, VDEWLP	*Pseudemoia*	*cryodroma*	Alpine bog skink
	Expert	*Pseudemoia*	*pagenstecheri A*	Tussock skink
	DEWA Prov	*Pseudemoia*	*rawlinsoni*	Glossy grass skink
	QLD	*Pygmaeascincus*	*sadlieri*	Magnetic Island dwarf skink
	Expert	*Rankinia*	*diemensis*	Mountain dragon

Group	Prioritiser	Genus	Species	Common name
	Expert	*Saiphos*	*equalis*	Three-toed skink
	DEWA	*Saltuarius*	*kateae*	Kate's leaf-tail gecko
	DEWA Prov	*Saltuarius*	*moritzi*	Moritz's leaf-tailed gecko
	DEWA Prov	*Saltuarius*	*wyberba*	Granite leaf-tailed gecko
	Expert	*Saproscincus*	*mustelinus/ oriarus*	Weasel skink
	Expert	*Saproscincus*	*rosei*	Rose's shade skink
	Expert	*Silvascincus*	*murrayi*	Murray's skink
	NSW, SA	*Varanus*	*rosenbergi*	Rosenberg's goanna
	VDEWLP	*Varanus*	*varius*	Lace monitor
Birds	DEWA, QLD, NSW	*Menura*	*alberti*	Albert's lyrebird
	NSW	*Calyptorhynchus*	*banksii banksii*	Red-tailed black cockatoo (coastal subspecies)
	SA	*Stagonopleura*	*bella samueli*	Beautiful firetail (sfr, mlr, ki)
	NSW	*Petroica*	*boodang*	Scarlet robin
	DEWA, QLD, VDEWLP	*Dasyornis*	*brachypterus*	Eastern bristlebird
	SA	*Hylacola*	*cauta halmaturina*	Shy heathwren (ki)
	SA	*Anthochaera*	*chrysoptera*	Little wattlebird
	NSW	*Daphoenositta*	*chrysoptera chrysoptera*	Varied sittella
	NSW	*Ninox*	*connivens*	Barking owl
	QLD	*Cyclopsitta*	*diophthalma coxeni*	Coxen's fig-parrot
	VDEWLP	*Lathamus*	*discolor*	Swift parrot
		Platycercus	*elegans*	Crimson rosella
	DEWA, VDEWLP	*Climacteris*	*erythrops*	Red-browed treecreeper
	DEWA, NSW	*Callocephalon*	*fimbriatum*	Gang-gang cockatoo
	DEWA Prov	*Pycnoptilus*	*floccosus*	Pilotbird
	NSW	*Calamanthus*	*fuliginosus*	Striated fieldwren
	SA	*Calyptorhynchus*	*funerea*	Yellow-tailed black cockatoo
	SA	*Pandion*	*haliaetus cristatus*	Eastern osprey
	NSW	*Falco*	*hypoleucos*	Grey falcon
	Expert	*Malurus*	*lamberti*	Variegated fairy-wren
	DEWA, QLD, NSW, VDEWLP (KI subsp - DEWA, SA)	*Calyptorhynchus*	*lathami*	South-eastern glossy black-cockatoo
	VDEWLP	*Meliphaga*	*lewinii*	Lewin's honeyeater
	NSW	*Tyto*	*longimembris*	Eastern grass owl
	DEWA, SA	*Zoothera*	*lunulata halmaturina*	Western bassian thrush
	NSW	*Turnix*	*maculosus*	Red-backed button-quail
	NSW	*Ptilinopus*	*magnificus*	Wompoo fruit-dove
	DEWA, QLD, SA,	*Stipiturus*	*malachurus*	Kangaroo Island subsp & southern emu-wren
	NSW	*Turnix*	*melanogaster*	Black-breasted button-quail
	SA	*Glyciphila*	*melanops*	Tawny-crowned honeyeater
	DEWA	*Monarcha*	*melanopsis*	Black-faced monarch

Group	Prioritiser	Genus	Species	Common name
	VDEWLP	*Gerygone*	*mouki*	Brown gerygone
	DEWA, SA	*Psophodes*	*nigrogularis lashmari*	Kangaroo Island western whipbird
	NSW	*Dromaius*	*novaehollandiae*	Emu (NSW North coast)
	VDEWLP, NSW	*Tyto*	*novaehollandiae*	Masked owl
	DEWA Prov	*Menura*	*novaehollandiae*	Superb lyrebird
	NSW	*Podargus*	*ocellatus*	Marbled frogmouth
	NSW	*Pachycephala*	*olivacea*	Olive whistler
	SA	*Lewinia*	*pectoralis*	Lewin's rail
	NSW	*Petroica*	*phoenicea*	Flame robin
	DEWA, VDEWLP	*Anthochaera*	*phrygia*	Regent honeyeater
	NSW	*Parvipsitta*	*pusilla*	Little lorikeet
	QLD, NSW	*Erythrotriorchis*	*radiatus*	Red goshawk
	NSW	*Petroica*	*rodinogaster*	Pink robin
	DEWA, QLD, NSW	*Atrichornis*	*rufescens*	Rufous scrub-bird
	DEWA	*Origma*	*solitaria*	Rockwarbler
	VDEWLP, NSW	*Ninox*	*strenua*	Powerful owl
	VDEWLP, NSW	*Tyto*	*tenebricosa*	Sooty owl
	SA	*Turnix*	*varius*	Painted button-quail
	DEWA, QLD, VDEWLP	*Pezoporus*	*wallicus*	Ground parrot
Bat	NSW	*Chalinolobus*	*dwyeri*	Large pied wattled bat
	NSW	*Chalinolobus*	*nigrogriseus*	Hoary wattled bat
	VDEWLP	*Falsistrellus*	*tasmaniensis*	Eastern falsistrelle
	QLD	*Hipposideros*	*diadema reginae*	Diadem leaf-nosed bat
	NSW	*Miniopterus*	*australis*	Little bent-winged bat
	VDEWLP,NSW	*Miniopterus*	*orianae oceanensis*	Eastern bent-winged bat
	NSW	*Myotis*	*macropus*	Large-footed myotis
	NSW	*Ozimops (Mormopterus)*	*lumsdenae*	Northern free-tailed bat
	DEWA Prov	*Phoniscus*	*papuensis*	Golden-tipped bat
	DEWA, VDEWLP	*Pteropus*	*poliocephalus*	Grey-headed flying-fox
	VDEWLP	*Rhinolophus*	*megaphyllus megaphyllus*	Eastern horseshoe bat
	NSW	*Scoteanax*	*rueppellii*	Greater broad-nosed bat
	NSW	*Syconycteris*	*australis*	Eastern blossom-bat
	SA	*Vespadelus*	*darlingtoni*	Large forest-bat
	SA	*Vespadelus*	*regulus*	Southern forest-bat
	NSW	*Vespadelus*	*troughtoni*	Eastern cave-bat
Marsupial	VDEWLP	*Acrobates*	*pygmaeus*	Feather-tailed glider
	NSW	*Aepyprymnus*	*rufescens*	Rufous bettong
	Expert	*Antechinus*	*agilis*	Agile antechinus
	DEWA	*Antechinus*	*argentus*	Silver-headed antechinus
	Expert	*Antechinus*	*arktos*	Black-footed dusky antechinus
	Expert	*Antechinus*	*flavipes*	Yellow-footed antechinus
	DEWA	*Antechinus*	*mimetes*	Mainland dusky antechinus
	Expert	*Antechinus*	*mysticus*	Buff-footed antechinus

Group	Prioritiser	Genus	Species	Common name
	Expert	*Antechinus*	*stuartii*	Brown antechinus
	Expert	*Antechinus*	*subtropicus*	Subtropical antechinus
	DEWA, NSW, VDEWLP	*Burramys*	*parvus*	Mountain pygmy possum
	Expert	*Cercartetus*	*concinnus*	Western pygmy possum
	SA	*Cercartetus*	*lepidus*	Little pygmy possum
	VDEWLP, NSW	*Cercartetus*	*nanus*	Eastern pygmy possum
	QLD	*Dasyurus*	*hallucatus*	Northern quoll
	DEWA, QLD, NSW, VDEWLP	*Dasyurus*	*maculatus maculatus*	Spotted-tailed quoll
	VDEWLP, NSW, SA	*Isoodon*	*obesulus obesulus*	Southern brown bandicoot
	DEWA, NSW	*Notomacropus*	*parma*	Parma wallaby
	VDEWLP	*Perameles*	*nasuta*	Southern long-nosed bandicoot
	DEWA, NSW, VDEWLP	*Petauroides*	*volans*	Greater glider
	DEWA, NSW, VDEWLP	*Petaurus*	*australis*	Yellow-bellied glider
	Expert	*Petaurus*	*breviceps*	Sugar glider
	NSW	*Petaurus*	*norfolcensis*	Squirrel glider
	DEWA, NSW, QLD, VDEWLP	*Petrogale*	*penicillata*	Brush-tailed rock-wallaby
	NSW	*Phascogale*	*tapoatafa*	Brush-tailed phascogale
	DEWA, VDEWLP, SA	*Phascolarctos*	*cinereus*	Koala
	NSW	*Planigale*	*maculata*	Common planigale
	DEWA, VDEWLP, NSW	*Potorous*	*longipes*	Long-footed potoroo
	DEWA, QLD, NSW, VDEWLP	*Potorous*	*tridactylus*	Long-nosed potoroo
	DEWA, SA	*Sminthopsis*	*fuliginosus aitkeni*	Kangaroo Island dunnart
	VDEWLP, NSW	*Sminthopsis*	*leucopus*	White-footed dunnart
Monotreme	DEWA, SA, VDEWLP	*Ornithorhynchus*	*anatinus*	Platypus
	DEWA, SA	*Tachyglossus*	*aculeatus multiaculeatus*	Kangaroo Island echidna
Rodent	VDEWLP	*Hydromys*	*chrysogaster*	Water rat
	DEWA, NSW, VDEWLP	*Mastacomys*	*fuscus mordicus*	Broad-toothed rat
	Expert	*Pseudomys*	*delicatulus*	Delicate mouse
	DEWA, NSW, VDEWLP	*Pseudomys*	*fumeus*	Smoky mouse
	NSW	*Pseudomys*	*gracilicaudatus*	Eastern chestnut mouse
	DEWA, QLD, VDEWLP	*Pseudomys*	*novaehollandiae*	New Holland mouse
	DEWA, NSW, QLD	*Pseudomys*	*oralis*	Hastings River mouse
	SA	*Rattus*	*lutreolus*	Swamp rat

Appendix 3: Assessment workflow followed by expert panels



Appendix 4: URL to come?

Appendix 5: Species with detailed genetic assessments in the confidential appendix.

Common name	Scientific name
BIRDS	
Glossy black cockatoo	*Calyptorhynchus lathami*
Albert's lyrebird	*Menura alberti*
Superb lyrebird	*Menura novaehollandiae*
Eastern ground parrot	*Pezoporus wallicus*
Western ground parrot	*Pezoporus flaviventris*
Western whipbird	*Psophodes nigrogularis*
Western whipbird	*Psophodes leucogaster*
Southern emu-wren	*Stipiturus malachurus*
MAMMALS	
Agile antechinus	*Antechinus agilis*
Silver-headed antechinus	*Antechinus argentus*
Black-footed dusky antechinus	*Antechinus arktos*
Yellow-footed antechinus	*Antechinus flavipes*
Mainland dusky antechinus	*Antechinus mimetes*
Buff-footed antechinus	*Antechinus mysticus*
Brown antechinus	*Antechinus stuartii*
Subtropical antechinus	*Antechinus subtropicus*
Mountain pygmy possum	*Burramys parvus*
Western pygmy possum	*Cercartetus concinnus*
Little pygmy possum	*Cercartetus lepidus*
Eastern pygmy possum	*Cercartetus nanus*
Platypus	*Ornithorhynchus anatinus*
Greater glider	*Petauroides volans*
Yellow-bellied glider	*Petaurus australis*
Sugar glider	*Petaurus breviceps*
Brush-tailed rock wallaby	*Petrogale penicillata*
Koala	*Phascolarctos cinereus*
Long-nosed potoroo	*Potorous tridactylus*
Smoky mouse	*Pseudomys fumeus*
New Holland mouse	*Pseudomys novaehollandiae*
Hastings river mouse	*Pseudomys oralis*

Common name	Scientific name
REPTILES	
Alpine She-oak skink	*Cyclodomorphus praealtus*
Cunningham's skink	*Egernia cunninghami*
Yellow-bellied water-skink	*Eulamprus heatwolei*
Alpine water-skink	*Eulamprus kosciuskoi*
Blue Mountains swamp-skink	*Eulamprus leuraensis*
Southern water-skink	*Eulamprus tympanum*
Rainforest cool-skink	*Harrisoniascincus zia*
Broad-headed snake	*Hoplocephalus bungaroides*
Stephen's banded snake	*Hoplocephalus stephensii*
Nangura skink	*Nangura spinosa*
Alpine bog-skink	*Pseudemoia cryodroma*
Moritz's leaf-tailed gecko	*Saltuarius moritzi*
Orange-tailed shadeskink	*Saproscincus rosei*
Rosenberg's goanna	*Varanus rosenbergi*
FROGS	
Marsupial frog	*Assa darlingtoni*
Eastern common froglet	*Crinia signifera*
Wallum froglet	*Crinia tinnula*
Giant burrowing frog	*Heleioporus australiacus*
Eastern banjo frog	*Limnodynastes dumerilii*
Booroolong frog	*Litoria booroolongensis*
Bleating tree frog	*Litoria dentata*
Ewing's tree frog	*Litoria ewingii*
Littlejohn's tree frog	*Litoria littlejohni*
Olongburra frog	*Litoria olongburensis*
Whistling tree frog	*Litoria verreauxii*
Southern barred frog	*Mixophyes balbus*
Red and yellow mountain frog	*Philoria kundagungan*
Masked mountain frog	*Philoria loveridgei*
Pugh's Mountain Frog	*Philoria pughi*
Richmond range mountain frog	*Philoria richmondensis*
Sphagnum frog	*Philoria sphagnicola*
Brown broodfrog	*Pseudophryne bibronii*

Rockwarbler. Image: JJ Harrison CC BY-SA BY 4.0 Wikimedia Commons

Further information:
http://www.nespthreatenedspecies.edu.au

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Threatened Species Recovery Hub

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