Report 2009-2012 Naturalis

Research and Education

Naturalis
Biodiversity
Center

Naturalis Biodiversity Center (Duistermaat, L. & van Tol, J., editors), 2014.
Report 2009-2012 Naturalis Research and Education

Contents

Introduction

Not many natural history museums in the world have changed so much as *Naturalis Biodiversity Center* since 2009. In this report we present over 50 larger and smaller projects of the last four years, providing an overview of the huge variation in the expertise and interest of the scientific staff of Naturalis.
This report also provides an overview of the research staff per department, as well as the publications of the permanent, temporary and honorary staff of 2009 up to 2012.
Naturalis is a merger of the Nationaal Natuurhistorisch Museum (*National Museum of Natural History*), the Zoölogisch Museum van de Universiteit van Amsterdam (*Zoological Museum of the University of Amsterdam*), and the Nationaal Herbarium Nederland (*National Herbarium of the Netherlands*), with branches in Leiden, Utrecht and Wageningen. These organizations will officially be placed under one directorate in 2013, but the process of joining buildings and research infrastructures has already been successfully implemented during the last few years.
The significant steps we made in our national and international visibility in biodiversity research was strongly facilitated by a grant of the Netherlands government of 30 million euro from the Fonds Economische Structuurversterking (Economic Structure Enhancement Fund), intended for the physical integration of the collections of the founding institutions of Naturalis, for digitization of the collections, and for establishing a new research infrastructure, partly in collaboration with CBS-KNAW (Netherlands Mycological Institute).
Additional funding for the research infrastructure was allocated from a starting grant from the Ministry of Education, Culture and Science. The additional budget for research thus totally amounted to 15.3 million euro for the years 2010-2015, which we invested in new molecular and morphological laboratories, and an EMP / Electron microprobe. Special attention was paid to appoint new researchers and PhD candidates focusing on biodiversity research not represented in Naturalis until then. During the second phase of this programme (2013-2015) Naturalis will focus on opportunities for implementing the knowledge of staff in application-oriented studies, for instance in the topsectors Agri & Food or Human Health.
These developments have been instrumental in the increasing scientific success of our institute. We have been successful in obtaining grants from NWO and EU, and both the number and impact of our publications have increased significantly during the last five years. The organization of our research has also changed. While systematic, taxon-oriented studies are the primary domain of the departments, the so-called focusprojects mainly deal with problem-oriented studies. Three programmes have been defined, viz., Evolution of species interdependencies, Dynamic biodiversity and Character evolution. Two other programmes are intended to coordinate all activities on *Nature of the Netherlands* and *Bioinformatics and biodiversity informatics.*
The programme *Nature of the Netherlands* even oversees initiatives in other sectors of Naturalis, while special attention is paid to partnerships with other professional and amateur organizations in this field.

Koos Biesmeijer
Erik Smets
Jan van Tol

Departments, focus projects and programmes

Lilium bulbiferum L. Govelin, Germany. Photo: Jan van Tol.

Botany

The past period for the department of Botany / NHN has been in the spirit of the transition to the new organisation of Naturalis. This entailed extra efforts, but of course brought also many positive effects, including the wider financial opportunities.

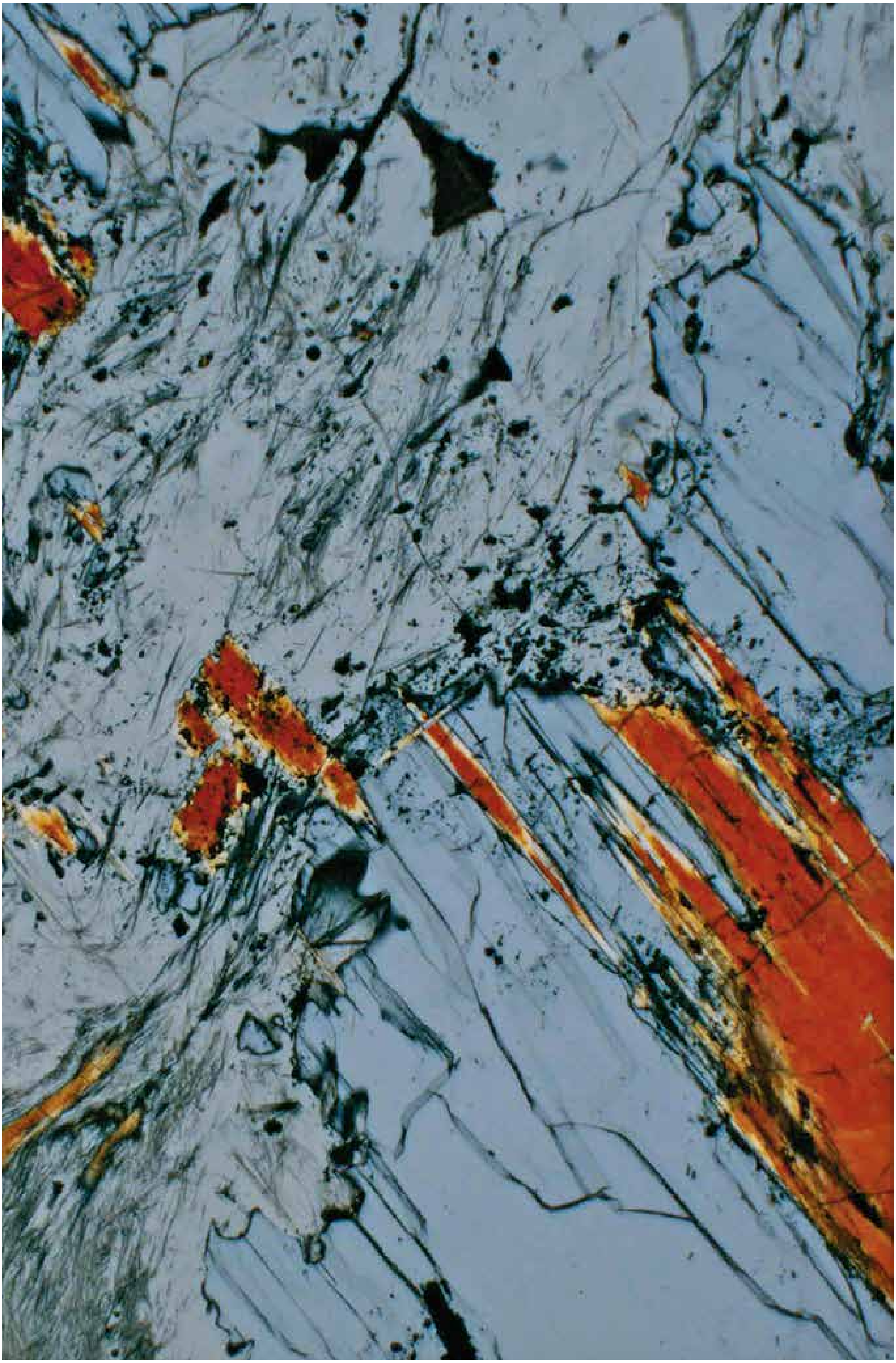
Much attention has been paid to long term continuity of taxonomic strongholds as expressed in the five large, international flora projects that are coordinated by the department of Botany, viz., Flora Malesiana, Flore du Gabon, Flora of the Guianas, Flora Agaricina Neerlandica and Heukels Flora van Nederland. Coordination was intensified and an important start was made towards renewal of a digital and internet-based means of cooperation and publication. The enormous amounts of biodiversity data that are thus made available form the basis of Naturalis in international biodiversity initiatives.

The expansion of our staff with research fellows and postdoctoral researchers was very fortunate, as we were thus able to attract extra expertise and to contribute more to the focus projects. This concerns e.g. modelling of collection data for the analysis of species distributions and spatial biodiversity patterns, the economic botany, the evolution and morphogenesis of wood, and the evolution of the symbiosis of fungi and plants.

Clear successes were project proposals, and application oriented activities. Highlights are the acquisition of the EU subsidy for pro-iBiosphere, as well as a VENI and a VIDI scholarship, a NWO-post doc project, and a Biodiversity Assessment project on Halmahera. The latter is strongly related to the ongoing progress of importing data in our collection databases and the use of them. Next to morphology based diagnostics, molecular diagnostics (next generation sequencing) is increasingly being applied. Because of this, the last few years the scope of Botany has been broadened considerably, e.g. towards cryptic and arctic biodiversity.

Noteworthy is that by bringing together the NHN wood collections supplemented with those of the Koninklijk Instituut voor de Tropen, we now preserve the world’s largest scientific collection for the purpose of wood research.

This has all led to a significant increase in internal cooperation within Naturalis, and strengthening of the multidisciplinary character of our research and of external networks of experts. This manifests itself especially in the field of global change biogeography and the modelling of species distributions. Growing opportunities can be identified for invasive species, ethnobotany and plant use, flower morphology and pollination patterns, and the wide use of functional traits. Concrete shifts of output towards high impact publication have taken place, while a certain continuity in Flora output remained. Also, a significant increase is seen in both the number and the rate of success of applications for externally financed project and programs. The development and use of taxonomic e-tools, and the wide application of spatial analysis methods and models have been put a significant steps forward. At the educational level a number of new items have been designed in cooperation with Institute of Biology Leiden and Institute of Environmental Sciences. These concern floristic education, the accreditation of a minor, and MSc-tuition.



Microscopic view (3 × 2 mm) of a metamorphosed sedimentary enclave (xenolith) transported from 10 km depth to the surface in a Neogene volcano, Mar Menor, Spain. Photo: Leo M. Kriegsman.

Geology

The Department of Geology of Naturalis has six full-time palaeontologists, two full-time mineralogists and one part-time palaeobotanist with a professorship at Leiden University. Palaeontological research has a focus on the Netherlands and adjacent regions, Southeast Asia, and the Caribbean and Mediterranean. Thematic research builds on the taxonomic expertise of staff members, that includes (fossil) foraminifers, molluscs, echinoids, vertebrates, and plants, and covers most of the Phanerozoic. Mineralogical research focuses on the Mediterranean and Precambrian basement areas of former Gondwana. The department houses the Netherlands Gemmological Laboratory, the only major gemmological facility in the Netherlands.

Highlights

- Willem Renema and Frank Wesselingh were succesful in attracting an EU funded ITN on the Indonesian Throughflow, an international project that allowed employing two PhDs (Sonja Reich, Vibor Novak).
- Frank Wesselingh was one of the leading authors on a Science paper and a book in 2010 on the ancient origin of modern Amazonian biodiversity.
- Kenneth Rijsdijk was employed on a project basis until June 2011 to lead an international project on the reconstruction of the world of the dodo at Mauritius that has led to many joint publications.
- National infrastructure funding (NCB/FES) allowed to expand the geological lab; new facilities include a FEG-SEM with EDS module, a micro-CT scanner, and micro-Raman.
- The same funding was used as matching to purchase, with Utrecht University and the Free University of Amsterdam, a nanoSIMS and a FEG-EMP, that wil be hosted in Utrecht and operated via a national consortium.
- Martin Brazeau started as a Research Fellow in 2011, studying character evolution in fossil fish, with a focus on Devonian specimens from Mongolia. In 2012, he was succesful in attracting an ERC Starting Researcher grant for a project on the evolution of jaws in early vertebrates; on this grant, a post-doc, two PhDs and a lab assistant can be employed.
- Willem Renema attracted national research funding (NWO) for a post-doc to work on biotic and abiotic drivers of shifting marine tropical biodiversity hotspots during the Eocene-Oligocene.
- A covenant was signed late 2011 with Utrecht University, on scientific collaboration, student supervision and shared labs; it also forms the basis for appointments of staff at the university.
- Staff in the department collaborated in many international projects: (i) reconstructing the living environment of hominids from the Liang Bua cave on Flores (Indonesia); (ii) Permian palaeobotany and -geography of central Sumatra; (iii) Caribbean palaeontology and -geography; (iv) the Eocene Azolla event in the Arctic; (v) deep crust underneath Morocco; and more.
- John de Vos and Frank Wesselingh co-authored a paper in the Journal of Human Evolution on the relevance of aquatic environments for hominins, using the famous Trinil site as a case study.
- After co-authoring several key publications on Neogene stratigraphy and vertebrate biogeography, Lars van den Hoek Ostende now plays a prominent role in an RCMNS working group on terrestrial ecosystems.
- Hanco Zwaan authored the first ever paper in Gems and Gemology that was published as an iPad app; the paper on Brazilian emeralds was also awarded a special prize for its quality.
- Steve Donovan published a paper in Geology on bivalve predation on crinoids, revealed through micro-CT scanning of gut contents; and a paper in the same journal on crinoid autotomy.
- the department hosted a number of foreign based scientists for one or more months: Evelyn Kustatscher, Cindy Looy, Daniela Kalthoff, Leon Claessens, Johnny Waters, Hunya and Cihat Alcicek, Thierry Rakotonandrasana, Mike Crow, and Laura Cotton, leading to many joint pulications.
- Leo Kriegsman led Naturalis efforts within the EU programme SYNTHESYS and the EDIT Network of Exellence, with two project staff (Minke van Det, Christiane Quaisser) until early 2011.

The pigmy seahorse *Hippocampus denise* Lourie & Randall, 2003, on the gorgonioan *Annella reticulata* (Ellis & Solander, 1786). Mansuar Island, Raja Ampat, West Papua, Indonesia. Photo: Bert W. Hoeksema.

Marine
Zoology

Research in the department of Marine Zoology is strongly collection-based. It is integrative by combining field surveys with the application of morphological and molecular methods. Fieldwork is mostly focused on specific coral reef taxa and leads to collection improvement with regard to these specific groups. The major research topics include

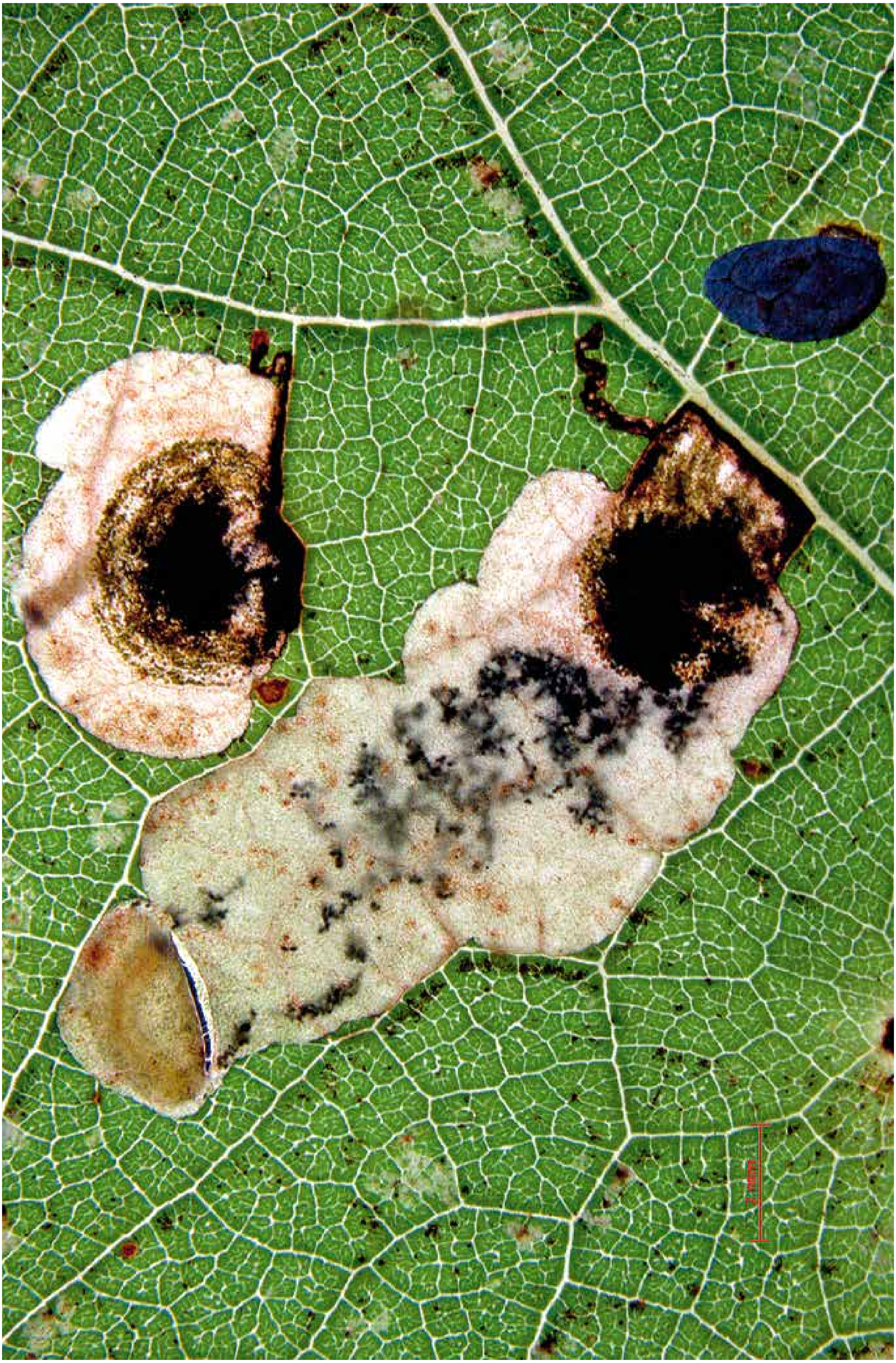
- Patterns of marine biodiversity in and around the Coral Triangle
- Evolution of species interdependencies
- Biodiversity along onshore-offshore gradients
- Historical collections and changing marine faunas
- Reef invertebrates as producers of bioactive compounds
- Conservation of marine biodiversity
- Exotic and invasive species
- Tropical marine lakes
- Fish fauna of Lake Victoria
- Climate change and its effect on coral reef faunas
- Shallow marine interstitial fauna
- Marine phylogeography

Marine biodiversity studies

Most marine taxa concern tropical organisms, especially invertebrates living on coral reefs.
An important key to the species richness of coral reefs is formed by the complex of species interdependencies. Most coral reef organisms live in symbiosis with other animals and plants. Phylogeny reconstructions of both partner taxa can be made to examine their co-evolution. The study of the evolutionary history of species associations (phylogenetic ecology or phylo-ecology) may help to clarify the origin of species-rich ecosystems, for which a knowledge of both the host and symbiont groups is required. Close cooperation between taxonomists dealing with the host group (e.g. hard corals, soft corals, sponges) and the associated group (e.g. algae, commensal shrimps, coral gall crabs, parasitic snails) is essential. Phylogeny reconstructions require the application of molecular (DNA) techniques, which also may help to distinguish sibling species. The results are important for understanding patterns of marine biodiversity: a high number of hosts species is a condition for a rich associated fauna, especially if symbiotic species are host-specific. However, owing to their architecture (size and shape) some host species have more associated species than others, whereas species that produce toxic bioactive compounds may have very few symbionts. A better understanding of biodiversity patterns and the occurrence of a rare species may eventually be applied to their conservation.

Coral reef biodiversity and conservation

The delineation of the Coral Triangle, the Southeast Asian - West Pacific Centre of Maximum Marine Biodiversity, is studied through biodiversity surveys of selected target taxa that serve as model groups (proxies). These surveys are usually performed in close collaboration with local nature conservation organizations with an interest in marine biodiversity and rare endemic species. The origin of the Coral Triangle is studied through phylogenetic biogeographical analyses of these taxa in combination with information on sea level fluctuations, currents and plate tectonics. Environmental variability is an important factor for regional species richness.
This is clearly reflected in the presence of unique ecosystems, such as marine lakes, which harbor many rare and endemic species. In order to have a better understanding of the role of environmental variation ("habitat diversity"), surveys are executed along environmental gradients, e.g. from onshore to offshore. Museum collections are used to find historical baselines to discern the local disappearance of species or the appearance of invasive species.
Unsustainable fisheries methods and the effects of elevated seawater temperatures and ocean acidification (resulting from climate change) are major threats to marine ecosystems. Taxonomic expertise can be applied to study their effects on various reef coral species.



Leaf mines and larvae of *Antispila oinophylla* Van Nieukerken *et al.*, 2012. Photo: E.J. van Nieukerken.

Terrestrial Zoology

Evolution of molluscs of limestone outcrops in Southeast Asia, pollinators and climate change, reconstruction of the phylogeny of damselflies using molecular characters, a small invasive moth species on grapevines, a revision of the velvet spiders, a book portraying the biodiversity of the Netherlands, and descriptions of many species of parasitic wasps from China and adjacent areas.

A wide range of topics as well as taxa all studied by researchers of Naturalis' department of Terrestrial Zoology.

Although several research lines are continued, we have also taken up several new topics. Research fellow Professor Koos Biesmeijer started a study of the dynamics in the distribution of pollinators and plants in Europe. Using the Naturalis collection and advanced statistical methods, shifts in occurrence of bees, butterflies, hoverflies and plants is documented. The results contribute significantly to externally funded international studies on the causes and effects of these declines.

The extended molecular laboratories play a significant role in many of our systematic projects. These laboratories were realized using allocated resources of the *Economic Structure Enhancing Fund* (Fonds Economische Structuurversterking), awarded to Naturalis in 2009. They play, for instance, a key role in a project organized by Professor Menno Schilthuizen on Mount Kinabalu (Sabah). A group of more than 30 taxonomists, both from Sabah and the Netherlands, collected specimens along a transect from sea level to the 4000 m high top of this mountain. Besides being interested in the huge diversity of plants and animals of this region, they also wished to assess whether the recently evolved species inhabit higher altitudes than their ancestral species, or can particularly be found at sea level.

Many Lepidoptera were sequenced both for global and local Asian DNA barcoding and phylogenetic studies, attempting to reconstruct the evolution of leafminers in relation to their hostplants (Dr Erik van Nieukerken and PhD student Mr Camiel Doorenweerd).

Biodiversity studies are traditionally based on huge amounts of data, including morphological measurements, photographs, and distributional data. The field of biodiversity informatics is developing rapidly, and expands our research options every year. Naturalis taxonomic expertise is now easily and effectively shared with the global biological community. Entomologists of Naturalis contributed to the EU-funded *Fauna Europaea* project with species lists per country for Lepidoptera, Hymenoptera, Diptera and Odonata, while they also contributed to the *Catalogue of Life* and set up information systems using *Scratchpads*, another EU-funded project.

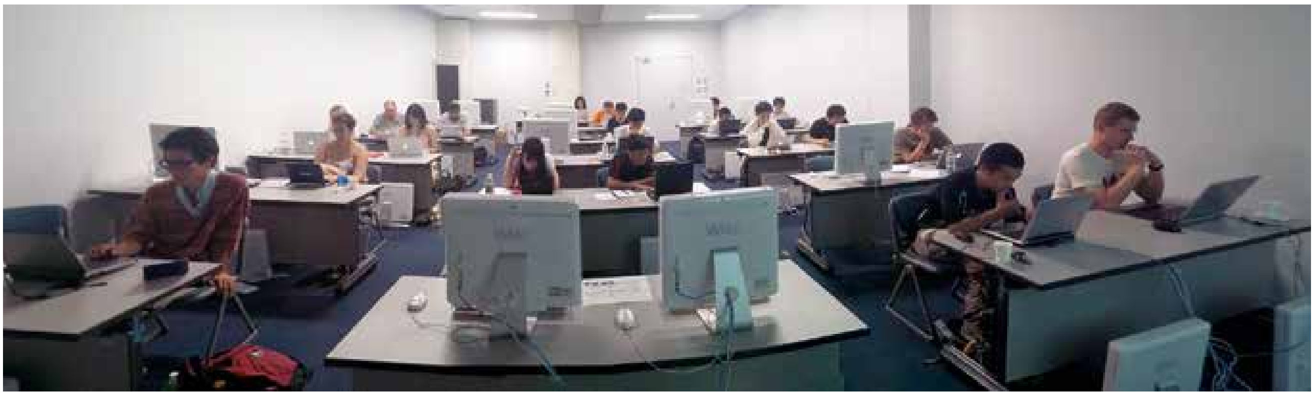
Our studies of the fauna of South and Southeast Asia provide a steady flow of publications describing new taxa, and understanding the historical biogeography of this region. Again, the data provided by our molecular lab are indispensible for these studies.

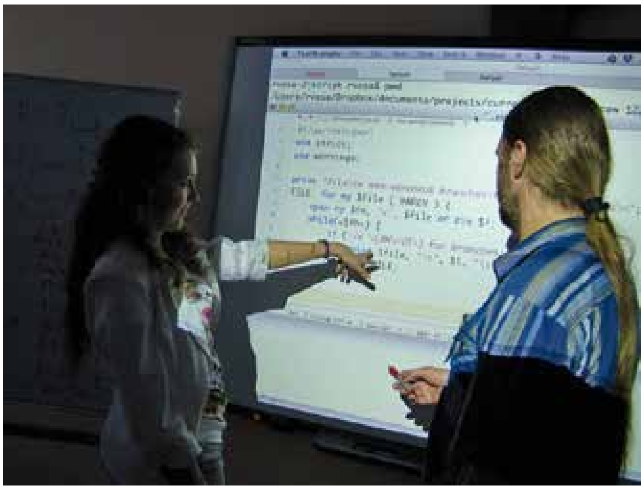
Dr Jeremy Miller, collaborating with colleagues from Vietnam and adjacent countries, started a project comparing the invertebrate fauna of undisturbed forest, disturbed forest and forest plantations. Using DNA barcoding and next generation sequencing, students assisted to this labour-intensive comparative study.

Dr Pim Arntzen continued his studies on the amphibian fauna of Europe, focusing on speciation and hybrid zones. Dr Freek Vonk, a specialist of snake venom, started his activities for Naturalis in 2012. He received the prestigious Eureka Prize for Science Communication of the Netherlands Science Foundation NWO in 2012.

During the report period, the department of Terrestrial Zoology of Naturalis merged with the department of entomology of the Zoological Museum of the University of Amsterdam. Three researchers continued their studies in Leiden, with specialists of Lepidoptera and Hymenoptera (Dr Sandrine Ulenberg), Diptera (Dr Herman de Jong) and applied entomology (Tom Hakbijl). Also Dr Ronald Sluys from the ZMA Department of Vermes and Deuterostome Invertebrates joined our department, and continued his studies on the phylogeography of Mediterranean freshwater flatworms.

For the coming years, the promising lines developed recently will, together with the strong presence in systematics and the increasingly digitized collections, form a strong basis from which we will further develop the profile of the department.





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Bio-informatics

Aims

Biology is becoming a computationally intensive science: data sets that are analyzed to answer biologically meaningful questions are growing in volume and complexity; analytical methods are becoming increasingly sophisticated. The bioinformatics program at the Naturalis Biodiversity Center, started in 2012, seeks to respond to this trend by developing informatics-oriented research projects and by supporting Naturalis researchers in developing computational research methodologies.

Activities

Research - The tools and technical skills of the bioinformaticists are brought to bear on a number of research projects at Naturalis. Over the last year, the bioinformaticists have, among other things, demonstrated evidence of natural selection acting on important genes in the genomes of orchids and venomous snakes, selected candidate plant accessions for sequencing by automating the analysis of digital images of herbarium sheets and developed a platform for large-scale phylogenetic inference. In addition, we have supported researchers in preprocessing their high-throughput DNA sequencing data, in deploying complex analytical software and in exploiting newly acquired high-performance workstations.
Software development - A large component of the bioinformaticists' activities is software development. To this end we have deployed two source code repositories, one for open source products[1] and one for confidential source[2]. In the last year, a number of in-house produced tools have been added to the public repository. For example, a pipeline for identifying DNA sequences obtained from CITES-controlled species, a pipeline for image analysis of herbarium sheets, a data format for structuring natural language from flora descriptions, and so on.
Capacity building - To support these activities, capacity building both in terms of personnel and in terms of computational infrastructure is an ongoing process. Over the last year this has resulted in the appointment of an additional bioinformaticist, Youri Lammers, and in the application for (and granting of) access to national infrastructure for parallel, high-performance computing tasks at SARA. Lastly, in close collaboration with the ICT department and the CIO, Naturalis bioinformaticists are identified as "key users" in the deployment of a virtualization platform that will enable economies of scale in the acquisition of additional computing hardware.
Teaching and training - In ongoing collaboration with the university of applied sciences (Hogeschool Leiden), Naturalis bioinformaticists are training students during their internships and collaborating with HS teachers in developing bioinformatics research. In addition, bioinformaticists have over the last year taught hands-on workshops in informatics at LUMC, the Gulbenkian Institute (Portugal), Moscow State University and the Kenya Medical Research Institute.

Collaborations

The Naturalis bioinformaticists participate in a number of national and international research collaborations. At the national level, we participate in the Virtual Laboratory for Plant Breeding, to which we are contributing a white paper on high-throughput DNA sequencing data retention. At the European level, Naturalis bioinformaticists are "key users" in the BioVeL project for biodiversity informatics pipeline development, for which Naturalis implements work packages on taxonomic service sets and outreach. Internationally, Naturalis bioinformaticists are co-organizers of the PhyloTastic project to make Tree of Life knowledge re-usable and lead the development of the SUPERSMART platform for sequence data mining, integration and automated inference of "exa-scale" (i.e. very large) phylogenies.

[1] http://github.com/naturalis

[2] http://bitbucket.org/naturalis

Nature of the Netherlands

The suprasectoral programme **Nature of The Netherlands** started in July 2011 intending to improve the coordination and visibility of Naturalis activities focusing on the Dutch flora, fauna and geology. The launched programme concerns both a consolidation of existing activities and an expansion with various new and promising projects. As such, it serves as an umbrella for ongoing and new projects, projects with clear objectives and measurable deliverables.

Ambition

Naturalis wants to make a significant contribution to the knowledge of and appreciation for nature in The Netherlands. This will be achieved by generating, assembling, managing and disseminating knowledge about the geological and biological diversity of the present and the past. Complex knowledge will be translated for several user groups.

Position

Naturalis conducts research on taxonomy, phylogeny and biogeography. In collaboration with professional and non-professional partners we develop identification keys and thesauri, we study the dynamics of distribution patterns, we examine ecological relationships, and we provide platforms to disseminate knowledge such as websites, journals, book series and exhibitions.

Exemplar projects

Dutch Species Catalogue

Naturalis maintains the national thesaurus of the (multicellular) species of the Netherlands, see www.nederlandsesoorten.nl. We are expanding this online catalogue to a digital flora and fauna. In 2012 we started a major revision of the taxonomic information for all species groups, an activity that will continue in 2013. Species information of the bees and vascular plants of The Netherlands was added. We are linking to the National Database Flora and Fauna to synchronize their taxonomic thesaurus of field records and to present dynamic distribution maps in the species catalogue, a collaboration with the Dutch Nature Authority.

Identification tools

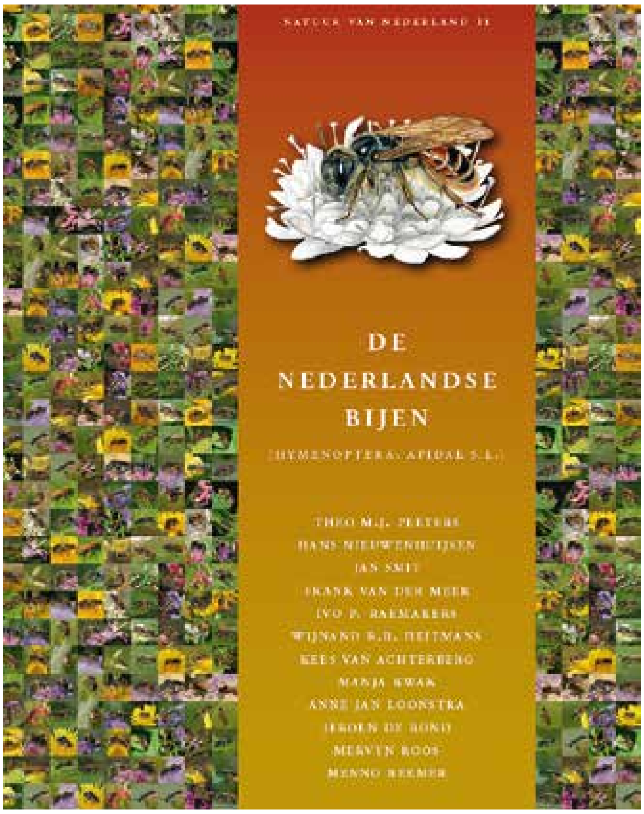
Together with the popular television show for children 'Het Klokhuis' and with Naturalis-based NGO EIS-Nederland, Naturalis created an animal identification tool for pupils at primary schools, as well as twelve television shows. The dierenzoeker (*animal tracker*) is available at www.dierenzoeker.nl. We received the 'Nationaal Groenfonds Natuurprijs 2012' for this initiative and were nominated for another prize, de 'Gouden apenstaart', for the best website for children.

For professional and non-professional scientists we started the development of a generic identification module with multi access keys in the Dutch Species Catalogue. The first prototype containing long-horned beetles is available at http://determineren.nederlandsesoorten.nl/boktorren. This project will take two years and will result in twenty multi access keys, available on internet and by apps. Collaborating organizations are the NGO's EIS-Nederland and Stichting ANEMOON, de Nederlandse Jeugdbond voor Natuurstudie (NJN) and ETI Bioinformatics.

DNA activities

In the past two years collaboration started with several NGO's to collect fresh specimens for our DNA barcoding project. We are generating DNA barcodes from at least 27 000 specimens, about half of them will be based on specimens from the Netherlands. By the end of 2012 we had received over 12 000 well-identified Dutch specimens from more than 200 volunteering experts. Our aim is to build a reference structure to improve reliability and speed of identification of species relevant for society, such as biological control, invasive species, birdstrikes and wildlife forensics, in which various stakeholders were involved.

One possible application of the DNA reference structure is monitoring species with environmental DNA. Naturalis and EIS-Netherlands started a pilot project in 2012 to monitor the occurrence of the



NATUUR VAN NEDERLAND 11

DE
NEDERLANDSE
BIJEN
(HYMENOPTERA: APIDAE S.L.)

THEO M.J. PEETERS
HANS NIEUWENHUIJSEN
JAN SMIT
FRANK VAN DER MEER
IVO P. RAEMAKERS
WIJNAND R.B. HEITMANS
KEES VAN ACHTERBERG
MANJA KWAK
ANNE JAN LOONSTRA
JEROEN DE ROND
MERVYN ROOS
MENNO REEMER

The cover of part 11 of the series Natuur van Nederland.

The homepage of the DierenZoeker app.

waterbeetle *Dysticus latissimus* by environmental DNA, a species of the EU Habitat Directive. In 2013 this will be expanded by all macrofauna species that are indicators for the EU Water Directive, using next generation sequencing.

Publications and literature

A new volume in our successful book series Nature of The Netherlands on the bees of the Netherlands was published in December 2012. This massive work contains information of over 350 species of bees, with chapters on their ecology, the relationships with their environment and the services they provide for ecosystems and society.

An initiative worth mentioning is our digitizing project ‘natuurtijdschriften’, focusing on journals with relevant information of nature in The Netherlands. The digitized files are made accessible in a repository with a central search engine and will be linked to the species catalogue. In the next two years we will expand the project with an extra 25 journals.

Exhibits in visitor centres

Together with IVN (Institute for Environmental Education), Artis (zoo), EIS-Nederland, Staatsbosbeheer en Natuurmonumenten (nature reserve managers), Naturalis implemented an exhibit in visitor centres in four major nature reserves. These exhibits contain a microscope, invertebrates (in glass) and an identification game. The aim of the project was a best practice to value invertebrates and make them visible for a larger audience. The project was financed by the Ministry of Economic Affairs.

Character evolution

Naturalis Biodiversity Center aims to archive, exhibit, catalogue, and understand the diversity of life. The most eye-catching aspect of this biodiversity is the endless variety of size and shape in living organisms. A fascination with this richness of form is, of course, the primary drive for most researchers in Naturalis, and this leads to the obvious and inescapable research focus on the evolution of form.
From the sheer endless diversity of morphological traits we select a limited array of “key innovations”: crucial changes in shape and structure that have opened the way to new evolutionary trajectories. At the moment, we focus on three such key innovations, namely: (1) secondary woodiness in plants, (2) skeleton innovations in the earliest vertebrate animals, and (3) left-right asymmetry (chirality) in the reproductive organs of plants and animals.

Secondary Woodiness

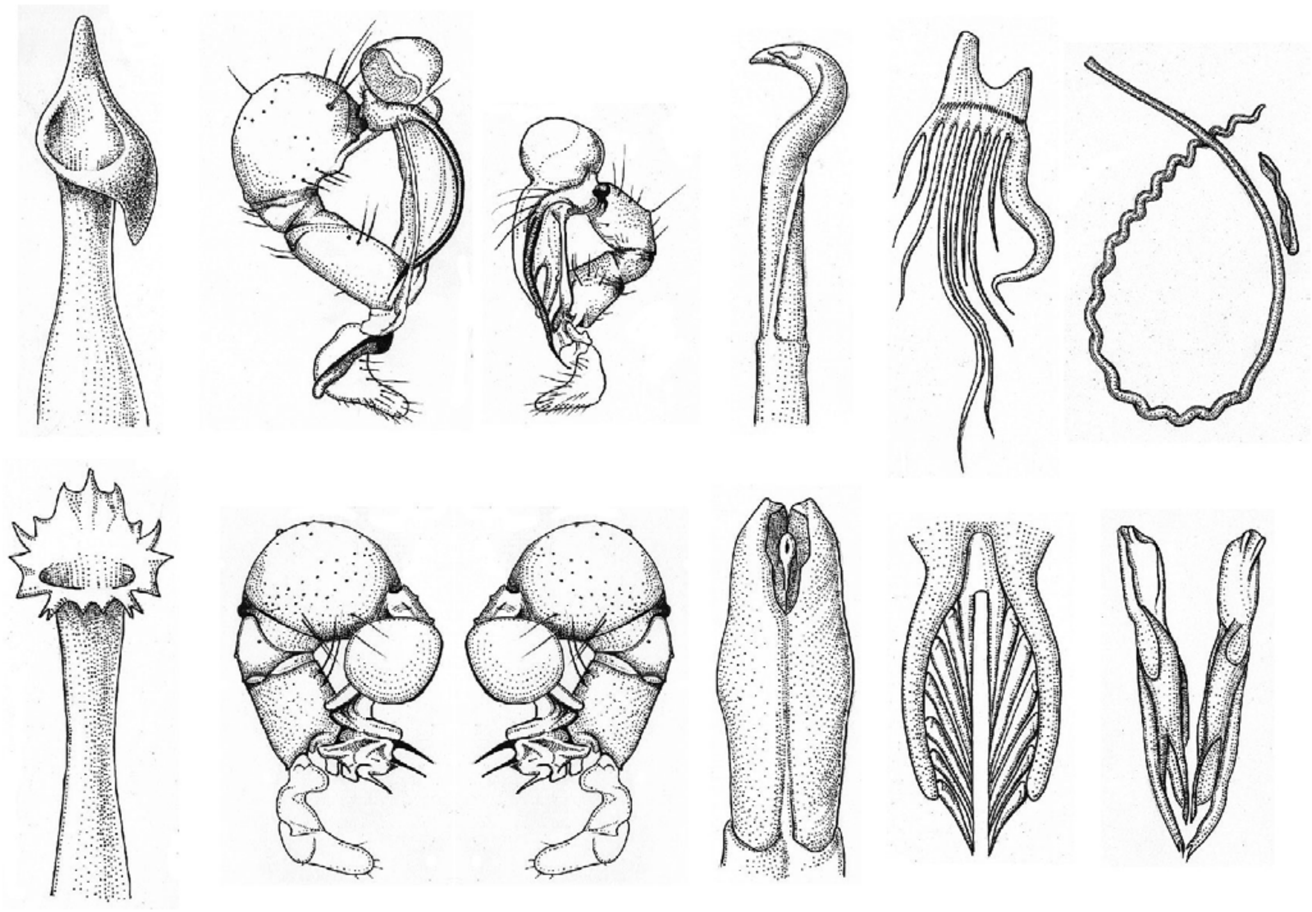
Secondary woodiness (the evolution of woody plants from herbaceous ancestors) often appears on islands. The group of Frederic Lens is studying whether this is caused by a demand for greater drought resistance, and they also investigate which genetic switches are involved. Using genetic modification, it might eventually be possible to turn herbaceous food crops into drought resistant shrubs, which might be necessary to cope with climate change. Also, lignin (the chief compound of wood) is an important future source of biofuel because of its high energy content.

Skeletal Innovations in the Earliest Vertebrate Animals

The team of paleontologists led by Martin Brazeau uses advanced imaging techniques to wrest new information from fossils of the earliest vertebrates – which they excavate in, for instance, the Mongolian desert. In doing so, they unravel how a series of innovations in skeleton structure has precipitated the origin of modern vertebrates (including ourselves). Research into our distant ancestors speaks to the imagination, one of the reasons why Brazeau’s work has appeared three times in *Nature* in the past few years. A welcome by-product of this work is the improvement of imaging techniques – such as synchrotron radiation CT-scanning – that may be applied to other materials and structures.

Left-Right Asymmetry in Reproductive Organs in Plants and Animals

Nature often places a premium on perfect external symmetry, for the stability it affords the body and its organs. That is why it also plays a role in reproduction: symmetry is sexy. Yet, the external reproductive organs of animals and plants are often strongly asymmetric. Two teams of researchers are trying to understand why this should be so. Barbara Gravendeel’s team studies whether orchids evolve asymmetric flowers to trick their pollinators. And the project by Menno Schilthuizen’s group on asymmetric animal genitalia has medical implications: in mammals, genitals are the only organ systems that are symmetric in some species, asymmetric in others. Developmental problems during ontogeny often result in disastrous deviations from symmetry. Studying organ systems like genitalia that easily evolve to cross this adaptive valley may help understand the regulatory mechanisms that maintain the delicate balance between symmetry and asymmetry in a body.
Besides these three projects, the focus group Character Evolution also forms a platform for scientific debate and exchange of information. We have regular meetings and seminars and also a monthly journal club held in café Meneer Jansen. We also do not shy from exploring possible applications of our morphological research. Think of the shock absorbers and zip-locks in the carapaces of small crustaceans (Dirk Platvoet’s work), or the optimalised prey catching apparatuses of pitcher plants (Rachel Schwallier).



Highlight

Asymmetric (top row, see fig.) and symmetric (bottom row) genitalia (from Schilthuizen, M., 2013. Something gone awry: Unsolved mysteries in the evolution of asymmetric animal genitalia. Animal Biology, 63: 1-20).

Dynamic biodiversity

Most will agree that biodiversity is an important life-support system for humanity and in addition that it represents a valuable part of the earth system by itself. We cannot envision a future without biodiversity. However, we are experiencing a global biodiversity crisis. Our natural ecosystems are being degraded and transformed, which affects the livability of our planet for generations to come. The magnitude of the current decline in not completely clear, the consequences for natural systems is largely unknown and impact on ecosystems services and livability remain to be established.

The Naturalis Biodiversity Center research focus Dynamic Biodiversity aims to document the patterns in species occurrence and diversity in space and time. This includes anything from single species to whole ecosystems and includes not only patterns of change, but also the drivers of change, the impacts of change and understanding the mechanisms of change. As such the theme encompasses a very wide range of research themes and brings together a wide range of researchers with very different expertise. Naturalis Biodiversity Center harbours a unique range of experts from deep time geologists to zoologist and botanists to species modelers and ecosystem service experts. More than 30 staff, about 30PhDs and 9 postdocs are currently active in the research area around the world. Much of the research is based on our extensive collections and databases which allow for detailed comparisons of temporal and spatial diversity patterns in marine and terrestrial environments. Our varied backgrounds allows us to assess the reaction and recovery of biota from past perturbations using the geological record. Furthermore, we are capable to track changes in diversity on human timescales from a vast network of observations and collections. We have been involved in the study of processes with a societal impact such as the consequences of invasive species or the shifting ranges of plant pollinators on biodiversity.

Our principal shared interests lay in understanding the processes and settings under which biodiversity is generated, maintained, or modified and destroyed, and what processes are relevant at what scales. By understanding the natural variability of biodiversity change (turnover) and the governing processes and settings we should be able to assess the human role in the current decline.

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Fig. 1. Using extensive databases we are the first to document large-scale shifts in plants and their insect pollinators, and are currently studying what is driving these shifts, e.g. land use, climate change, biotic interactions.

Fig. 2. Amazon forest: The Amazon forest is arguably the richest terrestrial biome. With a network of 150 scientists and 1400 plots well spread across the region we document tree diversity and composition of these forests, work with conservation agencies and aim to predict how global change may affect this area.

Evolution of species interdependencies

The interactions between species have been essential in the generation of the Earth's biodiversity: most organisms require coevolved interactions with other species to survive and reproduce. These interactions can involve a wide range of species that form complex networks of interdependencies. Networks of interdependent species are often heterogeneous and have architectures that are well-defined by the phylogenetic relationships between the interacting species. However, little is known about the evolutionary processes that generate these interdependencies.

Hypotheses

To increase our understanding of species interdependencies and their importance for biodiversity maintenance ongoing research at Naturalis aims to address the following general hypotheses:

1. Phylogenetic relationships are a determining factor in shaping the architecture of species interdependencies.
2. Both cospeciation and host shift events are important mechanisms for speciation of interacting species.
3. The signature of species interdependencies (e.g. mutualism, parasitism, commensalism) shapes the architecture of the phylogenies of the associated taxa.

Research

These hypotheses are tested by determining the phylogenetic structure of species interdependencies in a wide array of communities. Our research focuses on the species interdependencies in coral reef organisms, mycorrhizae, and plant-insect interactions. In each of these systems phylogenetic relationships between interacting species of specific target groups are inferred using DNA data and patterns of interdependencies are evaluated with a variety of analytical methods.

Coral reef organisms

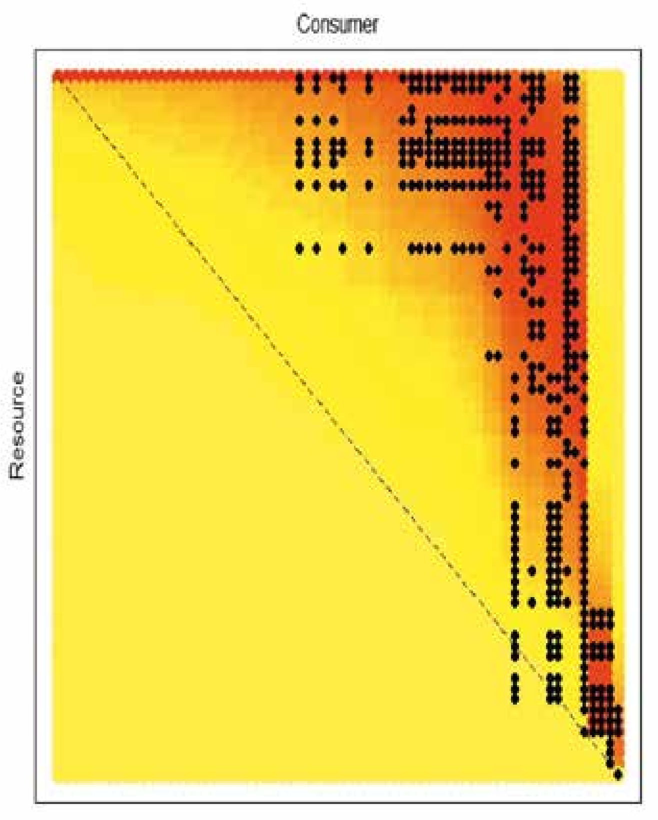
Coral reefs are the world's most species-rich marine biotopes. Due to climatic change and human impact the coral reefs are under pressure. Siltation resulting from deforestation, pollution due to urbanization, and coral bleaching linked to elevated seawater temperatures, are seen as major human-induced impacts on marine species diversity that play a role in tropical marine coastal areas. An important key to the species-richness of coral reefs is formed by the complex of species interdependencies. Host-symbiont relationships appear very specific. Thus the loss of a single host species (coral, sponge or tunicate) may also result in the disappearance of dependent species. At Naturalis species interdependencies between corals and parasitic coral gall crabs, parasitic ovulid snails, and pontoniine shrimps are assessed through the work of Bert Hoeksema, Charles Fransen, Sancia van der Meij, and Bastian Reijnen.

Mycorrhizae

The most widespread diffuse mutualism is the mycorrhizal association between plants and fungi. In this interaction, the plants exchange carbon for fungal nitrogen and phosphorus. Mycorrhizae are generally diffuse symbioses because a mycorrhizal plant typically associates simultaneously with multiple fungi and a mycorrhizal fungus often associates simultaneously with multiple plants. However, in several groups of plants specialization towards narrow clades of mycorrhizal fungi exists, particularly in orchids and plant lineages that exploit mycorrhizal symbioses ('mycoheterotrophs'). Evolutionary patterns of mycorrhizal specialization and their role in plant speciation is studied in mycorheterotrophic plants (Vincent Merckx and Constantijn Mennes) and orchids (Adam Karremans and Barbara Gravendeel, in collaboration with Lankester Botanical Gardens in Costa Rica).

Plants-insects

Plant-insect interactions are temporally, spatially, and ecologically dynamic, resulting in complicated patterns of interdependencies that range from mutualisms (pollination, protection and seed dispersal) to herbivory and carnivory. These interdependencies play a major role in the diversification of both groups. The observed nonrandom patterns of phylogenetic congruence between interacting plants and insects are produced by a combination of cospeciation, host switching, and tracking of particular resources or traits. At Naturalis, research on plant-insect interactions focuses on pollination interactions (Pleurothallidinae orchids by Adam Karremans and Barbara Gravendeel, and in Malesian Euphorbiaceae by Peter van Welzen), herbivory (leafmining Lepidoptera by Erik van Nieukerken, Nymphalid butterflies by Robin van Velzen, and adaptation to non-native plans by Menno Schilthuizen, Erik van Nieukerken, Kim Meijer & Leo Beukeboom (Rijksuniv. Groningen), Baudewijn Odé (Floron), and Roy Kleukers (EIS)), and carnivory (tropical pitcher plants by Rachel Schwallier and Barbara Gravendeel).



Highlight

Visit of Dr. Rudolf Rohr (Doñana Biological Station, Spain) on 12 & 13 June 2012 for a workshop on studying species interactions in R (see figure).

Research contributions

Medicinal and ritual plants
Illustrated field guide for Suriname

Tinde van Andel[1] & Sofie Ruysschaert[2]

[1] *Naturalis Biodiversity Center, Leiden*
[2] *Universiteit Gent*

Which herbs do Surinamese people use against diabetes? What does busi-blaw (*Indigofera suffruticosa*) look like and why does it protect you against the evil eye? What flowers are offered during Hindu services? Why do certain barks attract malicious forest spirits and how can you chase them away? The illustrated field guide *Medicinale en Rituele Planten van Suriname* (Fig. 1), based on traditional knowledge of the Surinamers themselves, provides answers to all these questions.
Suriname is a country with a great cultural and biological diversity. The interior rainforest houses a treasure chest of medicinal plants. During the past centuries, enslaved Africans and Asian wage laborers introduced many other useful plants to the country. Amerindians, Creoles, Maroons, East Indians, and Javanese: each ethnic group has its own language, religion, rituals, and ideas about health and illness. Nevertheless, there is ample exchange of plant knowledge between these groups. Traditional Amerindian crops end up in Creole herbal baths to call indigenous spirits, while Javanese magic shrubs are planted on Maroon graveyards. For many Surinamese, the use of medicinal herbs is essential for their physical and mental well-being. At present, thousands of Surinamers, especially Maroons, earn a living with the trade in medicinal plants (Fig. 2).

Medicinale en Rituele Planten van Suriname is the result of several years of scientific research by the National Herbarium of the Netherlands (Naturalis) and Ghent University (Belgium) on medicinal and magical plant use. We based the book on traditional knowledge of Surinamers from the regions Paramaribo, Pará, Wanica, Marowijne and Brokopondo and of Surinamese migrants in the Netherlands, complemented with data from literature and herbarium collections. This field guide contains scientific and vernacular names, botanical and use descriptions of almost 400 different plant species. We paid special attention to the translation of local names and the historical background of plant uses. Many honorary staff members of the NHN contributed to the book with plant and wood identifications, taxonomic descriptions and color photographs. Line drawings by botanical artists Hendrik Rypkema and Wim Hekking (†) further illustrate the book (Fig. 3).

The greatest part of this research was funded by the NWO-ALW Open competition grant “*Medicinal plants of Suriname-Changes in plant use after migration to the Netherlands*”. After the publication of several scientific papers on Surinamese ethnobotany that resulted from it, the authors decided that the raw data - traditional plant knowledge preserved over centuries by oral tradition - should be made available in an accessible format to the people that shared their knowledge with them.
The book is published in Dutch to serve its main public: readers in Suriname and the Surinamese migrant community in the Netherlands. An English translation is foreseen to serve a broader reader community. After the official book launch on the 8th of September 2011 at the Naturalis Auditorium, the book received ample coverage in the Dutch and Surinamese media. Apart from the regular bookstores, the book is also sold in Surinamese herb shops in Amsterdam, Rotterdam and The Hague.

Andel, T.R. van & S. Ruysschaert. 2011. Medicinale en rituele planten van Suriname. KIT Publishers, Amsterdam. ISBN 9789460221392.

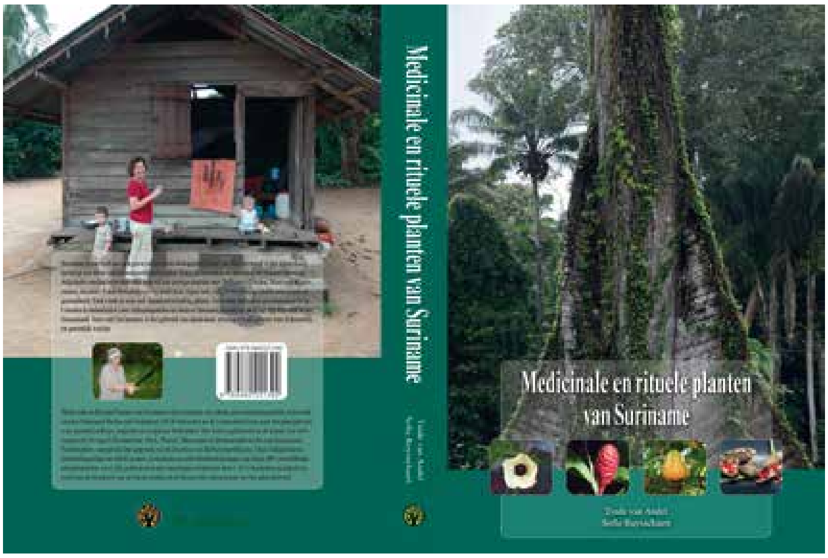


Fig. 1. Book cover of the illustrated field guide *Medicinale en rituele Planten van Suriname.*

Fig. 2. Harvesting *Dicranopteris flexuosa* in Pará, Suriname. This fern is believed to possess magic power and used to break up people's marriages. It is sold at the medicinal plant market in Paramaribo.
Photo: C. van der Hoeven.

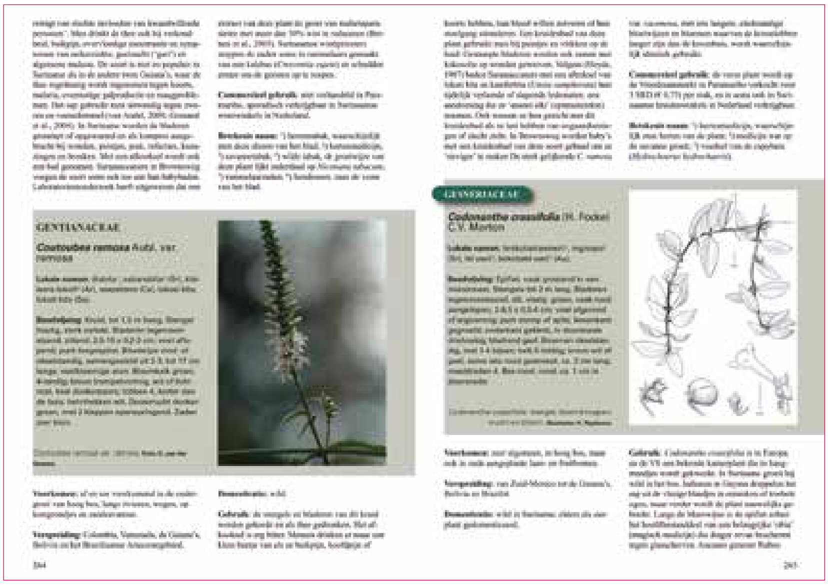


Fig. 3. Example of the treatment of *Coutoubea ramosa* and *Codonanthe crassifolia* in the book.

Wood science
In the service of legal timber trade

Pieter Baas[1], Elisabeth Wheeler[2], Frederic Lens[1] & Erik Smets[1]

[1] *Naturalis Biodiversity Center, Leiden*
[2] *North Carolina State University, Raleigh NC*

Microscopic wood structure harbours a host of diagnostic features suitable for identifying unknown wood samples to family, genus or even species.
For the enforcement of international or national protection measures to limit the logging and trading of endangered species it is crucial that their woods can be reliably identified by customs officers or their specialist consultants. The International Association of Wood Anatomists (IAWA), of which the editorial office has been hosted by the Leiden Herbarium since 1977, has played a leading role in developing user-friendly standard terminology for both hardwoods (1989) and softwoods (2003) and in supporting the web-based identification facility www.InsideWood (2004 onwards). Gasson, Baas and Wheeler (2011) are the first to provide detailed microscopic images together with coded wood anatomical descriptions using the IAWA Hardwood and Softwood Lists for all 27 CITES-listed taxa for which the international trade has been limited by international law. The result is an especially useful 44-page *microscopic atlas of all CITES-listed tree species*.
This publication is not only useful, but also striking because of the beautiful wood anatomical patterns it portrays for these endangered species that deserve our protection (Fig. 1 and 2).
The publication forms a chapter in a book containing the proceedings of a successful symposium on *"Practical and scientific efforts to combat illegal logging"* held in Madison, WI, USA, in June 2010 (Fig. 3). At the symposium, invited world experts addressed the many and diverse ways in which wood science is relevant for law enforcement to help protect forest ecosystems and endangered tree species and to support the CITES convention, restricting the international trade in endangered species. The first chapter surveys the interfaces of wood science and forest and timber policy.
Six chapters contain contributions from wood anatomy, including automated "machine vision", and another four explore the increasing importance of contributions from molecular biology (DNA analysis) and chemistry (especially infrared spectroscopy).
Wood anatomy at the National Herbarium section of the Naturalis Biodiversity Center has a strong international position, which explains why this book was published and co-edited in Leiden.
The strong international position increased even more, when on 22 September 2011 Naturalis marked the merger in Leiden of all major institutional wood collections (xylaria) in the Netherlands to constitute the now largest wood collection in the world (120,000 specimens) with a successful Wood Symposium. On this occasion, Erik Smets, Pieter Baas, Frederic Lens (all from Naturalis Biodiversity Center) and René Klaassen (from the Foundation Wood Research, SHR in Wageningen) lectured on the importance of wood collections for fundamental and applied research.

Alex C. Wiedenhoeft & Pieter Baas (editors). 2011. *Wood Science for Promoting Legal Timber Harvest*. Special Issue of the *IAWA Journal* 32(2) 121-296.
Including a chapter by Peter Gasson, **Pieter Baas** & Elisabeth A. Wheeler. Wood anatomy of CITES-listed tree species. *IAWA Journal* 32: 155-198.

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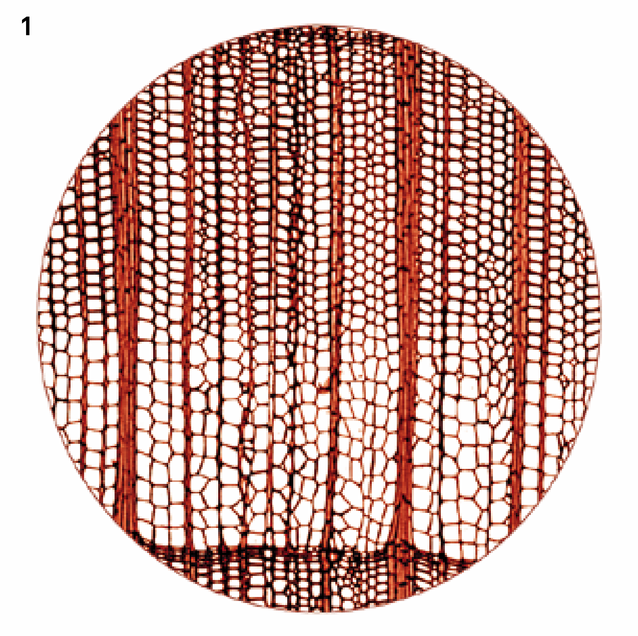

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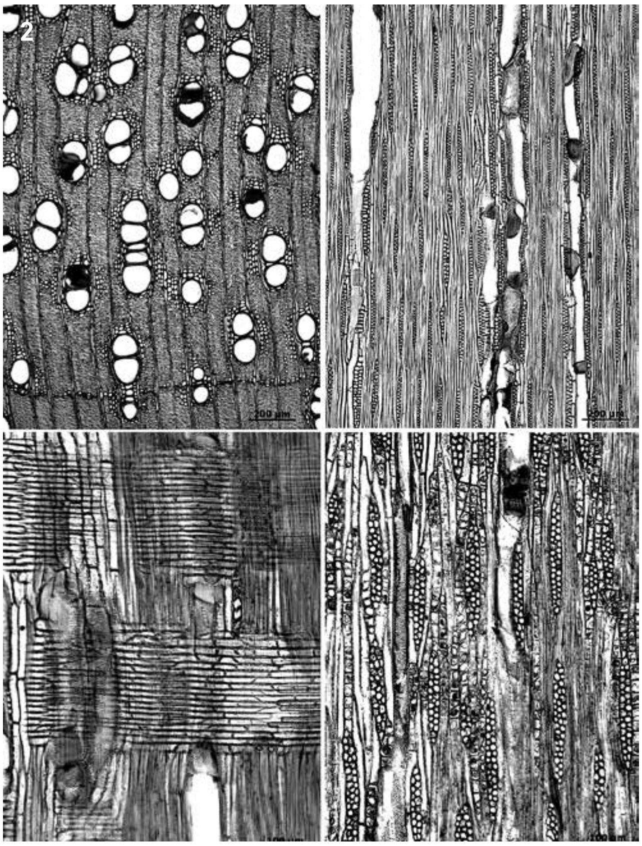

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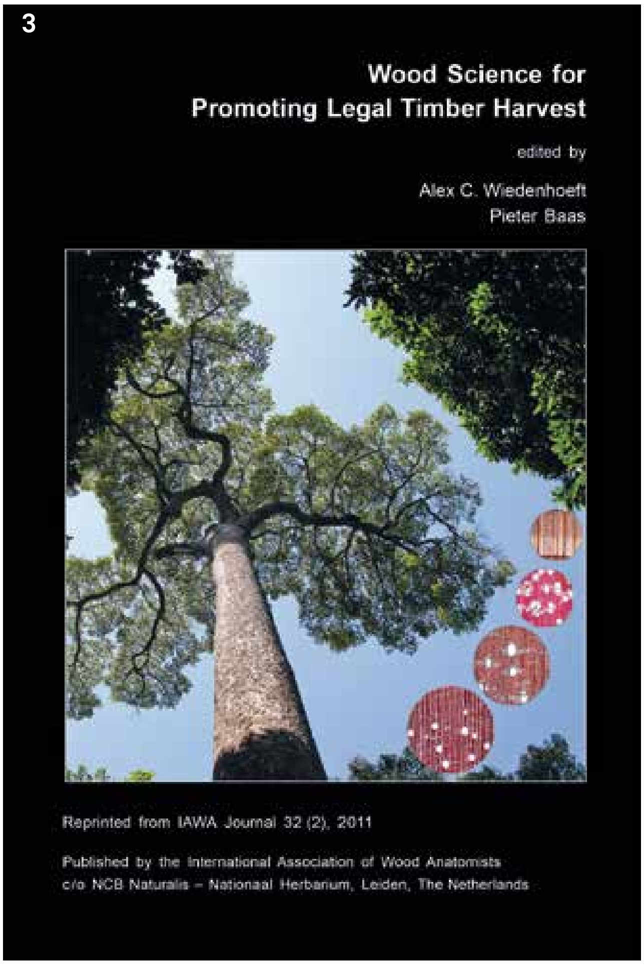

Wood Science for
Promoting Legal Timber Harvest

edited by

Alex C. Wiedenhoeft
Pieter Baas

Reprinted from IAWA Journal 32 (2), 2011

Published by the International Association of Wood Anatomists
c/o NCB Naturalis – Nationaal Herbarium, Leiden, The Netherlands

Fig. 1. Transverse section of the wood of *Tetracentron sinense* Oliver, a CITES-listed timber species from China and Japan
Fig. 2. Plate of *Caesalpinia echinata* – Brazilwood or Pernambuco, A CITES-listed timber species from Brazil.
Fig. 3. Cover of special issue.

Brokopondo Lake Suriname:
Floristic assessment on its islands

Chequita Bhikhi[1], Frits van Troon[2], Gunovaino Marjanom[3], Fabian Diran[3], Idris Fredison[4] & T. van Andel[1]

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[3] *Anton de Kom University of Suriname, Paramaribo*
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The Prof. Dr. Ir. W.J. van Blommensteinmeer or Brokopondo Lake is an artificial lake located in district Brokopondo in Suriname, about 90 km south from the capital city of Suriname. The bordering landscape of the Brokopondo Lake is part of the Hilly Lowland with locally iron stone and bauxite at the soil surface, mixed with sand, stones, clay, loam and gravel. It encompasses an area of 1560 km^2 and a water level between 47 and 50 meters above sea-level. The former landscape of the area was hilly with tops of about 100 m and a wide basin in the centre. The original vegetation of the lake basin was studied by Van Donselaar (1989) from 1964 to 1972. Now the lake contains more than 1100 islands of different sizes and standing dead tree stems along the borders. The forest on the hills, except for Tonka Island, has not been investigated before. Between January and April 2011 we embarked on an expedition to the Brokopondo Lake with two main goals: 1) to study the floristic composition and diversity of the lake islands and of the bordering mainland and 2) to train students in plant identification, collecting and processing techniques.

The expedition took place over a period of 60 days from January to April 2011. The expedition crew consisted of a group of 9 members; three students, a field-botanist, an assistant, two game-wardens, one boatman and the first author of this article. We performed general plant collecting surveys to obtain baseline data on the floristic composition of the lake and its islands. Fertile plants were collected from 87 randomly selected islands, beaches, and the mainland. A GPS coordinate was acquired for each collected specimen which were displayed on a map using GIS programs Manifold 8® en ArcMap 9.3.1 (Fig. 1). We also established eleven 0.1 hectare plots on several islands and on the bordering mainland to collect baseline data for the tree-alpha-diversity of the area. In these plots, we inventoried and sampled all trees with a diameter at breast height (dbh) of 2.5 cm. All plant parts were processed in the field using standard techniques and identified at the NHN-Leiden by the author and by botanical specialists, specialized in the Guianan region. Duplicates of eight plant families were sent to their respective botanical specialists for identification. We determined the number of new species records for Suriname by comparing our plant list with the checklist of the flora of the Guianas of Funk *et al*. (2007), and different internet dataportals.

Vegetation types

We encountered eight different vegetation types, primary forest, secondary forest, creek forest, riverine forest, swamp wood, swamp forest, mountain savanna forest and savanna forest. Most islands were covered with primary intact forest. Secondary forest dominantly occurred on islands close to villages, small settlements and in areas where gold mining activities took place. The wet forest types were found in the creeks and swamps in the lake. Riverine forest was found along the Suriname River. Mountain savanna forest and savanna forest was found on islands with a granitic soil. Large granite boulders were also found on the surface and shores of these islands. Island beaches were dominated by pioneer species such as *Mimosa pellita*, *Spermacoce alata, Sarcostemma clausum*, *Piriqueta cistoides*, *Passiflora foetida var. hispida*, *Ipomoea squamosa* and *Scoparia dulcis* (Fig. 2).

Families and species

During the expedition we collected 992 specimens, of which 98% is identified to species level. The majority (589) of these plants belong to trees and a smaller proportion (274) to lianas. The identified plants belong to 93 families, 307 genera and 597 species. Fabaceae contained by far the largest number of species (94), followed by Bignoniaceae (26), Myrtaceae (26) and Sapindaceae (25).

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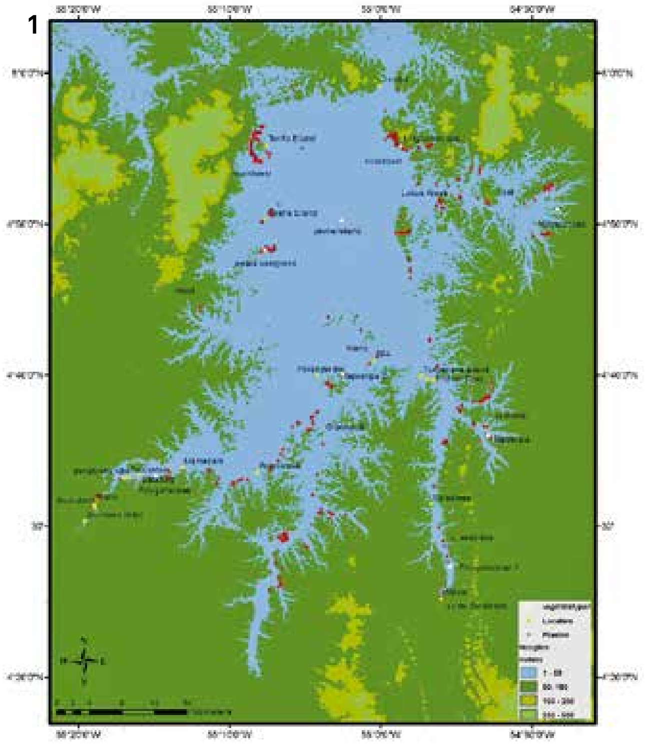

Fig. 1. GPS locations of collected plants specimens and villages in the Brokopondo Lake (January-April 2011) (by Niels Raes (NHN) 2011).

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Fig. 2. Colonization of island beaches with *Spermacoce alata*.
Fig. 3. Large abundances of *Ludwigia sedoides* in the Saracreek.

The expedition added 286 new plant species and 8 families to the checklist of the area.

New plant species

The expedition added 14 new plant species records to the checklist of Suriname, including three, *Machaerium multifoliolatum*, *Paullinia livescens*, and *Eugenia warmingiana* new for Suriname, Guyana and French Guiana. We also recorded a possible *Calyptranthes* (Myrtaceae) species new to science (*pers. comm.* Eve Lucas, Myrtaceae specialist of KEW botanical gardens). The new records *Tynanthus polyanthus, Tetrapterys megalantha, Ludwigia sedoides, Polygonum ferrugineum, Chiococca alba, Crepidospermum goudotianum, Protium morii, Protium opacum, Hirtella davisii, Inga alata, Psidium cattleianum* were collected on the shores of islands or in the lake. Extensive mats of *Ludwigia sedoides* were found in the Saracreek (Fig. 3). This species is native to Brazil and was possibly introduced to the area by Brazilian gold miners which are active in the area. *Polygonum ferrugineum* dominant in the creeks and gullies in northern Suriname also grows in dense mats in the Saracreek and in the transition zones between lake, river and creeks.

Discussion and conclusions

The number of new species for Suriname in such a short distance (90 km) from the capital city of Suriname shows that the area was little explored. The fact that we found some of these new species in large abundances indicates that inundation of the valley created a number of new habitats with opportunities for new species to establish. The lake location is mentioned as a white spot on a spatial distribution map for botanical collections (Haripersaud 2009), suggesting that few botanical inventories took place in the area over the years. The plant diversity in this area is thus of great importance for science. Further analyses of the plot data, collected during this expedition, will contribute significantly to the knowledge of plant diversity in the area. The Surinamese government, however, is planning to extend the southern part of the lake to increase the capacity for hydro electricity.
It means that the rising water level will again bring changes in the floristic composition of the lake.
We aim to study the vegetation of the Lake in more detail and to predict future vegetation changes due to Lake Expansion through a new project in the future.

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Invasive species
A Dutch information system

Leni Duistermaat[1], Johan van Valkenburg[2], Edu Boer[1] Tanja Speek[3], Roelf Pot, Clemens van de Wiel[3], René Smulders[3], René van Moorsel[1] & Bert Lotz[3]

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Leiden University: Marie-Anne Frenken, Thijs Groenewegen, Carlo Tomas
University of Groningen: René Cappers, Renée Bekker
Hortus Leiden: Paul Kessler
Illustrations (Naturalis): Ben Kieft, Anita Walsmit Sachs, Esmée Winkel

[1] *Naturalis Biodiversity Center, Leiden*
[2] *Nederlandse Voedsel en Waren Autoriteit, divisie Plant, Wageningen*
[3] *Plant Research International, Wageningen UR*

The last few decades have shown a strong increase of non-native species in the Dutch flora (Tamis, 2005). The majority of these new-comers are very modest and do not lead to problems. Floating pennywort (*Hydrocotyle ranunculoides*) (Fig. 1), however, is a clear example of a species that does cause problems. Species that through strong expansion of their distribution become problematic, having a negative impact on economy, public health or safety, are called invasive species. Invasive species, after habitat destruction, are worldwide seen as the second cause of biodiversity decline.

Many exotics have been imported via trade, either intentionally e.g. as ornamentals, or unintentionally e.g. as weed in potted plants or as contamination in seed products. As it is better to prevent than to cure, it seems logic to try to prevent the introduction of potentially invasive species. Therefore, the Dutch Ministry of Economic Affairs, Agriculture and Innovation provided a 4-year subsidy from the FES-programme "Versterking Infrastructuur Plantgezondheid" to build an information system on potentially invasive exotic species. The aim is to deliver information that could form the basis of an estimation of the chance that a species will develop invasive behavior upon introduction in The Netherlands, and to provide tools with which these species can be identified. Focus is on vascular plants, with special attention to aquatic plants because of acute problems in this group. The information system forms part of Q-bank, an identification and detection reference database for phytosanitary organizations (http://www.q-bank.eu/).

Selection of species

We included both species that are not yet present but could form a risk for the ecoregion that includes The Netherlands, species that are already present but with a management perspective, and species that are naturalized but for which strategic actions apply. Furthermore, we included species regulated in third countries. Export and transit of plant material is a considerable part of our economic motor, and contamination is not uncommon. Control of shipments on undesired or banned species before departure prevents possible problems at import in the third country. The degree of coverage differs from species to species. Fifty are fully treated: presenting information on taxonomy, bibliography, morphology, illustrations, uses, look-alikes, distribution (native and actual), biochemistry and molecular data, ecology, and invasion risk and control. Another 140 species are treated in less detail, while about 300 species are included in the identification keys only. We tried to include photos of all species, made by Ben Kieft in the studio (Fig. 2), by the researchers in the field, or obtained from others.

Distribution is described, as well as presented in maps. A world map is presented for 200 species based on literature, and for 50 species justified with herbarium collection data. For 50 species we present detailed maps of the Netherlands based on field recordings (FlorBase: NHN / FLORON) and herbarium collections (NHN). Because of the dynamic character of both trade, science and flora, we shall have to review the selection of species regularly.

Identification

To facilitate identification of invasive plant species, we developed interactive keys in the software package Lucid http://www.lucidcentral.org/. The keys are

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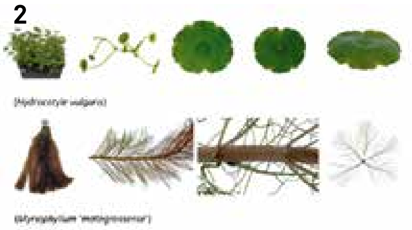

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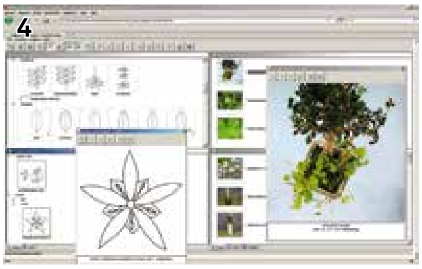

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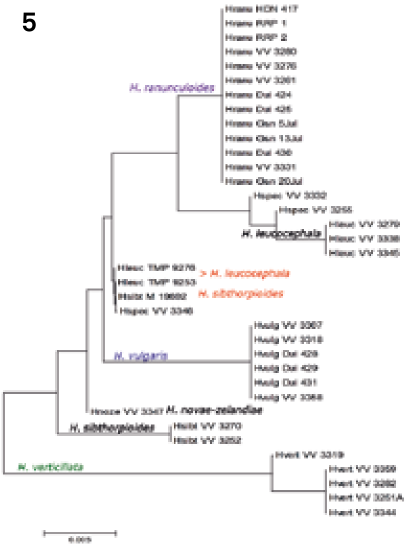

Fig. 1. *Hydrocotyle ranunculoides* (Floating pennywort): an invasive species in The Netherlands. (Photographer: B. Kieft, NHN Leiden)

Fig. 2. Examples of standardized pictures: *Hydrocotyle vulgaris* (upper row) and *Myriophyllum tuberculatum* (lower row).

Fig. 3. Digital identification key to seeds: identification of *Ambrosia artemisiifolia*.

Fig. 4. Digital identification key to weeds in bonsai plants: identification of *Centella asiatica*.

Fig. 5. Dendrogram based on *trnH-psbA*-sequences in *Hydrocotyle*.

intuitive, work visual and avoid the use of technical terminology. Artists Anita Walsmit Sachs and Esmée Winkel prepared illustrations of the features.
The user can start the identification by selecting the most obvious characters of the plant. The result of the choices (species in the selection, species out of the selection) is directly visible. We have prepared five keys, available on internet and with free access (www.q-bank.eu/Plants/, under the button *Identification*): seeds of invasive plants (in cooperation with the University of Groningen; Fig. 3), weeds in bonsai plants (Fig. 4), seedlings of invasive plants, invasive aquatic plants, and invasive terrestrial plants.
We include look-alikes that do not pose a risk but can be mistaken for the (potentially) invasive or quarantine species, to preclude '*false positives*'.
To distinguish invasive from non-invasive species based on morphology alone can be hard at a vegetative stage, as is commonly how material is met in inspection situations. DNA barcoding could be an alternative for reliable identifications, for which the CBOL Plant Working Group proposed the chloroplast sequences *rbcL* and *matK*. We performed a few pilot studies and additionally tested the *trnH-psbA* locus, as it is more variable than *rbcL* and more reliably amplified for sequencing than *matK*. Using *trnH-psbA* alone, we were able to distinguish the invasive *Hydrocotyle ranunculoides* from at least six other species from the genus *Hydrocotyle* (Van de Wiel *et al*., 2009; Fig. 5). We were also successful in the genera *Ludwigia* (*L. grandiflora* and *L. peploides*), *Myriophyllum* (*M. heterophyllum* and *M. aquaticum*), *Cabomba* (*C. caroliniana*), and four species of the Hydrocharitaceae (*Egeria densa*, *Elodea canadensis*, *Elodea nuttallii*, and *Lagarosiphon major*), Ghahramanzadeh et al. (2013). At the moment, DNA-barcoding still requires processing in a special laboratory. We foresee, however, that in the near future determination of DNA sequences may become a matter of routine that could be performed by customs and inspectors in the field, allowing for identification of species independent of external features.

Prepared for the future

The information system for (potentially) invasive plant species as in Q-bank is a reliable tool to support inspections, not only during import and export, but also within the framework of the 'Covenant Waterplanten'. With the increasing interest for the 'Groene Ruimte', the system is essential for education purposes. Knowledge concerning invasive plant species will be considered basic for both the inspector in the field and the policy officer dealing with the invasive plant species (inter)nationaly. With this system NVWA is prepared for future regulations from Brussels concerning invasive plant species in Europe.

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Surviving climate changes
The case of arctic mycorrhizal fungi

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Recent and future climate changes have major impacts on biological diversity. This is especially true in the Arctic that is already exposed to the most extreme changes. As a result, there are serious concerns among scientists and the public alike related to the future of arctic biodiversity. As a response to warming temperatures, shifts in land surface vegetation have already been observed. For example, increases in the abundance and extent of shrubs have been reported in various areas of the Arctic. Because future climate warming is expected to cause the distribution area of many arctic plant species to shift further north, long-distance dispersal capabilities of individual species will have a major influence on the composition of future arctic ecosystems. Thus, it is important to determine whether or not species will be able to track their climatic niche by assessing their long-distance dispersal capabilities.

Mycorrhizal fungi in arctic ecosystems

Fungi play a central role in the functioning of all terrestrial ecosystems due to their roles as root-associated symbionts (e.g. mycorrhizae) and decomposers. This is particularly true in the Arctic, wherealmost all plants are highly dependent on mutualistic relationships with mycorrhizal fungi for survival in these nutrient-poor environments. Ectomycorrhiza (ECM) is the predominant mycorrhiza type in arctic and alpine environments and ECM fungi are crucial for the survival of arctic shrubs, e.g. dwarf birch (*Betula nana*), mountain avens (*Dryas octopetala* and *D. integrifolia*), and various dwarf willows (*Salix* spp.). Therefore, ECM fungi are expected to play an important role in arctic vegetation change, particularly shrub expansion. However, fungal communities in the Arctic have been largely unknown and even such basic information as the estimated number of species has been unavailable before our study. Furthermore, based on studies on temperate and tropical ECM species, it has been generally assumed that typical ECM plant and fungus symbionts require overland routes for migration, possibly as a consequence of the strong reliance of the shrubs on the ECM fungi and *vice versa*. Therefore, in theory, long-distance dispersal and establishment of either the mycorrhizal fungus or the host plant in isolation has been considered unlikely, because the simultaneous arrival of fungal spore and host plant seed are presumed necessary. Indeed, the vast majority of temperate and tropical ECM fungi seem to be restricted to a certain continent, often even to a small geographic region. On the other hand, it was not known before our study whether or not arctic ECM fungi fit this conventional picture.

Svalbard: a model system

The Svalbard Archipelago (a group of islands ranging from 74° to 81°N and 10° to 35°E) represents a good model system for studying long-distance dispersal in the Arctic, because it was fully glaciated repeatedly during the glacial cycles of the Pleistocene, with virtually no vegetation surviving *in situ* in the archipelago. Genetic studies of arctic plants indicated that colonization by plants occurred after the glacial retreat. This is in agreement with geological reconstructions suggesting an extreme ice cover that excluded the local survival of most terrestrial plant species, and with palaeorecords that show evidence for arctic vegetation only after the end of the last ice age (ca. 10,000 years ago).

In this study, which is the first large-scale attempt to characterize the fungal communities of Svalbard, we analysed more than 3000 DNA sequences, derived from soil samples and collected fruiting bodies ('mushrooms'). Despite Svalbard's geographic

Fig. 1. *Cortinarius favrei*, one of the numerous ectomycorrhizal symbiont of the polar willow (*Salix polaris*) that colonized Svalbard via long-distance dispersal (Photo: Geml).
Fig. 2. Arctic tundra landscape in Svalbard (Photo: Geml).
Fig. 3. Machiel Noordeloos collecting fungi in Svalbard (Photo: Geml).

Fig. 4. József Geml on fieldwork in northern Alaska (Photo: Timling)
Fig. 5. Polar willow (*Salix polaris*), one of the most important arctic ectomycorrhizal host plants (Photo: Geml).
Fig. 6. Ny-Ålesund, the northernmost village of the world, is a unique scientific research community. The twin buildings of the Netherlands Arctic Station are visible in the foreground (Photo: Geml).

isolation and harsh arctic climate, we found that ECM fungi are surprisingly diverse, with at least 109 species, and more will likely be discovered with future expeditions to areas not yet sampled. For comparison, the total number of flowering plant species is ca. 165 for Svalbard. Of the species that we found, several are newly discovered. The most species-rich genera are *Thelephora/Tomentella*, *Cortinarius* and *Inocybe*, followed by *Hebeloma*, *Russula*, *Lactarius*, *Entoloma*, *Sebacina*, *Clavulina*, *Laccaria*, *Leccinum* and *Alnicola*(all in the phylum Basidiomycota).

Arctic fungi have been selected for mobility

Because previous studies on arctic fungi were limited in scope and scale, there is very scarce published information available on the distribution of arctic fungi. Therefore, we compared our DNA sequences from Svalbard to ca. 30,000 DNA sequences generated by our research group from sites along the North American Arctic Transect (NAAT), which spans more than 1000 km from northern Alaska to Ellef Ringnes Island in the Canadian Arctic.
Our results suggest that the vast majority of ECM fungi in Svalbard also occur in other areas of the Arctic and likely colonized the archipelago in post-glacial times, similar to arctic plants. In fact, based on what we know from plant fossils, it is very likely that ECM fungi had been present in Svalbard during many previous interglacial periods, but they were probably wiped out repeatedly by the glaciations, and then recolonized Svalbard again and again as the ice retreated. Our evidence suggests that, contrary to the prevailing view on the dispersal capabilities of ECM fungi, long-distance dispersal has probably played a major role in the evolutionary history of many ECM fungi at high latitudes in the Northern Hemisphere. It is very likely that many arctic fungi, similarly to arctic plants, have been selected for mobility during the glacial cycles and have the potential to track their climatic niches in the changing Arctic.

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An arctic community of symbiotic fungi assembled by long-distance dispersers: phylogenetic diversity of ectomycorrhizal basidiomycetes in Svalbard based on soil and sporocarp DNA.

Fungi in mammoth dung
DNA reveals very high diversity

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Little is known yet about the species richness of fungal communities of the mammoth steppe as fossil fungi are often difficult or even impossible to identify. This hampers progress in scientific insight since many species are either plant- or animal-associated, or both, and more information about their past distributions could provide better knowledge about climate-driven changes in biodiversity.
Fossil dung fungi are rather difficult to identify based on morphology (van Geel *et al.* 2011).
Using morphological features of ascospores and fruiting-bodies, so far only a few species could be identified from frozen mammoth dung (Fig. 1).
Ancient amplifiable fungal DNA has been shown to survive for several thousand years in fossil permafrost (Taberlet *et al.* 2012).
In the present study , we explored the diversity of fungal communities associated with dung of extinct mammoths (Fig. 2). Plant assemblages of the mammoth steppe were quite different from present-day Arctic communities and experienced very different grazing pressures (Blinnikov *et al.* 2011). Our study provides a molecular survey of fungi present in the mammoth steppe at two different sampling localities (Alaska and Siberia) by recently developed massive parallel Roche 454 pyrosequencing (Margulies *et al.* 2005) of permafrost-preserved mammoth dung dated to 18,560 ± 50 BP and 12,300 ± 70 BP, respectively.

Dung fungi

Our DNA barcoding analyses not only confirm the presence of three of the taxa that had been recognized by their spores in fossil mammoth dung, but add much more detailed identifications to the species level. A total of seventeen additional dung fungal genera comprising over 180 species were retrieved. These findings are in accordance with the number of dung fungal genera found in dung of extant boreal moose and deer. They support the view that mammoths had a wide food choice since a more species-rich diet generally correlates with higher dung fungal species richness. The high diversity of dung fungi retrieved from the mammoth dung samples analyzed here is probably also caused by the fact that mammoths ate dung, in this way further increasing uptake of fungal spores.

According to our phylogenetic analyses, several fungal species identified in the fossil dung analyzed are closely related to species known to occur on elephant and horse dung. These host associations are not surprising since typical grazers roaming Eurasia during the Pleistocene in large numbers included the musk-ox (*Ovibos moschatus*), mammoth (*Mammuthus primigenius*), woolly rhinoceros (*Coelodonta antiquitarius*), horse (*Equus* spp.), Steppe bison (*Bison priscus*) and saiga antelope (*Saiga tatarica*) (Guthrie, 1990).

Comparison between fossil and extant fungi

After abrupt climate shifts occurring between 15,000 and 11,000 years ago (Lowe *et al.* 2008), the vegetation of Alaska and northern Siberia changed from a grass-dominated steppe with many species of large herbivores in high densities during the Last Ice Age into a shrub-dominated tundra.

First of all, only very few matches could be found between the dung fungal genera nowadays recorded from Alaska and Siberia and the genera

Fig. 1. *Carex* infected by coprophilous *Sordaria* found in fossil mammoth dung. **Fig. 2.** Permafrost preserved mammoth dung analyzed.

Fig. 4. Uninfected moss (*Polytrichum*) remains found in fossil mammoth dung.

Fig. 3. Uninfected moss (*Bryum*) remains found in fossil mammoth dung (photographs fig. 1-4 by Jan van Arkel).

retrieved that occurred in the same area 18,000-12,000 year ago (this study, Pirozynski *et al*. 1984). Secondly, we found that dung fungi associated with large mammalian herbivores may have declined after the end of the Last Ice Age. DNA-based diversity assessments of fungi in modern dung samples from Spitsbergen further support this conclusion.

Contrary to the large diversity in coprophilous fungi found, no bryophilous fungi were found in the fossil mammoth dung analyzed. Bryophilous fungi grow on mosses and liverworts. Of genera occurring on moss species eaten by mammoths, many reference nrITS sequences are availale in NCBI GenBank. Our molecular survey should therefore have detected these fungi if they had been present in the fossil dung. The fact that we did not retrieve any of these genera by DNA barcoding of the fossil dung might indicate that bryophilous fungi, in contrast with coprophilous fungi, were not common in the Mammoth steppe (Figs 3 and 4). Since bryophilous fungi are currently frequently encountered it might be that Arctic fungal coprophilous species were partly replaced by bryophilous species and other plant associated groups of fungi such as mycorrhizae and rusts after mammoths and other large megafauna went extinct.

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First fully sequenced orchid
Mining the genome of *Erycina pusilla*

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The emerging field of evolutionary and developmental biology ('evodevo') investigates how changes in the number, sequence and expression of developmental genes are driving the evolution of morphological novelties (Mondragon *et al*. 2009). Orchids are excellent evodevo case studies as they radiated into one of the largest and most diverse plant families on earth during the last 80 million years (Ramirez *et al*. 2007). Over 20,000 species have been described and many more are being discovered every year. Orchid flowers are highly modified and examples of spectacular co-evolution between plants and pollinators by their large variation in colours, fragrances, lifespans and shapes (Gravendeel *et al*. 2004). Unfortunately, the genetic basis of orchid development and evolution is still poorly understudied. One of the main reasons for this is that no fully sequenced orchid genome is yet available. Orchid genomes are large and often complex due to polyploidy which makes it difficult and expensive to analyze using traditional Sanger sequencing.

We embarked on sequencing the nuclear genome of *Erycina pusilla*, a species in the Oncidiinae (Epidendroideae) which is easy to maintain under laboratory conditions because of its extremely small size (Fig. 1). Its relatively small (1.475 Gb) and diploid genome and short generation time of only 6 months make this species an ideal model for studying orchid evolution and development. We applied a hybrid approach for *de novo* sequencing of its genome by combining short (100 bp) Next Generation Illumina HiSeq with longer (1500 bp) Pacific Bio reads. After assembly, we compared the results obtained with available data on floral developmental genes retrieved from earlier sequenced and annotated plant genomes (Fig. 2). These included both established plant genetic models such as barley (*Hordeum*), corn (*Zea*), rice (*Oryza*) and wheat (*Hordeum*) as well as other emergent orchid models such as bee orchids (*Ophrys*).

Gene duplications drive orchid floral evolution

We sequenced genes coding for orchid floral colour, fragrance, lifespan and shape. Copies of these genes found in the genome of *Erycina pusilla* ranged from one up to eight. According to our phylogenetic analyses, most copies were the result of recent duplications with the exception of the duplications of the floral shape genes which were found to be very ancient. Changes in expression and mutational rates indicates that many gene copies retrieved new (sub) functions after duplication (Wang *et al*. 2001; Tsai *et al*. 2004; Han *et al*. 2006; Křeček *et al*. 2009; Chiou *et al*. 2010; Mondragon and Theissen, 2011; Mondragon and Trontin, 2011; Schluter *et al*. 2011). Our results show that gene lineage diversity in this first fully sequenced orchid genome is extremely high, supporting the hypothesis that duplication and subfunctionalisation of developmental genes are indeed important drivers of morphological novelties.

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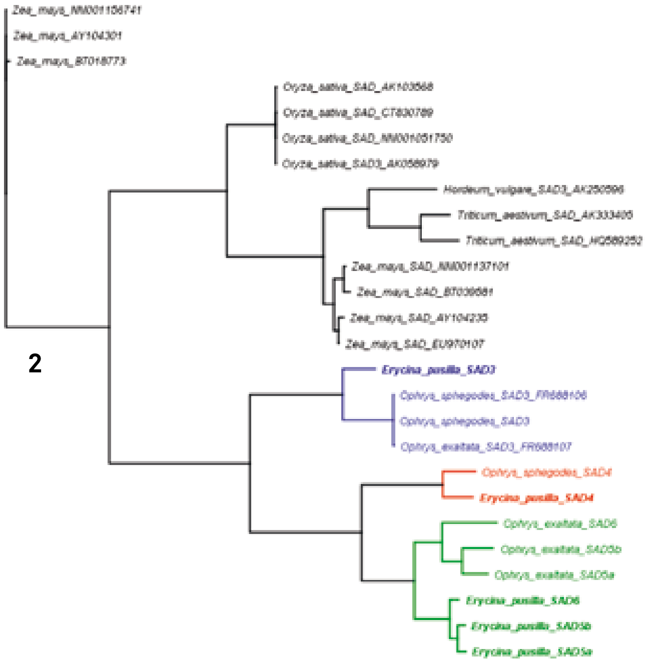

Fig. 1. Different developmental stages of *Erycina pusilla* sequenced (photographs by Rogier van Vugt). Mature plants are 5 cm high.

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Enigmatic plant fossils
An extinct type of seagrass

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Seagrass communities are important ecosystems in relatively warm, shallow seas. They are well-known for their high biodiversity, and many aspects of seagrass biology and ecology have been studied during the last decades. Seagrasses are flowering plants that successfully invaded the marine environment. They include members of three separate clades within the monocot order Alismatales, and share a number of traits that enable them to survive in a marine habitat: tolerance to salinity, an adequate aeration system and a capacity for underwater reproduction and anchorage.

Monocots diversified considerably during the Early Cretaceous, and seagrasses probably evolved from freshwater monocots during the Late Cretaceous. Worldwide, seagrass fossils are rare, but locally they are relatively common, for instance in the type area of the Maastrichtian Stage (SE Netherlands, NE Belgium). *Thalassocharis bosquetii* stems from this same area resemble those of the modern genus *Cymodocea* (Cymodoceae). The probably belonging leaves are always found incomplete and detached from the stems. They were described as *Thalassotaenia debeyi*. Comparison of these fossil leaves with leaves of extant seagrasses shows that there is not an easy match with any of them. *Amphibolis* and *Thalassodendron* (Cymodoceaceae) and *Posidonia* (Posidoniaceae) show the greatest resemblance.

Deviating seagrass stems

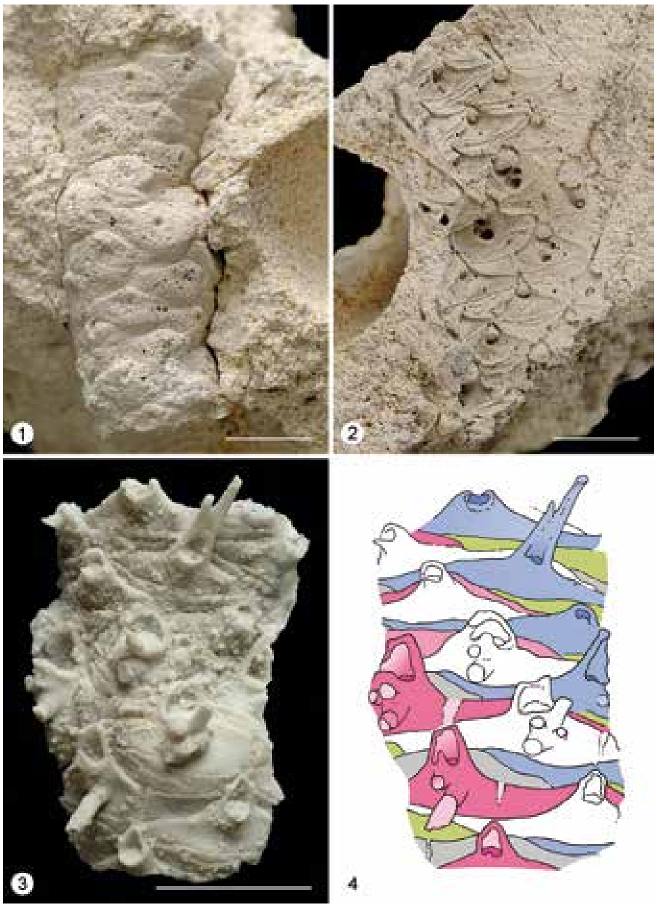
During the revision of extensive new seagrass stem material from the Maastrichtian type area, we found some deviating axes with spiral phyllotaxis (Fig. 1-6) among the distichous seagrass specimens. Several of these axes were labelled as 'seagrass', others as 'twig of *Cycadopsis cryptomerioides*' (a fossil conifer), as 'conifer?' or as 'alga??'. However, the fossils do not adequately match any of these groups.
The available material (35 specimens up to 2009) originates from quarries and temporary exposures in the western part of the area. Most of this material comes from the upper part of the Meerssen Member of the Maastricht Formation. Two specimens originate from the slightly older Emael Member. During fieldwork along the Albertkanaal in 2009 we collected much additional material (ca. 400 specimens) from the uppermost part of the Meerssen Member (Fig. 7).

The Emael and Meerssen Members consist of rather coarsely grained biocalcarenites deposited in, respectively, shallow and very shallow waters far off the coast. Macrofossils associated with the deviating material include seagrass stems with attached roots (*Thalassocharis bosquetii*), echinoids, bryozoans, a coral, foraminifers, serpulids (also epibiontic on the stems), glycymerid, ostreid, pectinid and other bivalves, gastropods, and ammonites. Remains of terrestrial animals or plants were not found.
A palynological sample taken from the matrix of stem fragments from uppermost part of the Meerssen Member is rich in aquatic palynomorphs; index taxa confirm the assignment to the very latest Maastrichtian. Terrestrial palynomorphs were not recorded.

While the stem fragments originate from the Emael and Meerssen Members, a piece of chert from an intermediate level (Nekum Member) contains several loose leaf fragments and a stem apex with attached leaf fragments, which all would fit well onto the stem fragments found in the Emael and Meerssen Members. Associated macrofossils include some of the species also found with the stem fragments.

3-D and taxonomical puzzle

The abundant material eventually permitted the description of a new genus and species: *Mosacaulis spinifer*. The genus name *Mosacaulis* is derived from Mosa (Latin for Maas, the river after which the city Maastricht, the Maastrichtian Stage and also



Figures. 1-4. *Mosacaulis spinifer*. NHMM RH 904 (holotype). Albertkanaal, temporary exposure. Bar = 5 mm. **1.** Internal stem-cast in matrix, showing a locally constricted stem fragment with densely-spaced leaf-bases. At the right is the imprint of an ammonite fragment (*Hoploscaphites constrictus*). Counterpart shown in Fig. 2. **2.** External stem-cast in matrix, showing densely-spaced leaf-bases with acuminate lateral extensions. Counterpart shown in Fig. 1. **3.** Artificial cast of the impression in Fig. 2, showing densely-spaced leaf-bases, each with a spiny structure, and several leaf-bases with 1-3 attached roots. Most spines and roots broke off during removal of the cast from the impression (compare with Fig. 4). **4.** Schematic drawing of the artificial cast in Figure 3, showing the spiral arrangement of the densely-spaced leaf-bases with acuminate lateral extensions. The five clockwise spirals have been given different colours, successively from the lower left left to the upper right side: red, white, blue, green and grey (green and grey series largely hidden at the back of the cast).

Figure 5. *Mosacaulis spinifer*. NHMM RH 933 (paratype). Geulhem, Curfs Quarry. Internal stem-cast in matrix, showing a long stem fragment with densely-spaced leaf-bases with spiny structures. Bar = 1 cm.

Figure 6. *Mosacaulis spinifer*. Renkens 27/11/09. Albertkanaal. Piece of matrix (just after collecting; see Fig. 7) with impressions and internal casts of various stem fragments. Several cross-sections show a central strand of vascular tissue. Bar = 1 cm.

Figure 7. Fieldwork along the Albertkanaal, 27 November 2009, during which we (Sjir Renkens on photo) could collect much additional material of *Mosacaulis spinifer* from the uppermost part of the Meerssen Member.

the marine reptile *Mosasaurus* have been named) and caulis (stem). In order to understand the three-dimensional structure of the stem-wall, we prepared artificial casts of a few stem impressions. We interpret *Mosacaulis spinifer* as a plant with cylindrical, dichotomously branching (pseudo) herbaceous axes with a central strand of vascular tissue, intermittant growth and densely-spaced, semi-amplexicaul leaves arranged in low spirals, with reproductive structures (sporangia?, prophylls associated with flowering axes?) attached to the adaxial sides of the leaf-bases. Adventitious roots are often attached near the centres of the larger leaf-bases. The possibly belonging leaves lack stomata. We interpret them as single-veined.

We consider *Mosacaulis spinifer* as a vascular plant of unknown systematic affinity, showing resemblances with such disparate lineages as lycopsids (e.g. *Isoetes*, *Quillwort*) and flowering plants (e.g. the basal order Nymphaeales). Its seagrass-like habit, gregarious occurrence, the association with seagrass and a diverse marine fauna (including epibionts), and the absence of any terrigenous material, remains of land plants and terrestrial palynomorphs strongly suggest that *Mosacaulis spinifer* grew in a shallow but fully marine environment. Defining a seagrass as a vascular plant adapted to survive in a fully marine environment would then designate *Mosacaulis spinifer* as a new, though extinct type of seagrass. See reconstruction on page 140.

The fern genus *Nephrolepis*
Its phylogeny and biogeography

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Most people know ferns of the genus *Nephrolepis* only as the tufts of greenery that are frequently offered at cut-rate prizes in supermarkets and garden centers. Indeed, *Nephrolepis* plants are among the most widely cultivated ferns. They have given rise to a highly dedicated branch of horticulture where a large number of selections are propagated by tissue culture and grown to marketable size by specialized fern growers. Few people, however, realize that the genetic basis for this industry is extremely narrow: virtually all cultivated plants are derived from a single plant originally found in the United Sates in the late 19th century (hence the common cultivar name "bostoniensis"). The entire genus *Nephrolepis* has a world-wide tropical and subtropical distribution, with a total number of species of the genus estimated to be 40 or 50, but with a considerable uncertainty about the actual number and the actual distribution of the species.

By their frequent occurrence, the cultivated *Nephrolepis* plants also have come to represent the general idea of "fern", although they are, actually, very atypical ferns. They have creeping stems (stolons) that are neither roots nor normal stems – other ferns have only roots and stems. They have leaves that continue to grow on at the tip – other ferns have mostly leaves that grow to the mature size, then stop growing.
In the wild species of *Nephrolepis*, the stolons show a number of modifications and adaptations: subterraneous tubers occur in some species, adapted to survive long dry seasons; long climbing stems occur in others, and can form dense jungles of twining plants. One species has become invasive, and is classified officially as a threat in parts of America.

The object of our research is to form a coherent picture of the variability and evolution of *Nephrolepis*. Our results would help to address a variety of topics. Fern growers can search effectively for a wider genetic base for the *Nephrolepis* industry, regulators can assess the potential for invasiveness of the cultivated species, and scientists can explain the driving force behind the curious morphological diversification.

To start with, we need an accurate overview of the entire genus, the species, their characters, distributions and ecological requirements. In a combined effort, a complete overview of the genus *Nephrolepis* was presented for the first time (Hovenkamp & Miyamoto, 2005), including 19 species, 3 of which have a world-wide distribution.

With his overview, it was also possible to provide reliable identifications for many of the samples of *Nephrolepis* that had been used for studies of phylogeny and evolution of ferns. In the phylogenetic study into the evolution of *Nephrolepis* by Sabine Hennequin, this turned out to be crucial for the interpretation of the results. In all cases where specimens of a single species appeared in different places of the cladogram this could be plausibly ascribed to incorrect identifications of sequences that were deposited earlier in GenBank.
With the help of the collections of *Nephrolepis* in the Hortus botanicus Leiden, and of many fern collectors throughout the world, we were able to include almost all known species of *Nephrolepis* in a comprehensive analysis of the phylogeny and biogeography of *Nephrolepis* (Hennequin et al., 2010). As a result, we now can say the following about the evolution of *Nephrolepis*:
There is only one really invasive species of *Nephrolepis*, *N. brownii*, and the origin of that species is in South Asia. Its worldwide distribution is of very recent origin – the first records in South America are only from the 1930's.
Nephrolepis exaltata, the species that is usually regarded as the source for all the cultivated species of *Nephrolepis* is very likely of hybrid origin.

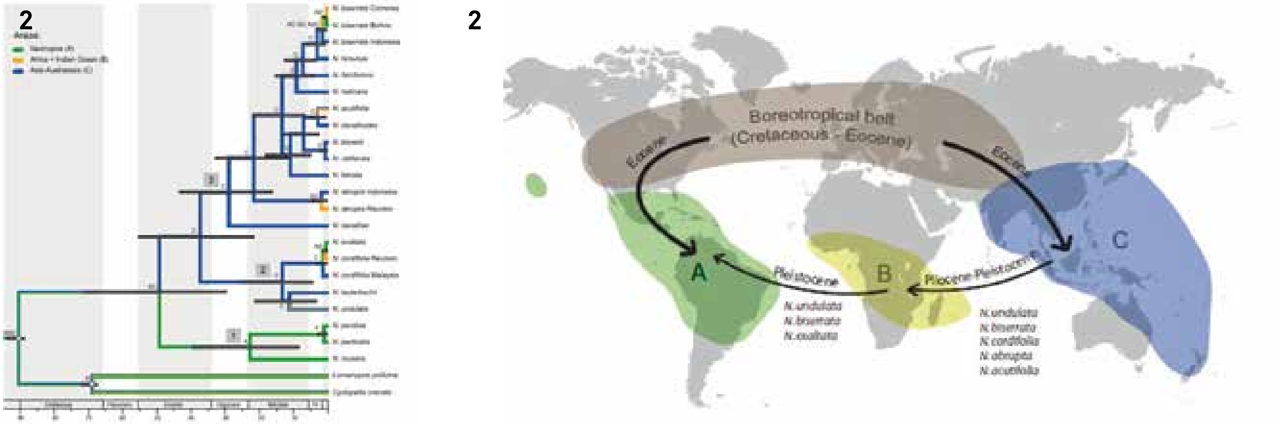

Fig. 1. Cultivated forms of *Nephrolepis* "*bostoniensis*". Source: growers' catalogues available on internet.

Fig. 2. Phylogeny and biogeographical history, reconstructed by Hennequin et al. (2010). Source available from Hennequin.

Fig. 3. Rhizomes of *Nephrolepis*. 1-4: *N. cordifolia*, with stolons, subterraneous tubers and plantlets sprouting from both; 5-6 *N. davallioides*, epiphytic plants attached with stout stolons. All photographs by Peter Hovenkamp, 1-4: South China, 5-6: Peninsular Malaysia.

Fig. 4. *Nephrolepis* in the wild. 1. *N. abrupta* Bory on exposed limestone summit in Peninsular Malaysia. 2. *N. acutifolia* on a tree in Singapore Botanical garden. 3. *N. biserrata* invading young secondary forest in East Borneo. All photographs by Peter Hovenkamp.

At least one of the two species with a naturally worldwide distribution, *N. biserrata*, is not a relict from Pangea, but has most likely attained its wide distribution more recently.
The diversification of *Nephrolepis* probably started when the tropical forests once present in North America and Europe disappeared, and the tropical plants inhabiting them had to retreat southwards.

A number of questions still remain, and are currently being studied:

- did subterraneous tubers as adaptations to seasonally dry climate arise only once in the evolution of *Nephrolepis*, or have they arisen several times on different continents in similar conditions?
- are the cultivated plants really derived from *Nephrolepis exaltata*, or perhaps from an independent event of hybridization?
- how recently have the widespread species been distributed over the world? Was that spontaneous, or were they, in some way, helped by man?

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Hennequin, S., P. Hovenkamp, M.J.M. Christenhusz & H. Schneider. 2010. Phylogenetics and biogeography of *Nephrolepis*- a tale of old settlers and young tramps. *Botanical Journal of the Linnean Society* 164: p. 113-127.

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Mosses as food

Biodiversity in the diet of arctic herbivores

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Mosses are an important part of the arctic tundra vegetation in terms of biomass and species numbers (Fig. 1). In general, mosses are rarely eaten by larger herbivores because of their low nutritional value. In the Arctic, however, mosses form a considerable part of the diet of certain herbivorous birds and mammals. This is probably because mosses are so abundant and recover earlier after snowmelt in the arctic spring than the more nutritious vascular plants. For example, the migratory bird species Barnacle goose relies on mosses as part of its diet after arriving in their breeding areas on the High Arctic archipelago of Svalbard (Spitsbergen), when little other food is available.

The Barnacle goose population in the Kongsfjorden area around the researcher village Ny-Ålesund on Spitsbergen (Fig. 2) has been intensively studied for the last 20 years, as part of the activities of the Arctic Centre of the University of Groningen and the Netherlands Arctic Station (www.arcticstation.nl). The classical way to study the diet components consisted of microscopic identification of plant fragments in the faeces. As Barnacle geese digest their food quickly and incompletely, fragments remain that can still be identified. In fact, it could be clearly shown in earlier studies that the geese eat grasses, other flowering plants, and few moss species. However, it remained unknown whether the geese foraged selectively on certain moss species and how representative the microscopic analysis was for the true diversity of species in the diet. We question the latter, as moss species are often difficult to identify even when the plants are in good condition. In the Arctic, moss plants tend to look very different because of the harsh environmental conditions (Fig. 3), which makes the situation even worse.

Using parts of the DNA as molecular markers is a powerful new tool for species identification (DNA barcoding) and for assessing the biodiversity in environmental samples. In the research programme BRYOARCT of the bryology group of the Botany section of Naturalis, we aim to, among other topics, improve the identification of arctic moss species and to infer the diversity of diet components by molecular analysis of herbivore faeces.

One of our three research projects, which all included fieldwork on Spitsbergen in the summer periods of 2008–2011, we devoted to the study of herbivore diets and the influence of grazing on the moss vegetation in the Kongsfjorden area. It was financed by the Netherlands Polar Programme of NWO and carried out in collaboration between Naturalis, Institute of Biology Leiden (K. Vrieling), and Arctic Centre Groningen (M.J.J.E. Loonen). In this project we sequenced DNA regions of the chloroplast genome from moss species growing in the study area to build up a reference database, which can be used together with the public database Genbank for comparison with the sequences that we could detect in herbivore faeces. For the DNA extraction and sequencing from Barnacle goose droppings we tested and optimized different protocols. In this testing stage we already detected a surprising diversity of mosses in the faeces, comprising at least ten different DNA sequence types (Stech et al. 2011). Subsequently, we used the more powerful ‘next generation sequencing’ to receive high numbers of sequences from selected droppings. We currently compare these with the results of microscopical analyses of the droppings to reach a detailed assessment of the Barnacle goose diet. One example of moss species identification from Barnacle goose faeces is shown in Fig. 4. The molecular analysis indicates that two DNA sequences obtained from next generation sequencing of faeces belong to the species *Meesia triquetra* of the moss family Meesiaceae. We also found fragments of this species during the microscopic analysis of the faeces. The total diversity of the Barnacle goose diet seems to comprise different species of grasses, other flowering plants, horsetails, and mosses.

As most adult Barnacle goose individuals present in the Kongsfjorden area during summer are ringed (Fig. 5), we could follow individual geese using a telescope and collect droppings that can be unequivocally assigned to specific individuals or at least families. We collected faeces samples from goose

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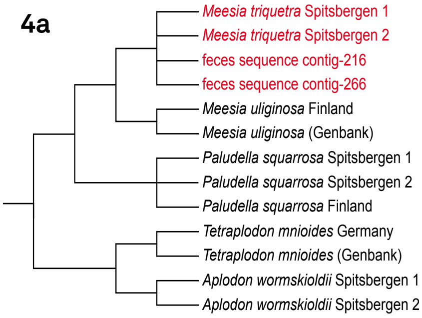

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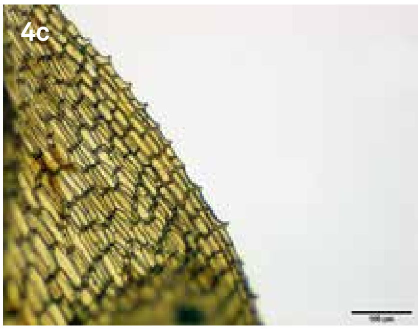

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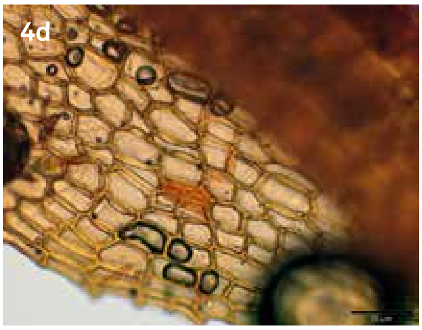

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Fig. 1. Wet moss tundra (photo: H. Kruijer).
Fig. 2. Barnacle geese on the tundra in Ny Ålesund, Spitsbergen (photo: M. Stech).
Fig. 3. Differences in size and branching pattern between temperate and arctic plants of the moss species *Hylocomium splendens* from Austria (left) and Svalbard (right) (photos: B. Kieft).

Fig. 4. Moss species identification from Barnacle goose faeces. a. Molecular tree showing two sequences obtained from faeces (contig-216, contig-266) in the branch of the moss species *Meesia triquetra*. b. *Meesia triquetra*, plants growing on the wet tundra near Ny-Ålesund, Spitsbergen. c. *Meesia triquetra*, leaf cells at basal part of leaf. d. *Meesia triquetra*, fragment of basal part of leaf from faeces (photos: E. Kolvoort, B. Cornelder, H. Kruijer).
Fig. 5. Barnacle goose, individual PCU (photo: M. Stech).

families (both parents and goslings), non breeding individuals, and from a selected tundra area during five weeks. In addition, we analyzed the moss vegetation from both grazed and ungrazed plots in the period 2008–2011.
Currently we analyse our data to answer questions as to how the diet composition changes in time and between different goose individuals, and how the grazing behaviour affects the tundra vegetation. The final results will provide new insights into processes in the food chains of arctic terrestrial ecosystems and allow to predict the impact of changes in the goose population on the tundra. At the same time it will result in improved tools for the identification of arctic moss species, which makes it possible for non-specialists to include mosses in future ecological research projects.

Reference

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Wood structure-function relationships

Correlating anatomy with hydraulics in maple trees

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[2] *Biology Department, University of Utah, Salt Lake City*
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The water transport system in plants plays a crucial role in determining the level of drought resistance of a species. Water in vessels is under negative pressure (tension) allowing water to be pulled upwards against gravity towards the leaves. One major issue with water under tension is that air bubbles can be formed spontaneously. The chance of air-bubble formation (cavitation) inside vessels is rising when the negative pressure becomes more negative due to a prolonged period of drought. When vessels are filled with air due to drought stress, the water transport within these vessels will be blocked, implying that the amount of water reaching the leaves will be hampered. Stomata in the leaves will sense this, and as a reaction close more often so that less CO_2 molecules will be taken up. Consequently, cavitation in vessels due to drought stress may not only lead to starvation because of hampered photosynthesis, plants also desiccate at the same time leading to branch sacrifice and ultimately plant death.

The structure - function gap

Only few integrative studies have combined anatomical and experimental approaches to investigate differences in cavitation resistance among trees. Furthermore, most of these studies lack in-depth anatomical observations. The present study bridges the structure-function gap using an anatomically comprehensive study based on transmission electron microscope (TEM), scanning electron microscope (SEM) and light microscope (LM) observations of seven *Acer* species, and link these observations with empirical measures of xylem hydraulics (Lens *et al*., 2011) (Fig. 1). By studying closely related species in a single genus, we reduced phylogenetic noise in anatomical traits. This facilitated the testing of a wide range of structure-function hypotheses, some of which have not been evaluated before.
Vessels are limited in length, often between 1 and 8 cm long in the *Acer* species studied, which means that water has to cross thousands of intervessel pits (comprizing mesh-like membranes) from roots towards leaves. It is known that cavitation resistance, i.e. the ability of plants to avoid air bubble spread from an air-filled vessel towards a water-filled vessel, depends on intervessel pits. Since this air bubble distribution requires the failure of only one intervessel pit, the greater the number of pits per vessel, the greater should be the probability of one pit failing (‘rare pit’ hypothesis). We tested whether pit quality characters (for instance pit membrane thickness and porosity) are more crucial than pit number per vessel to explain differences in cavitation resistance.
Other structure-function hypotheses are related to the mechanical strength of vessels. Vessels that are resistant to cavitation are likely to carry water under more negative pressures. These stronger tensions put a greater mechanical load on the vessel walls, which need to be more reinforced to avoid collapse. Vessel strength is a function of the “thickness-to-span” ratio, i.e. the double wall thickness per lumen diameter. Wood density is also strongly influenced by thickness-to-span ratio of the wood elements. Because both thickness-to-span and wood density increase with cavitation resistance in many broad-scale studies, we investigated whether these two mechanical parameters are also significant at the genus level. In addition, many of the in literature postulated correlational hypotheses between ecological wood anatomy and function have not been well evaluated experimentally and are tested here. For instance, more cavitation resistant species in *Acer* are thought to possess shorter vessel elements, more pronounced helical thickenings on inner vessel walls, and more and larger vessel multiples than their more vulnerable relatives.

Our results show a 2 MPa range in mean cavitation pressure (MCP) from -1.26 MPa in *A. saccharinum*

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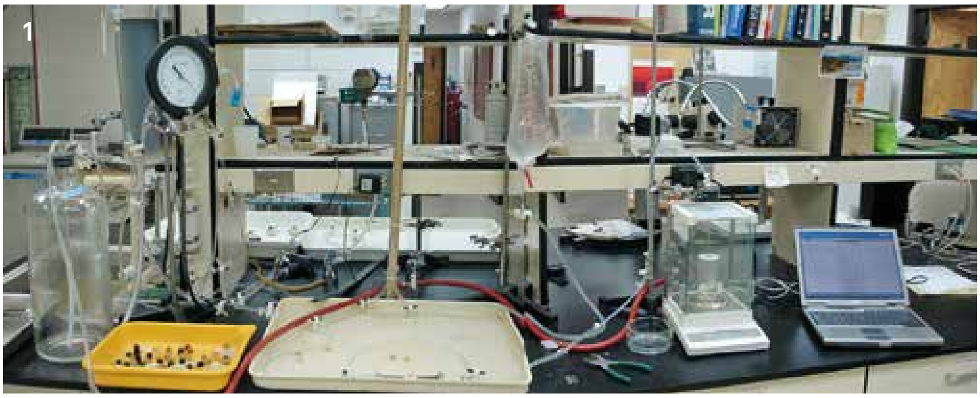

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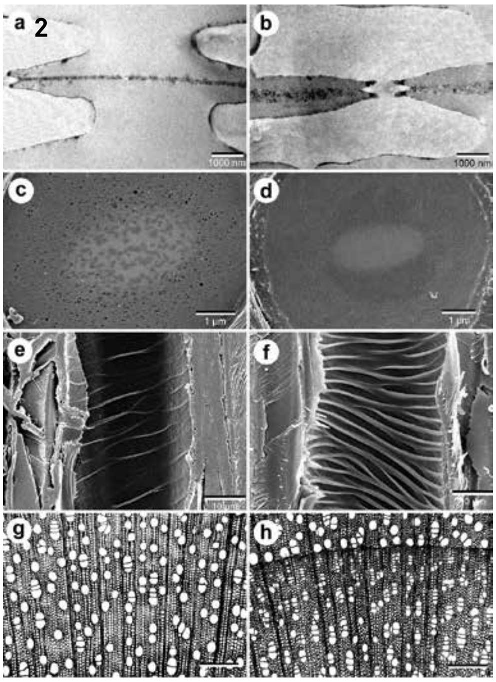

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Fig. 1. Experimental setup in the lab of prof. John Sperry (University of Utah, Salt Lake City, USA) used by dr. Lens to measure the water transport in maple stems. A single stem piece is connected to a system of hollow tubes through which water flows. The water flowing through the stem ends up in a container that is placed on a balance and connected to a computer. The computer calculates the amount of water that is flowing through the stem, indicated by the balance measurements and based on the known height difference between the two water levels.

Fig. 2. TEM (a, b), SEM (c-f) and LM (g, h) micrographs of the cavitation most vulnerable species (*A. saccharinum*; MCP: -1.26 MPa; left column) and the cavitation most resistant species (*A. grandidentatum*; -3.33 MPa; right column), showing anatomical characters that are crucial in regulating cavitation resistance within *Acer*: thickness of pit membranes (a, b), size of pit membrane pores (c, d), intensity of helical sculpturing on the inner vessel walls (e, f), number and size of vessel multiples (g, h).

Fig. 3. Dr. Frederic Lens (left) together with dr. Holly Slater, managing editor of *New Phytologist*, during the International Botanical Conference in Melbourne, summer 2011. Frederic is holding the issue of *New Phytologist* in which his Tansley awarding paper is published.

(most vulnerable species) up to -3.33 MPa in *A. grandidentum* (most resistant species). MCP is strongly correlated with intervessel pit quality characters: cavitation resistance increases with shallower pit chambers containing thicker pit membranes (Fig. 2a, b) with on average smaller pores (Fig. 2c, d). Also thickness-to-span ratio and wood density are strongly correlated with MCP. Likewise, resistance to cavitation increases strongly with the extent of helical thickenings on the inner vessel walls (Fig. 2e, f) and with vessel grouping (Fig. 2g, h). A highly significant opposite link is observed between xylem-specific conductivity and cavitation resistance. Vessel length, pit membrane thickness, pit chamber depth and aperture fraction are implicated in this safety-efficiency trade-off.

This integrative anatomical-physiological study clearly shows that the *Acer* species studied have maintained approximately similar pit numbers per vessel, and have adjusted their pit quality to achieve different MCP. At the tissue level, MCP is strongly correlated with vessel and wood strength parameters, which avoid vessel implosion due to stronger negative pressures. In addition, some of the first evidence for the functional role of vessel wall sculpturing and vessel grouping is provided here. The increased sculpturing of vessel walls in more cavitation resistant species has been previously demonstrated to enhance the wettability of the walls. This increased wettability is hypothesized to reduce the rate at which emboli are formed and to facilitate refilling of embolized vessels. Likewise, greater vessel multiples provide redundancy of the 3-D flow path, which would prove adaptive in xeric habitats where cavitation may be more likely. Xylem-specific conductivity is also strongly negatively linked with cavitation resistance, and this safety-efficiency trade-off is primarily established by vessel length and intervessel pitting traits.
In conclusion, cavitation resistance and hydraulic conductivity in *Acer* appear to be controlled by a very complex interaction between tissue, vessel network and pit characteristics.

Reference

Frederic Lens, John S. Sperry, Margareth A. Christman, Brendan Choat, David Rabaey, Steven Jansen. 2011. Testing hypotheses that link wood anatomy to cavitation resistance and hydraulic conductivity in the genus *Acer*. *New Phytologist* 190: 709-723.

TRY
A global database of plant traits

Frederic Lens

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Plant traits – the morphological, anatomical, physiological, biochemical and phenological characteristics of plants and their organs– determine how plants compete for resources, e.g. light, water and soil nutrients, and where and how fast they can grow. Ultimately, they determine how plants influence ecosystem properties, such as rates of nutrient cycling, water use and carbon dioxide uptake. Trait data thus represent the raw material for a wide range of research from evolutionary biology, community and functional ecology to biogeography. A major bottleneck to modelling the effects of climate change at ecosystem and whole-earth scales has been a lack of trait data for sufficiently large numbers of species. A database initiative, known as TRY (which is an expression of sentiment rather than an acronym) resulted in the publication of the world's largest database on plants' functional properties, or traits (Kattge *et al*., 2011; http://www.try-db.org). The database is hosted at the Max Planck Institute for Biogeochemistry in Jena (Germany) and developed under the auspices of IGBP (International Geosphere-Biosphere Programme) and DIVERSITAS (International Programme of Biodiversity Science), and jointly coordinated with the University of Leipzig (Germany), IMBIV-CONICET (Argentina), Macquarie University (Australia), CNRS and University of Paris-Sud (France). The contents rest on a worldwide collaboration of scientists from 106 research institutions (Fig. 1). After four years of intensive development, researchers compiled three million traits from 93 trait databases for 69,000 out of the world's ca. 300.000 plant species, with a focus on 52 groups of traits characterizing the vegetative and regeneration stages of the plant life cycle, including growth, dispersal, establishment and persistence. Naturalis contributed to this giant database using an extensive wood anatomical dataset that was generated by dr. Frederic Lens. TRY promises to become an essential tool for biodiversity research and Earth-system sciences.

What are the advantages of setting up such a large database? Three major examples can be given. The huge advance in data availability will lead to more reliable predictions of how vegetation boundaries and ecosystem properties will shift under future climate and land-use change scenarios. The TRY global database could potentially lead to revolutionize biodiversity research, resulting in a new understanding of how not only the numbers of species (biodiversity) but also the variation among species in their traits (functional diversity) together effect ecosystem functions and services. Statistical analyses of the TRY database demonstrate for the first time on a global scale that most of the observed trait variation is represented by differences among plant species. In contrast, plant functional types, such as used in global vegetation models, contribute much less to the trait variations, for several traits only as little as 25%. This illustrates the advantages of trait-based vegetation models, facilitating a more realistic and empirically grounded representation of terrestrial biodiversity in Earth system models. Such models may not only be helpful to predict the development of future climate, carbon sequestration or ocean levels but also provide a basis for mitigation strategies.

The TRY database provides unprecedented coverage of information on plant traits and will be a permanent communal repository of plant trait data (Fig. 2).

Fig. 1. Location of partner institutes (red) and sample cites (blue) of the TRY network.

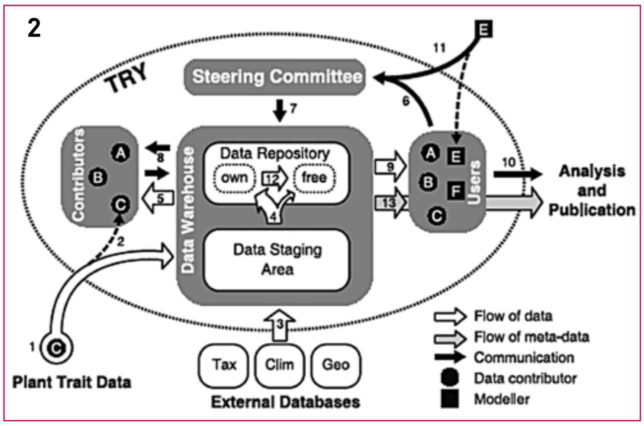

Fig. 2. The TRY process of data sharing. Researcher C contributes plant trait data to TRY (1) and becomes a member of the TRY consortium (2). The data are transferred to the Staging Area, where they are cleaned, checked for consistency and complemented with covariates from external databases (3) [Tax, taxonomic databases, IPNI/TROPICOS accessed via TaxonScrubber; Clim, climate databases; Geo, geographic databases]. Data are then transferred to the Data Repository (4). If researcher C wants to retain full ownership, the data are labelled accordingly. Otherwise they obtain the status 'freely available within TRY'. Researcher C can request her/his own data at any time (5). If she/he has contributed a minimum amount of data (currently 4500 entries), she/he automatically is entitled to request data other than her/his own from TRY. In order to receive data she/he has to submit a short proposal to the TRY steering committee (6). Upon acceptance (7) the proposal is published on the Intranet of the TRY website. Researcher C then contacts the contributors for permission to use the data (8). The permitted data are then provided to researcher C (9), who is entitled to carry out and publish the data analysis (10). Vegetation modellers (e.g. modeller E) – one of the pioneering motivations of the TRY initiative – are also allowed to directly submit proposals (11) without prior data submission provided the data are to be used for model parameter estimation and evaluation only. We encourage contributors to change the status of their data from 'own' to 'free' (12) as they have successfully contributed to publications. With consent of contributors this part of the database is being made publicly available without restriction. So far look-up tables for several qualitative traits have been published on the website of the TRY initiative (http://www.try-db.org). Metadata are also provided without restriction (13).

The first analyses presented here confirm two basic tenets of plant comparative ecology and vegetation modelling at global scale: (1) the aggregation of trait data at the species level represents the major fraction of variation and (2) the plant traits cover a relevant fraction of trait variation to represent functional diversity in the context of vegetation modelling. The scale of the challenges we are facing demands new ways of doing science, both in terms of the size of the networks and databases, and the high degree of collaboration. The improved availability of plant trait data in the unified global database is expected to support a paradigm shift from species to trait-based ecology, offer new opportunities for synthetic plant trait research and enable a more realistic and empirically grounded representation of terrestrial vegetation in Earth system models.

J. Kattge, S. Díaz, S. Lavorel et al. 2011. TRY - a global database of plant traits. *Global Change Biology* 17: 2905-2935 (IF 2010: 6, 346)

Good relationships going bad

Are some fungi easier cheated?

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[4] *University of California Berkeley, CA*

Mycorrhizas are ancient, widespread associations between soil fungi and the roots of many species of plants. The mycorrhizal association is probably the most important symbiosis in nature and plays an essential role in the maintenance of all terrestrial ecosystems. Both the plants and the fungi benefit from this association: the plants obtain water and nutrients from the fungi and in return the fungi obtain carbohydrates from the plants. However, several unrelated groups of plants evolved an ingenious way to cheat this interaction. Instead of supplying their root-associated fungi with carbohydrates these plants steal carbohydrates from their fungi without giving anything in return. This particular lifestyle is referred to as 'mycoheterotrophy'. Since mycoheterotrophic plants obtain all carbohydrates they need for growth and reproduction from their associated fungi they do not perform photosynthesis. As a result they can grow in absence of sunlight and thrive in the dark understorey of dense forests, where other plants fail to survive due to the lack of light. Most mycoheterotrophic plants occur in tropical rainforests. Many species are considered to be extremely rare and have been observed only a few times. However, in some cases our knowledge about the occurrence of mycoheterotrophic plants may be considerably biased by the plants' ability to remain unnoticed by collectors: they are generally very difficult to spot due to their small size and hyaline coloration (Fig. 1). They often fail to protrude above the dense leaf litter and remain covered by fallen leaves, even when flowering.

Due to their hidden life mycoheterotrophic plants remain poorly understood. Only during the last two decades we have started to identify their fungal hosts. This has revealed that cheating mycorrhizal fungi for survival comes at a certain cost. In general, the mycorrhizal association between plants and fungi is not very specific: a plant typically associates simultaneously with multiple fungi, and a mycorrhizal fungus often associates simultaneously with multiple plants. Thus every fungus has many potential plant partners and vice versa. In contrast, research has demonstrated that mycoheterotrophic plants are often growing only with very specific mycorrhizal fungi. This fits the view that host specialization is a common consequence of the evolution of parasitic lifestyles. Yet, it is unclear what the drivers behind this mycorrhizal specialization are. Some research suggests that mycoheterotrophic plants of different plant groups grow with similar fungi. This has let to the view that mycoheterotrophic plants generally target only a very specific group of mycorrhizal fungi and raised the hypothesis that there is a group of 'naïve' fungi, which are easier to cheat than others.

To investigate this hypothesis we identified the mycorrhizal fungi in the roots of several mycoheterotrophic plant species from French Guiana, Gabon, and Australia by sequencing a part of their fungal ribosome genes. To increase the coverage, we added all previously published DNA data of fungi living in the roots of mycoheterotrophic plants from all major rainforest regions. We compared these sequence data to a comprehensive database of DNA sequences of mycorrhizal fungi obtained from the roots of green plants. Evolutionary analyses showed that at least 20% of all known groups of mycorrhizal fungi are prone to exploitation by mycoheterotrophic plants. Since the number of sampled mycoheterotrophic plant species in this study remains low, it is likely that even more fungi can be used by mycoheterotrophic plants. The results demonstrate that specialization of mycoheterotrophic plants towards particular groups of fungi is not influenced by the evolutionary relationships of the fungi. Therefore we are able to confidently reject the existence of a 'naïve' group of mycorrhizal fungi.

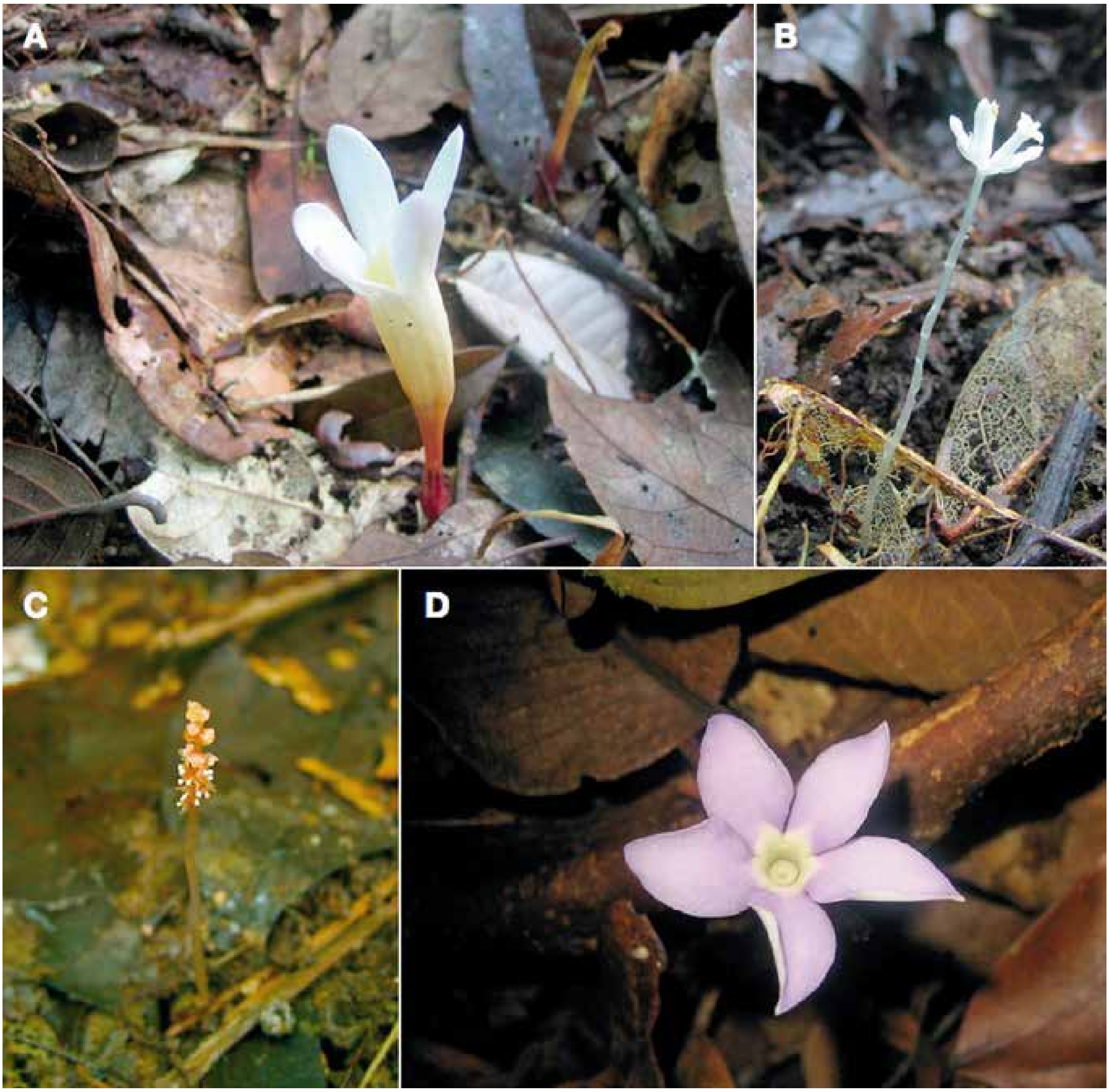

Fig. 1. Mycoheterotrophic plants from different rainforests around the world. A. *Voyria clavata* (Gentianaceae) growing at Savane-Roche Virginie, French Guiana. B. *Campylosiphon congestus* (Burmanniaceae) photographed on Mount Kupe, Cameroon. C. *Kupea martinetugei* (Triuridaceae) growing on the eastern flanks of Mount Cameroon, Cameroon. D. *Voyria caerulea* (Gentianaceae) observed at Trésor, French Guiana. Photos: Vincent Merckx.

This research was recently published as:

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Exploring plant diversity in 50 million ha of Amazonian pristine forest

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The Guianas are embedded in the largest stretch of tropical forest on earth, the Amazon, in Northern South America. The three countries forming the Guianas - Guyana, Suriname and French Guiana - have more than 85% of their political territories covered by pristine forest, ca. 50 million ha.

The Flora of the Guianas Programme bears the vision that taxonomic data provides the essential background for the great majority of the biological research in the region, playing therefore an important role in conservation and sustainable use of natural resources. Lead by the Nationaal Herbarium Nederland, in Naturalis, the programme is formed by a consortium of nine institutes in Europe, North America and the Guianas, aiming:
1) to generate and publish accurate taxonomic data, by collecting, identifying, cataloguing and describing plant specimens of the Guianas;
2) to train botanists and students, particularly in the Guianas, by offering courses of systematics of Neotropical plants and biodiversity metrics.

The book series *Flora of the Guianas* is the main product of the programme. Currently coordinated and edited in Naturalis, and published by Kew Publishing, UK, the book series has attained a steady production, with an average of one fascicle per year. Starting in the eighties, 36 fascicles of the Flora were published until now, covering 74 plant families in series A: Phanerogams; 6 families in series B: Fern and Fern allies; all moss families in series C: Bryophytes; and 3 families in series E: Fungi and Lichens.

The total number of species treated in the *Flora of the Guianas* in the last 30 years corresponds to approximately 25% of the known plant diversity in the region. Taking into account the regular finding of new species in the area, it is estimated that more than 15000 plant species still have to be treated, distributed in more than 150 families.

The completion of the Flora, i.e., the ideal situation where all plants cited for the region are described in taxonomy treatments, must be viewed not as an end product, but as part of a broader strategy for studying biodiversity, based on well curated and systematically organized taxonomic information. As such, the activities of the Flora are part of a framework of related research on biogeography, biodiversity and ethnobotany in Naturalis and in the partner institutes.

The latest fascicles

In these two first years of the Flora in Naturalis, between 2011 and 2012, three new fascicles were published:

- Mimosoideae (Flora of the Guianas Series A, 28), with 163 species occurring in the Guianas and four additional species expected to occur in the region.
- Musci IV (Flora of the Guianas series C, 2), with 271 species, is the completion of the moss flora. The fascicle also offers an update of the families treated in previous publications, by adding species recently recorded.
- Sapindaceae (Flora of the Guianas Series A, 29), with 114 species, presents four new species, *hot off the press*, encountered during the elaboration of the treatment.

Enchanting diversity: new species for science

Besides the formal hypothesis testing framework of scientific research, the process of preparing a taxo-

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Fig. 1. Panorama Brownsberg

Fig. 2. *Eperua falcata* Aubl. (Photo: L. Westra)

nomic treatment for a Flora frequently leads to unexpected novelties, such as the discovery of new species, either in the herbarium or in the field.

The preparation of the latest two fascicles of the Flora of the Guianas led to the description of, respectively, four and ten species new to science, published in electronic journals (Acevedo-Rodríguez 2012; Sipman & Ahti 2013).

Looking into the future

The demand for primary biodiversity data - such as the one offered by Floras - has increased as soon as computing age allowed analysis of very large datasets. This is simply because, once produced and made available in large volumes, primary biodiversity data can be reutilized to enable research in many different fields. Most of this data is the product of taxonomic work and has been organized in hard copy publications or digitized text files. Methods to support data basing, management, algorithmic exploration, and analysis of taxonomic information have been developed in the two last decades (Soberon & Peterson 2004) and the technology available has also a central role in increasing species description rates and taxonomic efficiency (Costello *et al*. 2013). The digital format allows the maintenance of quality and reusability of the data provided, the quick gathering of large volume of data by end users, and the links with other databases in related fields, collections and literature.

During 2012 biennial meeting of the Flora of the Guianas Programme, in Leiden, the board members agreed upon the transference of the data/ content of the published fascicles from text to a relational database format. A text format for prospective literature - future submissions - that facilitates the transference of data to an e-taxonomy platform is also being prepared.

The challenge posed for the future of the Flora is to increase the production of fascicles, concomitantly with a modernization of the workflow and the data dissemination channels.

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Entolomataceae of Tasmania

Fungi of World Heritage Forests

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Tasmania, the island state of Australia, lies between 40° and 43°40' south of the equator and is separated from the mainland of Australia by Bass Strait. The island, with an area of 68,200 km^2, is approximately the same size as Sri Lanka and a little smaller than Ireland. Its climate can be described as modified marine Mediterranean. Broadly speaking, the vegetation can be classified either as austral montane, temperate rainforest (Fig. 1) or sclerophyll forest (Fig. 2). However, within these three broad formations there is a complex mosaic of vegetation types across the island due to the geology, edaphic factors, precipitation and fire history of the island. In general, the island of Tasmania is divided into a wet western half and a dry eastern half, although there are gradations within this broad division. The vegetation has plant species in common with New Zealand and South America that are either relicts from an ancient Gondwanan flora or resulting from a more recent dispersal from these regions.

Covering an area of over 1 million hectares, the Tasmanian Wilderness constitutes one of the last expanses of temperate rainforest in the world.

It comprises a contiguous network of reserved lands that extends over much of south-western Tasmania including several coastal islands. The core area was inscribed on the World Heritage List in 1982 on the basis of all four natural criteria and three cultural criteria, satisfying more criteria than any other World Heritage property on Earth.

The *Entolomataceae* (>100 spp.) constitute a dominant part of the macrofungi in these forest types, together with *Hygrophoraceae* (50 spp.), and *Cortinariaceae* (>300 spp). An effort of 14 years of collecting *Entolomataceae* in the various forest types of the wilderness area of Tasmania, Australia resulted in several thousands of well-annotated collections. Although initially involving only the Tasmanian residents Genevieve Gates (Fig. 3) and David Ratkowsky, who made twice- or thrice-weekly forays into the forests throughout the year, the project was subsequently joined by agaric specialist Machiel Noordeloos from the Netherlands, and by fungi photographer Michael Pilkingtonfrom the United Kingdom (Fig. 4, 5). Our collections form the basis of the monographic treatment of the family for Tasmania (Noordeloos & Gates, 2012), including 90 *Entoloma* species and 10 *Clitopilus* species. Earlier contributions of Tim Baroni (University of Cortland, US) and Genevieve Gates to the Tasmanian *Rhodocybe* species (Baroni & Gates, 2006) stood at the basis of the revision of the now expanded concept of *Clitopilus*. The species are well documented with standardized descriptions, line drawings of fruit bodies (Fig. 6, 7) and diagnostic microscopic characters, and, when available, with colour photographs (Fig. 8-14). Thanks to the intensive fieldwork, it was possible to illustrate most species in colour. Dichotomous keys facilitate identification of the species. Brazilian Ph.D. candidate Fernanda Karstedt thoroughly tested the keys to the *Entoloma* species during her visit of several months in 2010. Anita Walsmit-Sachs prepared the line-drawings on the base of field scetches, photographs, and micrographs.

This monograph essentially uses a morphological species concept (Kuyper in Bas *et al*. 1988), defining a species on two supposedly independent characters in which it differs from similar (related) taxa. In the long taxonomic practice of the Leiden agaricologists, this has proved to be a practical and feasible approach.

Similarity in morphology may easily lead to the use of European or North American names, as has been done frequently in the past. However, our increasing knowledge of other groups makes it clear that many agaric species do not have a world-wide distribution, but are often geographically restricted (Geml *et al*. 2004, 2006; Nuytinck *et al*. 2006; Matheny *et al*. 2009). Ongoing molecular / phylogenetic studies in *Entoloma* also show that the Tasmanian species often form a clade of their own, sister to a clade with another geographic origin.

The *Entolomataceae* mycota of Tasmania appears to be fairly unique. As many as 73 out of 90 species of *Entoloma* and 5 out of 10 *Clitopilus* species are new to science, with the majority of the remaining species shared with Mainland Australia and New

Fig. 1. Habitat Tahuna rainforest : impression of a mixed temperate rain forest of *Eucalyptus* and *Nothofagus*.
Fig. 2. Kermandi Falls lower track: sclerophyll forest; typical habitat for *Entoloma*, open places with much leaf litter.

Fig. 3. Genevieve Gates, in rain forest with giant Eucalyptus oblique, rich habitat for Entolomataceae.
Fig. 4. Photographer Michael Pilkington in action.

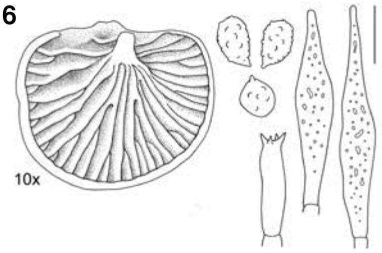

Fig. 5. Team: from left to right David Ratkovsky, Genevieve Gates, Machiel Noordeloos, Michael Pilkington; sitting Fernanda Karstedt.
Fig. 6. Line drawing of *Clitopilus conchatus* by Anita Walsmit Sachs.

Zealand. Similar species occur in the *Nothofagus* zone of South America, which leads to the conclusion that the group concerned typically is Gondwanan. Only a few taxa have characteristics that match those of European species, and might have been introduced from Europe.

The current state of knowledge, despite intensive collecting in Tasmania, New Zealand, and Australia is still insufficient to make reliable statements about endemism. Of the more than 100 species in the current treatise, at least 15 are also found in New Zealand, including several species that Horak (2008) cited as endemic to New Zealand, and we have unpublished information that some of our species also occur on mainland Australia in similar habitats. Eventually, detailed biogeographical studies in a larger area, including New Zealand, Australia and the *Nothofagus* zone of South America (i.e. Patagonia), will make it possible to decide whether or not certain species are endemic.

Because the majority of *Entolomataceae* species are decomposer species (saprobs), they are often associated with broad-leaved (soft-leaved) tree species such as *Pomaderris apetala* Labill., *Olearia argophylla* (Labill.) F. Muell., *Bedfordia salicina* DC and *Zieria arborescens* Sims. In contrast, the narrow-leaved (hard-leaved) understorey species of the genera *Pultenaea* Sm., *Epacris* J.R. Forst. and *Hakea* Schrad. & J.C. Wendl. appeared to be unfavourable for species of *Entoloma*. Collecting *Entolomataceae* has been most successful in two types of native forest, viz.: wet sclerophyll (the understorey consists of just broad leaved shrubs) and mixed forest (the understorey consists of rainforest species) dominated by the tall wet eucalypt species *E. obliqua* and *E. regnans*, and lowland temperate rain forest dominated by *Nothofagus cunninghamii* which is the climax of a wet sclerophyll or mixed forest that has not been affected by wildfire for 400-500 years.

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Flore du Gabon

Diversity of an African hotspot

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Gabon is a central African country, situated on the equator. About 85% of its surface is occupied by lowland tropical rain forest, which harbors the highest density of flowering plant species in the whole of Africa. This is probably linked to the fact that, in climatically less favorable periods during the Pleistocene, parts of Gabon remained forested, whereas in many other parts of tropical Africa such forests disappeared. Gabon, therefore, is recognized as a refuge area for plants, but also for insects, forest birds, land snails, frogs, etc. Many such species are endemic, only found in Gabon (Fig. 1). About 11% of all flowering plant species present in Gabon are endemic to this country.

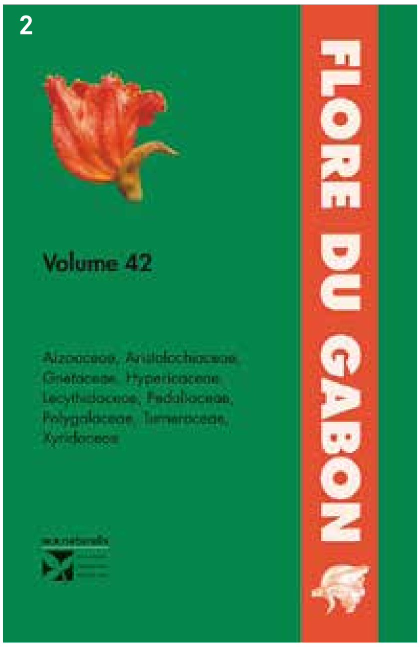
About 11% of the 267.668 km^2 surface of Gabon has a protected status, as National Park or Reserve. With a population of only 1.5 million soles, most of which live in a few larger cities, the interior of the country is almost empty and forms a true paradise for biologists. In order to properly manage the protected areas and to wisely use the botanical resources, one must first of all know which plant species are present, and how to recognize them. This is where the Flore du Gabon program fits in. The main output of this series of books are detailed descriptions, illustrations and identification keys with which anyone with some botanical knowledge should be able to tell which plant one has at hand. Apart from that, the Flore du Gabon gives information on geographical and altitudinal distribution, rarity, uses, vernacular names, core literature and the correct scientific name for each species. Hence, an indispensable tool for anyone performing botanical research in Gabon, be it a forester, ecologist, ethnobotanist or conservationist, or even zoologists who want to know which plants are eaten by the animals they study.

However, the multivolume series Flore du Gabon is far from complete. Since 1960, 45 volumes were published treating only 52% of the 5000 plant species known to exist in Gabon. Volumes 1-37 were published by the Muséum nationale d'Histoire naturelle in Paris. In 2005, the Wageningen branch of the National Herbarium of the Netherlands, now part of Naturalis, having had a strong program of over 30 years of botanical research in Gabon, upon request took over the production of the series.

We created a new editorial team, involving two Gabonese botanists, and adopted a new, more simple, format. Then, we invited a large number of specialists to contribute and to help reach the ambitious goal to finish the Flore du Gabon by 2018. To date, a network of some 60 botanists are involved in the endeavor. Progress is taking up and since the re-vitalization in 2008 five volumes were published, volume 42 in 2011 (Sosef *et al*. 2011) (Fig. 2, 3), and three more in 2012.

Now, before one can write a Flora for any given region, we need to investigate which plant species are present in that region. The first plant ever collected in Gabon dates back to 1848, and to date some 85,000 plant specimens have been collected in that country. These represent over 5,000 species. However, still every year plants never observed before in Gabon pop up. We now estimate the total number of species at some 7,000. Thus, Gabon is, despite all these efforts, botanically speaking still a poorly explored country.

The above not only shows that major efforts are still needed to finish the Flore du Gabon, but also that volumes already published since the 1960s should in fact be updated with newly gathered information. Even before we took over the production of the Flore du Gabon, we coordinated the digitization of the data related all plants ever collected in Gabon. This database is 95% complete, available on the internet (http://dps.plants.ox.ac.uk/bol/Gabon) and formed the foundation for the first Checklist of Gabonese Vascular Plants (Sosef *et al*., 2006) listing all species known to occur in Gabon, along with some information about its distribution and all specimens belonging to it. As such, it represents a great tool for those who now start up their efforts to finish the Flore du Gabon.



FLORE DU GABON

Volume 42

Aizoaceae, Aristolochiaceae, Gnetaceae, Hypericaceae, Lecythidaceae, Pedaliaceae, Polygalaceae, Turneraceae, Xyridaceae

naturalis

Fig. 1. *Begonia aspleniifolia* (Begoniaceae), a fern-leaved begonia in Waka National Park.
Fig. 2. Cover volume 42.
Fig. 3. *Vismia guineensis* (Hypericaceae), drawing by Hans de Vries.

Fig. 4. Collecting team and local guides in eastern Gabon.

Fig. 5. Marc Sosef and famous tree-spotter Yves Issembe in the Doudou Mountains.
Fig. 6. Pulcherie Bissiengou (PhD student) and locally trained para-taxonomist pressing plants in Waka National Park.
Fig. 7. The National Herbarium of Gabon.

Our second major action now is the development of an electronic and web-based version of the Flore du Gabon. We scanned all volumes, converted them into a text format and currently these are being transformed into a database format developed within the EDIT program (European Distributed Institute for Taxonomy), funded by the EU. This will allow specialists as well as Gabonese botanists to edit and improve the information provided within the Flore du Gabon series at any time. Unfortunately, Gabon has very few trained botanists. Therefore, we plan to develop a broad and long-term training program that will cover general training in botany, performing inventory work (Fig. 4, 5, 6), producing family treatments for the Flora, managing herbarium collections (Fig. 7), but also updating the specimen database information and becoming acquainted with the new web-based system.
The first training that seven Gabonese botanists recently received resulted in treatments of eight smaller families for the Flora, and several more are in progress. This is the first time Gabonese botanists contribute to the production of their Flora, which is a very positive first step towards a situation where finally they will be able to study their own flora, and produce their own updated volumes of the Flora du Gabon. On the other hand, it is clear that such developments, as well as finishing the Flore du Gabon by 2018, will need strong financial support from external sources. A first contact with a high official in the Gabonese government seems to open some potentials at least.

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Reconstructing dodo forest
Past vegetation & climate of Mauritius

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During the excavation of a mass grave of extinct animals in a filled-in lake at *Mare aux Songes* (MAS) in Southeast Mauritius (Fig. 1, 2) an important number of very well-preserved bones of dodos was discovered, as well as micro- and other macro-faunal remains. In the same site an abundance of sub-fossil (waterlogged) wood, seeds, fruits and pollen was found.

Unique preservation of wood

Based on the amount, sizes and quality of the botanical material we conclude that we are dealing with the remains of a local woody vegetation (Fig. 3) that formed the setting of the unfortunate adventures of dodos and other animals. This event can be dated around 4200 years ago, when the whole African region was presumably suffering under a mega drought.

We processed ca. 350 waterlogged wood finds (Fig. 4), collected between 2005 and 2011 by the *Dodo Research Program*, and have identified most: they belong to at least 25 different taxa, some of which are at species level. In order to analyse the wood finds microscopically, we thin-sectioned them and made them into semi-permanent slides.

The wood-anatomical characters that could then be perceived we compared with reference material from wood and microscope slide collections at the National Herbarium of the Netherlands and abroad. Since many of the trees, shrubs and woody-based lianas growing on the island don't occur anywhere else, the availability of correctly identified samples from the native woody vegetation is especially important in establishing the identity of any sub-fossil wood. For this purpose we brought together a collection of Mauritian/Mascarene woods, which is now >90% complete, thanks as well to recent additions by staff members of the Mauritius Herbarium (MH) who survey the various vegetation types on a regular basis (Fig. 5).

The taxa that we recognized from MAS sub-fossil wood until now represent dry coastal vegetation to upland wet forest (or even heath), with many of the species covering part or all of that range.

We especially noted the presence of *Ficus* sp. (Fig. 6), a medium to large-sized tree (sometimes a strangler), in at least 25% of the finds. Today, five native species of this genus are known, of which three endemic to Mauritius and the neighbouring island of Reunion. *Ficus* species, some of which are very rare today, could have been an important plant for frugivores (for instance bats, parrots and pigeons) feeding in the vicinity of the lake. Some of our other discoveries include *Cassine orientalis* (Celastraceae), *Zanthoxylum* or *Vepris* (Rutaceae) and the rare *Hornea mauritiana* (Sapindaceae).

Wood anatomy indicating drought?

In many of the wood samples we saw faint to distinct growth rings (Fig. 7), which in tropical lowland regions are an indication of seasonal differences in the availability of water (temperature having little effect here as opposed to temperate climates). Interesting in this respect is the hypothesis of the mass mortality at MAS being caused by recurring droughts that led to drying-up (as well as salinization and toxicity) of one of the scarce fresh water resources in that part of the island (Rijsdijk *et al*. 2011).

Studying and comparing growth rings in the stems of both sub-fossil and living trees can provide us insight into seasonal variations in rainfall that occurred in the past. To this end in November/December 2011 with the help of the Mauritius Herbarium and the Forestry Service of Mauritius we started a so-called cambial marking experiment (the results of which are to be expected in 2013) in places with remaining native dry forest on Mauritius. We repeatedly wounded the cambium of a small number of the commonly occurring *Cassine orientalis* or 'bois d'olive' (Fig 8), with intervals of exactly three months. Hence, the series of wounds (visible as scars in the wood) will provide us with a timescale for the amount and type of wood that is formed throughout the year, under different climatic conditions.

Fig. 1. Location of *Mare aux Songes* (MAS) (map elaborated from: ELP Resource Atlas).
Fig. 2. The team from Naturalis, NHM London, TNO, Hollandia Archaeology and IBED (Photo: A. Kromhout).

Fig. 3. 'A day in the life of the Mare aux Songes' (painting by Julian Pender Hume).
Fig. 4. Well-preserved sub-fossil branches and roots, after cleaning.
Fig. 5. Kersley Pynee (MH) and conservationist Gabriël d'Argent inspecting native plants.

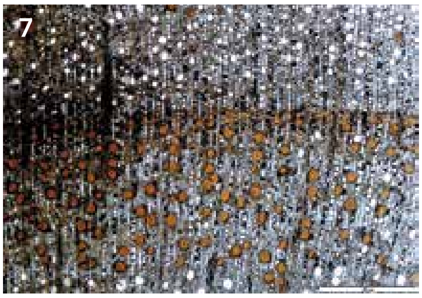

Fig. 6. Transversal section of a sub-fossil branch of *Ficus* sp. (scale bar: 500 μm).
Fig. 7. More or less distinct growth rings in sub-fossil *Cassine orientalis* (scale bar: 500 μm).
Fig. 8. Tree with fresh pinmark. The pinning device - a nail - has been pulled out.

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Thai Floristic districts
The influence of climate change

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The NHN/Naturalis participates in the Flora of Thailand project since its start in the 1950's. About 50% of the flora is presently critically revised. Species distributions within the project are traditionally given for seven flora districts (Fig. 1a). However, the recognisability of the areas was doubtful, it was uncertain that the districts could be characterized by typical species. In order to test this, two, almost independent databases were compiled, one listing the species distributions per province as recorded in the Flora of Thailand, the other comprising collecting localities of plant specimens. This second database was used for Species Distribution Modelling (SDM), not only for the present day distributions, but in combination with a climate model also for 2050. SDM adds areas to species distributions if climate, altitudinal and soil conditions are more or less similar as in the collecting localities.
Both databases (Fig. 1b, c) show that ca. four floristic regions are present, the most southern and northern ones are the most distinct and these only partly overlap with the areas in the flora (Fig. 1a).
In 2050 the number of floristic areas increases to five; the northern area splits into two and in the central part the boundaries are completely different (compare Figs. 1a and 2). The climate in 2050 is expected to be wetter and at most 2° C warmer, but with more extreme dry periods. This results in a forecasted high loss of biodiversity between now (Fig. 3a) and 2050 (Fig. 3b) in especially the northern floristic region (Fig. 3c). Gains are present in the southern and eastern parts (Fig. 3c).
Figures 1-3 seem to show an unlimited plant cover. However, when land use is taken into account (Fig. 4, white areas), then only few forests appear to be present, mainly along the borders. The grey shadings in Fig. 4 show that every floristic region (four areas nowadays, Fig. 4a; five in 2050, Fig. 4b) has protected areas. These protected areas, few as they are and only covering a limited amount of land, will be crucial to maintain Thailand's high biodiversity, now and in the future.

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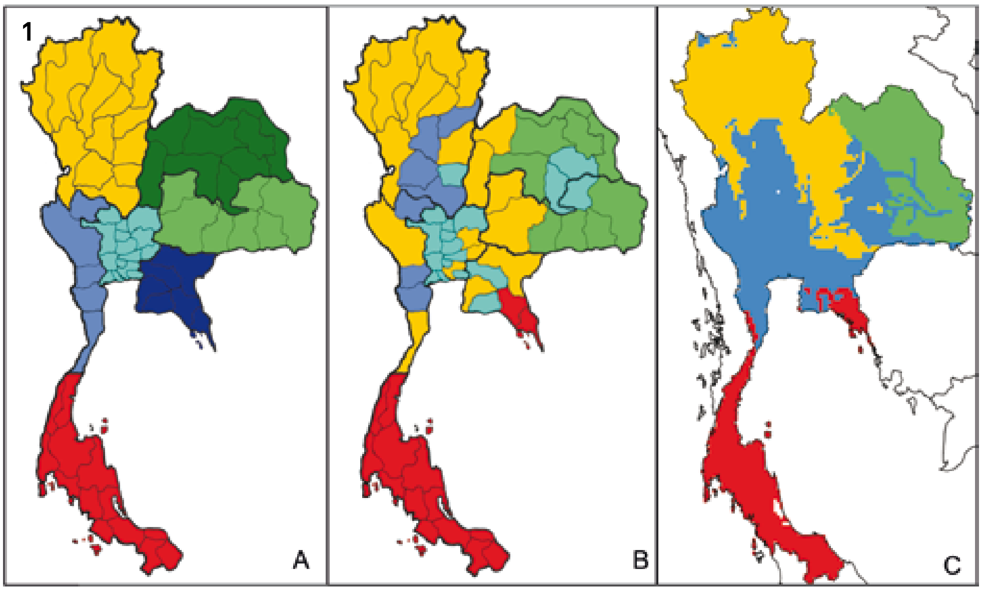


Fig. 1. Floristic areas. A. As used in the Flora of Thailand; B. Cluster analysis of database 1 (presences per province from the Flora of Thailand; C. Cluster analysis of Species Distribution Models.

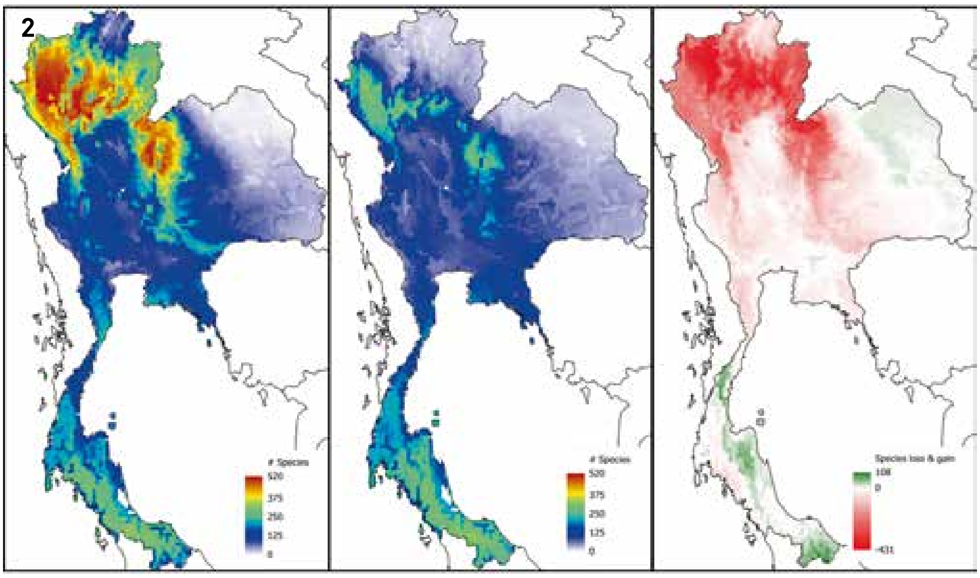
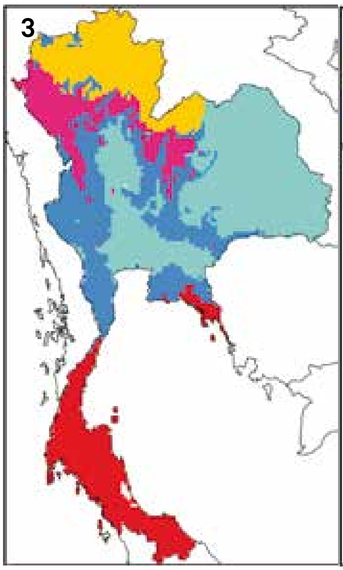


Fig. 2. Floristic regions in 2050 based on Species Distributions Models.



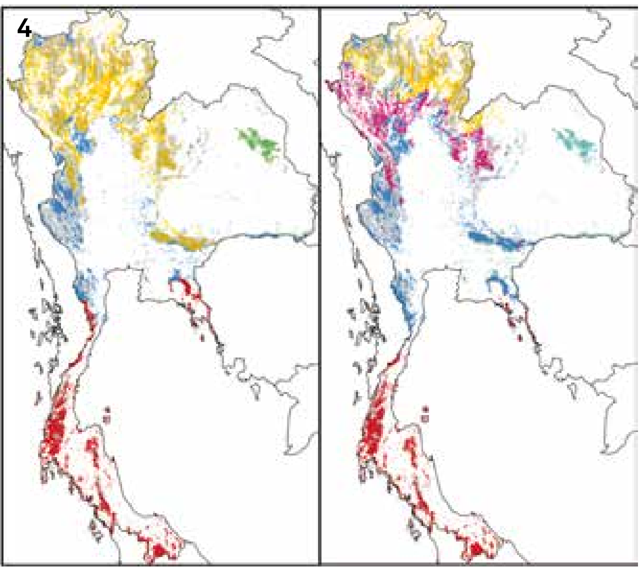


Fig. 3. Biodiversity (numbers of species) at present (A), in 2050 (B) and A subtracted from B showing loss (red) and gain (green) in C. Species numbers per 10 by 10 km grid cells.

Fig. 4. Human land-use (cities, agriculture, industry, etc.) is shown as white areas, the coloured areas show the remaining forests, whereby the colours indicate the different floristic regions nowadays (Fig. 1c) and in 2050 (Fig. 2). Protected areas are hatched with grey.

Attacking the hot potato
Hymenostegia s.l. (Leguminosae)

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The Legumes are one of the most important plant families, both in terms of species numbers (nearly 20,000) and economically. In the temperate regions of the world, legume diversity is mostly represented by herbs and shrubs from the papilionoid subfamily which commonly, but not always, have typical pea-like flowers. However, in rain forests, especially those of Africa, another group of legumes has become dominant: trees from the tribe Detarieae (the caesalpinoid subfamily). More than half the trees in the canopy layer of some rain forests in Africa are species of this tribe, a phenomenon often attributed to the symbiotic relationships with ecto-mycorrhizal fungi that these trees are able to establish (Newbery *et al*, 1997; Wieringa, 1999). The fungi absorb and pass on vital nutrients to the trees which is a great advantage to them as they grow on the typically nutrient poor rainforest soil. Within the Detarieae, there were several 'hot potatoes' present: i.e. genera with a problematic generic or specific circumscription. Several of these have been dealt with in the past 20 years; e.g. the *Anthonotha* group (Breteler 2010; 2011), *Berlinia* (Mackinder & Pennington, 2011), and the *Monopetalanthus*-group (Wieringa, 1999). For the past couple of years we have taken up the task to get the *Hymenostegia* group resolved. In several phylogenetic studies based on chloroplast markers (e.g. Bruneau *et al*., 2008, Mackinder *et al* 2010a), *Hymenostegia* came out as a polyphyletic group, but in a part of the phylogeny where the resolution is pretty low. A part of *Hymenostegia*, including its type, forms a monophyletic group in such studies, and has been re-defined morphologically by us as well (Mackinder *et al*. 2010a) as *Hymenostegia* sensu stricto. It is related to another tropical African legume tree genus *Talbotiella*, and in a recent treatment clarifying the borders between the two genera, we transferred one species of *Hymenostegia* to *Talbotiella*, while at the same time we described 4 species new to science in the later (Mackinder *et al* 2010b).

Next we started to study the species within *Hymenostegia* s.s.. So far we described three new species of *Hymenostegia* (Wieringa & Mackinder 2012, Mackinder & Wieringa 2013; Figs 1-2), but more new entities are still hiding under currently accepted names.

Since about half of the species traditionally classified as *Hymenostegia* prove to be not congeneric with the genus as we now circumscribe it, we also started to find new homes for these species.

This task is not as simple as it seems. First of all, the eight "out-species", as we call them, do not form a single monophyletic group but seem to comprise at least 6 different groups. We tried to find shelter for them in related genera like *Loesenera*, *Plagiosiphon* and *Scorodophloeus*, but without success.

Another problem that rises over the horizon is the also related, pan-tropical genus of *Cynometra*. As currently circumscribed, *Cynometra* contains about 90 species, but preliminary evidence suggests that *Cynometra* will prove just as polyphyletic as *Hymenostegia*, and we may discover that some species of *Cynometra* are actually closely related to some of our *Hymenostegia* out-taxa. To investigate possible relationships between our out-taxa and other Detarieae, we have added a considerable number of species to those already present in previous molecular studies, and plan to publish these new molecular findings in the coming years. First results of this study indicate that some of our out-taxa will need to be placed in yet to be described new genera. Although they are sisters to clades containing several other genera, merging all into a single genus would result in genera that would make no morphological sense, so we abandoned that option.

As the molecular study progresses and sheds more light on the new entities that we will need to recognise, we plan to revise them one after the other, including the description of any new species that belongs to them. At present, we are aware of at least 6 more new species in the *Cynometra*-*Hymenostegia* group that need to be described. It is remarkable that so far we have not had a single case where we needed to synonymize a name. Our studies have already shown that the diversity of Detarieae trees in

Fig. 1. *Hymenostegia robusta* Wieringa & Mackinder. A) several twigs with axillary flowering shoots; B) flowering shoot, inflorescence subtended by 2 leaves; C) inflorescence; D) inflorescence with leaf base and stipule. All *Wieringa 2783*. (Photographs by J.J. Wieringa)

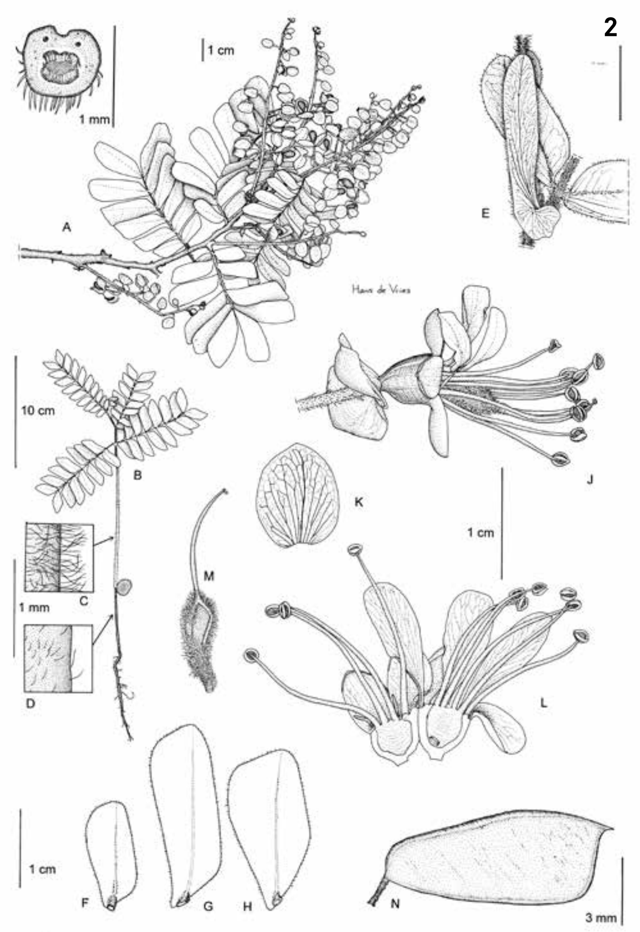

Fig. 2. *Hymenostegia viridiflora* Mackinder & Wieringa. a) Flowering branch; B) seedling; C) detail of epicotyl; D) detail of hypocotyl; E) stipule; F) basal leaflet; G) middle leaflet; H) apical leaflet; I) cross-section of leaf rachis; J) flower; K) bract from inside; L) dissected flower from inside; M) ovary with stipe and style; N) pod. (Drawings by H. de Vries)

Africa is much larger than previously recognized, both at the generic and specific levels.

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Cucurbitaceae
Revised for Flora Malesiana

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Taxonomic research at NHN-Leiden focusses on the flora of the Malesian region. Including precursors, about 50% has been treated, by which more than 100 families have been revised in 23 volumes. Recently, we revised another family for the series Flora Malesiana, the Cucurbitaceae (de Wilde & Duyfjes, 2010, vol. 19: 1-333), treating 121 native species and several cultivated species as well, belonging to 37 genera. The treatment contains an overview of all Cucurbitaceae, wild and cultivated, for the Malesian area. The account is illustrated with 97 drawings by Jan van Os (Fig. 1), recipient of the Jill Smythies Award of the Linnean Society, and 32 full colour photo plates (Fig. 2), and it is accompanied by a digital key on CD-Rom (Fig. 3), constructed by the editor, H.P. Nooteboom.
Cucurbitaceae is a family of climbing plants to which *melons*, *pumpkins*, *gourds* and *cucumbers* belong; it also includes crops such as *squashes*, *watermelons* and *chayotes*. They are predominantly distributed in and near the tropics, and species with edible fruits were amongst the earliest cultivated plants in both the Old and the New World. *Trichosanthes* is the largest genus in the Cucurbitaceae family, with 43 species in Malesia; its name alludes to the long threads on the petals (Fig. 4).
Cucurbits rank among the most important plant families, providing food (and medicines) for humans like *Cucumis sativus*, the *cucumber*, probably the most commonly used source of raw, or cooked vegetable or *Citrullus lanatus*, the *watermelon*.
Of many species the shoots, leaves and young fruits e.g. of *Sechium edule*, the *chayote* or *Luffa aegyptiaca*, the *vegetable sponge* can be eaten as greens, of others the mature fruits or seeds, like e.g. *Cucurbita moschata*, the *pumpkin* serve as staple food.

Cucurbitaceae in the wild are more or less evenly dispersed over the tropical world, and comprise about 100 genera with over 800 species. For Asia the taxonomically most challenging genera were *Trichosanthes* (100 species) and a group of small statured climbers formerly mostly called *Melothria* but now divided into several distinct genera (with several new species), e.g. *Indomelothria*, *Pilogyne*, *Zehneria.* Recent molecular research, mainly at Munich, brought better insight into the relationship of genera, including a wider concept of *Cucumis,* directing attention to wild growing species possibly useful in commercial breeding. The alleged wild progenitor of the Cucumber, *Cucumis hardwickii* (from India) was recently also discovered in Thailand, and could be compared in detail with very similar plants cultivated by hill tribes in SE Asia (fig. 5a-b).
Malesian cucurbits are all climbers, most of them of small to medium length, but some reaching the tall forest canopy. In general they prefer to grow in or near primary rainforest or in other primary conditions and always in the vicinity of (running) water. They are rather difficult to study in the wild: many are small climbers, often only flowering during the night, and in addition they are dioecious.
Mount Kinabalu (Malaysia) and surroundings appeared to be a hotspot for the genus *Trichosanthes*, where during the last 15 years 10 new species were discovered, for instance *Trichosanthes postarii* (fig. 4b).

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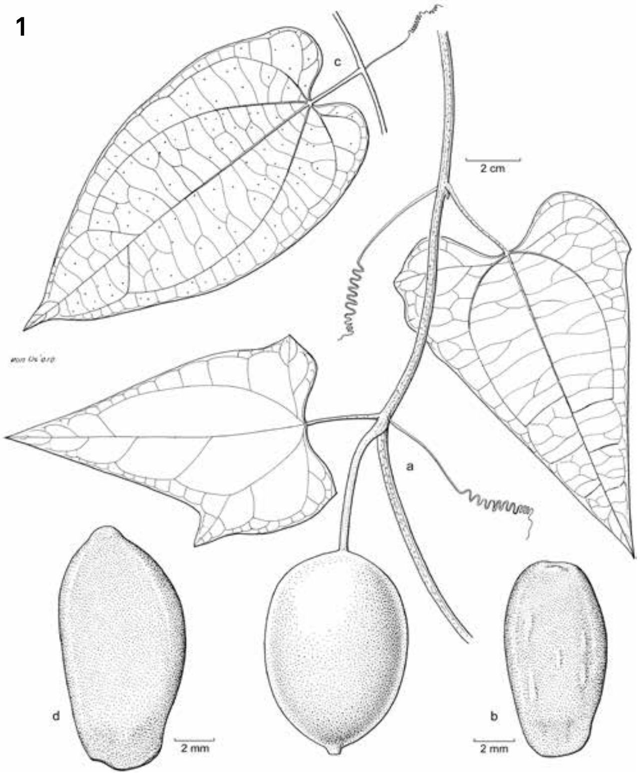

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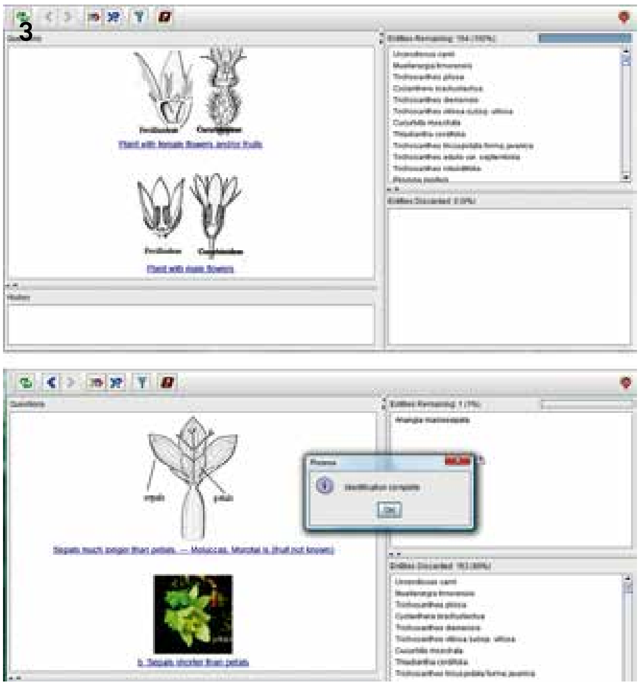

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4a

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Fig. 1. *Trichosanthes pedicellata* W.J.de Wilde & Duyfjes, drawing by Jan van Os.

Fig. 2. *Kedrostis monosperma* W.J.de Wilde & Duyfjes, photo by the authors.

Fig. 3. The digital key in use.

Fig. 4. Examples of flowers with long threads on the petals. a. *Trichosanthes pilosa* Lour.; b. *Trichosanthes postarii* W.J.de Wilde & Duyfjes

Fig. 5a-b. *Cucumis sativus* L. (feral form).

5a

5b

Forests vulnerable to drought
Predict response to climate change

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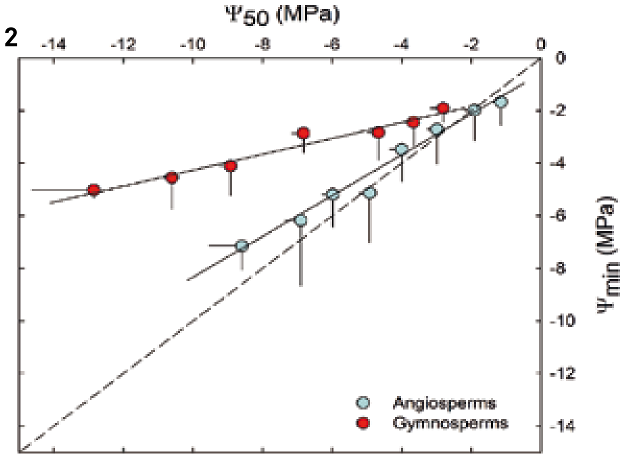
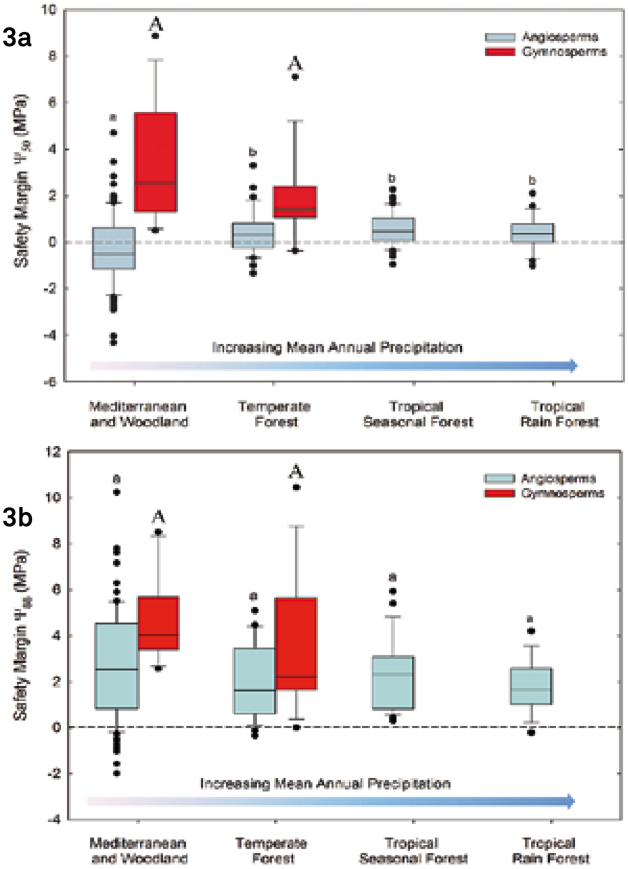
Beneath the bark of world's trees pulses a finely tuned vascular system that transports billions of litres of water to the skies every day. This plant hydraulic system depends on a unique but unstable mechanism that is continuously challenged by environmental stress. New research in *Nature*, lead by the University of Western Sydney and Ulm University in Germany in collaboration with 20 other institutes including Naturalis Biodiversity Center, has found most trees, even those in rainforests, operate very close to their hydraulic safety threshold leaving them highly vulnerable to droughts of increased severity. What kind of impact does these results have in the light of the current climate change scenario predicting more periods of increasing drought for many parts of the world?

Risky business

Drought is one of the major forces shaping our forest ecosystems (Fig. 1). Over the last century, drought has been responsible for many incidences of large-scale forest dieback around the world. To make effective predictions of how the forest landscape may change in future, we need to first understand how plants work. One of the main problems that plants face during drought is to keep their 'plumbing' working. In order to take up carbon dioxide for photosynthesis and to cool their leaves, plants must transpire very large amounts of water every day. This water is absorbed from the soil and transported through a network of thread-like pipes that connect the roots to the leaves. An important force enabling this upwards pulling of water is tension that acts as a suction force created in the leaves. As soil dries, the water in these pipes comes under an even larger tension that can cause breakage of the liquid threads inside the plumbing system. This so-called "cavitation" of the liquid continuum inside the plant vascular system can cause an air blockage, similar to the embolisms that can block the human circulatory system. As drought stress increases, the rate of embolism formation in water conducting cells increases until the plant desiccates and dies. The difference between the critical point at which embolisms exponentially increase, often called P50 or the pressure needed to induce 50% loss of hydraulic conductivity, and the daily tension that plants experience to pull water against gravity is the so-called safety-margin (Figs 2, 3).
An international team of 24 plant scientists organized via the ARC-NZ Research Network for Vegetation Function compiled a global data synthesis examining all existing measurements of plant embolism resistance in forest species. Vulnerability to embolism (Fig. 4) is known to be one of the main factors determining drought effects on trees.
As expected, species growing in wet forests were less resistant to embolism than those growing in arid areas. While plants vary greatly in their embolism resistance, their vulnerability to drought is the same across all forest types. Seventy percent of 226 forest species from 81 sites in the worldwide study operate with narrow hydraulic safety margins against potentially deadly levels of drought stress. The team found safety margins are largely independent of mean annual precipitation, illustrating global convergence in the vulnerability of forests to drought, with all forest types equally vulnerable to hydraulic failure regardless of their current rainfall environment (Figs 1-2). The findings provide insight into why drought-induced forest decline is occurring not only in arid regions but also in wet forests not normally considered at drought risk. Trees take a 'risky' hydraulic strategy in a trade-off that balances growth with protection against the risk of mortality.

For trees, and the planet, the consequences of longer droughts and higher temperatures are potentially dramatic. For example, rapid forest collapse via





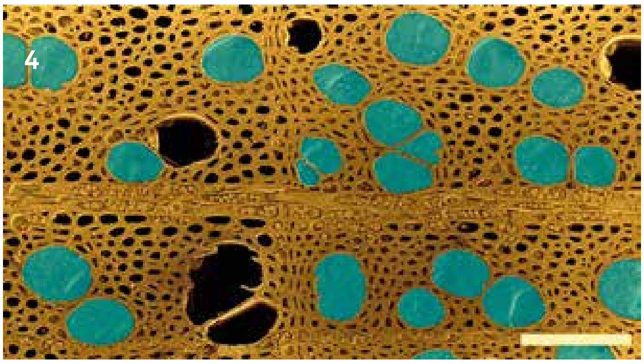


Fig. 1. Forest near Trieste (Italy) showing large-scale tree mortality due to drought stress during the summer of 2012. Species affected included *Fraxinus ornus*, *Quercus pubescens*, and *Ostrya carpinifolia*, while Pine trees, *Prunus mahaleb*, and *Pistacia terebinthus* remained perfectly healthy. Photo credits: Dr. Andrea Nardini (University of Trieste, Italy).
Fig. 2. Minimum xylem pressure (Ψ_{min}) as a function of embolism resistance (Ψ_{50}) for 191 angiosperm and 32 gymnosperm species. The dashed line indicates the 1:1 line. The safety margin is the distance between each point and this line. Error bars show standard deviation. Points were binned in 1.0 MPa increments for Ψ_{50}. Bins were pooled with the next lowest bin if they contained only one sample. Regression lines shown were fitted to raw data (angiosperms $r^2 = 0.57$, $P < 0.0001$, gymnosperms $r^2 = 0.59$, $P < 0.0001$).
Fig. 3. Box plot of hydraulic safety margins for angiosperm and gymnosperm species across major forest biomes. The Ψ_{50} ($\Psi_{min} - \Psi_{50}$) safety margin is shown in Fig. 2a, and the Ψ_{88} ($\Psi_{min} - \Psi_{88}$) safety margin in Fig. 2b. Boxes show the median, 25th and 75th percentiles, error bars show 10th and 90th percentiles, and filled symbols show outliers. Gymnosperm species were not represented in tropical forests. Significant differences ($P < 0.01$) between biome means are indicated by different letters above boxes with angiosperms (lowercase) and gymnosperms (uppercase) considered separately.
Fig. 4. Electron microscopic picture of wood from a *Prunus sargentii* tree showing water-transporting cells that are either functional (blue colour) or embolised (i.e., air-filled, dark colour). Drought stress increases the likelihood of embolism, reduces photosynthesis, and may eventually lead to plant death. Scale bar = 100 µm. Photo credits: Dr. Yuzou Sano (Hokkaido University, Japan).

drought could convert the world's tropical forests from a net carbon sink into a large carbon source during this century, and thereby enhancing the climate change scenario. However, the results of the study do not necessarily point to forest Armageddon. A forest may respond to climate change in a number of ways. For instance, some species may be able to evolve quickly enough to keep pace with a changing climate in one location, while others may spread into new locations, tracking their preferred conditions. Survival is largely dependent on species having enough time to respond to changes in the environment. The new dataset will be useful to better predict the balance between a declining or a healthy forest. It will also provide a better understanding of which species are likely to persist and which are likely to suffer and potentially disappear.

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Macaranga and *Mallotus*

Reliable fossils in Euphorbiaceae?

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More than 50 fossil specimens of *Macaranga* and *Mallotus* are described in literature, ranging from pollen grains to wood, seeds and especially leaf imprints. This collection should be sufficient to find fossils with which a phylogeny of both genera can be dated and to get an indication of the palaeontological distribution of the genera.

An evaluation of the fossils, in close cooperation with experts, gave a very negative result. Most fossils could not reliably be identified, at most only up to a group of genera. The results were published (Nucete *et al*., 2012) as a warning to be prudent with the use of fossil plant fragments in phylogenetic and historical biogeographic studies.

Fossil wood shows a too general pattern to even reliably call it Euphorbiaceous. The seed type of *Macaranga* and *Mallotus* is very general, thus not helpful for identification and pollen is only typical for a group of genera to which *Macaranga* and *Mallotus* belong. The leaf imprints mainly showed venation patterns and these were unfortunately also very general and found among various tropical plant families. Only a few leaves showed enough detail for a reliable identification, e.g. glandular scale hairs and extra-floral nectaries were present.

For dating, the next problem is to link the fossils to a place in the cladogram. A fossil from Ethiopia closely resembled the present day species *Macaranga kilimandscharica* Pax (Fig. 1) and could be associated with the African *Macaranga* clade. A group of New Zealand specimens showed a high similarity with *Mallotus nesophilus* Müll.Arg. (a species occurring in Australia, but unknown for New Zealand; Fig. 2). Finally, a Japanese fossil (*Mallotus hokkaidoensis* Tanai) could be linked to a clade of *Mallotus* species typical for secondary habitats. With these fossils and a starting date of the clade *Macaranga/Mallotus* from literature the dating was successful, but to be presented later.

Figure 3 shows the present day distribution of *Macaranga* and *Mallotus* and the fossils are plotted on the map. Quite a number of fossils occur within the contemporary distribution ranges, especially in India, but many are from outside the present day distribution. A problem with the latter is that these fossils are at most difficult to identify, only the New Zealand fossils probably belonged to a former, wider distribution of *Mallotus*. It is also likely that some of the E. Asian fossils belong to *Mallotus* (*Macaranga* seemingly needs more tropical conditions). However, we are completely uncertain about the European and American fossils. One fossil from Alaska has recently been redescribed as a *Platanus*.

Knowledge of ancestral distributions is a predicament in historical biogeography. Methodologically, ancestral species could never have lived outside the distributions of the present day species. Fossils can indicate otherwise, but there are generally too few to offer a complete picture. A combination with species distribution modeling for various geological times might provide a solution, though the models will show less resolution than present day models due to a lack of or less precise climate data.

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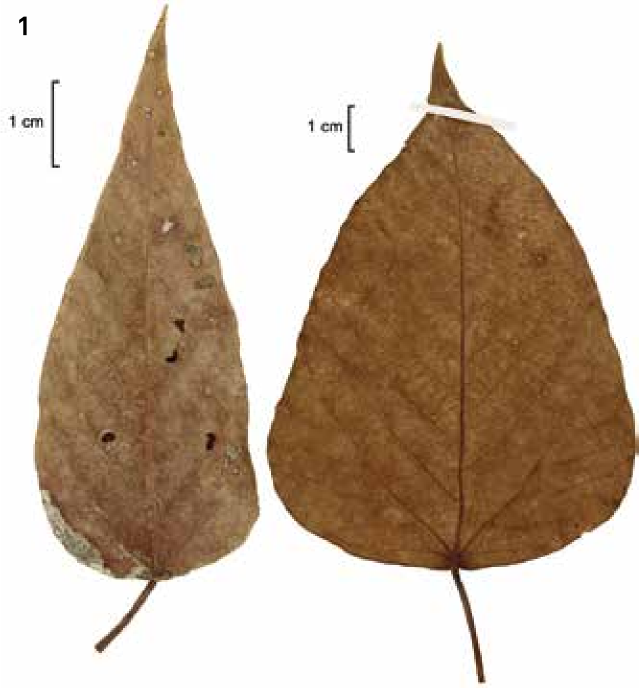

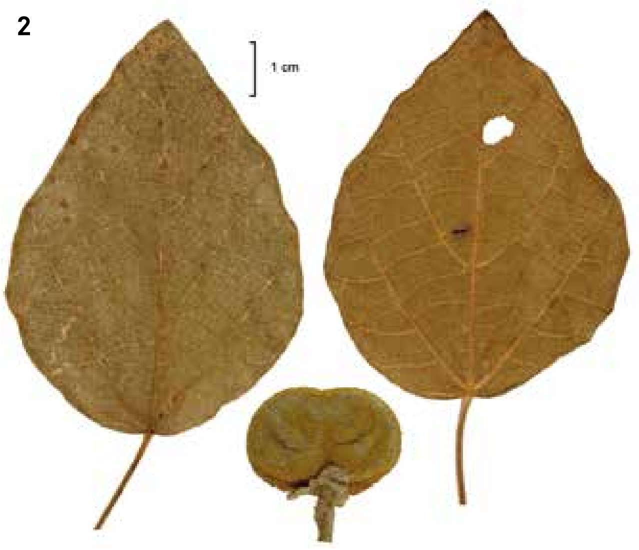

Fig. 1. Upper (left) and lower (right) surface of leaves of *Macaranga kilimandscharica* Pax.
Fig. 2. Upper (left) and lower (right surface of leaves of *Mallotus nesophilus* Müll. Arg., fruit (centre) c. 5 mm.

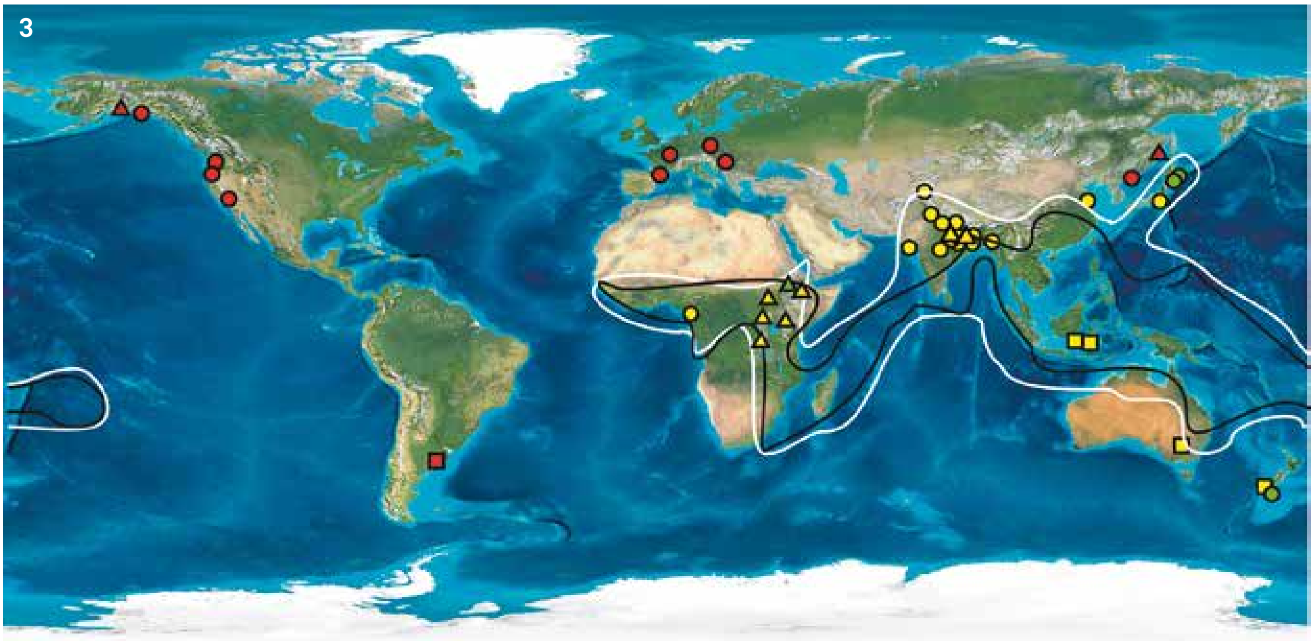

Fig. 3. Present day distribution of *Macaranga* (black line) and *Mallotus* (white line) and locations of fossils discovered; ▲ = *Macaranga* fossils; ● = *Mallotus* fossils; ■ = *Macaranga* or *Mallotus* fossil; Green = identified fossil; Yellow = 'unidentifiable within the present day distribution'; Red = 'unidentifiable outside the present day distribution'.

Ethnobotany of Gabon

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From June to December, 2012, Diana Quiroz and Alexandra Towns carried out fieldwork for their PhD study in Gabon. In the beginning, when exploring the forests near the capital Libreville, they were assisted by several students and researchers (Fig. 1). The team started with a survey of the medicinal herbs, barks and roots sold at the Libreville market. To find out whether these species are harvested in a sustainable way, students Guinee and Boogmans followed market vendors in the field to see where and how they collected their plants (Fig. 2). This will result in a quantitative description of the trade in herbal medicine in the country and a shortlist of commercial species with conservation priority. After their students and supervisor left, Quiroz and Towns headed for remote parts of the country like the southeastern Bateke Plateaus bordering Congo-Brazzaville and the isolated lakes of the Ogooue river delta. Quiroz, who focuses on ritual plant use, witnessed initiation rites based on the hallucinogenic roots of *Tabernanthe iboga* and interviewed some 40 traditional healers on plants used for spiritual diseases, witchcraft and sacrifices (Fig. 3). She worked with people of 14 different ethnic groups, among which were the Babongo Pygmies living in the forests of Waka National Parc. Towns studies plants used for women's health and child care. She interviewed 80 women on plants used to treat reproductive health problems and children's diseases. She discussed her results with 20 gynecologists, general practitioners and pediatricians in the Libreville hospitals to better understand cultural-bound disease concepts like closing fontanels and post-partum uterus cleansing, and evaluate the possible risks and benefits of using traditional medicine. With student van Vliet, she accompanied her informants into the forest and home gardens to compare the proportion of cultivated, domesticated and wild plants used by rural and urban women.

Currently, the researchers are analyzing their data and about to publish their first results.
Some important findings are:

- Although rural women were expected to use more wild plants than urban women as they had better access to the forest, both groups used similar percentages of cultivated and wild plants. Urban women had easy access to wild plants, because they could purchase them on the market. Wild species were preferred by both groups.
- Bark of the rainforest trees *Annickia affinis, Bailionella toxisperma* and *Aucoumea klaineana* was offered for sale in large quantities on the medicinal plant markets in Libreville. Resin of the latter species was also an important commercial item. The yellow *Annickia* bark is a well-known remedy for malaria, while the bark of *Bailionella* is used to treat male circumcision wounds. Both resin and bark of *Aucoumea* were used against sorcery. Traditional beliefs, such as the *bwiti* religion play a large role in the trade in herbal medicine in Gabon.
- Thanks to Gabon's low population density and extensive forest cover, most medicinal plant species seem to be harvested sustainably. The majority of the herbal medicine is either domesticated or harvested from secondary vegetation. However, the rainforest trees mentioned above, and species like *Copaifera religiosa* and *Pterocarpus soyauxii* may be threatened in the future, as they are exploited for timber on a large scale. Most of Gabon's interior is divided into logging concession or national parks. This means that local people may have less access to culturally important species in the future.

Fig. 1. The research team at the Forêt Classée Raponda-Walker, Gabon. From top left to bottom right: Diana Quiroz (PhD student WUR), Sofie Ruysschaert (Univ. Ghent), Tinde van Andel (postdoc UL), Britt Boogmans (BSc student UL), Lieke Guinee and Esther van Vliet (MSc students UU) and Alexandra Towns (Phd student UL). It is probably the first all-female (ethno-) botanical team in history.
Photo: Diana Quiroz.

Fig. 2. Market vendor preparing a medicinal plant bundle.
Photo: Diana Quiroz.

Fig. 3. Traditional bwiti priestess, Gabon. Her face is painted red with sawdust of *Pterocarpus soyauxii*.
Photo: Diana Quiroz.

This research is carried out in the framework of the NWO-Vidi project "Plant Use of the Motherland-Linking Afro-Caribbean and West African Ethnobotany", headed by Tinde van Andel (Naturalis / UL).
In Gabon, the team was supported by the Herbier National and the Institut de Pharmacopee et de Medecin Traditionnelle in Libreville.

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Amischotolype (Commelinaceae)

Taxonomic revision for Asia

Leni Duistermaat

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A revision of the the Commelinaceae (Spiderwort family) for Flora Malesiana, a family of about 650 species in 41 genera with a cosmopolitan distribution (although with no native species in Europe; Faden 1998), has been hampered by difficulties to revise the genus *Amischotolype* solely from herbarium collections. While based in Singapore, when I had the opportunity to study several species of this genus in the field, I took up this challenge.

Generic delimitation

The first species were described from Java by Blume in *Campelia*, but the genus is best known as *Forrestia.* The correct name for the genus, however, is the unpronounceable name *Amischotolype* Hassk. The name refers to the sessile glomerules of flowers, the character that immediately distinguishes it from the American species of *Campelia* (which are now united with *Tradescantia*).

Hong described the genus *Porandra* from China as closely related to *Amischotolype*, differing by its climbing habit with branched and basally 'woody' stems, and by having thecae opening by apical pores (hence the name). These characters, however, are not unique for *Porandra*, as noted by Faden, and confirmed in the present revision. However, for now, pending results from on-going molecular studies, I keep the genera separate.

Need for revision

Amischotolype has a paleotropical distribution and the species typically grow in a forest environment, even surviving for a long time after disturbance of the forest, on rather dry to swampy soils. The most recent monographic revision of the genus was that of Clarke, dating back to 1881. Since then, 12 more species have been described. The African species are excluded from this revision. There is no overlap in species between Africa and Asia. Nomenclature and species delimitation in local Asian flora treatments differ considerably. Several considered the amount of indument on the sheath and the lower surface of the leaf blade of high taxonomic importance, but in my revision these proved to be variable within many species.

Characters that I proved valuable for the delimitation of Asian species of *Amischotolype* include the indument of the internodes, and upper surface and margin of the leaf blade, the inflorescence position, the (relative) length and indument of the sepals, the length of anthers, and size and indument of the capsules. In the present revision of *Amischotolype* I recognise 22 species for Asia, of which eight are new. *Amischotolype glabrata* is the most widespread species, occurring from E Pakistan through China to S. Japan (Ruykyu Islands) and south to Nusa Tenggara (Lombok), excluding the Philippines and Sulawesi.

I managed to include colour photographs of 11 species (Fig. 1). For the eight new species, Anita Walsmit Sachs produced detailed line drawings (Fig. 2), as well as flower and fruit details of the other species. To facilitate identification, I produced a dichotomous identification key including the 22 species of *Amischotolype*, as well as the two species of *Porandra*. To allow for quick comparison between species of both genera, I also developed a character synopsis for vegetative, inflorescence, flower and fruit characters, and distribution.

Published as

Duistermaat, H. 2013. A taxonomic revision of *Amischotolype* (Commelinaceae) in Asia. *Gardens' Bulletin Singapore 64:* 51-131.

Reference

Faden, R.B. 1998.Commelinaceae. In: Kubitzki, K. (ed.) *The Families and Genera of Vascular Plants.* 4: 109-128.

Fig. 1. *Amischotolype monosperma* (C.B.Clarke) I.M.Turner. Detail of inflorescence showing opened flower with cream-coloured red-hairy sepals. Photograph by André Schuiteman from *HBL* (*Vogel*) *960236*.

Fig. 2. *Amischotolype parvifructa* Duist. **A.** Habit. **B.** Flower with fruit. Drawing by Anita Walsmit Sachs, from *Chew W.L. 837* (L).

Fungi in Andean cloud forests
DNA in soil reveals many new species

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The Andean cloud forests (i.e. the Yungas) are a system of tropical and subtropical montane forests developed on the eastern slopes of the Andes.
The Yungas are extremely diverse and rich in endemic species. For example, despite covering only 2% of the area of Argentina, they harbour about 50% of the country's biodiversity. Unfortunately, the Yungas are among the ecosystems most threatened by anthropogenic pressure and climatic changes. Globally, the majority of biodiversity studies and conservation efforts are focused on vascular plants and vertebrates, while soils remain a relatively unexplored, yet presumably significant source of biodiversity.
Fungi represent one of the largest groups of living organisms. Already well before the routine use of DNA methods, their true diversity was estimated to be around 1.5 million species, while more recent estimates suggests there may be as many as 5 million fungal species. Although there are differences among the estimates, it is clear that with the appr. 100,000 described species, an estimated >90% of all fungi are still unknown. Such lack of knowledge is particularly unfortunate, because fungi play central roles in the functioning of terrestrial ecosystems as decomposers and as symbionts of plants and animals.. Similarly, previous mycological works in the Argentinian Yungas focused on macrofungi (e.g., agarics, polypores) and mycorrhizal symbionts of *Alnus acuminata*, while diverse fungal communities in the Yungas still remain virtually unexplored. This lack of adequate taxonomic and ecological knowledge now severely compromises our ability to conserve and utilize biodiversity and to recognize and to respond intelligently to recent and future environmental changes.

High diversity and strong habitat preference

We carried out a massive next-generation sequencing project of soil samples to provide the first kingdom-wide fungal biodiversity assessment for the Yungas. Based on previous mycological studies, about 150 fungal species had been recorded from this region. We collected soil samples in 2011 May in the Calilegua National Park in Jujuy province near the Bolivian border (Figs. 1-2).
The selected sites represented three major forest types along an altitudinal gradient: the piedmont forest (400-700 m above sea level), the montane forest (700-1500 m asl), and the montane cloud forest (1500-3000 m asl).
We found ca. 2000 fungal species in our soil samples, while the total number of fungi is likely even higher in this ecosystem (Fig. 3). Despite the presence of more than 100,000 fungal ITS sequences in public databases, ca. 50% of the OTUs in our samples could not be identified to species level. This number is even greater if we consider those sequences for which highly similar but not fully identified matching sequences were found. Because of the rigorous quality checks applied while processing the sequence data, our conservative estimates clearly indicate the need for further fungal diversity research in the Yungas in particular and in the Neotropics in general. Many fungi at the sampling sites likely are still undescribed, while others may remain unidentified because of the unavailability of reference sequence data from known species due to the time lag in type strain and specimen sequencing.
The composition of fungal communities were clearly different among all three forest types, with many species showing strong preference for a certain altitudinal forest zone (Fig. 4). Besides elevation, soil pH, N and organic matter contents, and C:N ratio strongly correlated with fungal community structure as well, although these were all

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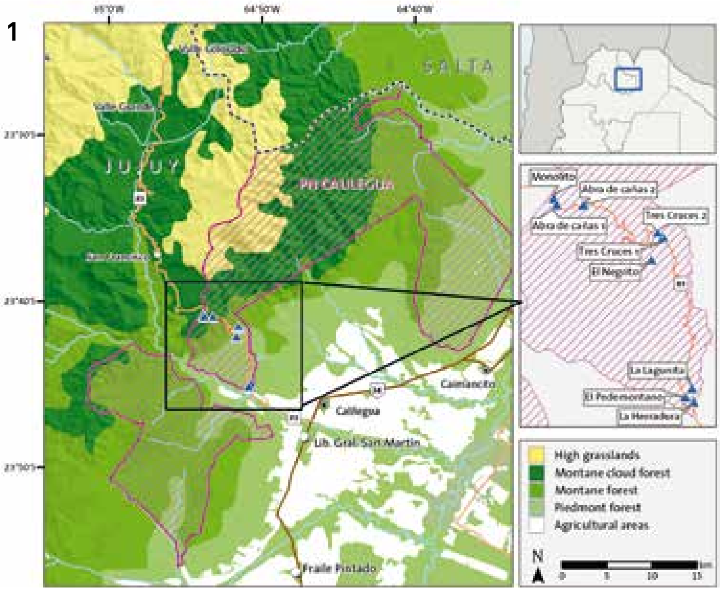

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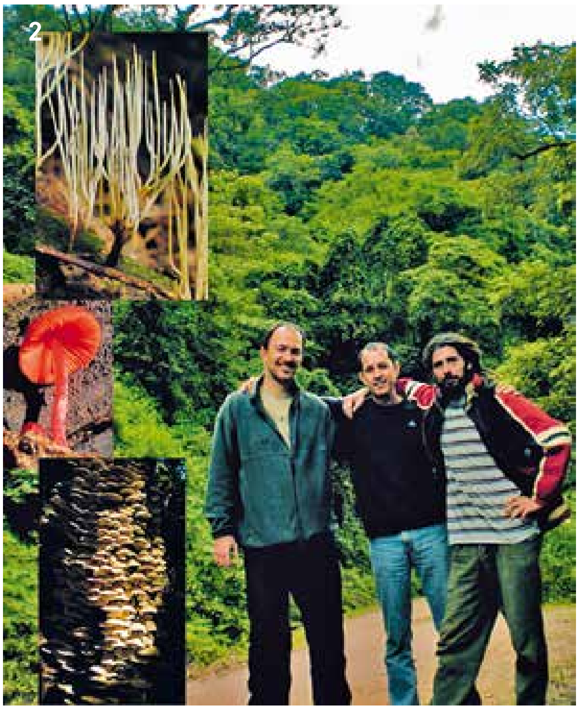

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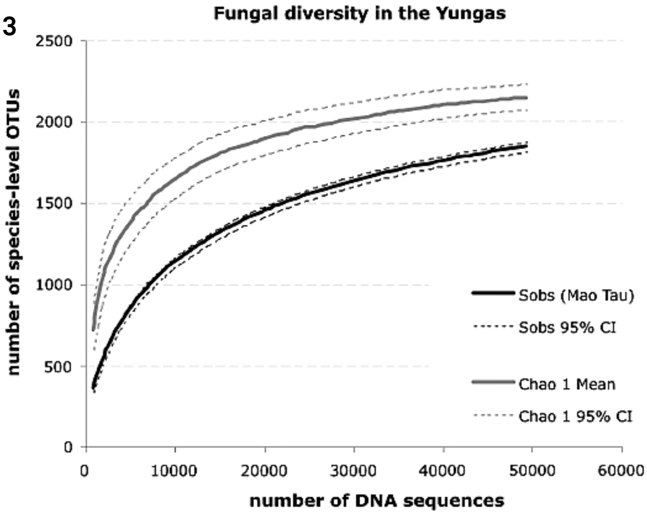

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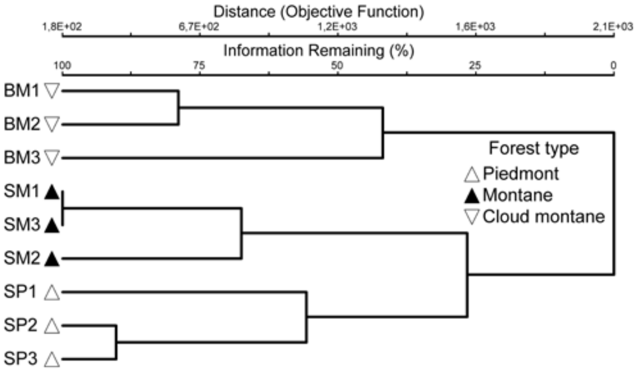

Fig. 1. A map showing the sampling sites in Calilegua National Park in Jujuy province (Argentina) with the altitudinal forest zones indicated.

Fig. 2. Fieldwork in Calilegua National Park, l-r: József Geml, Eduardo Nouhra, Lisandro Fernandez (Photo: Pastor) with various fungal species shown in the inserts (Photos: Geml).

Fig. 3. Species accumulation curves showing the observed (Sobs) and estimated (Chao 1) number of fungal species detected in our samples from the Yungas.

Fig. 4. Cluster dendrogram showing compositional similarity of fungal communities among elevational forest zones.

co-correlated with elevation and forest type. Our project offers an unprecedented insight into the fungal biodiversity of the Yungas and into the zonal changes in fungal community structure, with potential applications in conservation strategies to preserve the unique biodiversity of the Andean forests.

Presented at

Mycological Society of America Annual Meeting, Yale University, New Haven, CT, U.S.A., Inoculum 63(3): 18.

Original title

Mycota of the Andean Yungas forests: Assessments of fungal biodiversity and habitat partitioning in a threatened ecosystem

The Catalogue of Life
Essential for biological sciences

Jan van Tol, Rob van Soest & Nicole de Voogd

Naturalis Biodiversity Center, Leiden

'How many species live on Earth' is without doubt one of most frequently asked questions to taxonomists. And the answer is both simple and uncomfortable: 'We don't know'. For many years biologists estimated that the number of species of multicellular organisms could be as high as 50 or even 100 million, but more recent studies consider a number of ten million more realistic. Then, of course, we like to know how many species have been described up to know, and the answer is still again rather disappointing.
With the number of taxonomists declining, at least in the northern hemisphere, it became evident that taxonomy needed a complete new methodology than used up to recently to complete the inventory of the world's organisms. The taxonomic impediment not only consisted of the declining number of taxonomists, but also by the poor infrastructure for many colleagues new in the field. Old books and series of journals, especially of hundred years old and more, are only available in a small number of libraries in Europe and North America. Likewise, natural history collections, also from the southern hemisphere, are mainly preserved in Europe and North America. Several initiatives now try to lay a sound basis for taxonomy outside these continents.

Information technology plays an important role in the new taxonomy. Old literature is made available through the *Biodiversity Heritage Library,* digitizing millions of pages of books and journals for distribution via internet. Many collections are digitized and the data made shared with the *Global Biodiversity Information Facility*. The *Catalogue of Life* is an initiative for one single database of all species of the world. And the *Encyclopedia of Life* tries to link all these data via one portal.

Naturalis is involved in several of these projects, but we focus here on our involvement in the *Catalogue of Life*. This project has been supported several times by the European Union (recently 4D4Life and i4Life), and also by the American government via ITIS. The success of the Catalogue of Life can be attributed to many years of intensive coordination activities of Professor Frank Bisby of the University of Reading UK, who died unexpectedly on 25 October 2011. One of the success factors of Species 2000, the managing body for the Catalogue of Life, is its decentralized nature. It actually is a consortium of more than hundred professional and amateur taxonomists, each bringing together all knowledge of the taxonomy and classification of a particular group of plant or animals, such as mosses, or flies. One of the larger expert groups is the *World Register of Marine Organisms* (WoRMS). Naturalis researchers Rob van Soest and Nicole de Voogd keep the Global Species Database (GSD) of the sponges (Porifera) for WoRMS, while Jan van Tol is the curator of the GSD of Dragonflies and damselflies (Odonata; Fig. 1), which is directly contributing to the Catalogue of Life. Typically, these databases not only include all the names of species described in that particular group, but also the status of these names, for instance whether they are valid names or just synonyms. Preferably, all names in a Global Species Database have been checked against the original publication, and the status of the names is updated on a regular basis. Some databases also include data of the type specimens, further references, habitat, distribution or common names.
It was estimated that just one record in a taxonomic database costs about 30-60 minutes to enter and check, so at least 20 euro per record. The present Catalogue of Life on DVD (Bisby et al., 2012) includes 1.4 million species from 115 databases, thus representing an investment of more than 26 million euro. This immensely useful information system is now used by several high-profile projects to organise their data, including GenBank, Barcode of Life, Encyclopedia of Life and GBIF. Some private companies agreed on the use of the Catalogue of Life as a basis for their own information system on taxonomy.

Naturalis will continue to invest in taxonomy as one example of collection-based research. Furthermore,

Fig. 1. Photographs of Odonata (dragonflies and damselflies).
1a. *Crocothemis servilia*;
1b. *Euphaea basalis*;
1c. *Rhinoneura villosipes*.
Photos: Jan van Tol.

the institute wishes to contribute to the global biodiversity informatics infrastructure, e.g., the Catalogue of Life, the Global Biodiversity Informatics Facility and the Encyclopedia of Life. Naturalis will also house the secretariat of Species 2000 from the summer of 2013. These international initiatives will also be linked with our own projects, such as the Dutch Species Register (www.nederlandsesoorten.nl). Our expertise on ontologies and thesauri will also be shared with other institutions in the cultural sector in The Netherlands.

These high ambitions can only be realized with our staff of taxonomists, in close cooperation with biodiversity informaticians, and IT staff.

Red Hills Road Cave, Jamaica

A diverse Pleistocene fauna

Stephen K. Donovan

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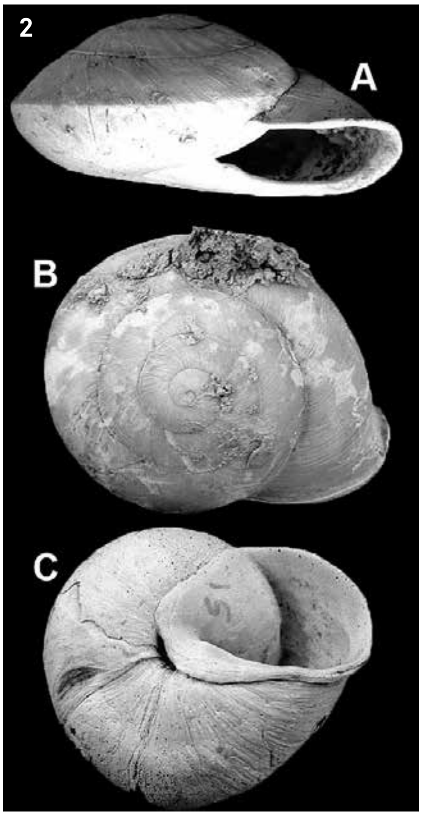
Jamaica has more caves than there are holes in a piece of Swiss cheese. Jamaica was a carbonate platform, perhaps similar to the Bahamas at the present day and with limestones accumulating in a variety of shallow- to deep-water environments, between 50 and 10 million years ago. The island was uplifted about 10 million years ago and today about two thirds of Jamaica is covered by limestones. High precipitation and high temperature have led to extensive dissolution, and with most drainage of limestone areas being subterranean, the limestones are now riddled with caves and other solution features.
Jamaican caves vary in size and complexity, but, as a palaeontologist, my favourites are those that produce fossils. A particularly fossiliferous example is found close to Kingston, in the Red Hills Road Cave (RHRC) (Fig. 1). The remains of the cave are small, but its included fauna is of unusual diversity and includes remains of some fossils unique to the Late Pleistocene of the Antilles. The remnants of the cave are flask-shaped and exposed in vertical section, with a narrow opening at the apex. It was exhumed and truncated when the road was built. The cave was dissolved into well-lithified limestones, and is partially infilled with dripstones, fallen limestone boulders and siliciclastic sediment. The last is probably largely derived from the *terra rossa* soils that are prevalent in this area, hence the name Red Hills. Preliminary dating suggests that the deposit is about 20,000-40,000 years old.

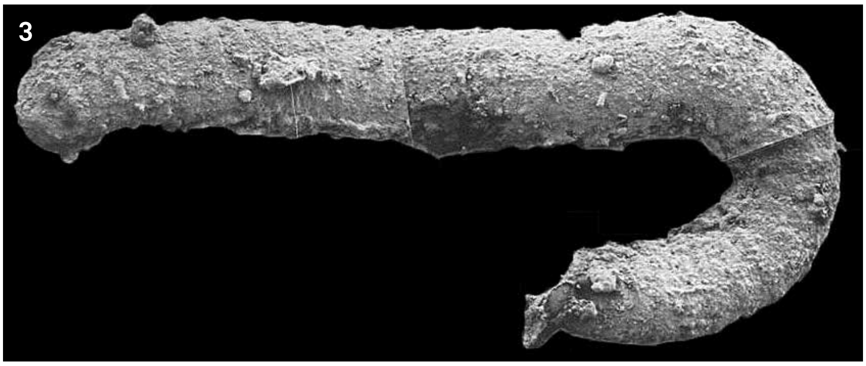
Jamaican Pleistocene cave faunas, and that of the RHRC is no exception, tend to be dominated by vertebrates and land snails. The fossil fauna of terrestrial gastropods (land snails) from the RHRC is the richest yet reported from the caves of Jamaica with approximately 60 species (Fig. 2). Jamaica has a diverse fauna of extant terrestrial gastropods with over 500 nominal species, making it a biodiversity hot spot for land snails. Previous studies of Pleistocene and Holocene fossil snail faunas concluded that these endemics had maintained their local distributions over the last 40,000 years, apart from Holocene and Recent extinctions due to the development of drier conditions or, in some cases, as a result of forest clearance by humans. But comparison of the fossil and Recent faunas at RHRC gives quite a different pattern of occurrence. Not only are there local endemic species in the fossil fauna that no longer live in the area, but there are also several local endemic species in the Recent fauna that are unknown from the cave deposits. Of a total of 80 endemic species recognized, only 30 (37.5 %) are shared between both the fossil and Recent faunas. This suggests that significant migration of snails has occurred in the Red Hills area and that the geographic distributions of local endemic snails are not as stable as had previously been assumed.

Vertebrates from the RHRC include amphibians (very few small bones), reptiles (small lizards and iguana), birds (several medium- and small-sized species) and mammals (disarticulated bones). The last group includes bat jaws. Fossil bats occur in the RHRC as delicate fossils, particularly jaws and jawbones, of three species. They are a rare component of the RHRC fauna, but are receiving detailed study in – Naturalis Biodiversity Center.

The RHRC is the only Jamaican Pleistocene cave to have yielded a diversity of terrestrial arthropods, including millipedes (Fig. 3), isopods, claws of non-marine crabs, ostracods and fly pupae. Fossil terrestrial arthropods are virtually unknown from the West Indian islands, apart from the notable exception of the Miocene amber deposits of the Dominican Republic. But it is only in Pleistocene deposits that terrestrial animals are moderately common fossils throughout the region, particularly those accumulated in caves. The RHRC arthropods are noteworthy for their excellent three-dimensional preservation. This is an uncommon feature in fossil terrestrial arthropods, usually limited to specimens encased in amber.

A model to explain the morphologically contrasting yet chemically similar modes of preservation in the RHRC is related to climatic patterns in Jamaica (Fig. 4). Annual rainfall in mountainous eastern Jamaica is 760 to 6500 mm yr^{-1}. Rainfall in the Red Hills region is concentrated into two rainy seasons per year, with irregular occurrences of tropical storms and hurri-





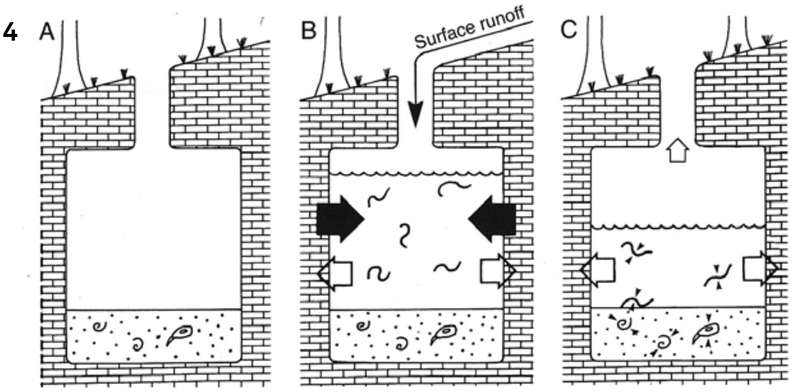


Fig. 1. General photograph of the remains of the RHRC, Jamaica. The cave was probably excavated when the road was cut through. It is narrow and tall, with an opening at the top. Chris Paul provides a scale as while sieving for land snails.

Fig. 2. A typical fossil land snail from the RHRC, *Pleurodonte subacuta* (Pfeiffer). **(A)** Apertural view, width of shell 44 mm. **(B)** Apical view, diameter 44 mm. **(C)** Umbilical view, diameter 40 mm.

Fig. 3. Fossil millipede from the RHRC. A complete specimen of *Rhinocricus* sp., head to the left. Length about 32 mm. Scanning electron micrographs of specimens coated with 60 % gold-palladium.

Fig. 4. Postulated depositional sequence for calcitic preservation of millipedes and isopods in RHRC. **(A)** Dry/damp conditions. The cave acts as a bottle trap for any organisms that fall into the opening in the roof, but accumulation of infill is slow. **(B)** Hurricane/tropical storm conditions. The cave fills with water from surface runoff and from the karstic aquifer (large black arrows; smaller open arrows indicate outflow into karst). Millipedes and other organisms washed in and drown. **(C)** After the storm. Water level drops by evaporation (small arrow) and karstic runoff. Calcareous skeletons in, on and floating above the sediment (mainly gastropods, vertebrates and arthropods) act as substrates for calcite precipitation (small black arrows). Uncalcified organisms and soft tissues rot away.

canes. Particularly during periods of high rainfall, the bottle-shaped cave may have been partially or entirely filled with water (Fig. 4A, B), causing any live animals washed in to drown. Water flowing off the vegetated catchment would have been acidic, with a high carbon dioxide content. This water would presumably be rich in dissolved calcium carbonate (calcite) from the surrounding limestone, as would be the water moving through the karstic aquifer.

As the cave dried out (Fig. 4C), dissolved calcite would have precipitated preferentially on calcium-rich substrates such as the walls of the cave, bones, snail shells, isopods and millipedes, the last four now presumably largely buried in or resting on the wet sediment.

Millipedes and isopods, both arthropods with a relatively calcite-rich skeleton, have a higher potential for preservation by calcification than other soil arthropods. Yet their occurrence as fossils in the Red Hills Road cave was favoured by a particular set of circumstances. These include the bottle-shape of the cave with an apical opening, the surrounding limestone, the clastic infill and the seasonality of precipitation, particularly the high rainfalls that occur during tropical storms and hurricanes. This suite of conditions is not necessarily unique, but is apparently rare and most likely to occur in the tropics. While caves are common in temperate regions, precipitation is spread throughout much of the year, and major storm events are rarer and less energetic.

Donovan, S.K. & C.R.C. Paul, 2011. A diverse terrestrial fauna in the Pleistocene of Jamaica: the treasures of the Red Hills Road Cave. *Geology Today* 27: 173-180.

Under the volcano

Along the Spanish-Moroccan hot line

Leo M. Kriegsman

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The Earth's deep continental crust, roughly 20-40 km deep, plays an important role in volcanism, notably of the most cataclysmic type, and in mountain building processes. As for the first aspect, the most explosive and potentially hazardous volcanoes, so-called "super-volcanoes", occur in continental settings and contain large amounts of crustally derived melts and fluids. As for the second aspect, the presence of melt in the deep crust is regarded as a key factor in so-called "hot orogens", in which it determines the rate of deformation and the overall topography of mountain chains. Research on deep continental crust addresses both issues and helps to improve risk assessments of volcanism.

Information on the deep crust is mainly based on three types of observation: (i) geophysical (e.g. seismic) data on the current deep crust; (ii) ancient roots of mountain belts that have been uplifted and eroded and are now exposed at the surface (e.g, Scandinavia and many parts of former Gondwana); and (iii) crustal xenoliths (solid fragments) transported from great depths to the surface by lavas. Xenoliths have a different origin from their lava host and are unique in that they provide relatively fresh samples of the deep Earth, not modified by processes during uplift of mountain belts. In that sense, volcanoes can be regarded as drill cores directly sampling the deep Earth.

I am studying a volcanic "hot line" that starts from the active volcanic islands of Gran Canarias, transects Morocco, and ends in the Neogene Volcanic Province of southeastern Spain. For several years I studied together with dr. Antonio Álvarez Valero (now at Salamanca University) xenoliths in the last domain (Fig. 1) that show evidence for high-temperature (*c.* 850°C) melting in the deep continental crust (Álvarez-Valero & Kriegsman, 2007, 2010). We showed that the depth of melting decreases from 20-25 km in the southwest to 9-12 km in the northeast over a 160 km long zone. This level matches a deep crustal zone of low seismic velocity just above the crust-mantle boundary (The Mohorovičić Discontinuity, or Moho) where a significant melt proportion is still present (Álvarez-Valero & Kriegsman, 2008). A spin-off of this research was an improved method for the interpretation of melted rocks (Kriegsman & Álvarez-Valero, 2010).

In mid-2010 research shifted to the Moroccan part of the volcanic "hot line", that transects crustal domains ranging in age from 30 to 650 million years and shows hundreds of Miocene to Plio-Pleistocene volcanic vents. We enlarged the team with colleagues from Fes University (drs. Dahire, Driouch, Moukadiri and Ntarmouchant) and Toulouse University (drs. Duchêne and Severac), with their MSc students, and involving MSc students Joost van Hoeflaken & Ingrid van Namen (Utrecht University) (Fig. 2). Preliminary results on the Middle Atlas in Morocco are: (i) all crustal xenoliths found have been derived from 30-35 km depth, near the current Moho; (ii) they show evidence for peak temperatures up to 1000°C at that level around 300 million years ago, in large contrast with the surface geology, followed by slow (tens of millions of years) cooling without significant uplift; and (iii) very fast (days!) transport of the xenoliths to the surface by the Quaternary lavas, as documented by garnet breakdown (Fig. 3). Preliminary results on the samples from northern Morocco are: (i) dominance of sub-volcanic and magmatic enclaves, absence of mantle xenoliths; (ii) much lower peak pressures (2-3 kbar = 7-10 km depth) in the rare crustal xenoliths; (iii) similar ages as the Middle Atlas.

Within the next 3-4 years the project aims to build a coherent model for the deep crust along the Moroccan part of the volcanic "hot line". We expect the model and its underlying dataset to deepen the general understanding of patterns and processes in the deep continental crust. We also hope to contribute significantly to improving models of explosive volcanism.

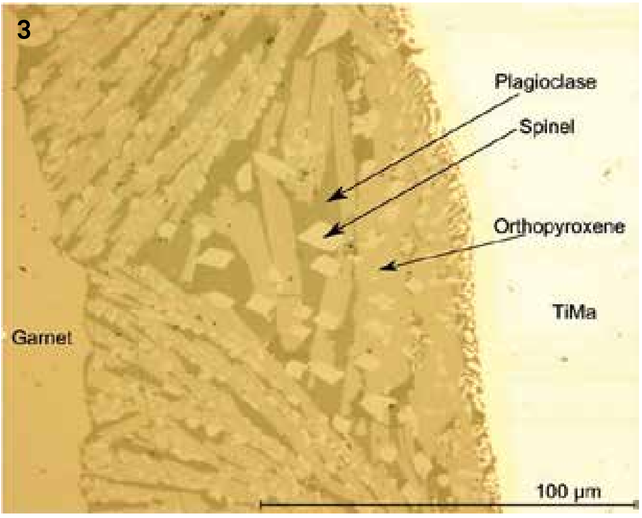

Fig. 1. Crustal xenolith in a lava, Cerro de Hoyazo, southeastern Spain.
Fig. 2. Part of the research team taking a break on the explosive breccia rimming a volcanic maar in the Middle Atlas, Morocco.
Fig. 3. Garnet breakdown to a fine-grained intergrowth of three other minerals, indicating very rapid uplift of a xenolith from the Middle Atlas, Morocco.

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Cenozoic evolution of the Indonesian Throughflow and the origins of Indo-Pacific marine biodiversity

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SE Asia contains the most diverse shallow marine biota on Earth, yet the factors responsible for the origins and maintenance of this diverse biota remain unknown. Molecular phylogenetic studies suggest that most extant taxa evolved during the Miocene (5-23 Mya). However, the fossil evidence currently available to document this pattern and its geographic context is sparse, and primarily consists of small collections of fossils and publications from the late nineteenth and early twentieth centuries. The collection of Naturalis Biodiversity Center is one of the most important and contains much type material from the region. The existing data demand taxonomic and stratigraphic revision to accommodate advances in these fields over the past century, but most importantly there is a crucial need to collect new data.

To investigate the relation between global and regional environmental change and the roots of the biodiversity maximum seven European institutes cooperate in the FP7-funded Initial Training Network 'THROUGHFLOW'. The scientific objective of THROUGHFLOW is to reconstruct the biological and environmental history of shallow marine habitats in southeast Asia. This region includes the most diverse extant marine biota in the world as well as the Indonesian Throughflow (ITF) - the sole tropical ocean gateway with a significant influence on global climate. However, the origins of this biodiversity 'hotspot', and the significance of the ITF as a control on regional diversity remain to be fully understood. As a novel association of earth and life scientists, the THROUGHFLOW project is a multidisciplinary study of key sections in Java and Kalimantan that will integrate data from geology, geochemistry, ocean modelling, and palaeontology to understand the Neogene history of the region. Furthermore, we aim to improve awareness in the broad scientific and general community of the value of ancient biotic response to environmental change to aid the prediction of outcomes of ongoing anthropogenic global environmental change on coral reefs and associated ecosystems.

THROUGHFLOW started in 2010 with hiring 11 Ph.D students, two of whom (SR and VN) are employed by Naturalis. Sonja Reich's thesis focuses at the evolution, turnover, and paleoecology of Miocene molluscan faunas associate with seagrasses.
The stratigraphical framework of all THROUGHFLOW localities, as well as the paleoecology of Oligocene-Miocene shallow marine carbonate rich environments will be the topic of Vibor Novak's thesis.
In 2011 Sonja Reich won the poster award at the 82nd annual meeting of the German palaeontological society for her poster entitled "Molluscs from meadows - An Early Miocene seagrass mollusc association from Java, Indonesia".

In November/December 2010 and June/July 2011 we conducted two large expeditions in East Kalimantan (Fig. 1). Together with the Geological Agency in Bandung, we coordinated field parties of 11 PhD students and some 20 scientists. This resulted in a total of more than 1000 field days, almost 4000 samples (Fig. 2), weighing more than 7000 kg (about half of which are now stored and investigated in Naturalis), from almost 200 outcrops. During these expeditions we were able to relocate some key outcrops that we identified from fossil material available in our collections, as well as outcrops in new areas. Initial assessment of the data indicates that most of these outcrops range in age from ~20-5 Million year ago and allows us to study a time interval critical to the development of the modern fauna (Fig. 3).

Fig. 1 The biodiversity team is sampling one of our newly discovered ~10 million year old localities, this section is particularly rich in seagrass dominated molluscan faunas.

Fig. 2. A sieved residue of a sample collected at the site of Figure 1. Note the abundant well preserved corals (*Seriatopora*, *Porites*) and molluscs (*Rhinoclavus*, *Columbella*, *Vexillum*). This 10 million years old sample contained > 125 species of molluscs. The inset shows two species of the genus *Smaragdia*, *S. semari* (left) and *S. gelingehensis* (right).

Fig. 3. Most of the fossil reefs we discovered consist of platy coral and large benthic foraminifera in a muddy environment, indicating that they grew in low light conditions in a deltaic environment.

Tobleria biscuspis reconstruction

3D model of Early Permian strobilus

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[2] *Breda University of Applied Sciences, Breda*

Compressed cones were found (Van Waveren *et al*., 2007) in close association with dispersed material on the same rock fragment. The dispersed material on different rock fragments had previously been described as *Tobleria biscuspis*, and interpreted as the seeds scale complexes of a probable conifer (Jongmans and Gothan, 1935). The coherence between the dispersed material and the attached material was the object of a statistical study that led to two possible reconstructions of the cone and their ontogenetic developments.

The dispersed and attached material consisted of 235 Fertile Units (104 free, 66 on dispersed scales and 65 in cones), 146 Scales (46 were dispersed and carried paired FU's, 89 were dispersed and Empty and 11 were measured in cones). To establish an inventory of the fertile scale complexes variability we used relations between length, width, height of the point of attachment of the fertile units and apex length. This variability indicated a continuum ranging from small relatively elongated scales with short apices and small fertile units attached at their base into large scales with long apices and bean shaped paired fertile units attached centrally (see Fig. 1).

A size shape diagram of all the fertile scales indicated that broader scales carried immature fertile units often attached to the scale ribs, while the more elongated scales carried mature seeds, that corresponded in distribution and size to the dispersed seeds. We converted the relations for these seeds being shed into a large number of parameters that served to reconstruct the seed scales complexes.

The position of each of the scale complexes along the cone axis was established by direct comparison with the length of the scales on the compressed cones. The cone base that was not preserved and that carried the broader scales is not included in the reconstruction.There were no clues on the actual physical appearance of the cone axis in the fossil remains of the *Tobleria* sample. Luckily this part of the cone is usually completely hidden by attached fertile scale complexes. For phyllotaxy we relied on what is found in modern cones using the Fibonacci polynomium that gives the closest packing of objects placed in a spiral.

We considered the size range of fertile units and scales to be the result of arrested development because scale size distribution in *Tobleria* was comparable to that of a modern Pinaceae cone. This allowed us to conceive an ontogeny of the fertile scale complex and translate information from the fossilized plant material into a dynamic simulation using a software package for procedural animation, called SideFX Houdini. The procedural animation allowed for apical growth where smaller scales grow into larger. We defined three areas in the cone where the scales would undergo varied development velocities: a basal area where scales would fully develop, a small apical area where the development would slow down to a minimum and a central area in between.

This model would represent a very early occurrence of a pinaceous conifer cone, considered in literature (Rothwell *et al*., 2005, Anderson *et al*., 2007, Taylor *et al*., 2009,) as the result of numerous reductions, yet it occurs previous to numerous other early conifers *Schizolepis permensis* (Heer, 1876) is comparable to *T. bicuspis* with respect to the position, the attachment of the two seeds, the deeply incised scale and its occurrence in the Late Permian, *Coricladus quiteriensis* from the Lower Permian of Brazil has bifid scales and paired anatropous ovules (Jasper *et al*., 2005).

Various features observed both in the cones and in the dispersed material of *Tobleria biscuspis* indicated possible stacking of fertile scales. This radically different cone architecture necessarily indicates an extra reduction of a shoot, thus bringing early conifer evolution in a more complex context than was previously thought, and giving some insight in the ancestors of the pinaceous conifers. This second new reconstruction is visualized in another configuration of the dynamic model (with the ontogeny of its scale and cone).

While a stacked scale architecture never was described before, a female cone with a bract an ovuliferous scale with paired seeds truly is a very derived architecture and would place the dichotomy between

Fig. 1. Modelling the ontogeny of the stacked scales of *Tobleria biscuspis.*

the Pinaceae and the Conifer II (Gugerli *et al*., 2001, Ran *et al*., 2010) in the Late Carboniferous. The zonation of scale types in the cone, may be considered functional, in which case *Tobleria biscuspis* would represent a form ancestral to both the Pinaceae and the Conifer II.

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On the ancient origins of Amazon biodiversity

Frank Wesselingh

Naturalis Biodiversity Center, Leiden

The Amazonian rain forest is the most species rich biome in the entire world. But also the rivers and lakes of Amazonia house by far the greatest numbers of aquatic species, the fish species even outnumber the species of the Atlantic Ocean. The timing of, and the processes behind the sheer diversity in Amazonia have been vigorously debated in the biological and geological scientific communities over the past decades. In 1969, Jürgen Haffer, proposed an elegant model where much of the terrestrial diversity was explained as the result of repeated fragmentation of the forest into isolated forest-islands during the Quaternary ice ages. During these periods, the previously continuous ranges of species were fragmented into forest refugia and could therefore speciate. This refuge hypothesis has been long the standard model to explain much of the Amazonian diversity, but the underlying evidence became increasingly discarded.

In 2010 a large team led by Carina Hoorn & Frank Wesselingh assembled the current knowledge on the geological and landscape history of the Amazon, the diversity patterns and insights into processes that have shaped Amazonian biodiversity (Hoorn & Wesselingh, 2010; Fig. 1). An updated review about the origin of Amazonian diversity appeared in the journal Science (Hoorn et al., 2010; Fig. 1). In that review, the molecular phylogenetic record, the fossil record, the sedimentary record and biodiversity assessments were combined in order to investigate the correlation of modern patterns with landscapes, climate zones and to seek causations in the geological history of Amazonia.

All the evidence points to pre-Quaternary origins of most of the Amazonian diversity. Rain forests existed in northern South America already 60 million years ago. Amazonian landscapes were dominated by rivers draining the very ancient cratonic hinterlands until about 25 million years ago, and became increasingly dominated by Andean rives. The modern Amazon established only some 10 million years ago (Fig. 2). In between, megalakes developed in western and central Amazonia, sometimes invaded by the sea, that housed spectacular radiations of aquatic biota (Fig. 3).

Much of the terrestrial diversity can be explained in terms of diversification of landscapes and increased edaphic heterogeneity. This landscape diversification has been driven mainly by the increasing influence of relatively nutrient rich Andean derived fluvial deposits in the past 25 million years. Thus a link between Andean tectonic uplift and diversification in lowland Amazonia can be made. However, the various groups of plants and animals show different diversification histories and processes behind diversification are diverse as well.

Today, the Amazon is a threatened ecosystem. Timber extraction, hunting and fishing and conversion to agriculture all are encroaching this biggest and most species rich ecosystem on earth. We have shown that the generation of such diversity is a matter of very long time scales and complex processes. We can only hope that such understanding will contribute to place greater value to the preservation of Amazonian nature.

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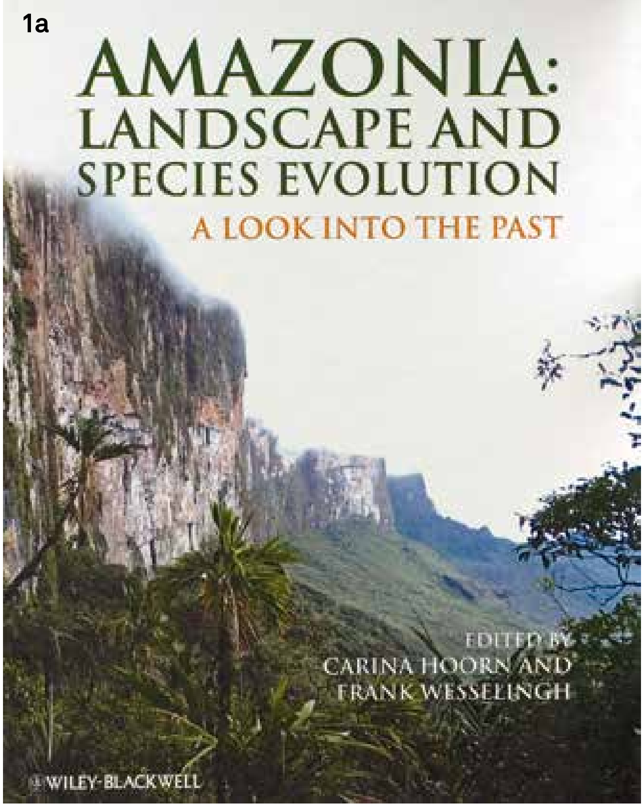

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REVIEW

Amazonia Through Time: Andean Uplift, Climate Change, Landscape Evolution, and Biodiversity

C. Hoorn,[1]* F. P. Wesselingh,[2] H. ter Steege,[3] M. A. Bermudez,[4] A. Mora,[5] J. Sevink,[1] I. Sanmartín,[6] A. Sanchez-Meseguer,[6] C. L. Anderson,[6] J. P. Figueiredo,[7] C. Jaramillo,[8] D. Riff,[9] F. R. Negri,[10] H. Hooghiemstra,[1] J. Lundberg,[11] T. Stadler,[12] T. Sarkinen,[13] A. Antonelli[14]*†

The Amazonian rainforest is arguably the most species-rich terrestrial ecosystem in the world, yet the timing of the origin and evolutionary causes of this diversity are a matter of debate. We review the geologic and phylogenetic evidence from Amazonia and compare it with uplift records from the Andes. This uplift and its effect on regional climate fundamentally changed the Amazonian landscape by reconfiguring drainage patterns and creating a vast influx of sediments into the basins in Amazonia. We explore the origins of Amazonian ecosystems and biodiversity with the use of a combination of geologic (including paleontologic) and ecologic data sets as well as dated molecular phylogenies. Through schematic representation of these findings, we summarize the geologic evolution of this area, outline the age structure of its biodiversity, and provide a guideline for future integrated geologic, biogeographic, and conservation studies.

Amazonia Prior to Andean Influence: An Ancient, River-Dominated Landscape

The area known today as Amazonia was once part of a much larger "pan-Amazonian" region, which, before the late Miocene [until 10 million years ago (Ma)], included the area of the present Amazon, Orinoco, and Magdalena drainage basins

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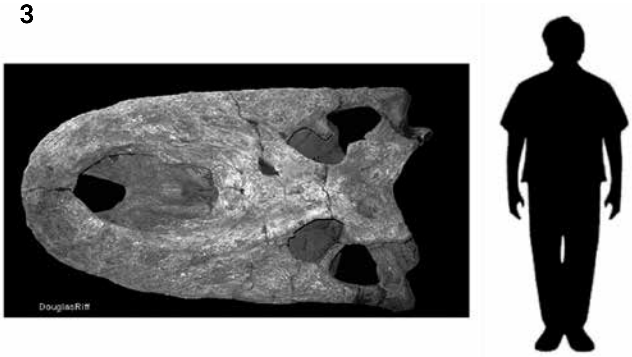

Fig. 1. Cover of "Amazonia, landscape and species evolution" and of the Science review paper by Hoorn et al., 2010.

Fig. 2. Landscape evolution of Amazonia in the past 65 million years. From Hoorn et al., 2010. Graphics by Frank Wesselingh.

Fig. 3. The Amazonian megawetlands hosted 10 million years ago the largest crocodiles ever living on earth, including the giant *Purussaurus*. Artwork by Orlando Grillo.

Fossil shells
of the Dutch coast

Frank Wesselingh

Naturalis Biodiversity Center, Leiden

For over a century, collectors have found fossil shells on beaches in the southern part of The Netherlands (Fig. 1). These shells derive from shallow Neogene and Quaternary layers that are eroded by tidal currents. Since the 1930ties also huge amounts of fossil shells have been dredged for the production of shell grit. The latest part of a major assessment of the fauna was completed in 1984 and a serious overhaul was long overdue.

In 2010, a major new work appeared, “the fossil shells of the Dutch beaches” (Moerdijk et al., 2010; Fig. 2). Written by 17 authors, among them various world renown amateur specialists, this book treats 323 bivalve species, 10 scaphopod- and 8 chiton species. The previous assessment in 1984 contained 253 bivalve species, and six scaphopod species and no chitons were known at the time. Many of the new findings derive from amateur collectors, several of whom have developed remarkable skills in recognizing deviating material. Often such findings were discovered on identification meetings organized for this project (Fig. 3). The book is therefore the result of as well as a tribute to the efforts of these collectors.

The fossil fauna contains a diverse pre-Ice age fauna with several North Sea endemic species and representatives of geological episodes of our history with arctic climatic conditions as well as paratropical conditions. Most material originates of Quaternary and Pliocene layers. Smaller numbers of Miocene, Oligocene and Eocene species are almost exclusively found in the southernmost part of the coastal zone. During the work on this book a number species new to science were discovered and subsequently described (e.g., Pouwer, 2009; Fig. 4).

Currently we are working on a second part of the “fossil shells of the Dutch coast”. This work contains gastropods, the latest assessment of which was published in 1965. We expect the number of species of gastropod to possibly double, from 213 species to more than four hundred species. The first chapter of the new fossil gastropod project was published in 2011 (Wesselingh & Pouwer, 2011). It may take some six years to complete, even with the help of many amateurs.

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GEOLOGIE VAN NEDERLAND

DE FOSSIELE
SCHELPEN
VAN DE
NEDERLANDSE
KUST

P.W. MOERDIJK, A.W. JANSSEN,
F.P. WESSELINGH, G.A. PEETERS,
R. POUWER, F.A.D. VAN NIEULANDE,
A.C. JANSE, L. VAN DER SLIK (†), T. MEIJER,
R. RIJKEN, G.C. CADÉE, D. HOEKSEMA,
G. DOEKSEN, A. BASTEMEIJER, H. STRACK,
M. VERVOENEN & J.J. TER POORTEN

NCB naturalis

Fig. 1. An assambly of fossil shells *in situ*.

Fig. 2. Cover of the book “the fossil shells of the Dutch beaches”.

Fig. 3. One of the meetings organised to identify fossil shells of the Dutch beaches.

Fig. 4. Pencil drawing from the book.

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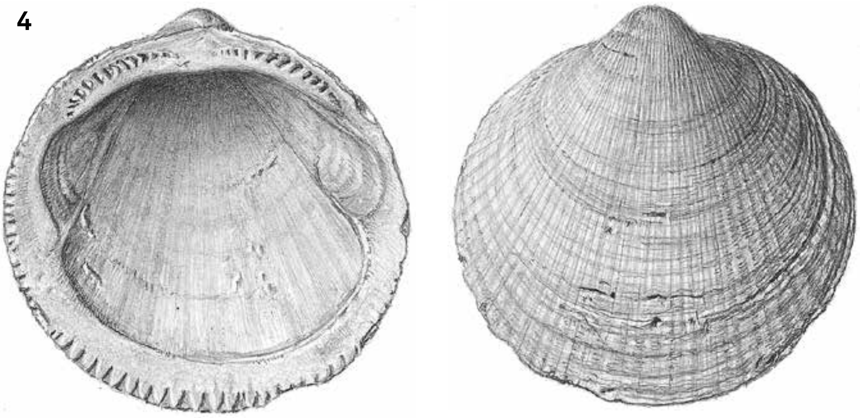

New emerald deposit
Sustainable mining in Fazenda Bonfim [Brazil]

Hanco J.C. Zwaan[1], Dorrit E. Jacob[2], Tobias Häger[2], Mário T.O. Cavalcanti Neto[3] & Jan Kanis[4]

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Brazil is an important gem producing country. It produces 100 different gemstone varieties of which 80 percent is exported. Brazil does much to strengthen the position of small mining companies and to develop local gem-cutting centers. At the same time there are strict rules the mines must adhere to; the focus is on developing programs for ethical, environment-friendly, and sustainable mining of gems, particularly motivated by the ever growing pressure on the Amazon rain forest and other nature reserves by the continuous search for more resources.

In this respect, a great example of modern mining is the Belmont emerald mine in Minas Gerais (Fig. 1). The company seeks minimal environmental burden by applying reforestation and re-use of water. The mine also emphasizes proper risk management and is heavily investing in good knowledge of geology, which is vital to properly conduct feasibility studies of mining operations, but also to environmental conservation. 'When you know where to go', based on sound geologic knowledge, emeralds can be mined with minimal environmental impact. This is where science comes in: understanding the fundamental processes in the Earth's crust that lead to the formation of these gems contributes to effective exploration and sustainable mining. Sustainable gem mining may serve as an example for mining operations involved in other raw materials, such as (rare) metals, that are vital to our high-tech industry.

New emerald deposit

A team led by Mário T.O. Cavalcanti Neto recently discovered emeralds in the Fazenda Bonfim region, in Rio Grande do Norte State (Fig. 2). They found emeralds in an area where geologists had previously focused on gold and rare-element mineralization. Several mines in this region had produced beryl and/or columbite-tantalite (coltan ore) from pegmatites, but without any attention to the potential of ores related to ultramafic rocks next to the pegmatites (Fig. 3).

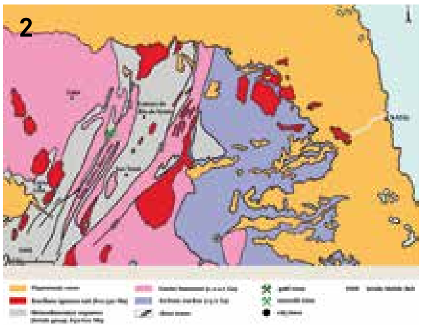
After the discovery of emeralds in the Fazenda Bonfim region, Mineração Vale Verde Ltd. acquired the mining rights and invested heavily in mineral exploration. In April 2010, a consortium of the Federal University of Rio Grande do Norte in Natal, the Geological Survey of Brazil, and other institutes including Naturalis, managed to get a grant from The National Council for Scientific and Technological Development (**CNPq**) of Brazil for a project entitled 'Characterisation of the emerald province and associated ultrabasic rocks of Eastern RN, Brazil'. Unfortunately, due to legal disputes, we could only start our fieldwork in the end of 2011. Our goal in this 4-year project is to unravel the geologic history of the emerald and gold bearing area in detail.

The results of our geological study will contribute to the development of an underground operation, which will prevent unnecessary movement of material and digging of huge open pits, which would have a major impact on the landscape.

Results

Geological Map. Geologists of the Federal University of Rio Grande do Norte in Natal, and the Geological Survey of Brazil mapped the area around Lajes on a 1:100,000 scale, to exactly locate the ultramafic bodies and pegmatitic bodies. This map will be the basis for our detailed geological studies.

The ultramafic rocks associated with emerald mineralization appear to be restricted to an old geologic basement (age 2,200-2,000 million years) mainly consisting of metamorphosed granites. However, we need to look in detail at the age and tectonic relations between gneisses, ultramafic rocks, the major 'Santa Monica' shear zone and pegmatites. We will also need to examine the ultramafic rocks for the existence of associated beryl-rich pegmatites:



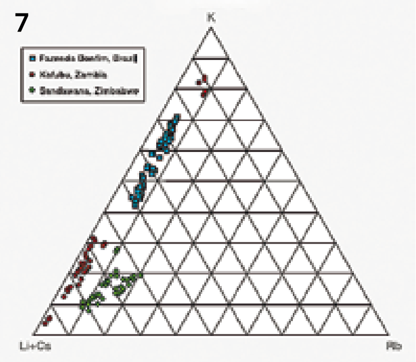


Fig. 1. The Belmont emerald mine, located in the Itabira district, Minas Gerais, Brazil, is a perfect example of modern, sustainable gem mining with minimal environmental impact.

Fig. 2. Geological sketch map with the location of the new emerald deposit in the Fazenda Bonfim area, Rio Grande do Norte, Brazil.

Fig. 3. Emeralds at the Fazenda Bonfim deposit occur in association with recrystallized pegmatites that intruded a sheared succession of dark ultramafic rocks, adjacent to a granitic gneiss (the weathered unit at the top). A small recrystallized pegmatitic body (white) is visible on the left side.

Fig. 4. Some of the first emerald crystals and fragments obtained from material processed for exploration purposes is shown here. The large crystals on the lower right are 5 cm long. Courtesy of Mineração Vale Verde Ltd.

Fig. 5. The polished emeralds studied represented a range of sizes, from 0.17 to 3.89 ct, and were an attractive saturated bluish green.

Fig. 6. Fluid inclusions were dominant in Bonfim emeralds. Raman microspectroscopy showed the presence of CO_2 within large gas bubbles in hexagonal-shaped negative crystals (a. image width 0.8 mm). The fluid inclusions may contain captured minerals (b. image width 0.3 mm), which after Raman analysis turned out to be carbonate and mica along with bertrandite in the carbonate.

Fig. 7. Chemical analysis combined with optical data and information from inclusions may pinpoint the geographic origin of gemstones. This ternary diagram shows the concentrations of K, Li+Cs, and Rb in emeralds from Fazenda Bonfim, Kafubu, Zambia, and Sandawana, Zimbabwe. The Fazenda Bonfim emeralds show intermediate K and Li+Cs content and are clearly distinguished from Zimbabwean emeralds and most Zambian emeralds that show enriched Li+Cs. The Zimbabwean emeralds have relatively higher Rb.

perhaps we can identify new promising emerald localities! It is our intention to finally create a Prospecting Guide for entrepreneurs involved in mining.

Emerald formation. Adding geochemistry and study of mineral relations and reactions will ultimately help to understand the processes that lead to emerald formation in this particular area. The first author extensively looked at these processes in Africa (Zimbabwe and Zambia; see http://science.naturalis.nl/zwaan) and it will be of great interest to see how the situation in this part of Brazil compares to existing models of emerald formation.
Advanced techniques, such as EPMA (Amsterdam), LA-ICP-MS (Mainz) and Raman microspectroscopy (Naturalis, FES investment in 2011), combined with microscopy and optical methods will distinguish emeralds of various localities (Figs. 6, 7).
This outcome is also an interesting side-result, of particular use in the Netherlands Gemmological Laboratory, part of Naturalis. The laboratory certifies diamonds, coloured gemstones and pearls both for the commercial trade and the general public, and also, on demand, issues 'country of origin' reports on gemstones.

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Sharks
in four dimensions

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Sleek and deceptively simple in their build, sharks have long been seen as primitive animals, virtually unchanged for 400 million years. In both popular accounts and technical considerations, this view has had a strong grasp on the imagination. Unfortunately, such ideas have been built on unfounded notions of evolutionary progress, naturally with humans at the top of a scale of being and the fishes down below. Modern sharks are remarkably sophisticated and diverse animals. Nevertheless, humans, sharks and other animals with backbones and jaws do have a common ancestor that was certainly fish-like. Our research is looking at the fish-like early history of animals with backbones from multiple angles. Some of the questions we ask include: in what ways are modern sharks very different from our last common ancestor with them? How have they evolved and adapted ecologically? And, if that ancestor was not a shark-like animal, then what kind of animal was it? How was it constructed and what did it do ecologically?

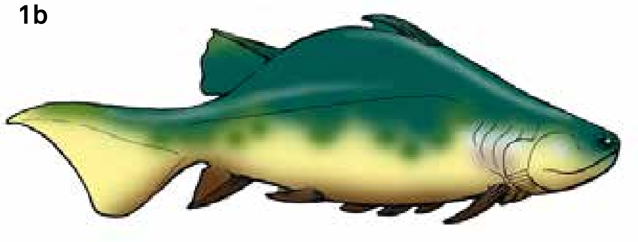
A new look at a fossil shark-like fish

The notion of sharks as 'living fossils' has influenced more than just the popular press, including scientific thinking. Since Haeckel's *Pedigree of Man* published in the 19th Century, the concept of sharks as the first backboned animals with jaws has influenced fields as far apart as palaeontology and developmental biology. The best place to test the 'living fossil' hypothesis of sharks is to look to the fossil record itself. Indeed, fossils of the earliest known fishes with jaws and teeth are beginning to show that modern sharks have many specializations that were probably not present in our common ancestor with all jawed fishes. Piece by piece, a more accurate picture of the origin of jawed fishes, and the nature of early fish evolution (including the early ancestors of sharks) is coming together.

Recently, Martin Brazeau re-described the anatomy of a fossil shark-like fish from the Early Devonian period (about 410 million years ago) of England (Brazeau 2012) (Fig. 1). The fossil, known as *Ptomacanthus anglicus* was originally discovered in the 1930s, but first formally described in 1973. It has traditionally been classified as a type of early jawed fish known as 'acanthodians'. This is much like some modern sharks, such as dogfish, but the 'acanthodians' had spines on nearly all fins, including the paired front and back fins. These superficially shark-like fishes with pointy spines on the leading edge of their fins have long evaded proper classification as either primitive relatives of cartilaginous or bony fishes.

The fossils of *Ptomacanthus* were found in a layer of siltstone in a quarry being worked for building stones. From this layer came many very well preserved fish fossils (Fig.1), many of which were complete from head to tail. In spite of being well preserved, many important details of the anatomy of *Ptomacanthus* went overlooked. Exceptional among these details was the impression of the bottom part of the braincase (Brazeau 2009). These details challenged some long-held preconceptions about *Ptomacanthus*, but its precise relationships have been difficult to establish. Brazeau's 2009 analysis of evolutionary relationships suggested *Ptomacanthus* may be an early member of the lineage of cartilaginous fishes: the line that would eventually lead to modern sharks, skates, rays, and chimaeras (rabbitfishes).

However, *Ptomacanthus* shows an interesting mix of features found in bony fishes and cartilaginous fishes. It has a rather shark-likeoverall shape,



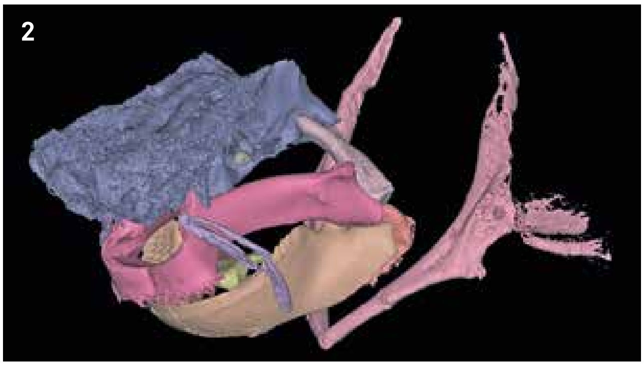


Fig. 1a. Natural History Museum (London) Palaeontology specimen 19998 of *Ptomacanthus anglicus* from the Welsh Border regions. Scale is 5 cm. **1b.** Reconstruction of *Ptomacanthus anglicus*

Fig. 2. Virtual 3D rendering of the skull, jaws, and shoulder girdle of a modern deep sea shark from the Indian Ocean.

tooth-like body scales, teeth that are arranged in whorl-like families, and spines on the fins just as we see in modern sharks. Quite unlike modern sharks, however, the skull of *Ptomacanthus* was covered in a mosaic of plates called "tesserae" (just like Roman pavement). The gills were covered by a series of blade-like plates, a feature we still see today in many living bony fishes. The jaws of *Ptomacanthus* were clearly fixed to the braincase, rather than having the ability to become detached from it and protrude forward, as we see in sharks. Together with information from other fossils, *Ptomacanthus* illuminates our understanding of the diversity of the early jawed fishes. It shows us that the anatomy of early members of the branch in the Tree of Life that would eventually give us sharks combined both shark-like features and features of other groups.

Ecomorphology of sharks in "4D"

The evolutionary history of shark ecologies poses some interesting questions. Very specialized modes of life, such as suspension feeding giants like basking sharks, whale sharks, and manta rays have clearly evolved independently, emerging in very distantly related families of shark and rays.
This raises interesting questions of whether shark evolution is marked by large bursts of evolutionary change followed by relative stasis (unchanging), or whether change is frequent, and perhaps very gradual.
To explore how modern sharks have diversified since their last common ancestor 200 million years ago, doctoral student Pepijn Kamminga is investigating the diversity in body form and the feeding apparatus of modern sharks. He is examining specimens of living shark species, many of which are housed in Naturalis ichthyology collections.
His measurements from these specimens capture the shape of the body, the fins, and mechanical properties of the jaws and teeth. Using computed tomography (CT) scanning, we can produce three-dimensional reconstructions of the skull and jaws of representatives of living shark families (Fig. 2). From this, Pepijn will be able to quantify the diversity of modern sharks in terms of their shape and adaptations to particular feeding strategies and modes of life. The data gathered in Pepijn's work will be studied in a comparative framework and using time-calibrated molecular evolutionary trees to study the relationship between diversification and body shape. The output of this work will address how these different models of evolutionary change apply to the history of sharks.

These projects reveal two very different looks at sharks, shark-like fishes, and their relationship to the evolutionary history of animals with backbones. The early fossil history of jawed fishes reveals animals with features resembling both cartilaginous and bony fishes, and resembling modern sharks only very superficially. The forthcoming work on modern sharks will deliver a more nuanced and modern perspective on shark evolution.

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Carideorum Catalogus
Decapod shrimps: all recent species

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Recently, an updated classification for the entire Crustacea Decapoda, including crabs, lobsters and shrimps, was published listing all known families and genera organized by higher taxonomic groups and including estimates of the number of species in every genus (De Grave et al., 2009). This compilation was based on lists that were just published or were in preparation by the leading taxonomists of the various higher taxa concerned. In this publication the estimate for extant decapod species is 14,756, whereas 2,979 are known exclusively as fossils. The counts of the shrimp-like decapods was based on a preliminary list (Fransen & De Grave, 2009) which counted 3,671 species. Since then numerous descriptions have appeared (see De Grave & Fransen, 2010). The present Carideorum Catalogus (De Grave & Fransen 2011) listed 4,048 valid species. Recently, this publication was used to update the taxonomic information on shrimps in the WoRMS (World Resister of Marine Species) (Appeltans et al., 2011) database and several other related databases. The list treats the four major groups of shrimp: the infraorder Dendrobranchiata and suborders Procarididea, Stenopodidea and Caridea. The focus of this compilation is on genera and species and is complementary with the books treating the higher classification published by Holthuis (1993) for the Stenopodidae and Caridea (including Procarididae) and Pérez Farfante & Kensley (1997) for the Dendrobranchiata. For each genus the reference to the original description as well as the type species, grammatical gender, and all synonyms are provided. For species and subspecies their original generic designation, original orthography as well as all known synonyms with reference to the original descriptions, type locality, and lectotype and neotype designations are included. The catalogue is illustrated with many photographs in colour of represetatives of the families included (Fig. 1).

The Naturalis library and archives proved to be very valuable for our work. We needed to consult all publications with original descriptions of the taxa. Many of these, sometimes obscure, works are present in the Holthuis Library of Naturalis. Another important source for names and synonyms, also present in Naturalis, were the archives of the late Prof. Holthuis who kept files of all references to shrimps in the literature. From these files we could trace many names for larvae, nomina dubia and nomina nuda.

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Fig. 1. *Aristaemorpha foliacea* (Risso, 1827). Photo by Tin-Yam Chan.
Fig. 2. *Benthesicymus tanneri* Faxon, 1893. Photo by E. del Solar.
Fig. 3. *Melicertus marginatus* (Randall, 1840). Photo by Tin-Yam Chan.
Fig. 4. *Sicyonia ingentes* (Burkenroad, 1938). Photo by Sammy De Grave.

Fig. 5. *Solenocera rathbuni* Ramadan, 1938. Photo by Tin-Yam Chan.
Fig. 6. *Lucifer* spec. Photo by Arthur Anker.
Fig. 7. *Sicyonella* aff. *maldivensis* Borradaile, 1910. Photo by Tin-Yam Chan.
Fig. 8. *Procaris hawaiana* Holthuis, 1973. Photo by Troy Sakihara.

Changing marine faunas

Importance of historical collections

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Natural history museums house botanical and zoological collections, often including specimens from centuries ago. These collections are becoming increasingly important for historical ecological research on the effects of global change and human impact on marine biota. Collections can also include specimens that represent expansions of currently known distribution ranges or species that have become locally extinct. Often, such local extinctions can be linked to human impact, including pollution, habitat change or the introduction of invasive species.

Baseline data are a crucial part of conducting studies on biodiversity changes. Early scientific expeditions to species-rich areas were organized to explore biodiversity and to discover unknown species. Large marine expeditions were often ship-based and consisted of collecting specimens indiscriminately by grabs and trawls, wading (Figs 1, 2), or sampling by professional divers without taxonomic training (Fig.3). Such methods may have missed rare species and cryptic taxa. The collected specimens were usually sorted and preserved on board and eventually deposited in museum collections (Figs 4, 5). Available material was identified and described in large series of floristic and faunistic monographs, which generated insights in marine species richness. Nowadays, collecting is primarily done by marine systematists themselves and therefore gives a better representation of the present biota. Botanical and zoological museum specimens may serve as proof that species that nowadays are absent in a particular area, actually did occur there in the past.

Research carried out by the Marine Zoology department focuses on shallow tropical coral reefs. These are among the most diverse and threatened pristine marine ecosystems of the world, but lack baseline studies, because *in situ* underwater observations only started relatively recently when dive equipment became available. Older information on species distributions was obtained from expeditions. Some of the oldest natural history museums and herbaria, however, harbour samples of coral reef fauna and flora that have been stored there for over 100 years. These specimens form the baseline for our historical studies. Moreover, species that are difficult to identify (cryptic or part of species complex) could have been represented in collections for a long time without being noticed. We show the importance of a collection-based approach to reconstruct changes over times in a few examples from our research.

Jakarta Bay & Singapore

Reefs in Jakarta Bay and Singapore have been subjected to anthropogenic impact for decades. Already in 1927 human impact was waseasured in Jakarta Bay. Both Jakarta and Singapore are large cities located near coral reefs, and witnessed a huge increase in their population size. Jakarta's population increased by a 10-fold over less than 100 years, and is now estimated to be over 12 million people or more than 23 million with inclusion of the Greater Jakarta Area. This urbanisation led to an increase of sewage, sediments and other types of pollution spilled into the Bay.

Our research, based on historical collections and recent observations, shows that the coral reefs of Jakarta Bay suffered from this anthropogenic stress, and that almost 50% of the reef coral species disappeared from the area (van der Meij *et al.*, 2010). For the molluscan fauna, the results are even more dramatic. More than 65% of the species recorded in 1937/38 disappeared from the area, including many edible species (van der Meij *et al.*, 2009).

For Singapore we conducted a similar study, but with a focus on mushroom corals. Four out of 19 previously recorded species disappeared from the area between 1860 and 2006 (Hoeksema & Koh, 2009).

Saba Bank

Saba Bank (Caribbean Netherlands) is a large submerged atoll covered by species-rich benthic

Fig. 1. Indonesian participants of the Snellius expedition collect specimens on a shallow reef flat.
Fig. 2. Small boats are used to transport people and material to and from the mother ship (Snellius expedition).

Fig. 3. Royal Dutch Navy diver collecting specimens at Saba Bank (Caribbean Netherlands) in 1972.
Fig. 4. The coral collections of Naturalis contain many specimens of the Snellius and Siboga expeditions.

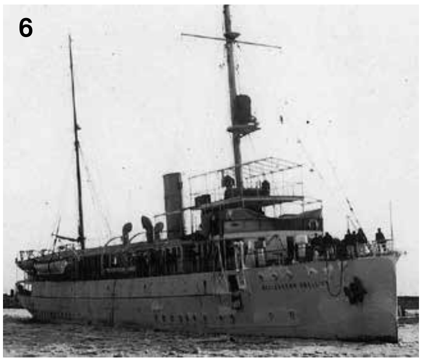

Fig. 5. Mollusks collections from Jakarta Bay, collected in 1938, now serve as a baseline for studies on biodiversity changes.
Fig. 6. The Hr. Ms. Willebrord Snellius.

assemblages, which have been under threat by anchoring oil tankers. So far, relatively little explorative research has been carried out on its reef assemblages. However, results of a recent survey (2006) showed that the zoological collections made at Saba Bank during a previous expedition (1972) have become valuable baselines to indicate possible losses of local coral and sponge species (Thacker *et al*., 2010; Hoeksema *et al*., 2011).

Snellius expedition

The Snellius expedition took place in 1929-1930 and lasted about 18 months. The expedition was named after the ship “Hr. Ms. Willebrord Snellius” (Fig. 6), which collected data on the geology, oceanography and biology of eastern Indonesia. A wealth of biological samples was eventually deposited in the Leiden museum. Many scientists worked on the material over the years, publishing large monographs on several taxa. The large staghorn genus *Acropora*, however, was largely ignored because of the urgent need of a revision, which became available only in 1999. This enabled identification of the Snellius material. We selected one *Acropora* ‘species group’ and identified all specimens to species level. Surprisingly, the material yielded new distribution records, including a record from a species previously only know of the western Indian Ocean and central Pacific Ocean (van der Meij & Visser, 2011).

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Soft corals and sea fans
Symbioses with Octocorallia studied

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Soft corals (Alcyonacea) and gorgonians or sea fans (Gorgonacea), together belonging to the Octocorallia, play a prominent role for other organisms on tropical coral reefs, where they act as hosts for snails, crabs and fish. These symbiotic species use their hosts as food source or as a shelter against predators. Either way, their appearance and life history are usually adapted to allow them to live in perfect symbiosis with their host coral. How specific such relationships are and how they evolved is one of the major research topics within the department of Marine Zoology at Naturalis.

One of our studies concerned the intricate relationships between gorgonians and pygmy seahorses. Most of these diminutive seahorses were discovered recently and are desired objects for underwater photographers owing to their photogenic appearance (Fig. 1). The taxonomy of their host corals is still troublesome owing to a lack of morphological diagnostic characters. Therefore the holotypes of the host species were compared with material collected in Indonesia and Malaysia. We discovered that pygmy seahorses live in symbiosis with more than the four octocoral species that were previously recognized as host and that these hosts were often misidentified in previous studies (Reijnen *et al.*, 2011).

Another study concerned the host specificity of ovulid snails (Ovulidae) living on octocorals.

We found that brightly and conspicuously coloured ovulid species on the Caribbean island Curaçao lived in association with hosts belonging to various Octocoral genera whilst the more inconspicuous and cryptic species were found on corals of only one or two different genera (Reijnen *et al.,* 2010).

We use ovulids and octocorals as model organisms to study the evolution of defence strategies, such as the use of camouflage by snails on specific hosts (Reijnen, 2010).

Since the species richness of ovulids and reef-dwelling octocorals is highest in the Indo-Pacific, our focus is on species interactions in this region. Field expeditions have already resulted in collections and photographs of many colourful ovulids and their host corals (Figs 2-5) as basis for publications on their co-evolution.

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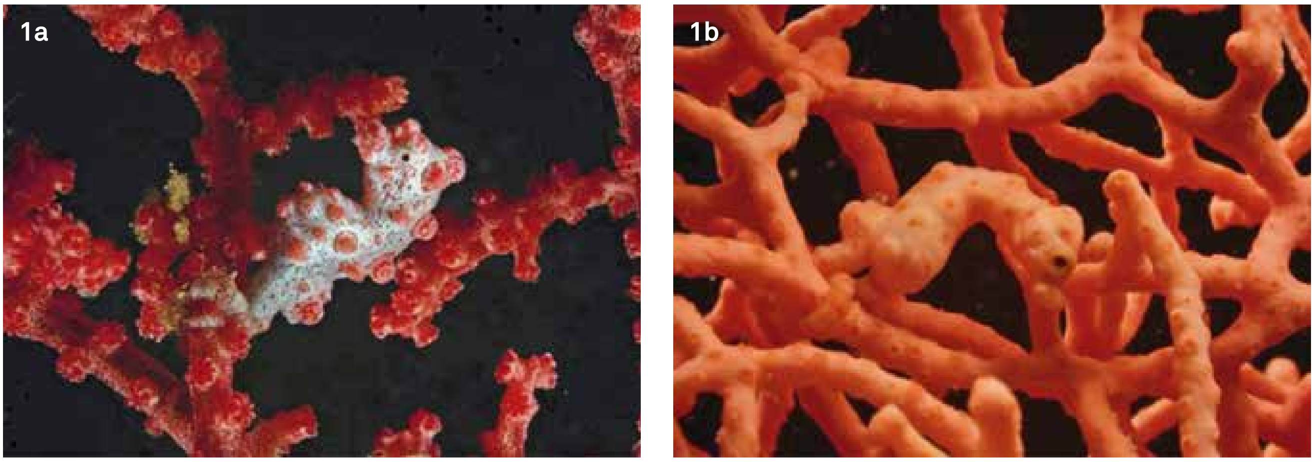

Fig. 1. The diminutive pygmy seahorses *Hippocampus bargibanti* (a) and *H. denise* (b) living in between the branches of respectively the octocoral *Muricella* sp. and *Annella* sp. Photo: B.T. Reijnen.

Fig. 2. A yellow gorgonian (*Melithaea* sp.) from Indonesia, a perfect host for Ovulidae snails. Photo: B.T. Reijnen.

Fig. 3. This tiny ovulid snail (*Prosimnia draconis*) mimicks the polyps of its host. Photo: B.T. Reijnen.

Fig. 4. A perfect mimick of the host polyps on the mantle of an ovulid (*Hiata* sp.), Photo: B.T. Reijnen.

Fig. 5. A brightly coloured and spotted ovulid (*Primovula rosewateri*) easily recognized on its host. Photo: B.T. Reijnen.

Reef invertebrates
Producers of bioactive compounds

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Natural products (also called secondary metabolites), are by-products with biological activity of metabolic pathways of living organisms. They have been exploited by people for a variety of purposes including the manufacturing of medicines, insecticides, pigments, fragrances, and even food. Although there is almost no ethnomedical history for this and because the sea is difficult to access, there is hope that substances of potential therapeutic importance or other use will be found in marine life forms. This expectation is based on two facts. First, with an estimated biodiversity of at least 200,000 species distributed over 30 phyla, and many more phyla in the sea than on land, the structural diversity in the sea is much higher than on land. Also, the percentage of anticancer leads with significant selective cytotoxic activity is much higher in marine animals than in other groups of organisms.

Marine biodiversity is particularly enhanced in coral reefs. No firmly established numbers on biodiversity of various marine habitats are available, but conservative estimates amount to at least equal species richness of coral reefs compared to the total of all other marine habitats. Coral reefs also comprise the habitat with most intense species interactions. These two factors contribute to the fact that coral reefs are the source of a disproportionately high yield of marine natural products. These substances generally act as chemical toxins if the producing organism uses them as defense against predation or as a weapon in the competition for space with neighboring organisms (Fig. 1).

The most important species groups that produce these toxins are sponges (Porifera), octocorals (Cnidaria: Octocorallia), and tunicates.

Taxonomic expertise is highly relevant for the identification of animals that are recognized as producers of these secondary metabolites, especially in marine taxa consisting of species that are difficult to identify. Each year we receive and identify many specimens of octocorals and sponges from which new important bioactive compounds were isolated (Figs 2, 3).

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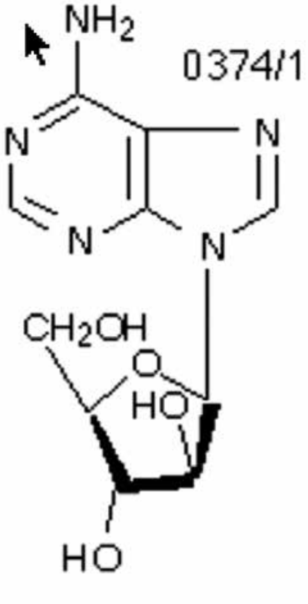

2

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Fig. 1. Spongouridine, the first compound from marine invertebrates to make it (synthesized and changed) to a generally used anti-viral medicine.
Fig. 2 Lobophytum *pauciflorum* (Ehrenberg, 1834). New isobiscembranoids were isolated from this species (Pengcheng et al., 2010a,2010b).
Fig. 3. *Agelas linnaei* de Voogd et al., 2007. Eleven new secondary metabolites were isolated from this species (Hertiani et al., 2010)

Coastal groundwater

Fauna survey of Maluku Utara, Indonesia

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Compared to the USA and Europe, the groundwater fauna (or stygofauna) of marine habitats in Indonesia is a white spot on the global map of life underground. It is expected to have a high diversity, as is common in tropical waters, with unique (or endemic) species. The importance of groundwater organisms in hydrology and nutrient cycling has often been demonstrated but the taxonomy and evolutionary aspects are fully open to new discoveries.

In October and November 2009 our marine stygofaunal research in the North Moluccas concentrated on collecting subterranean crustaceans in diverse habitats on different places on the islands (Fig. 1A). We sampled in coastal areas (Fig. 1C), wells, small brackish lakes, beaches, and mangrove fringes of Ternate, Hiri, Tidore, Maitara, Gura Ici Islands, and the west and east side of North Halmahera. Sampling gear consisted of a biophreatical BouRouch groundwater pump (BRh. pump) (Fig. 1B) and steel pipes, Cvetkovnet, dipnet, and shovel (Fig. 2). In beaches we placed the pump near to the waterline. Subterranean crustaceans are presumed to be poor dispersers and consequently their distribution patterns are expected to depend more on plate tectonics than on oceanic currents. Nevertheless, the subterranean beach environment may be very dynamic, even at secluded spots, and the fauna may move with the sediment, suggesting at least some dispersal within coastal areas. The present study on *Psammogammarus wallacei* sp. nov., a beach interstitial amphipod from the North Moluccans, and the locations of its geographical closest relatives (Japan, Middle East), suggest that this type of fauna of southeastern Asia is largely undiscovered, despite recent studies in Australia.

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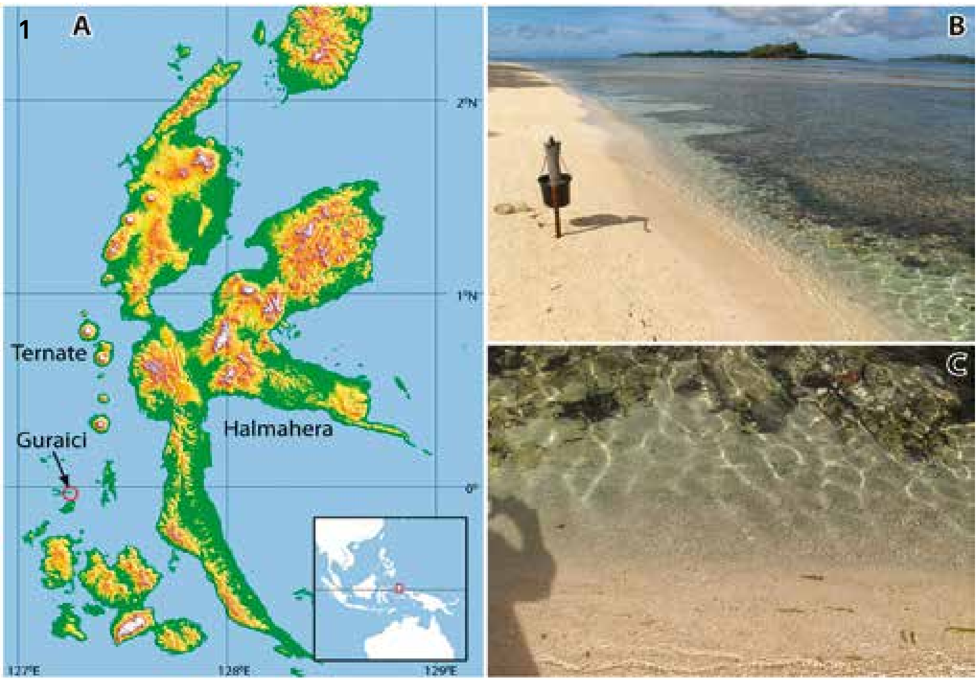

Fig. 1. Marine shallow interstitial fieldwork in Indonesia. A. Map showing locality of new species; B. Bou-Rouch phreatical pump placed in beach; C. border of moving sands between beach and reef flats containing high diversity of interstitial marine fauna. **Photo: R. Vonk**

Fig. 2. Superficial groundwater sampling on the island of Ternate, Tolire Kecil. Photo: S. Ishak.

Semporna Expedition SMEE 2010

Underwater explorations for nature conservation

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The Semporna reef complex is located at the east coast of Sabah (Malaysia) (Fig. 1), within the Coral Triangle, the centre of maximum marine biodiversity. Semporna has the largest concentration of reefs within Malaysia, which represent five major geomorphological reef types.

The Tun Sakaran Marine Park in this area contains eight islands and is the first marine protected area in Malaysia to include local communities within its boundaries. Sipadan Island's waters are proposed as a park and the intention to gazette was published in mid-2009.

Marine biologists from Malaysia, the Netherlands and the USA assessed the marine biodiversity and coral reef health during the expedition onboard MV Celebes Explorer at the end of 2010 (Fig. 2). The expedition was organized by WWF-Malaysia, Universiti Malaysia Sabah (UMS), Universiti Malaya (UM) and Naturalis Biodiversity Center.

High species diversity

The results show that Semporna rivals other top spots in the Coral Triangle in species numbers of corals, fish and shrimps. Mushroom coral species (Family Fungiidae) (Fig. 3) were counted as a proxy for coral species richness. A total of 44 species were recorded from 63 sites (Waheed & Hoeksema, 2013). The species composition at each site depended on the reef condition. Species diversity was generally higher at reefs close to the mainland. The total of 44 species of mushroom corals that have been recorded from this expedition surpasses other areas with very high biodiversity in the Coral Triangle and to date Semporna holds the record for the highest species diversity of this coral family.

The fish surveys also found high richness. The surveys focused on reef-dwelling fish (Fig. 4) and pelagics as encountered in the Semporna fish markets. The reef fish diversity of Semporna recorded during the roving surveys and in rotenone stations consistsed of 690 species belonging to 265 genera and 72 families. The number of species recorded from market surveys was 141, of which 78 were not recorded during the surveys, resulting in a combined diversity of 768 species for the entire expedition. This puts Semporna in the top 5 sites in the world for fish species richness.

Other taxa surveyed included shrimps (Fig. 5), gall crabs (Fig. 6; van der Meij & Hoeksema, 2013), and ovulid snails (Fig. 7). The surveys found 104 shrimp species, which ties with Ternate, Indonesia as the highest in the Coral Triangle. Three shrimp species were seen as co-inhabitants of the mushroom coral *Heliofungia actiniformis* (Hoeksema and Fransen, 2011). The surveys of gall crabs and Ovulidae have contributed to a growing literature on these relatively unknown taxa. The algae surveys found more than 130 species.

Reef damage

The reef status team surveyed 106 transects at 60 sites. The results show that for substrate cover, only 5 stations out of the 109 (5%) are found to be 'Excellent', 25 stations (23%) 'Good', 41 stations (38%) 'Fair' and 38 stations (35%) are at 'Poor' status. One reef area with low coral cover featured an exceptionally large aggregation of the tube worm *Filogranella elatensis* (Hoeksema and Ten Hove, 2011).

Damage to the reefs was mainly caused by unsustainable fisheries methods. The occurrence of blast fishing (Fig. 8) was obvious by fields of broken corals and by the sound of explosions. Discarded nets were observed to smother the reefs (Fig. 9), while fish traps were seen to be held at their place by coral boulders.

The conclusion from this expedition is that overall biodiversity is remarkably high, even within the

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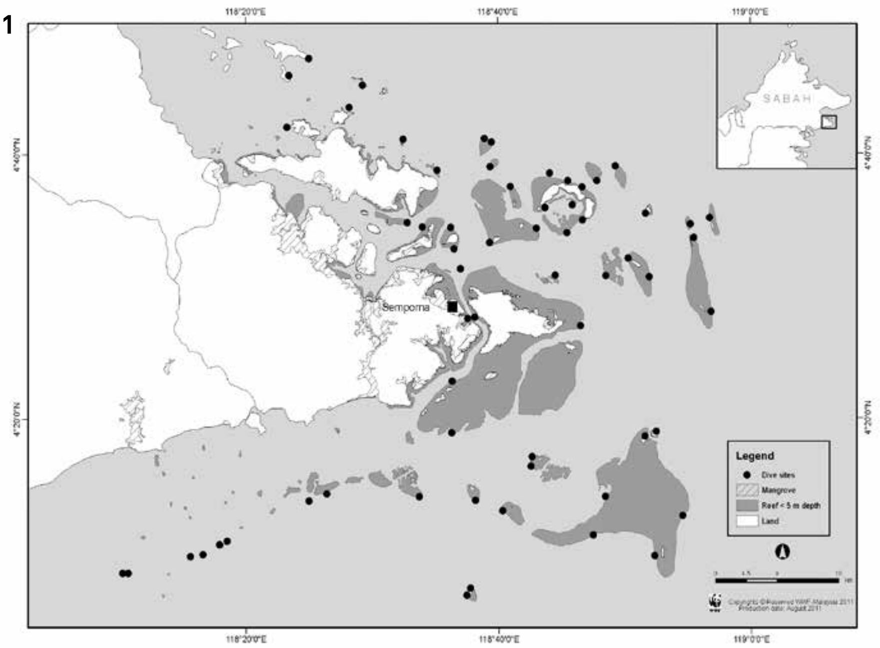

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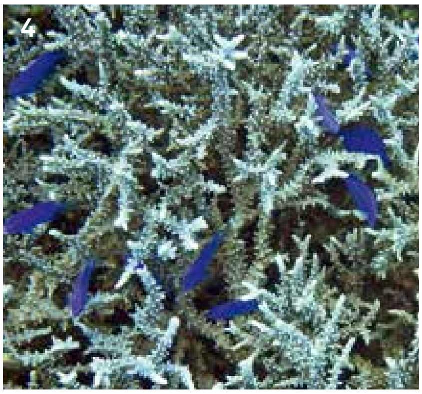

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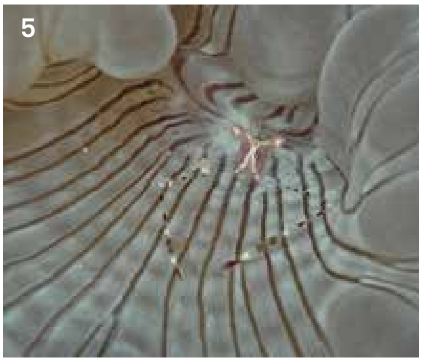

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Fig. 1. Research area
Fig. 2. The expedition team
Fig. 3. *Lithophyllon ranjithi*, a mushroom coral endemic to waters around northern Borneo

Fig. 4. Fish seeking shelter in between coral branches
Fig. 5. Commensal shrimp in a *Nemenzophyllia* coral

Fig. 6. Gall crab in *Turbinaria* coral
Fig. 7. Ovulid snail on octocoral host
Fig. 8. Divers examining a blasted reef
Fig. 9. Large net smothering a reef

Coral Triangle. Concerns for the future pertain to destructive fisheries and a possible impact of the diving industry on some popular reefs.

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Marine lakes of Indonesia

Leontine E. Becking & Nicole J. de Voogd

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Marine lakes are anchialine systems – a term first coined by a former curator at Naturalis, Dr. Lipke Holthuis,for land-locked seawater bodies that maintain a marine character through narrow subterranean connections to the sea (Fig. 1). Broadly speaking, I wanted to find out if marine lakes represent a type of island-system. Since Darwin, islands have played a key role in biology because they provide an explicit spatial and temporal context in which to study biodiversity. Similarly, the marine lake setting, with clearly delineated contours and known ages, provides a unique model to study key questions in marine ecology and evolution.

In order to determine whether marine lakes represent marine "island life", it first had to be established to what degree they are isolated systems. This can be illustrated by comparing marine lakes and the adjacent coastal habitats (reefs and mangroves) and measuring the following three aspects of isolation: 1. the degree of water exchange, 2. the degree of similarity in species composition, 3. the degree of genetic connectivity of populations. If the lakes would be in high connection to the adjacent sea and to each other, we would expect to find similar species composition and little genetic differentiation between populations, particularly between geographically close localities. Sponges were chosen to measure biodiversity, because sponges are one of the most diverse and dominant taxa in the lakes (Fig. 2) and also constitute important players in reef and mangrove systems in terms of diversity, biomass and filtering activities.

Expeditions

Previously, little was known about marine lakes in Indonesia as they are usually hidden inland, located in remote uninhabited areas. As a result much descriptive groundwork (e.g. discovering the lakes, describing their geographical and physical characteristics and describing species new to science) was a prerequisite before any further analytical studies could be performed.

With the aid of Google Earth satellite images, a water airplane, and old maps, a quest was started to find marine lakes during four expeditions to the regions Berau (East Kalimantan) and Raja Ampat (West Papua). For the work in Raja Ampat the extensive regional knowledge of Max Ammer from Papua Diving was crucial. Each time I was accompanied by students from the Free University Amsterdam, University of Amsterdam, Leiden University, University of Papua, as well as colleagues from Naturalis and Munich University (LMU). Once the lakes had been spotted by air from a water airplane (Fig. 3), we continued our search by boat equipped with GPS and aerial images. More often than not, our boat came to a halt in front of a seemingly impenetrable wall of sharp limestone covered in rainforest. Then commenced our ascent into the unknown. Each lake entry was a different adventure. Some came with muddy slopes or sharp loose rocks, others required advanced climbing skills, while others had us wading through smelly swamps. But as the lakes came into view we were always rewarded with magical sceneries (Fig. 4). At the lake's edge our scientific instincts soon would take over, and we started scanning the surroundings to determine what type of fauna and flora dominated. This included critically examining every log-like object from a distance, and hoping that everyone agreed that it was "kayu" (wood) and not "buaya" (saltwater crocodile). Once safety was confirmed, we would plunge into the water to record biodiversity, water characteristics, like depth and salinity, as well to collect samples.

Unique biodiversity

We discovered 50 lakes new to science of which 20 were surveyed for my doctoral work (Becking, 2012). As far as isolation goes, marine lakes represent a continuum from highly isolated to almost open systems, from brackish to almost fully marine. With respect to the question of islands, marine lakes do share important characteristics with is-

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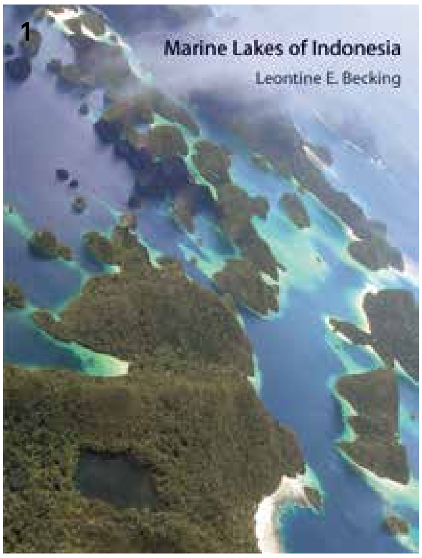

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Fig. 1. Cover of PhD-thesis "Marine Lakes of Indonesia" (photo by L. Becking, design by A. Hulskamp)
Fig. 2. Lisa Becking snorkelling in marine lake, note the 100% cover of colorful sponges (by N. Santodomingo)
Fig. 3. The Super Drifter water-airplane of the Raja Ampat Research & Conservation Center (by E. Dondorp)
Fig. 4. Marine lake in Misool, West Papua, Indonesia (by L. Becking)

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land systems: they are well-defined geographically, harbor unique biota with a large proportion of endemics and/or an abundance of species rare elsewhere, and isolated populations. We discovered that much of the biodiversity within marine lakes is restricted only to the lakes. This included over 30 species new to science of which we have described two and we are currently in the process of describing the remainder.
It is remarkable that marine lakes harbour such a unique diversity, while they are relatively young systems (<15000 year old). The question is how that could be possible. Our data indicates that the diversity within the lakes seems to have two origins: (a) recent divergence of rapidly evolving populations isolated from their ancestral population in the sea and (b) ancient lineages, which are probably relicts of the sea. In other words: the marine lakes appear to be both cradles and refuges of biodiversity!

Conservation

The findings of this PhD research also have important implications for conservation. Like island systems marine lakes are vulnerable to anthropogenic threats such as exploitation and alien species introduction. As a result of their many special features, marine lakes should play a prominent role in the marine conservation planning of both Berau and Raja Ampat.

Becking LE (2012) Marine lakes of Indonesia. PhD thesis University of Leiden, ISBN 978-94-6203-213-2, pp. 211.

Project funded by Earth and Life Sciences division of the Netherlands Organisation of Scientific research (NWO-ALW project # 817.01.008).

Shifting salamanders

Tracing the moving hybrid zone of two *Triturus* newts

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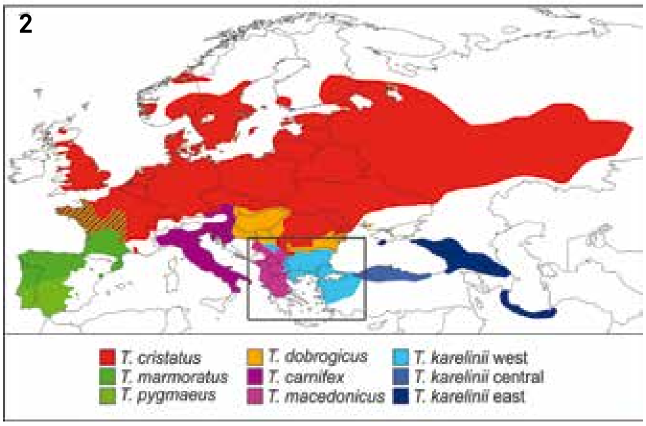
In our studies on phylogeny and historical biogeography, we use *Triturus* – marbled and crested newts (Fig. 1) – as a model. *Triturus* newts show an intricate distribution pattern (Fig. 2), with narrow hybrid zones separating their largely parapatric ranges. The *Triturus* taxa can be grouped in five different 'morphotypes'. Morphotypes reflect ecological specialization related to the time annually spent in the water to breed, with slenderness being correlated with aquaticness. The radiation of the four morphotypes that comprise the crested newts occurred in an evolutionary blink of an eye. Such a rapid, reticulate, adaptive radiation makes for an interesting struggle across space and time. This is exemplified by the case of *T. macedonicus* and *T. karelinii*, where a mix of competition and hybridization resulted in an intriguing biographical pattern that could only be deduced with the aid of molecular genetic methods.

Climate change forces species to shift their distribution ranges and can result in species displacing each other geographically. If a species overturn coincides with hybridization, this could cause mitochondrial DNA to be transferred across the species boundary, from the outcompeted into the invading species; a process known as asymmetric mitochondrial DNA introgression. We present a case involving two species of crested newts, distributed in the Balkan Peninsula of southeastern Europe, and in the west of Asiatic Turkey. We show that secondary contact and subsequent competition following the conclusion of the last glacial period resulted in mitochondrial DNA of *Triturus karelinii* to introgress into *T. macedonicus*. To explore how the two crested newt species shifted their distributions through time, we combine two distinctly different types of data: spatial genetic variation in the mitochondrial DNA and temporal variation in the environment.

We first conduct a phylogeographical survey, meaning we determine the geographical distribution of the mitochondrial DNA of *T. karelinii* and *T. macedonicus*. Based on the *T. macedonicus* populations that contain *T. karelinii* mitochondrial DNA, we delimit a ca. 54,000 km^2 zone of asymmetrically introgressed mitochondrial DNA (hatched blue-green in Fig. 3). The spatial genetic structuring of the mitochondrial DNA data of *T. karelinii* suggests that this species recently expanded its range considerably from Asiatic Turkey across the Balkan Peninsula, before it was outcompeted by *T. macedonicus* in the introgression zone. Additionally, the *T. karelinii* mitochondrial DNA that crossed the species boundary into *T. macedonicus* is still very similar, if not identical, to that found in *T. karelinii* itself. Hence, the mitochondrial DNA data provide two lines of evidence suggesting that the introgression zone was only established in the recent past.

To further explore the recent species overturn, we take a closer look to the two species' environmental requirements and their response to global climate change. Therefore, we conduct ecological niche modeling, which encompasses the approximation of the ecological requirements of the two crested newt species, based on the range of climatic conditions they experience at known localities. For locality data we use the populations for which we obtained genetic data, complemented with additional *T. karelinii* and *T. macedonicus* localities based on the literature, museum data and correspondence with colleagues. We project the models on current climate layers and reconstructions for the Last Glacial Maximum and the mid-Holocene. The introgression zone region only became hospitable for either crested newt species after the Last Glacial Maximum ended. At the mid-Holocene the area was relatively more suitable for *T. karelinii* than for *T. macedonicus,* whereas today it is the other way around. These results are in line with *T. karelinii* postglacially colonizing the introgression zone and subsequently being displaced by *T. macedonicus*.

Together, the two independent approaches applied – phylogeography and ecological niche modeling – support a scenario in which *T. macedonicus* displaced *T. karelinii* postglacially. Due to the changing climate, the two crested newt species came into spatial contact after the Last Glacial Maximum. Subsequently, the contact zone shifted, as *T. macedonicus* outcompeted *T. karelinii*. However, the



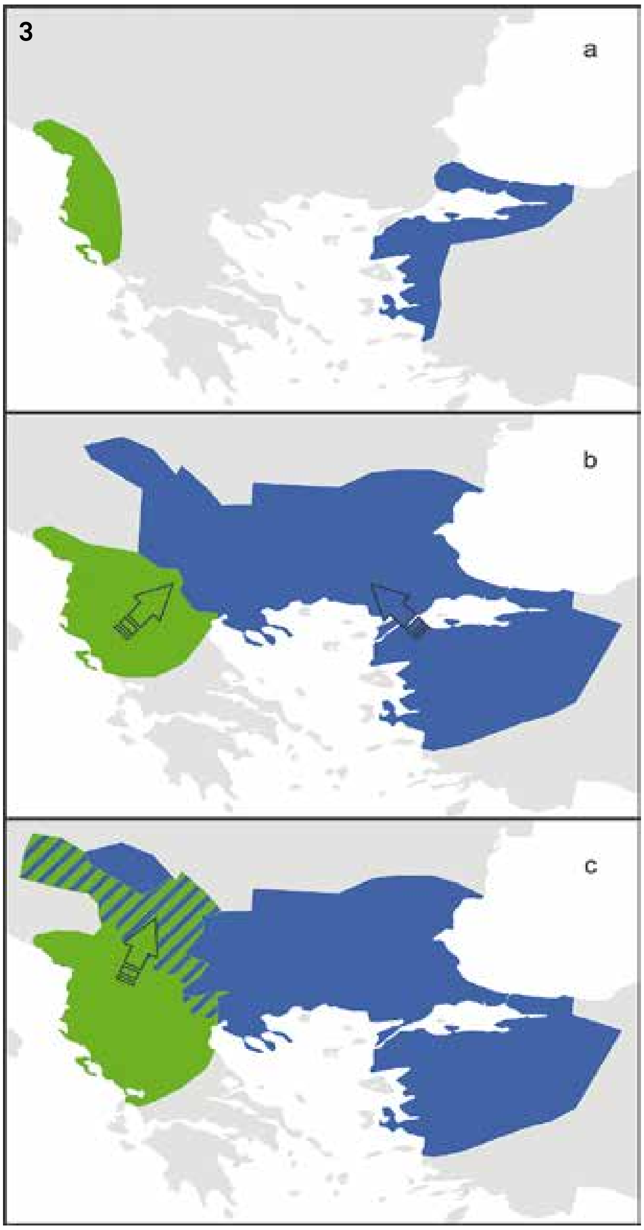


Fig. 1. A male *Triturus karelinii* (right) courts a female (photo by Max Sparreboom).

Fig. 2. Distribution of *Triturus* salamanders across Europe and Asia. The area of *T. karelinii* – *T. macedonicus* overlap is boxed and shown in detail in Figure 2.

Fig. 3. A scenario showing how the mitochondrial DNA of one crested newt species ended up in another. The area depicted is the Balkan Peninsula (Europe) and western Turkey (Asia). The range of *T. karelinii* is shown in blue. Green denotes the part of the range of *T. macedonicus* where it possesses *T. macedonicus* mitochondrial DNA. The green-blue hatched area is the region where *T. macedonicus* contains the mitochondrial DNA of *T. karelinii*. During the last glaciation, both species' ranges were contracted (a). After glacial conditions alleviated, *T. karelinii* colonized a considerable part of the Balkan Peninsula; *T. macedonicus* also expanded its range and the two came into spatial contact (b). Subsequently, *T. macedonicus* displaced *T. karelinii* over part of its range and, because of occasional hybridization with *T. karelinii*, took up *T. karelinii* mitochondrial DNA in the process, resulting in the mismatch between mitochondrial DNA distribution and species ranges observed today (c).

former distribution of *T. karelinii* was 'fossilized' as asymmetrically introgressed mitochondrial DNA. The invoked distribution dynamics, explaining the asymmetrically mitochondrial DNA introgression from *T. karelinii* into *T. macedonicus*, are summarized in Fig. 3.

Published as

Wielstra, B., Arntzen, J.W. 2012. Postglacial species displacement in *Triturus* newts deduced from asymmetrically introgressed mitochondrial DNA and ecological niche models. *BMC Evolutionary Biology* 12: 161.

The STEP-project
A future for European pollinators

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As newcomers to Naturalis, we have started to develop a Naturalis research field on pollinators and pollination, with emphasis on pollinator declines in Europe, distribution of pollinators in the Netherlands, and to improve our understanding of the role of pollinators in crop pollination and our food supply. Some of this work is part of a large EU Framework 7 research project called STEP, which stands for Status and Trends of European Pollinators (www.step-project.net) and started in 2010. The 5-year project consists of 22 partners across Europe and now, after the move of Koos Biesmeijer to Naturalis, includes Naturalis as an official partner. The project aims to (1) assess the trends in European pollinators (are pollinators declining? If so where? Which species? Can we predict future loss?); (2) improve our understanding of the factors causing change, such as land use, agricultural practices, climate change, invasive species); (3) identify the impacts of pollinator loss, such as deficits in crop pollination or wild plant pollination; and (4) find solutions for the problems identified in 1-3, including improving habitat and nesting for wild pollinators.

The Naturalis team in STEP (Koos Biesmeijer and postdoc Luisa Carvalheiro) is leading the research on assessing changes in plant and pollinator communities in Europe. This provides a natural link to the Naturalis collections and to the data holders of the Netherlands including EIS (The European Invertebrate Survey), de Vlinderstichting and FLORON (the plant recording society). The main problem in assessing change is that old data are needed to compare the current situation with. These data are often not available, but working with collections and data of amateur recording societies has resulted in 32 million records of plants and pollinators (bees, hoverflies, butterflies) for the Netherlands, the UK and Belgium, which makes it possible to analyze changes in the richness of bees, butterflies, hoverflies and plants over the last 60 years. Developing novel methods will also allow analysis of other biodiversity groups in addition to pollinators, e.g. all invertebrate groups treated by EIS, geological or marine collections.

Trends in species populations and communities

Making progress on assessing declines is important because halting biodiversity loss is a key international priority, and central to the Convention of Biological Diversity and EU policy. Much is known about well-studied groups such as birds, but the majority of European biodiversity is made up of insects with poorly known distributions, dynamics and threats. This ignorance concerning the status and trends of insects is worrying, but it is even greater concern for species that play important functional roles, such as pollinators. Pollination is an essential ecosystem service, vital to the maintenance both of wild plant communities (80% of plants are animal-pollinated; Fig. 1) and agricultural productivity (about 65% of major food plants benefit from insect pollination; Fig. 2). These pollination services depend on both domesticated and wild pollinator populations, and both may be affected by a range of recent and projected environmental changes, with unknown consequences. Even some simple questions are yet unanswered. We do not know, for example, which species are pollinating our crops, what is the loss in crop yield if pollinators disappear and how will climate change affect crop pollination and thus agricultural production?

Ecosystem services and conservation

These questions are addressed in STEP, but also in a large UK research project led by Koos Biesmeijer. One of the main modeling methods we use in this project is species distribution modeling (postdoc Chiara Polce, based at the University of Leeds).

Fig. 1. Many different insects visit flowers to collect nectar or pollen. In this process they pollinate more than 80% wild flowers. STEP investigates how and why wild pollinator populations are changing and the impacts of these changes.

Fig. 2. Two-thirds of our major food plant species need insect pollination. Both the quantity and the quality of fruits, vegetables and seeds are improved when pollinators are available in adequate numbers and diversity.

In parallel we are analyzing shifts in pollinator and plant distribution patterns in the past and future at Naturalis (Jesus Aguirre, PhD student). Comparison of the species models for the two countries (Netherlands and UK) is an excellent test to assess whether the models make sense and whether we understand the ecological and environmental needs of species well enough. Again pollinators are the main group of organisms we start with, but they are also an excellent way in to analyzing the importance of ecological interactions in species distributions. For example, does the distribution of a host plant limit the occurrence of its pollinator or is it the other way around? Now that the models are being developed, they allow us to address other questions related to plant-insect interactions in general (together with EIS for example and their extensive network of volunteer recorders).

Automated identification of pollinators

To make assessments of change easier in the future we need to improve the knowledge and research tools for monitoring pollinators and pollination. One way to achieve this is to develop automated identification systems for pollinators. We are starting with bumblebees, being important pollinators in decline in various parts of Europe, yet common enough for the general public to be attractive. Identifying even the commonest bumblebee species is not always easy. The common white-tailed bumblebee in NW-Europe can be any of at least four species. There are no easy morphological characteristics to separate them, but we now explore whether patterns in their wing venation can be used to identify the species (Fig. 3). Honeybee keepers use this method to see which subspecies of the honeybee they have in their hive, therefore we are confident that bumblebee species are different as well and can be identified based on such patterns. The idea is that, in the future, one could simply take a picture of a bee wing (on a smart phone for example) send it to an online database which then provides you with the name of the bee. Such a system would make monitoring of bumblebees (and later other pollinators) much easier and cheaper.

In summary, being a partner in a large European network of researchers has many advantages to Naturalis. Our students are embedded in a network and can benefit from all expertise available there and we can combine our strengths with external expertise to deliver even better research and address important question. Not all networks are open and open-minded, but the STEP consortium welcomes new members with good ideas any time and collaboration is the main method for making progress. Maybe this is inspired by the interaction between the bees and the plants!

Chinese wasps revisited
Family Stephanidae (Hymenoptera)

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The wasp family Stephanidae Leach, 1815, is a cosmopolitan family with 345 extant species.
It is considered to be the most basal group of the Hymenoptera-Apocrita. It occurs mainly in subtropical and tropical forests, but some species occur in moderate climate zones. Stephanidae are conspicuous by the “crown” on the head (Fig. 1a-c), the more or less modified pronotum (Fig. 1d, e), the shape of hind legs (especially the more or less swollen hind femur with ventral large teeth, the hind tibia widened apically) (Fig. 1f), the often present ivory streaks on the frons or temple and ivory or whitish subapical band of the ovipositor sheath in some genera (Fig. 1g). The species of Stephanidae are usually medium-sized to large, and the largest species are in the genus *Megischus*, with body length reaching up to 35 mm.
Presently, about 13 valid genera and 351 valid species (including 6 extinct species in 2 extinct genera) of Stephanidae are known worldwide and about half of the species occur in the Oriental Region. Stephanidae are generally considered to be rare or extremely rare, and nearly 95% of all stephanid species were described from a single specimen. The systematics of the family is imperfectly known; many types have never been studied since their descriptions. The species exhibit a rich, but often continuous morphological variation.
We are the first to have monographed the family Stephanidae for an area as large as China (Hong *et al*., 2011). We studied al type material, described and illustrated all species, summarized the full synonymy, and provided keys to the genera and within the genera to the species. The publication is an open access special issue of ZooKeys.
We recognized 21 species belonging to five genera which are known from 12 provinces or regions (Fujian, Guandong, Guangxi, Hainan Island, Henan, Henan, Hong Kong, Hubei, Shaanxi, Sichuan, Taiwan, Yunnan and Zhejiang) of China. 6 Species (or 29%) are new to science. However, the actual number of Stephanidae occurring in China may be considerably higher, since these wasps exist without doubt in more than the reported provinces of China.
Worldwide, only 303 specimens from China are available in museum collections. The rarity of collections may be explained by the fact that Stephanidae are not easily collected by traditional methods. Sweeping, Malaise traps and yellow pan traps, which are all staple methods for collecting many Hymenoptera, seem ineffective for stephanids. The use of blue pan traps was reported to be an effective trapping technique for Stephanidae in the New World. However, only seven stephanids were collected in 39 blue pan traps in China and further evidence is needed to prove the potential of such traps in the Old World.
Stephanidae are solitary idiobiont ectoparasitoids of wood boring beetle larvae of mainly Cerambycidae and Buprestidae. The actual biology of many species is unknown or nearly unknown and only two species absent in China, *Schlettererius cinctipes* and *Stephanus serrator,* are recorded from several hosts. Other recorded hosts belong to other families of Coleoptera such as Curculionidae, and to the hymenopteran family Siricidae (woodwasps), both larvae as well as solitary bees, but the latter needs re-confirmation.
Schlettererius cinctipes was once introduced from California to Tasmania to prove its potential value as a member of the parasitoid complex on *Sirex noctilio*; *Stephanus bidentatus* and *Stephanus tridentatus* were found on trunks of *Quercus* and *Toxicodendron* trees with Cerambycidae larvae and *Stephanus tridentatus* was ovipositing in Buprestidae larvae in an *Ulmus* tree. Obviously, Stephanidae can be of importance in biological control of coleopteran and hymenopteran pests in trees.
The paper has been made possible by the support of a 3-months Martin-Fellowship from Naturalis to the first author in 2010.

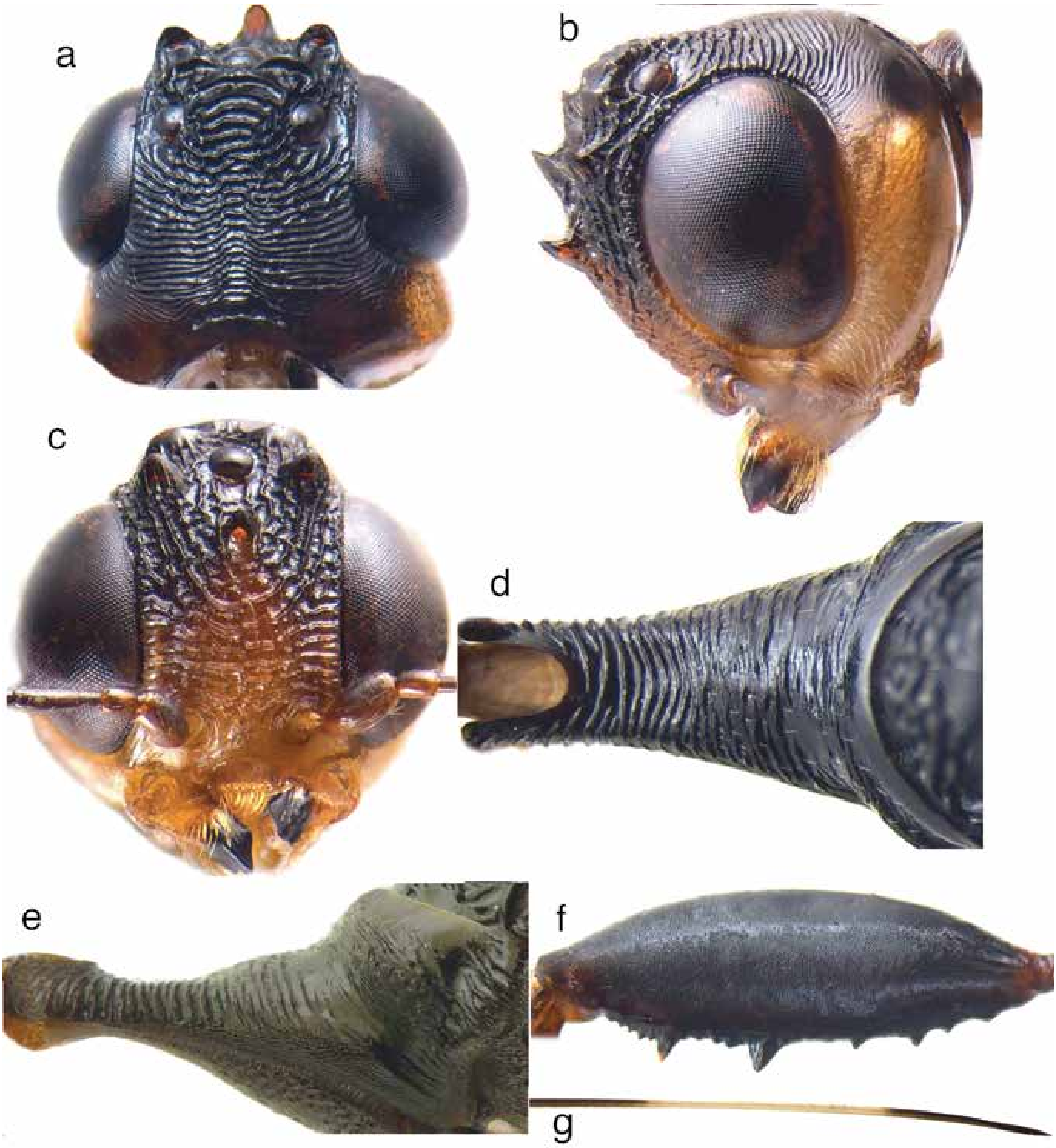

Fig. 1. *Foenatopus acutistigmatus* Chao, 1964, female, Mt. Nanling, Guangdong, S. China. **a** head dorsal; **b** head lateral; **c** head anterior; **d** pronotumdorsal; **e** pronotumlateral; **f** hind femur; **g** ovipositor sheath.

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Evolution of a brass band

The amazing shells of *Opisthostoma*

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Darwin's finches and peppered moths are commonly used examples in biology textbooks to illustrate evolution. Generations of students have learned about evolution processes from these famous case studies. Recently, the results of Campas *et al*. (2010) even suggest that it is possible to develop a formal, mathematical scheme to quantify morphological phenotype and relate it to both the genotype and the underlying developmental genetics.

However, the morphological transformations that occur during the evolution of Darwin's finches cannot be that simply transposed to other organisms.

Due to its relatively simple spiral geometry, the snail shell is more studied theoretically than any other biological shapes (Dera *et al*. 2008). In view of the diverse morphology of the shells, we chose the land snail genus *Opisthostoma* as a model to investigate the evolution of morphospace. To analyze the occupancy of a theoretical morphospace – the spectrum of all possible morphologies of a group of taxa – we first need to describe shape variation of all the individuals belonging to this taxa in a way that can be related to the genotype.

Diverse species morphology of *Opisthostoma*

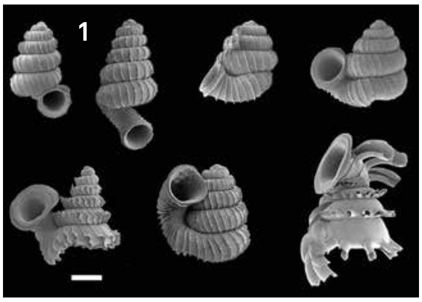
We started to compile the existing knowledge about the taxonomy, distribution, and ecology of *Opisthostoma* species. We identified a total of 134 *Opisthostoma* species, which together represent a large portion of shell diversity in the Gastropoda. Similar to most of the shelled Gastropoda, some *Opisthostoma* species have a dextral, regular, spirally coiled shell throughout their ontogeny (Figure 1a). However, many other *Opisthostoma* species have a shell form that changes halfway in their ontogeny - the last whorl of the shell detaches from the preceding whorls and coils in an opposite direction (Figure 1b-1g). These shell morphological transitions are extreme cases, but are known for many extant species and fossils (e.g. Okamoto 1988; Clements *et al*. 2008). Another characteristic feature of this genus is the radial rib ornamentation on its shell surface, which can vary greatly in form and intensity.

Convergent evolution of shell traits

We sequenced mitochondrial and nuclear genes for 53 *Opisthostoma* species, together representing the geographical distribution and shell phenotypes of this genus. Surprisingly, based on the resulting phylogenetic tree, the two major shell traits of *Opisthostoma* – coiling direction and shell surface ornamentations show convergent evolution. The same traits have independently evolved in several monophyletic *Opisthostoma* clades that are not closely related (Figure 2).

To our knowledge, *Atopos* slugs and Lampyridae larvae (glow worms) are two major predators of *Opisthostoma*. They attack *Opisthostoma* via the aperture – the only opening of shell. Thus, it is thought that the elongated tuba, which remains an open space when the snails retract deeply into the shell, prevents the predators from reaching the retracted snail body (Figure 3a & 3b). However, the slugs have developed a novel strategy to attack the snail by boring holes through the shell layers, judging from the holes that have been found in many shell remains of dead *Opisthostoma* snails (Figure 3c & 3d) (Schilthuizen *et al*. 2006). In response to this strategy, many *Opisthostoma* species have evolved stronger radial spines to make their shells less vulnerable to such predation techniques.

Although we are slowly unveiling the selection pressures driving the phenotypic evolution of the shell, the developmental and genetic basis of the morphogenesis that determines the coiling direction and shell surface ornamentations are still poorly known.



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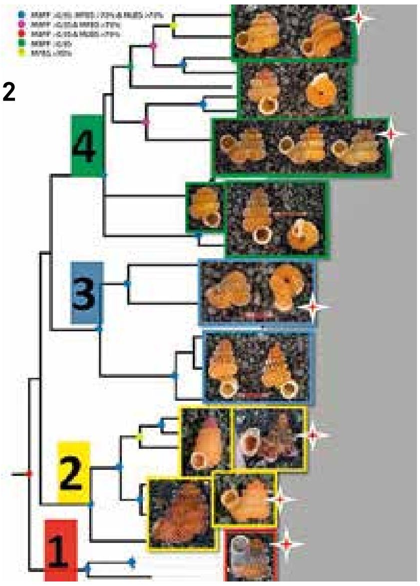

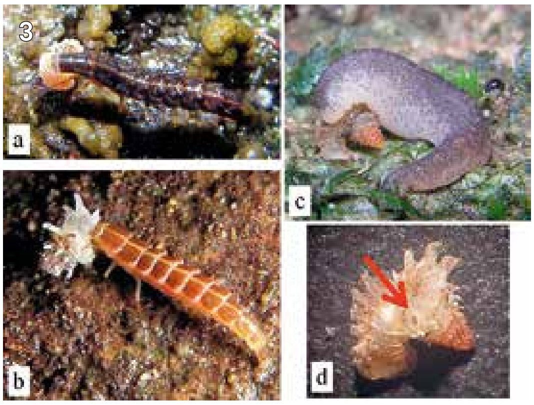

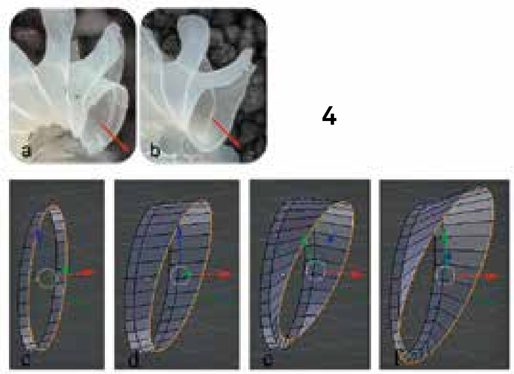

Fig. 1. Shell diversity of *Opisthostoma* species. Scale: 1 mm.

Fig. 2. Bayesian phylogeny for *Opisthostoma*. Nodal support: Bayesian posterior probabilities (MB), maximum-likelihood (ML), and maximum parsimony (MP). The cross label correspond to the species with irregular coiled shell.

Fig. 3. *Opisthostoma fraternum* attacked by beetle larva via the shell aperture; b: *Opisthostoma laidlawi* attacked by beetle larva via the aperture; c: an *Atopos* slug attacks *Opisthostoma concinnum* by boring a hole on the shell; d: hole on shell drilled by *Atopos*. The evolution of elongated tuba, changing of coiling direction and spines could have driven by these predators.

Fig. 4. Upper panel - Growth stages of Opisthostoma species: a) shell growing stage; b) spine or rib growing stage. Lower panel – major growth processes of shell, which are simulated by 3D computer graphics software - Blender: c) the primary aperture before new shell materials are added, yellow ring is the mantle edge; d) extrusion; e) rotation; and f) expansion. The red arrows indicate the growth direction of shell.

Shell morphogenesis

In order to gain a better understanding of shell morphogenesis, we investigate growth patterns and morphological changes in the shell along the ontogeny of the *Opisthostoma*.
As in all other snails, the shell of *Opisthostoma* follows an accretionary growth mode. The new shell material is continuously added at the shell aperture by mantle tissue with slight modifications of the existing aperture in terms of rate of expansion, rotation, and extrusion (Figure 4).
We will develop a refined shell geometry model, based on the growth vector model described in Urdy *et al*. (2010a,b), which will be used not only to simulate a shell phenotype, but also the growth processes. We shall then be able to identify the key transitions in growth processes that produce the various shell phenotypes. This model should provide a smooth mathematical way to describe the changes in growth processes and allow the comparison of all the *Opisthostoma* shell shapes, as Campas *et al*. (2010) exemplified in the case of Darwin's finches.

By using *Opisthostoma* as a model, we can provide more insight into how ecology, biogeography, genetics, development and evolutionary history influence the morphospace occupation of a whole genus.
We hope that *Opisthostoma* will pave the way for greater understanding of the evolution of other shell-bearing snails, including the accumulated fossil snail record over millions of years.

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Spiders in Southeast Asia
Communities and cybertaxonomy

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Scientists know less than you may think about the species that share this planet with us, where they live and what they look like. Conservationists and land managers have to set priorities based on which areas are relatively high in diversity and species with small distributions. Setting these priorities intelligently requires fairly even knowledge of the biodiversity across a large area. Regional scale biodiversity knowledge is typically only available for a few charismatic groups, like birds and flowering plants. However, these represent only a small part of the overall terrestrial biodiversity, which is in fact dominated by insects, spiders, and other arthropods. In my research, I use structured inventories to investigate patterns of spider biodiversity in some of the most species rich communities on Earth: tropical forests. This means intensive sampling of the spider community in an area.

Diverse tropical arthropod communities are generally characterized by a few common species and a *very* large number of rare species. Adequate sampling from such communities is problematic because the dominance of rare species makes it nearly impossible to obtain a complete census of the species present. It is only within the past several years that statistical methods have become available to compare communities between sites based on incomplete samples. I am applying these methods to learn how factors like distance, habitat, disturbance, and structural complexity affect diverse communities. I use a variety of approaches to obtain data on biodiversity patterns including morphology-based sorting, DNA barcoding, and next-generation sequencing of bulk homogenized samples.

My field research involves rapid inventories of spiders from protected forests in Southeast Asia. We collect every spider we can find using a variety of methods. These samples are then brought back to Leiden and sorted to “morphospecies.” We spend very little time at this stage investigating whether the species we found have been described before or what their scientific names are. We are sure that a substantial fraction of the species we collect are new to science, but our first priority is to describe the overall community pattern. We take a series of photographs of every species. We also obtain DNA barcode sequences for as many species as possible. The DNA and morphospecies results are cross-checked to look for inconsistency. Using these two independent methods to determine the number of species in our samples increases the accuracy and reliability of our results. In my lab, we currently have images of well over 250 Vietnamese spider species. Soon we will post all these images online, along with their DNA sequences in an expandable digital, open access resource for anyone with an internet connection and an interest in spider biodiversity of the region.

In a study currently underway I will compare arthropod communities from diverse protected forests and adjacent monoculture *Acacia* plantations in two regions of Vietnam (Fig. 1). I will use this study also to develop methods for rapid evaluation of the entire arthropod community, using insecticidal fogging (Fig. 2) and next-generation sequencing whereby the sample is homogenized and bulk sequenced. The result is tens of thousands of DNA sequences. From this, we can estimate the total number of species in the sample and classify them according to major arthropod taxon. This is a new approach and not yet thoroughly tested. So we are processing half of each sample in the traditional way described above (morphospecies sorting, DNA barcoding, and photography) and homogenizing the other half. From this, we will be able to test the reliability of the new method and, if necessary, propose methods to correct for biases. Our hope is that this method can be developed into a protocol for quickly obtaining vast amounts of data about arthropod communities that will help us to monitor the consequences of major ecological issues like conversion of forest land into plantations and climate change.

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Fig. 1. Bach Ma National Park, Vietnam, 2011. Arrow shows park boundary. Inside the park is a diverse forest with a mosaic of structure. Just outside the forest is monoculture *Acacia* plantation used for paper production.

Fig. 2. Tuan, a Vietnamese member of the sampling team, operates the fogger in an *Acacia* plantation.

Inventories of tropical arthropods generate specimens that can form the basis of taxonomic and phylogenetic research. My work in spider taxonomy follows a cybertaxonomic model. In addition to traditional publications, elements of my taxonomic work are distributed online in a variety of ways. This is important because scientists and students living and working in proximity to the greatest concentrations of biodiversity often have limited access to large academic libraries and collections, but access to the internet is increasingly widespread. Biodiversity is one of the most information-rich fields of human knowledge and online resources provide unprecedented power to make this aggregated information more accessible and relevant.

The Netherlands Biodiversity
47,800 species, new phylum and tree

Erik J. van Nieukerken, Roy M.J.C. Kleukers, Jinze Noordijk, André J. van Loon, Marco C. Roos & Charles H.J.M. Fransen

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The United Nations declared the year 2010 as the International Year of Biodiversity. For an institute with 'Biodiversity' in its name a year not to miss: not only was the new institute launched at the beginning of that year (see p. *), the end of that year saw the publication of a book covering the entire Dutch biodiversity (Noordijk *et al.*, 2010) (Fig. 1). Naturalis published and initiated this book together with the foundation 'European Invertebrate Survey – Nederland' (EIS-NL) which holds office at the Naturalis premises. The idea was to update an earlier book on the Netherlands Biodiversity (van Nieukerken and van Loon, 1995), now supported by the online Dutch species catalogue (Anonymous, 2011). We invited a large number of specialists and specialists organisations to write a chapter on their taxonomic group, including 26 of our staff members and 14 research associates. EIS-NL and Naturalis co-ordinated the project, and members of the editorial board filled in chapters on taxonomic groups that were not covered by specialists. The book was publicly launched on 25 November 2010, and received a lot of positive press coverage, including book reviews in international journals. All chapters are now also available as pdf online in the Naturalis repository (http://www.repository.naturalis.nl/).
Few countries have listed or counted all of their biodiversity, and a book with the same extensive coverage as ours is a unique document. It shows what we have and where knowledge is lacking. Here we highlight some of the interesting results.

All specialists, often being the global specialists, provided an estimate of global numbers of described species. As a result, we could publish an update of global numbers in Chapter 6, raising from a little less than 1.9 million in Chapman (2009) to 1.95 million in our book. Our figures were internationally recognised, since several were cited in the recent Zootaxa issue on Animal Biodiversity (Zhang, 2011a, b).

The Biodiversity of a small country
By summing up all expert counts and estimates of the species richness for their group, we arrived at the staggering number of 47,800 species from the Netherlands, composed of 45,939 established species and 1861 of which occurrence in the Netherlands is assumed. This number is composed of 27,146 (+ 612 assumed) Animalia, 10,300 Fungi, 3894 Plantae (red and green algae and land plants), 3016 (+1104) Chromalveolates (brown algae, diatoms, forams and various other unicellular groups), a few in the remaining groups of unicellular organisms and a low estimate of 1100 Eubacteria and Archaea. For the land plants, various groups of larger algae, most animals and larger fungi these figures are pretty accurate, but for large groups of unicellular organisms, bacteria, and microfungi we hardly have substantial data for the presence of species in the Netherlands.
The number of 47,800 represents 2.45% of our estimated global number of described species. We concluded that compared to the size of the country (0.02% of the world) we have a rich biodiversity (Noordijk and Koomen, 2011) (Fig. 2).

A new phylum

When checking whether all groups were covered, we realised nobody has searched for the recently (1995) discovered animal phylum Cycliophora in The Netherlands. These minute animals (max 300 µm long) live as commensals on mouthparts of lobsters, such as Norwegian lobster *Nephrops norvegicus*, a relatively common species in the North Sea. Prompted by this realisation, CF checked the collections and found many specimens of the cycliophoran *Symbion pandora* (Fig. 3) on a single Norwegian lobster, taken in 1936 west of the isle of Texel. We thus could report the spectacular news of the presence of a new phylum for the Netherlands (van Nieukerken, 2010).
We are now studying more collections to see how wide the phylum is distributed, not only in the Netherlands, and whether we can find a wider host range.

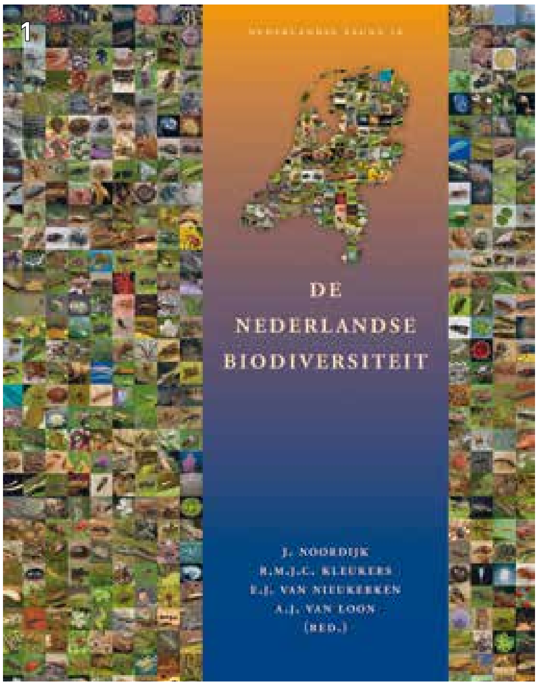

Fig. 1. Book cover.

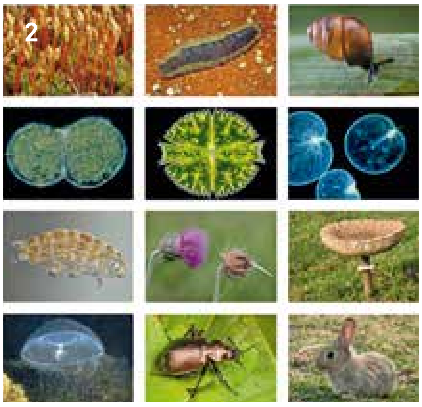

Fig. 2. An overview of the rich biodiversity (p. 57 of the book).

Fig. 3. *Symbion pandora*.

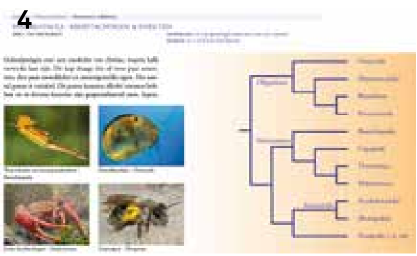

Fig. 4. Representative species and a cladogram of the Pancrustacea.

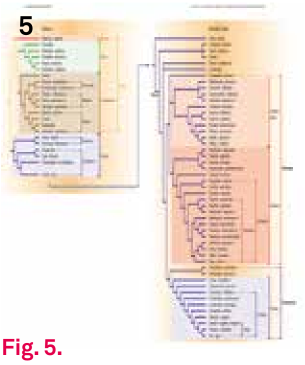

Fig. 5. Examples of cladograms.

Naturalis classification and Tree of Life

Authors have very different opinions as to classifications and phylogenetic relationships. For a book of this size, covering all life, we needed to find a common ground, a classification framework that does right to current scientific knowledge. The last 10 years we have seen drastic changes in the tree of life, mostly due to the increase of phylogenomics, where large numbers of genes for many taxa were analysed. Original divisions of life in animals, plants and fungi no longer do justice to current knowledge of the tree of life. We decided to build our "own" Naturalis tree of life and classification on the basis of the most recent knowledge. However, it should and cannot be conserved, as new data already have overruled some of our 2010 choices. Our choice for a strict phylogenetic classification also implied that we refrained from using traditional paraphyletic groupings such as "Algae", "Protists", "Crustacea", "fishes", or redefined them in cladistic terms (e.g. by adding birds to Reptilia). We introduced groups such as the monophyletic supergroups (including several phyla) Chromalveolata, Excavata and Unikonta, or at a lower taxonomic level the Pancrustacea (Fig. 4), combining insects and crustaceans. We document all our choices with references, and illustrated them by simple cladograms, of which we show some examples (Fig. 5).

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Willy awry
The mystery of the crooked genitals

Menno Schilthuizen[1,2], Paulien de Jong[1,2], Tamara Hoogenboom[1,2], Rick van Beek[1,2], Rik Lievers[1,3], Thijmen Breeschoten[1,2], Tom van Dooren[1], Michal Polak[4], Stefan van Dongen[5], Frietson Galis[1], & Leonardo Latella[6]

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Hunched over her microscope, Leiden University MSc student Tamara Hoogenboom sighs in desperation. “They are so fast!” she exclaims. Indeed, separating males and females of the small scavenging beetle *Sciodrepoides watsoni*, which requires a good look at the foretarsi (the “feet” on the first pair of legs) is not easy. The beetles, which she keeps in petri dishes with soil and a small bit of Limburg cheese for food, are fast runners and apt at avoiding the intruding eyes of the student. But eventually Tamara is satisfied that she has separated all the males from the females. This is crucial, for she is planning mating experiments, aimed at finding out whether female *S. watsoni* beetles prefer males with more or with less symmetric penises.

This may sound like the pinnacle of scientific frivolity, but is actually a crucial component of a research project on the evolution of asymmetric genitalia. This project, which forms part of the Left-Right Asymmetry programme (within the Focus Group “Character Evolution”), tries to find answers to the question why the reproductive organs in so many species of animals are asymmetric. This pattern is found across the animals: in insects, mammals, flatworms, earthworms, nematodes, snakes, and other animals that are bilaterally symmetric on the outside, male and female genital organs in many species are asymmetric. In the hoofed mammals, for example, deer (Cervidae) have symmetric penises, but many of their relatives (mousedeer, camels, pigs) have asymmetric two-pronged or corkscrew-shaped penises (Schilthuizen, 2011). The subfamily of beetles that *Sciodrepoides watsoni* belongs to, the Cholevinae (Lievers, 2012), are another good example. In *S. watsoni*, one of the species that is cultured in the incubators in the Van Steenis building, the penis is almost perfectly symmetric, but in its close relative, *S. fumatus*, it is always bent to the right with two unequal lobes at the end (Fig. 1). Similarly, the female of this species has an asymmetric twist to plates in the tip of her abdomen.

Nobody knows why this pattern exists. In fact, nobody sofar seems to have worried about it too much. Taxonomists have been using genital asymmetry as a handy way to recognise species, but seem never to have been surprised that asymmetry would evolve so often. But surprising it is: studies in the 1990s showed that symmetry is sexy. The more asymmetric a potential mate is, the less attractive (Van Dongen, 2006). So how could asymmetry in a sexually selected characteristic like genitalia begin to evolve? What advantage does an asymmetric penis or vulva have over symmetric ones, and why only in particular species?

To try to answer some of these questions, our team is tackling the problem from all sides in beetles. Tamara Hoogenboom works (Fig. 2) with our cholevine experimental system, hoping to find out what happens inside a mating pair of beetles and how asymmetry in that nether region could possibly be of benefit. Her class mate Paulien de Jong, who does her work in the DNAmarkerpoint (the Naturalis-IBL shared DNA lab), sequences the DNA of a large number of Cholevinae species to build a phylogenetic tree. At the same time, student Rick van Beek (Fig. 2) measures the genital asymmetry in males and females of all the species that Paulien is studying the DNA for. In March 2012, the three of them visited the Cholevinae-lab of Leonardo Latella, our collaborator in Italy, to collect species for their tree that do not occur in The Netherlands. And at the same time, BSc student Thijmen Breeschoten is doing the same in a group of rhinoceros beetles.

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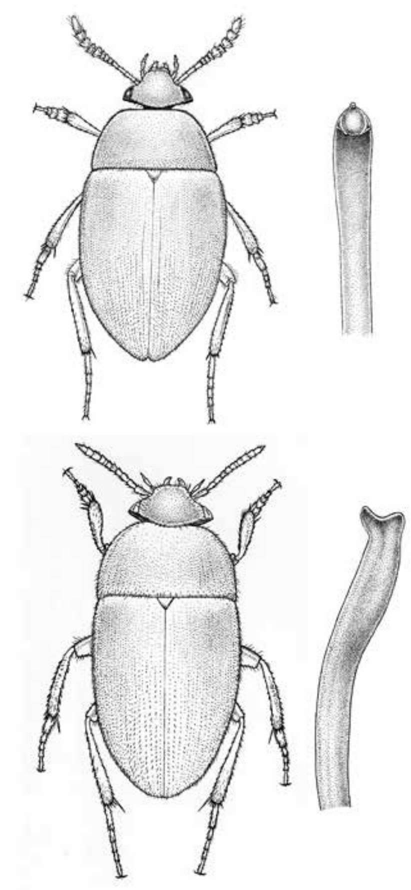

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Fig. 1. *Sciodrepoides watsoni* (top: with symmetric penis) and *S. fumatus* (bottom: with asymmetric penis). Artwork: Erik-Jan Bosch.

Fig. 2. Students Tamara Hoogenboom (left) and Rick van Beek (right) celebrating successful collecting of leiodid beetles with asymmetric genitalia in Italy. Photo: Paulien de Jong.

We hope that in the near future, the experimental work (which until now uses naturally occurring deviations from symmetry) can be enhanced with a kind of insect surgery. Our collaborator Michal Polak has developed a unique machine: a micro-laser with which minute structures on the genitalia of small insects can be zapped off (Polak & Rashed, 2010) or otherwise modified. Recently, we managed to persuade Michal to try something new with his laser: to sculpt the symmetric penis of a cholevine beetle in such a way that it becomes asymmetric. So far, he managed to do this with alcohol-preserved specimens quite beautifully. The next step is to do the same in live beetles and to see how conspecific females react to them.

Answering these questions does not only help us understand the evolution of genitalia (a rich field of research these days; e.g., Leonard & Córdoba-Aguilar, 2010), but also has implications for the control of body asymmetry and disease. Frietson Galis studies congenital defects in human embryos (Galis *et al*., 2006), including asymmetry in the vertebrae. Her work has shown that our bodies employ a delicately tuned “symmetry management system”: during development, some parts **must** remain symmetric (our limbs, our faces, our kidneys and gonads), but other parts **must** be asymmetric (our hearts, our intestines, and, to some extent, our brains). Deviations from this may result in spontaneous abortion, birth deformations, and disease. But in evolution, genitalia seem to flip between these two categories of control quite easily: in some species asymmetry is better, in others symmetry. When a species with symmetric genitalia evolves into a species with asymmetric ones, this means that evolution needs to force the symmetry management system to let go of symmetry control over the genitalia, while maintaining control over the organ systems around it. Understanding how evolution can do this so easily without going through an “adaptive valley” will give us a better understanding of the origin of symmetry-related disease in humans.

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Garden snail evolution
Response to climate change

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It was one of Naturalis's greatest events of the Darwin Year 2009: participating in the Evolution Megalab – a project to study the evolutionary change of shell colour in the variable garden snail *Cepaea* in Europe (Fig. 1). Brainchild of UK evolutionary ecologist Jonathan Silvertown (author of *Demons in Eden*), the project aimed to be a web-based citizen science project for the whole of Europe. By recording the colours of the shells of the *Cepaea* snails in their vicinity, people all over Europe could contribute to a study in which it would be possible to see if the shell colours in garden snails had evolved over time. This was made possible by comparing the 2009 data with older data for the same areas. The expectation was that yellow shells without any black bands would have increased because of climate change, since these are better at reflecting the sun's heat and thus the snails inside would better survive mid-summer overheating.

Naturalis volunteered to run the Dutch branch, and it became a great success. For much of the year 2008 and early 2009, the Dutch Megalab team was busy attending workshops in the UK, translating the web pages into Dutch, loading collection data into the data base, writing and editing school work books, preparing the launch, getting schools involved, and speaking to the press. And then when the project was launched in April 2009, we sat back and watched the data points accumulate steadily on the Google Maps interface on the website www.evolutionmegalab.org/nl (Fig. 2).

In the end of 2009, we had collected some 9,000 records, together representing the more than 250,000 individual snails that had been accumulated.
The analysis of these data proved harder than we had anticipated, due to identification errors and errors made when locality coordinates were manually typed in. So we had to filter those records out first. Finally, we had to reduce the data set to only those records that were based on a sufficient number of snails (ten or more).

The final result of the analysis (Silvertown et al., 2011) showed two things. First, there was indeed an increase in yellow snails, but only in one particular habitat: dune areas. This we could explain by the fact that dunes are very open habitats, where hiding before the sun is often not an option to snails – resulting in stronger natural selection. The other thing we found was a bit harder to explain: a Europe-wide increase over the past 50 years of snails with a single black band over the middle of the shell. Puzzled by this result (no known benefit exists for this one-banded morph), we decided to run a number of accurate, small scale tests. After all, the large scale of a citizen science project (we could never have collected a quarter of a million snails all over Europe ourselves within half a year) is traded-off against the disadvantage of inaccuracy (we may not have filtered out *all* the errors introduced by getting lay people do science) (Worthington *et al*., 2011). While Robert Cameron started some resampling of areas he had sampled himself in the 1960s, here in The Netherlands we turned to the legacy of Henk Wolda (Fig. 3).

Wolda was an evolutionary ecologist who worked at the Rijksuniversiteit Groningen in the 1950s and 1960s, and who was the Dutch exponent of the Europe-wide fashion of the time of using the shell colour polymorphism in *Cepaea* for population genetics. He and his team carried out many field studies in Groningen, Friesland, Drenthe, and Gelderland, which resulted in many papers. After he moved

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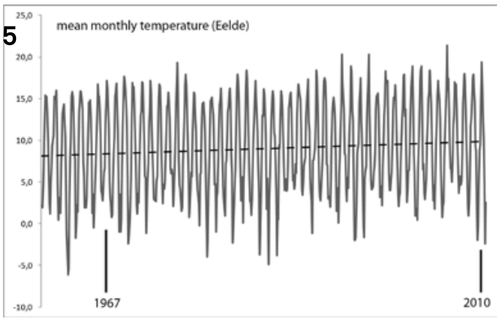

Fig. 1. Various colour morphs in *Cepaea nemoralis.*
Fig. 2. A screenshot from the Evolution Megalab website.
Fig. 3. A portrait of Henk Wolda in his *Cepaea* days.
Fig. 4. Resampling *Cepaea*.
Fig. 5. Temperature increase at Eelde.

to the Smithsonian Tropical Research Institute in Panama in the early 1970s, his samples of snail shells eventually were deposited in Naturalis.

In his collection we found several sets of samples that would be suitable for resampling. For example, some 3,000 shells from a small area around the village of Eenrum, all collected in 1967 and labelled very accurately with “Amersfoort coordinates”, in many cases with 10 × 10 m accuracy, provided a unique opportunity for resampling. We could return to those places, search for snails, and see how the colours had changed over those 43 years. And so we did. In the summer of 2010, we first scored the colour patterns on the museum specimens. Then, we drove to the exact localities where the Eenrum material had been collected and collected modern-day *Cepaea* snails there (Fig. 4), for which we also scored the colour morphs.

The results (Ozgo & Schilthuizen, 2012) were remarkable: in almost all sites, some evolutionary change had taken place. But for the most part, these were very local changes. In Ernstheem, for example, mid-banded went down from 0.14 to 0.02; while at Oude Tocht, pink went from 0.19 in 1967 to 0.49 in 2010. But only one colour morph went up everywhere: not mid-banded, but yellow snails without bands on the top of the shell. It is known that, in the full sun, such morphs stay up to 2°C cooler than snails with other coloration (Heath, 1975). And indeed, the weather records of the nearby airport Eelde show that the mean monthly temperature has steadily increased by 1.5°C over the period 1967-2010 (Fig. 5).

This year, we plan to continue our research into shell colour evolution in response to climate change on a smaller scale. VU-student Nikita van Zeijl will study snails in the so-called heat islands in big cities that were mapped by TNO (Klok *et al*., 2010) and look for signatures of heat-induced evolution in city-dwelling *Cepaea*. And who knows we will finally find a cause for the Europe-wide increase in mid-banded snails.

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European songbirds
Biodiversity hotspots

**Ronald Sluys[1], Mansour Aliabadian[2] &
Cees S. Roselaar[1]**

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Birds form an excellent indicator group for the identification of key sites for biodiversity conservation due to the fact that detailed information is generally available on their distribution. We created a database of digitized equal area distribution maps of 2,401 phylogenetic species of songbirds endemic to the Palearctic Region. The geographic distributions were interactively plotted on an equal area map of the Palearctic Region. The basic information on bird distribution was compiled over a period of 20 years from an extensive literature study, supplemented by data obtained from the examination of bird skins – and specimen labels – in numerous zoological collections. An example of such a map concerns the Bluethroat (Figs. 1, 2).

Hotspots of range-size rarity or endemism were calculated as the sum of the inverse of the range sizes. A species recorded from 1 cell has the maximum weight of 1, a species occurring in 10 cells scores 0.1, from 100 cells 0.01, etc. For each grid cell the weights are added up for all species occuring in this cell. Hotspots of species richness were chosen by counting the numbers of species in each grid cell, subsequently ranking the cells by this count, and selecting the higher scoring cells.

Geographic distribution of species richness delineated several hotspot regions in the Palearctic, mostly located in mountainous areas (Fig. 3). The index of range-size rarity generally identified similar hotspot regions as that for species richness, although it de-emphasized the large central-Siberian hotspot.

We tested the hypothesis that databases restricted to a non-natural biogeographic region, such as "Europe", will identify a different set of hotspots, as compared with a spatial analysis of a more natural biogeographic region such as the Palearctic.

For that purpose only those taxa from the dataset were selected that occur in the geographic region delimited by the EBCC atlas and the Climatic Atlas of European Breeding Birds, in total 516 taxa.

Our results revealed that European hotspots of species richness were slightly more prominent in the Palearctic dataset as compared with the European dataset of 516 taxa. The index of range-size rarity indicated a more pronounced difference between the hotspots identified by the Palearctic dataset and the European dataset, with little or no differentiation in the latter. Results of our qualitative analysis suggest that it is important for hotspot and conservation studies to examine a natural biogeographic region and not a geopolitical entity such as "Europe".

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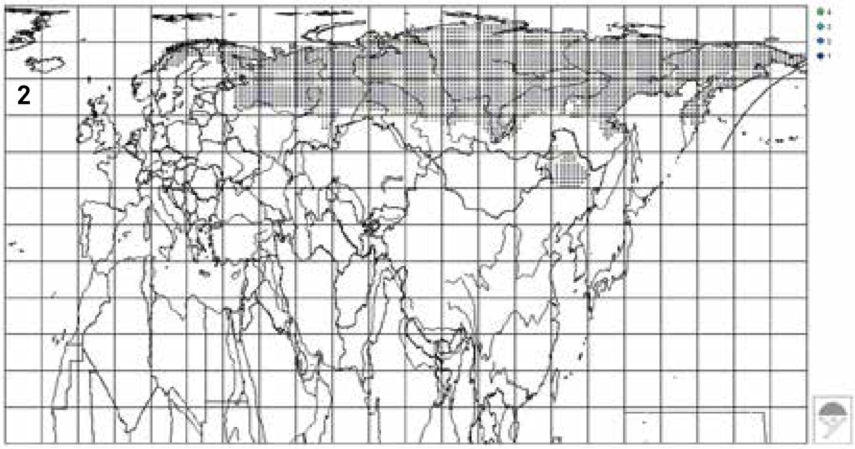

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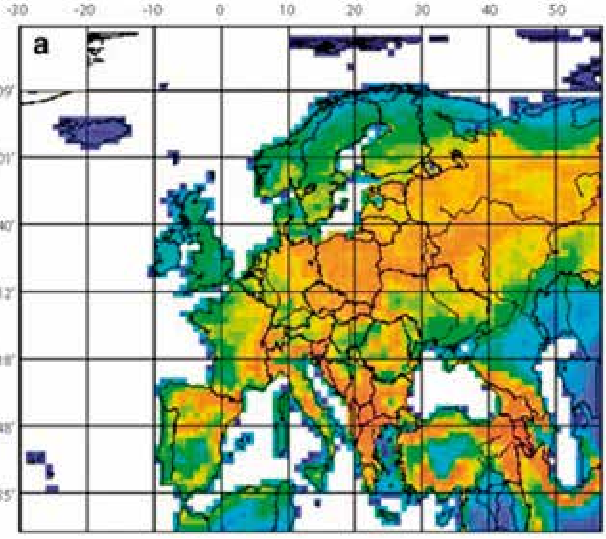

Fig. 1. Bird skin of the Bluethroat *Luscinia svecica svecia*.
Fig. 2. Distribution map of the Bluethroat *Luscinia svecica svecica*.
Fig. 3. Map of Species Richness among equal area grid cells in songbirds. Maximum richness shown in deep rufous and minimum in dark blue.

Published as

Sluys, R., M. Aliabadian & C.S. Roselaar 2011. European Hotspots as Evidenced by the Palearctic Distribution of Songbirds. In: Zachos, F.E. & J.S. Habel (eds), Biodiversity Hotspots – Distribution and Protection of Conservation Priority Areas, Springer, Heidelberg, Dordrecht: 165-173.

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New freshwater flatworms

From Iberian Peninsula and Greece

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Freshwater planarians are an ideal model group for historical biogeographic studies because they do not possess larval dispersal stages and do not tolerate salt water and thus need contiguous freshwater bodies to survive and disperse. Few studies have examined the diversity of freshwater planarians or flatworms in the Iberian Peninsula and Greece. We have searched extensively in the field for specimens, mainly in the Iberian Peninsula, and have reviewed the taxonomy and biogeography of the species. In total we collected 13 species, concerning 5 genera.We describe two new species of *Dendrocoelum* and six new species of *Phagocata* (Fig. 1). Further, we review the status of five other species and present distribution maps that summarize records of freshwater planarians in the Iberian Peninsula. Based on our findings we were able to recognize and describe three ecological groups of freshwater planarians in this area: (1) hypogean and ground water species, (2) spring- and cold stream dwelling species, (3) warm water species. We show that a rich, stream-dwelling freshwater planarian fauna is present, contrary to the findings of earlier studies. On the other hand, our findings do support the traditional viewpoint that European lake-dwelling species are scarce in Spain. The distribution pattern of the species *Girardia tigrina* is also discussed. This species is introduced in several European countries, including Spain. We conclude that the endangered status of *Schmidtea mediterranea* in this area is partly due to habitat alteration through human interference.

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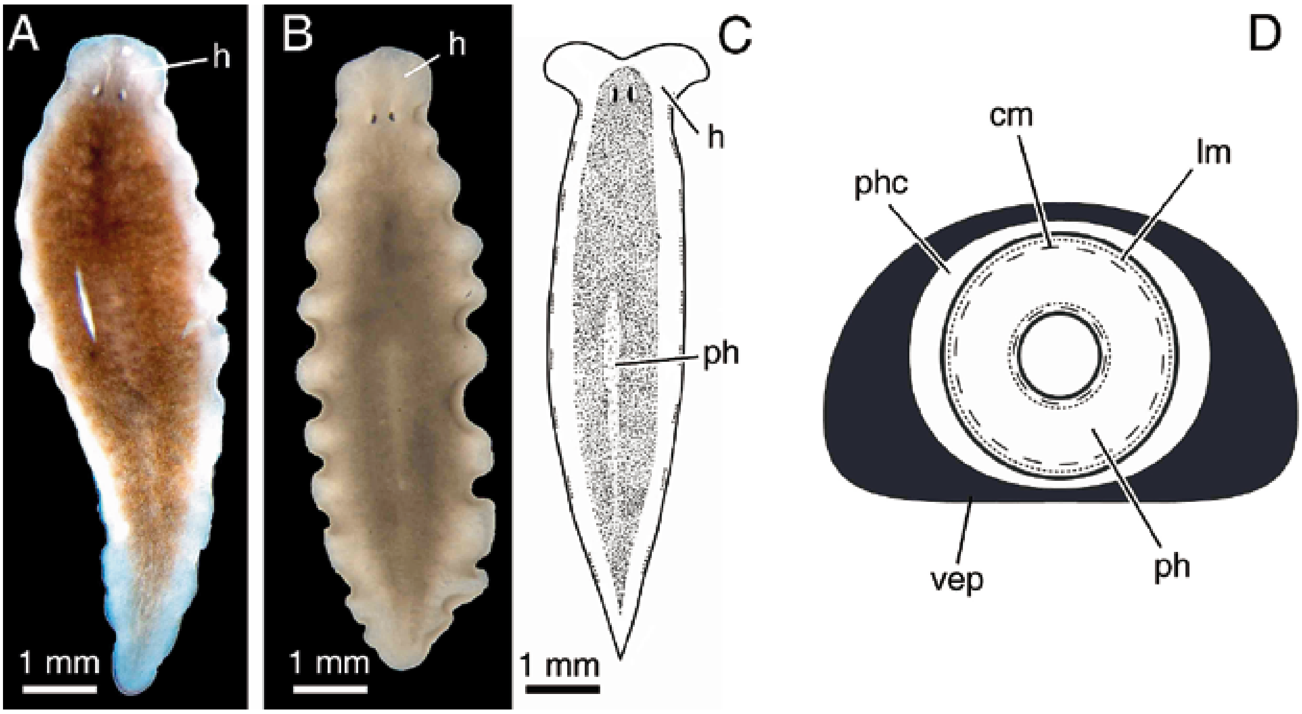


Fig. 1. The new species *Phagocata flamenca*.

Barcoding
Beetle diversity

Oscar Vorst & Camiel Doorenweerd

Naturalis Biodiversity Center, Leiden

There are over 350,000 described species of beetles (Coleoptera) worldwide. It is estimated that the number of species awaiting discovery is even several times larger. Even a small and relatively species-poor country as the Netherlands harbours over 4,100 indigenous species and many accidentally introduced. Although the Dutch beetle fauna has been intensively studied for over 150 years (Fig. 1), new species are still being discovered.

Their sheer number in combination with so many undescribed species makes reliable beetle identification a highly specialized task. Only taxonomists with knowledge of the extensive literature, access to reference collections, and years of experience are able to do so. Unfortunately it is becoming increasingly difficult to get a reliable identification as the number of professional taxonomists is worldwide in decline, and the Netherlands is no exception to this trend. Herein lies a threat to the quality of biological studies, as proper identification is an essential first step for any kind of biological study, be it evolutionary, taxonomically, ecologically or behaviourly.

DNA-based identification could in many cases offer an alternative to the classical morphology-based species identification. This so-called DNA barcoding technique involves the isolation of a small standardized DNA fragment of which the nucleotide sequence is then determined. Comparison of the base pair sequence, composed of the four nucleotides A, G, C & T, to known barcodes would then enable species recognition, similar to the way a supermarket scanner uses the black stripes of the printed barcode to recognize your purchases.

Prerequisite is the use of a single, standardized DNA fragment by all taxonomists worldwide, that is both variable enough to discern between species and well conserved within species. Another requirement is the availability of barcodes of as many species as possible for comparison.

Naturalis contributes in the International Barcode of Life (iBOL) initiative that aims to bring together barcodes of as many species as possible (Fig. 2). A fragment of cytochrome c oxidase I (COI), a mitochondrial gene, proved to be highly effective in identifying beetles and many other animal groups, and therefore was chosen as the barcode region. The resulting barcodes are stored in the Barcode of Life Database (BOLD; www.boldsystems.org), a public database that facilitates a simple web-based identification engine. Entering the barcode from an unknown organism will suffice to reveal its name.

At Naturalis a dedicated DNA lab was equipped to generate barcodes of 27,000 organisms within 4 year, focussing on the flora and fauna of the Netherlands (Fig. 3). Many of the Dutch taxonomic experts, either employed by Naturalis or from the Naturalis network, support the project by collecting and identifying specimens (Figs 4, 5, 6). This, in combination with the storage of voucher specimens in the Naturalis collection ensures the quality and verifiability of the barcodes generated. In the lab a tiny amount of tissue, for beetles and other insects commonly a single leg, of each specimen is taken for DNA extraction. The DNA extract is used to determine the organism's barcode, after which the remainder is stored for future research. High quality photographs are taken from all vouchers and uploaded to the public barcode database together with the barcode, species' identity and collecting data.

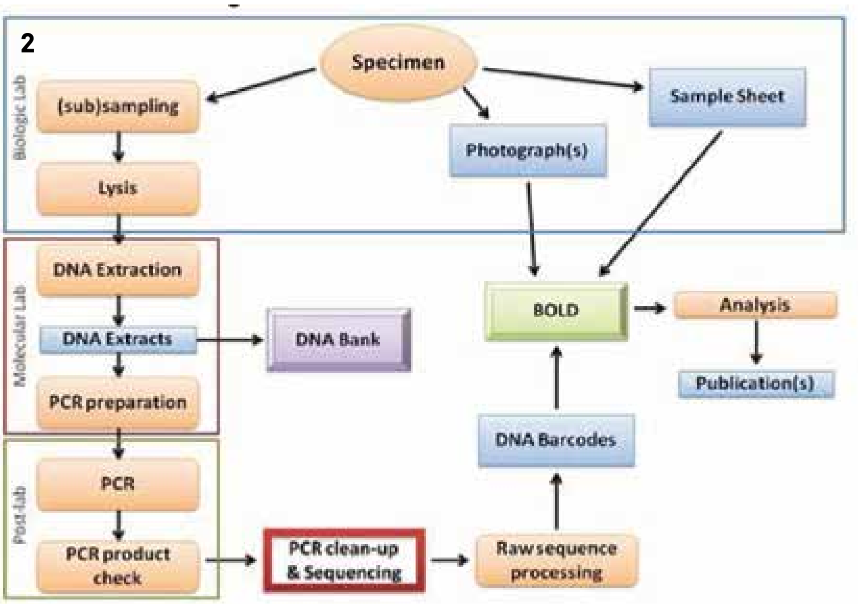
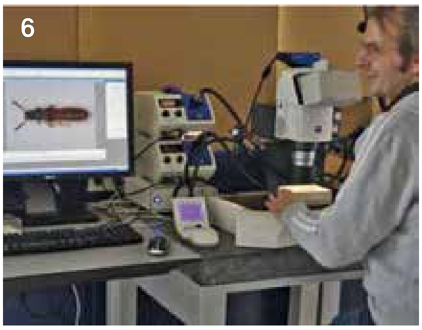


Fig. 1. Samuel Constant Snellen van Vollenhoven (1816-1880) conservator at the Rijksmuseum van Natuurlijke Historie (one of the forerunners of NCB) was the first to seriously study Dutch beetles.
Fig. 2. DNA barcoding workflow.
Fig. 3. The NCB barcoding team (LtRTtB): Oscar Vorst, Aline Nieman, Berry van der Hoorn, Kevin Beentjes, Els Baalbergen, Frank Stokvis and Camiel Doorenweerd
Fig. 4. Coleopterists afield, collecting beetles from wrack.
Fig. 5. *Heterocerus flexuosus*, an average sized Dutch beetle.
Fig. 6. Happy researcher at the NCB DNA lab.



As many specimens are newly collected – fresh material being the easiest way to ensure high quality DNA extracts – the project also updates the Naturalis collection with a large amount of well-identified material. We expect that taxonomists will find extra support for the recognition and description of new species in the barcodes database.

DNA barcoding will change taxonomy by enabling access to simple and reliable species identification to many. No longer is this the exclusive realm of taxonomic specialists. The implementation will not only be of benefit to other biologists, through the efficient identification of intact specimens, fragments, traces or even complex samples (soil, water, pancakes), it also will be of use in other fields of our society: e.g. in forensics, (agricultural) pest management, biomonitoring of species, as well as fighting trade in endangered species. Hopefully it will also highlight the role of taxonomy in our society and lead to the discovery of some fascinating new beetles.

Snail richness
A study across different scales

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Although the study of biodiversity has progressed greatly over the past 50 years, we are still a long way from a comprehensive understanding of the processes that determine species diversity in space. In fact, "What Determines Species Diversity" was considered one of 25 great unanswered questions which the journal *Science* highlighted on its 125th anniversary (Pennisi 2005).

Terrestrial gastropods as model group

Land snails are highly suited for testing several hypotheses about species diversity, especially when compared with a far more popular group, terrestrial arthropods, to whom they are second in species numbers within the animal kingdom. Like insects, they can be sampled exhaustively and in an unbiased fashion, not by trapping or fogging, but by collecting empty shells from the ground.

The much slower active dispersal of gastropods minimizes the problem of distinguishing between resident populations and migrants. The low vagility makes gastropods ideal indicator groups of environmental disturbances, as populations that were driven to local extinction by adverse environmental conditions are not immediately replaced. The slow recolonization, however, also increases the susceptibility of terrestrial gastropods to (regional) extinction from global change such as transformations in land use.

A slow exchange between locations can also cause a high beta-diversity and short-range endemism. This characteristic of the Gastropoda thus allows a larger range of relevant spatial scales and probably all relevant ecological and evolutionary processes to be encompassed with fewer efforts than in the case of arthropod studies.

In this study, we focus on calcareous outcrops. Calcareous outcrops are heterogeneously structured macrohabitats (Fig. 1). In addition, they fulfill one of the basic needs of snails, namely a high calcium availability.

Calcareous outcrops are remarkably rich in snail species (Nekola 1999). Species richness at calcareous structures even surpasses that of moisture-retaining structures such as coarse woody debris or historical mining pits of the same area (Kappes et al. 2012a). Besides, high gastropod densities on calcium-rich soils allow various statistical analyses, including species abundance distributions.

A multitude of spatial scales

The project is funded by the Netherlands Organisation for Scientific Research (NWO – ALW 821.01.002). Among its local cooperation partners are the Universiti Malaysia Sabah (UMS) and the Danau Girang Field Center. The latter organization kindly helped to gather a first data set from Batu Batangan, Borneo (Figure 2).

Sampling is performed in a spatially nested approach (Kappes et al. 2012b). For the nine smallest spatial scales (1 km² and below), we will select two mostly undisturbed limestone hills of approximately 1 km². Each will be divided into ten 0.1 km² sections, of which one will be further divided into ten 0.01 km² sections, and so on until the smallest spatial scale of 10 × 10 cm is reached (Figure 3).

For each hill, this gives us ten quadrats at each spatial scale (except for the 1 km² scale of the entire hill), giving a total of 162 quadrats. Throughout each quadrat (except perhaps the two smallest scales, where the quadrat size may be limiting), five liters of litter and top soil are randomly assembled and enriched by flotation.

However, limestones, or karst areas, can be found in different climatic conditions around the world. It thus appears promising to compare different climatic settings, evolutionary backgrounds, and

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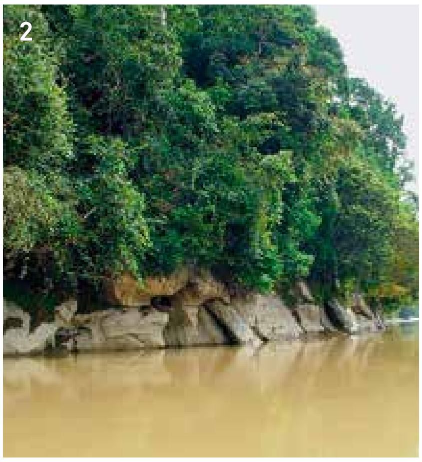

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Fig. 1. The Kakushöhle, an example of a temperate zone outcrop.
Fig. 2. The South-Eastern slope of Batu Batangan, facing the Kinabatangan River.
Fig. 3. An impression of the smallest scale, 10 × 10 cm, at Batu Batangan.
Fig. 4. Collection of living and dead snails from a sample of the Kakushöhle.

areas that differ in primary productivity. As a first step towards comparisons across biomes, the area around the Kakushöhle in the Eifel Hills of Northrhine-Westphalia was sampled in 2012 (Figure 4) using the same spatially nested sampling approach as developed for the outcrops in Sabah.

Theoretical and applied impact

The study described above will lay the foundations for building a model that incorporates the relative effects of niche differentiation, competition, dispersal, extinction, and speciation on the land snail communities at all relevant spatial scales. Such a model will not only be valuable for understanding biodiversity patterns in this study system (and act as a point of reference for similar studies in other systems) but will also allow direct application in conservation.
Karst forests world-wide and in Southeast Asia in particular, are under severe threat of destructive exploitation by quarrying for cement and disturbance by fire, logging, and cave-tourism. This is particularly worrying for taxa such as terrestrial Gastropoda that have high population densities on calcareous substrates, and for which limestone hills could form important targets for conservation of entire communities. However, conservation planning for karst systems so far is lacking sufficient information on the relevant spatial scales. Our study may help to elucidate if conserving a few large hills and sacrificing other smaller ones, or exploiting many hills, but only to a small portion, is the better option to conserve the biodiversity of gastropods, and possibly also of other mainly soil-associated forest organisms.

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Kinabalu-Crocker Range
Naturalis – Sabah Parks expedition

Leontine E. Becking, Vincent S.F.T. Merckx, Constantijn B. Mennes & Menno Schilthuizen

Naturalis Biodiversity Center, Leiden

From 10-25 September 2012 an international team of 50 scientists participated in the Kinabalu/Crocker Range Expedition to Sabah in Malaysia. This expedition was jointly organised by Naturalis Biodiversity Center and Sabah Parks (Fig. 1).

Malaysia is among the world's high-biodiversity countries, with much of this diversity found in pristine rainforests. In Borneo, the state of Sabah is home to some of the most spectacular montane forests. Prime among these are the Crocker Range Park and Kinabalu Park (both managed by Sabah Parks).Together they form a chain of forested peaks of over 2000 m altitude, crowned by Mount Kinabalu (4095 m), the tallest mountain between New Guinea and the Himalayas (Fig. 2). The flora and fauna of Kinabalu is fascinating. The mountain is – geologically speaking – young (only 1.5 million years), but its biological wealth is unique: thousands of species occur only there and nowhere else on earth. This type of spatially restricted species are referred to as endemics. The origins of these endemic species on Mount Kinabalu remain a mystery. They are either young: evolved from lowland ancestors by adaptation to the high elevation habitat, or old: relicts of a time when Borneo was much cooler. The aim of the Kinabalu - Crocker Range Expedition is to provide answers to the question whether the mountain is a biodiversity hotbed or rather evolution's storehouse.

From tropical heat to freezing cold

Zoologists, mycologists and botanists from Naturalis, Sabah Parks, Sabah Forest Research Centre, Wageningen University, University Malaysia Sabah, Royal Belgian Institute of Natural Sciences, and Natuurmuseum Fryslân joined their efforts to collect and identify specimens from sea-level to the summit of Mount Kinabalu and the Crocker Range mountains (Fig. 3). They stayed in eight stations in Kinabalu Park and the Crocker Range Park varying in comfort levels from fully furnished rooms to outdoor camping.

Each specialist had a different method of collecting in the forest, depending on the species they were hoping to catch. Plants and mushrooms were sampled and photographed during long day-hikes. At various elevations soil samples were taken to analyse the below-ground diversity. Some researchers needed to be near streams to find waterbugs, stalk-eyed flies, and water mites, while other had to take extended camping trips off the beaten path to find hidden populations of pitcher plants. During their activities many researchers involuntarily sampled leeches as well, thereby donating proteins to the jungle ecosystem.

After a long day of work everybody came together again at dinner sharing stories about their experiences and encounters with strange creatures. Though for some researchers their work only started after sunset. Armed with flashlights and healthy dose of enthusiasm they ventured into the dark to catch reptiles and amphibians. And while some participants set up light traps to attract moths and beetles expedition leader Menno Schilthuizen was placed in the spotlight to give live updates about the expedition for an intrigued crowd at Naturalis.

The intensive two-week expeditionresulted in plenty of highlights. The mycology team, for example, discovered a spectacular clump of glowing ('bioluminescent') mushrooms on a log near Inobong field station. The pitcher plant team bumped into an unknown population of the rare *Nepenthes rajah*, another botany team found several species of leafless plants that are new for the area.

DNA-barcoding

Almost 8000 samples were collected that represent over 1400 species of which at least 160 species are new to science. The fungi, spiders, watermites, and beetles had the highest number of undescribed species of all collected taxa. Now that all the exertion of collecting samples in the forest is over the equally hard though climatically easier part of the

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Fig. 1. Logo of Kinabalu / Crocker Range Expedition.
Fig. 2. Mount Kinabalu. Photo: M. Schilthuizen.
Fig. 3. Cloud-forest. Photo: C. Mennes.

research has commenced: the high-throughput DNA analysis lab at Naturalis will be used to obtain sequences for approximately 3,000 samples.
The only way to test whether the endemics are recent evolutionary offshoots from the species that live in the lowlands or relicts from times when Borneo was much cooler is by comparing evolutionary trees for a large number of plant, animal, and fungi species from Kinabalu and surrounding areas. 50 separate evolutionary trees will be constructed for taxa in which lowland species and closely related highland-endemics exist. By comparing DNA of the endemics to that of related, more widespread species, we can unravel the mystery of the mountain.

Mount Kinabalu provides a natural test case of evolution. All the different species that reside on the slopes of the mountain have very different life history strategies, but they all have experienced the same geological history. Each taxon represents an independent witness of the same shared history. If a similar evolutionary signal is observed within the different taxa, then a general answer can be inferred on the origin of the endemics. By the end of 2013 a manuscript will be submitted on this research, authored by all participants who provided samples and data.

Collaboration

The expedition was truly a joint effort between Naturalis and Sabah Parks. Both parties clearly benefitted from this collaboration and the collaboration will continue:in 2013 Sabah Parks scientists will visit Naturalis to obtain in-house training in DNA-technology and evolutionary analysis.

Media

The public interest in the expedition was high as illustrated by the great amount of media exposure that the expedition received.20 (inter)national newspapers and journals reported on the expedition, including NRC Handelsblad, Vrij Nederland, National Geographic Nederland and Science. There were furthermore 11 interviews on the radio and one interview on television on EenVandaag, and additional media exposure on international websites such as CNN and NBC. During the expedition active blogs were maintained on the websites of the Dutch National Geographic, Scientific American, Wetenschap24, and Naturalis.

Conservation

Mount Kinabalu houses an astonishing wealth of unique species. Endemics are generally of high importance for conservation as they are particularly vulnerable to extinction. The results from the expedition will provide important information to the conservation agencies that are active in Borneo: finally they will know how evolution shaped the endemic fauna and flora that lives within the boundaries of the Heart of Borneo and how future changes in climate and environment may affect this treasure of biodiversity. Or to quote the American scientist Carl Sagan: “You have to know the past to understand the present.”

Molecular taxonomy
and natural history collections

Dick S.J. Groenenberg

Naturalis Biodiversity Center, Leiden

Natural history collections started out as eclectic assemblages of curious objects ('rariteitenkabinetten'). With the increased acceptance of Linnaeus' Systema Naturae these collections got more and more ordered into natural groups. Traditionally, these groups were separated based on habitus and anatomical affinities, but nowadays groups are designed to reflect their historical origins. Using a wide diversity of animal taxa, this thesis (Fig. 1) illustrates how molecular data can elucidate genealogical and taxonomic questions.

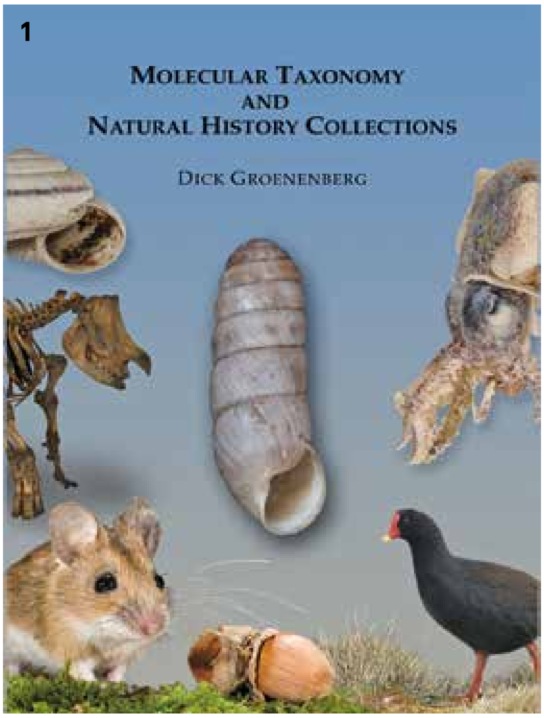
Most of the time, a clear congruence exists between morphologically and genetically recognized groups. In some cases, here demonstrated for a group of bobtail squids (Groenenberg 2012) more groups are distinguished based on DNA sequence data than on morphology. This is typically observed when undescribed (and possibly cryptic) species are involved. The opposite situation, where morphological differences do not reflect a difference in genealogy can also be true, as demonstrated for a group of mussels (Groenenberg 2012). One of the pitfalls of using DNA sequence data for addressing taxonomic issues is the trustworthiness of reference sequences. Generally, people use public databases such as GenBank for Blast searches (to identify their own sequences) or to obtain sequences of related taxa (to be used with phylogenetic analyses, for instance). Unfortunately, the vouchers for sequences in GenBank are not always identified correctly. In 2004, Steinke *et al*. published a controversial paper on the Western Palearctic Helicidae (a family of terrestrial snails) for which clear errors in GenBank are shown (Fig.2). Our analyses also showed mistakes (or contamination) in that study which must have occurred in the lab (contamination) or with the submission of the sequences to GenBank.

We introduce the term 'pseudo-voucher' for (part of) a specimen that differs from the specimen that was actually used for DNA analysis (Groenenberg 2012).

Occasionally, DNA sequencing of type-specimens can facilitate in settling ong-standing taxonomic disputes. The flightless moorhens of Tristan da Cunha (TdC, an island on the Mid-Atlantic Ridge between Africa and South-America) are an example of such a dispute. These moorhens (*Gallinula nesiotis*) were described by Sclater in 1861, but after a strong decline in the decades thereupon they were considered extinct by the end of the 19th century. In 1972, flightless moorhens were rediscovered on a remote part of TdC. Although some believed these to be survivors of the original population, others thought these were the descendants of an extremely similar moorhen (*Gallinula comeri*) from the nearby (ca. 400 km) island of Gough. Based on this similarity and the unlikeliness that the moorhens of both islands would have lost the ability of flight independently without differentiating in other characters, Eber (1961) considered *G. comeri* a junior synonym of *G. nesiotis* and controversy surrounded future illustrations of both taxa (Fig.3).

Our analyses (Groenenberg 2012) show that *G. nesiotis* and *G. comeri* are different taxa, that *G. nesiotis* indeed became extinct and that *G. comeri* now inhabits both TdC and Gough. Morphological characters can be indeterminate or unavailable if the used specimens are juvenile or if the objects are poorly preserved. In those instances, DNA sequences can be a useful tool for identification purposes (demonstrated for a fieldmouse and a rhinoceros; Groenenberg 2012). The drawback of the hitherto mentioned applications is that all required a substantial amount of polymerase chain reaction (PCR) product as input for Sanger sequencing. With the advancement of DNA sequencing technologies (such as the NGS platforms) it became possible to sequence complete genomes without PCR. The last chapter of this thesis shows how a mitogenome was sequenced without PCR from a collection specimen that had been in 70% ethanol for 8 years (Groenenberg 2012). This illustrates that NGS can be elementary in unlocking thus far inaccessible data from natural history collections and future, molecular phylogenetic studies.

1



MOLECULAR TAXONOMY
AND
NATURAL HISTORY COLLECTIONS

DICK GROENENBERG

2

3

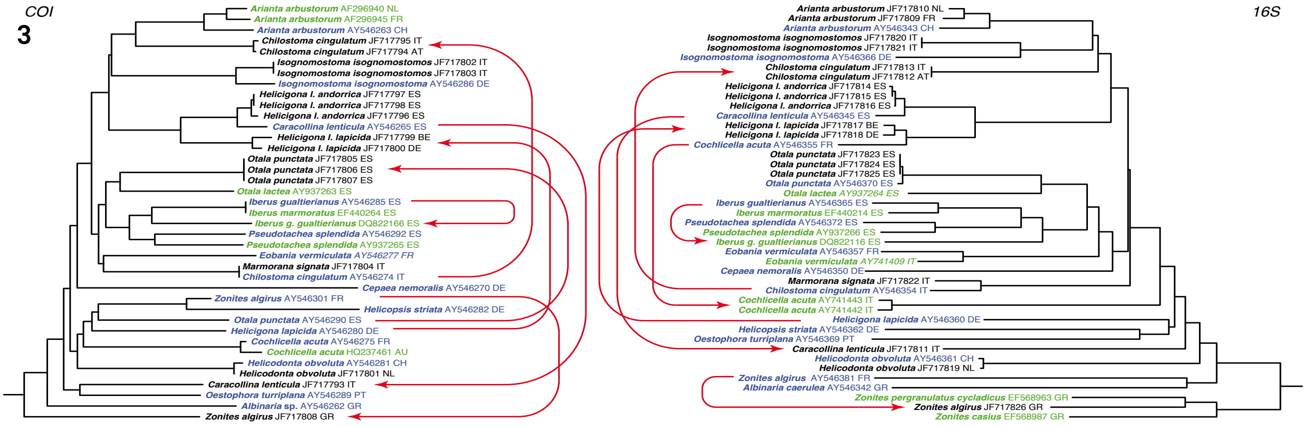


Fig. 1. Thesis cover – front view.

Fig. 2. A comparison of COI (left) and 16S (right) NJ phylogenies with a focus on the Helicidae s.s. In blue are sequences from Steinke *et al.* (2004), in green sequences from various studies (GenBank) and in black sequences from this study. The red arrow indicates erroneous or misidentified sequences and the correct sequences for the corresponding most closely related taxa in this figure.

Fig. 3. Illustrative stamps, issued in 1987 and 2005. (A) 2005: Text and illustrations belong together and are correct. (B) 1987: In Gough *G. comeri* occurs, not *G. nesiotis*; both names should not be synonymized. (C) 2005: The text correctly indicates G. nesiotis as from Tristan, but the bird itself most probably belongs to *G. comeri*, introduced from Gough, since *G. nesiotis* is now extinct on Tristan and not available to be pictured anymore.

Reference

Groenenberg, D.S.J. 2012. Molecular taxonomy and natural history collections. PhD thesis, Leiden University.

New taxa

Taxonomic studies of our team of researchers and honorary staff members over the years 2009-2012 has resulted in the description of over 240 new taxa, including species, genera and even a family. Here we present a representative selection of those new taxa, including those that have been selected in the Top 10 which is composed on a yearly basis by the International Institute for Species Exploration (IISE).

1. ***Opisthostoma vermiculum*** Clements *et al.*, 2008
   Clements, R., T.-S. Liew, J.J. Vermeulen & M. Schilthuizen, 2008. Further twists in gastropod shell evolution. *Biology Letters* 4: 179-182.

Top 10-2009 (http://species.asu.edu/Top10)
Photo: Reuben Clements.

2. ***Bulbophyllum nocturnum*** Schuiteman *et al*.
   Schuiteman, A., J.J. Vermeulen, E. De Vogel, & A. Vogel, 2011. Nocturne for an unknown pollinator: first description of a night-flowering orchid (*Bulbophyllum nocturnum*). *Botanical Journal of the Linnean Society* 167: 344-350.

Top 10-2012 (http://species.asu.edu/Top10)
Photo: A. Schuiteman.

3. **Kollasmosoma sentum** Gomez Duran & Van Achterberg, 2011
   Gómez Durán, J-M. & C. van Achterberg, 2011. Oviposition behaviour of four ant parasitoids (Hymenoptera, Braconidae, Euphorinae, Neoneurini and Ichneumonidae, Hybrizontinae), with the description of three new European species. *ZooKeys* 125: 59106.

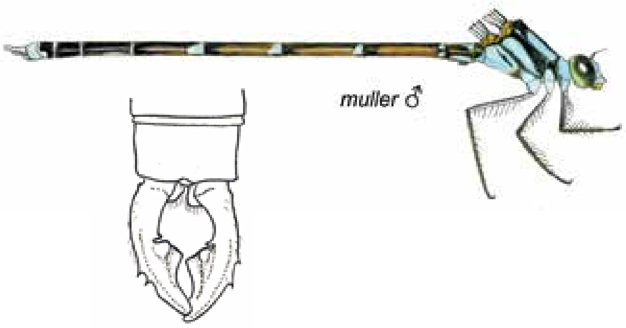
Top 10-2012 (http://species.asu.edu/Top10)
Photo: Naturalis Biodiversity Center.

4. **Antispila oinophylla** Van Nieukerken *et al*., 2012
   van Nieukerken, E., D. Wagner, M. Baldessari, L. Mazzon, G. Angeli, V. Girolami, C. Duso & C. Doorenweerd, 2012. *Antispila oinophylla* new species (Lepidoptera, Heliozelidae), a new North American grapevine leafminer invading Italian vineyards: taxonomy, DNA barcodes and life cycle. *ZooKeys* 170: 29.

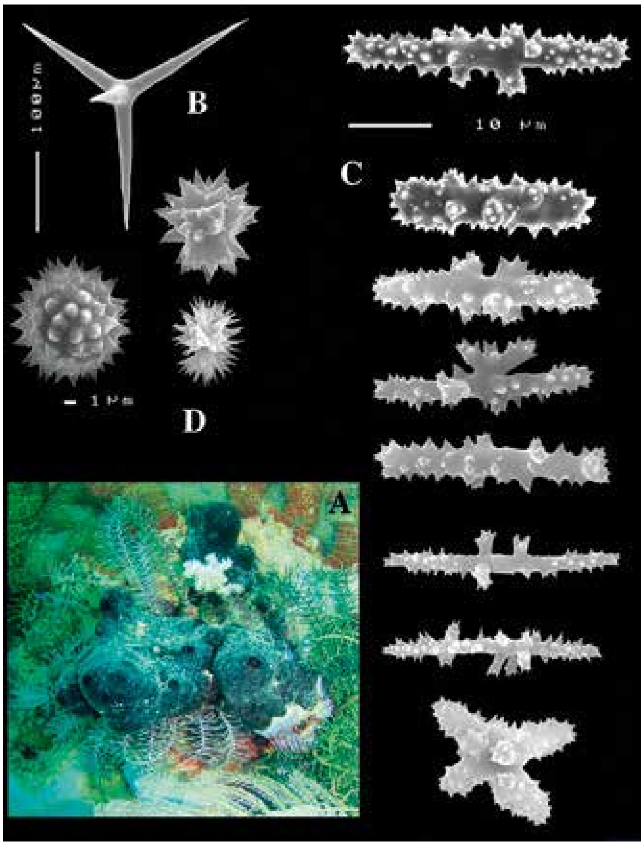
Photo: Naturalis Biodiversity Center.

5. **Argiolestes muller** Kalkman, Richard & Polhemus, 2010
   Kalkman, V.J., S.J. Richards & D.A. Polhemus 2010. Three new species of *Argiolestes*, with a key to the males of *Argiolestes* s. str. (Odonata: Megapodagrionidae). *International Journal of Odonatology* 13: 75-88.

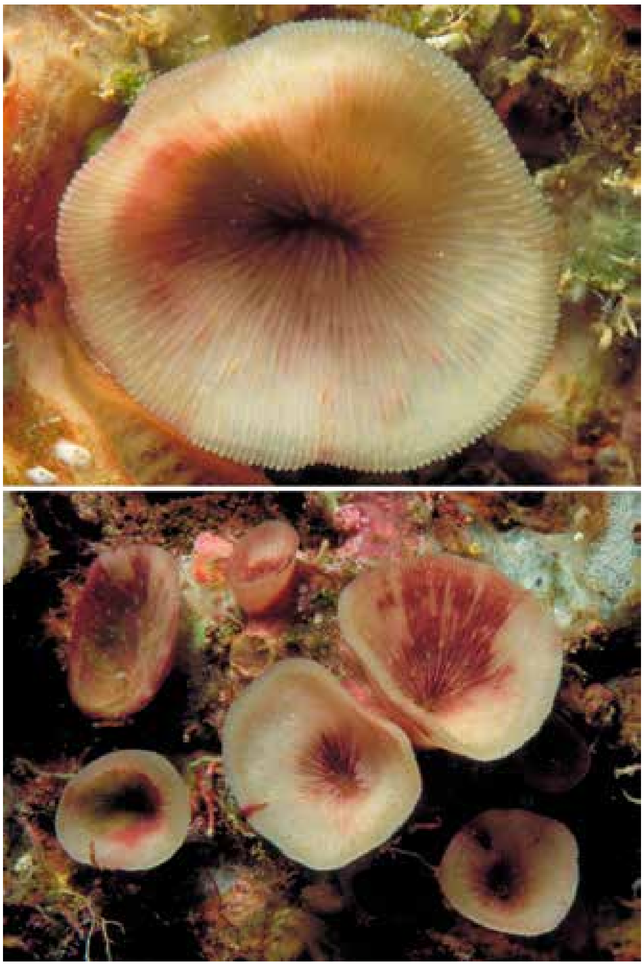
Drawing: A.G. Orr. / Photo: S.J. Richards.



6. ***Dercitus* (Halinastra) *berau*** Van Soest, Beglinger & De Voogd, 2010
Van Soest, R.W.M., Beglinger, E.J., De Voogd, N.J. 2010. Skeletons in confusion: a review of astrophorid sponges with (dicho-)calthrops as structural megascleres (Porifera, Demospongiae, Astrophorida). *Zookeys* 68: 1-88.
Holotype RMNH 4256, A, Habitus in situ, Berau region, Kalimantan, Indonesia; B-D, calthrops.
Photos: N.J. De Voogd.



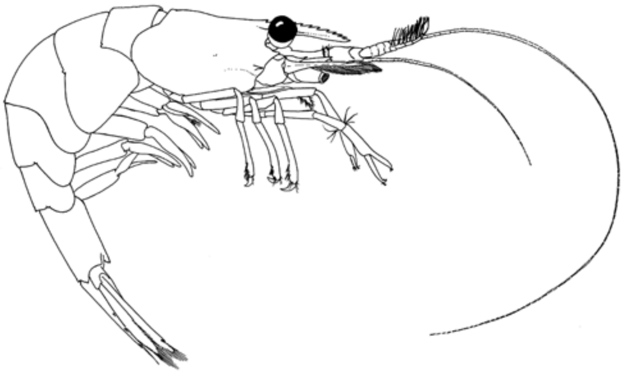
7. ***Leptoseris troglodyta*** Hoeksema, 2012
Hoeksema, B.W., 2012. Forever in the dark: the cave-dwelling azooxanthellate reef coral *Leptoseris troglodyta* sp. n. (Scleractinia, Agariciidae). *ZooKeys* 228: 21.
Photo: B.W. Hoeksema.



8. ***Eunephthya ericius*** McFadden & van Ofwegen, 2012
   McFadden, C.S. & L.P. van Ofwegen, 2012. A revision of the soft coral genus, *Eunephthya* Verrill, 1869 (Anthozoa: Octocorallia: Nephtheidae), with a description of four new species from South Africa. *Zootaxa* 3485: 1-25.

9. ***Neopontonides brucei*** Fransen & Almeida, 2009
   Fransen, C.H.J.M. & A.O. de Almeida, 2009. *Neopontonides brucei*, a new pontoniine shrimp species from Brazilian waters (Decapoda, Palaemonidae). *Crustaceana* 82: 837-846.

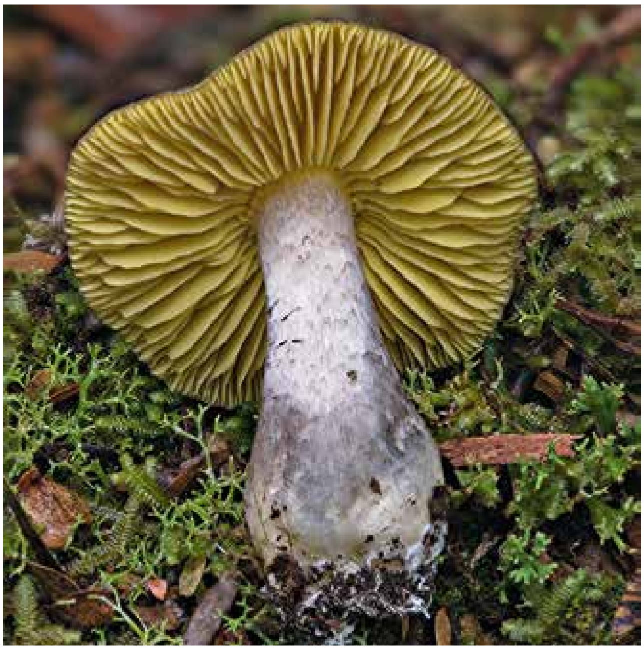
Drawing: C.H.J.M. Fransen.



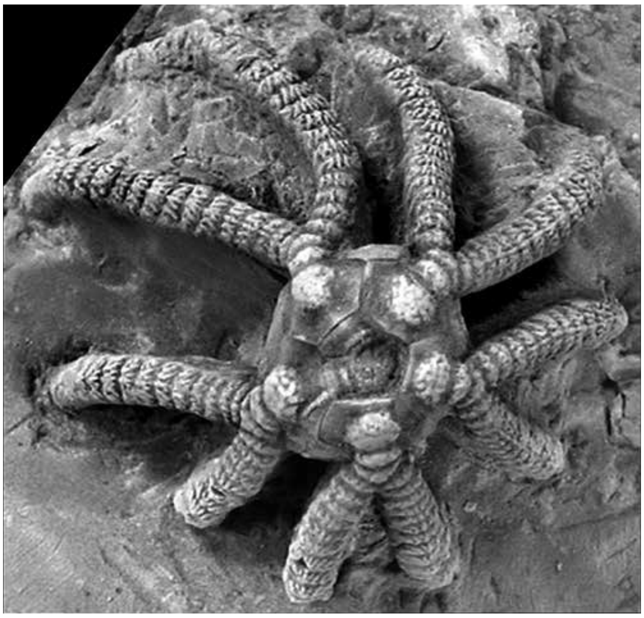
10. ***Amischotolype parvifructa*** Duistermaat
    Duistermaat, H. 2012. A taxonomic revision of *Amischotolype* (Commelinaceae) in Asia. *Gardens' Bulletin Singapore* 64: 51-131.

Drawing: A. Walsmit Sachs.

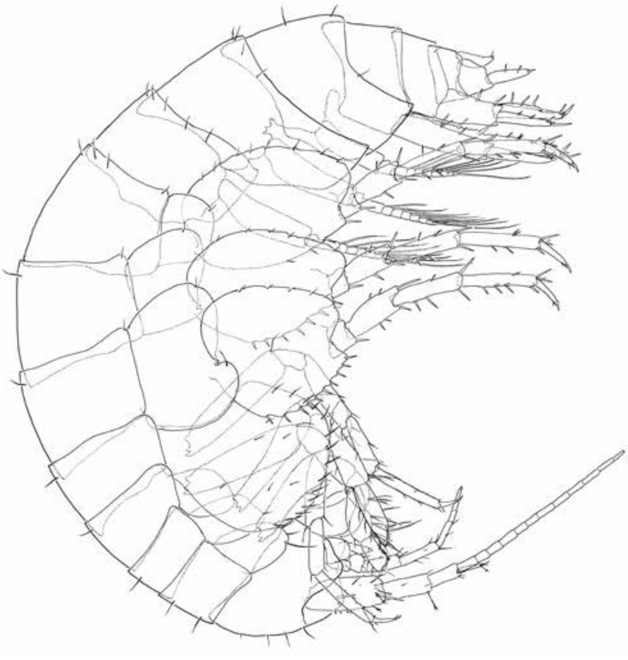
11. ***Entoloma mathinnae*** G.M. Gates, B.M. Horton & Noordel.
    Gates, G.M., B.M. Horton & M.E. Noordeloos, 2009. A new *Entoloma* (Basidiomycetes, Agaricales) from Tasmania. *Mycotaxon* 107: 175-179.
Photo: M. Pilkington.



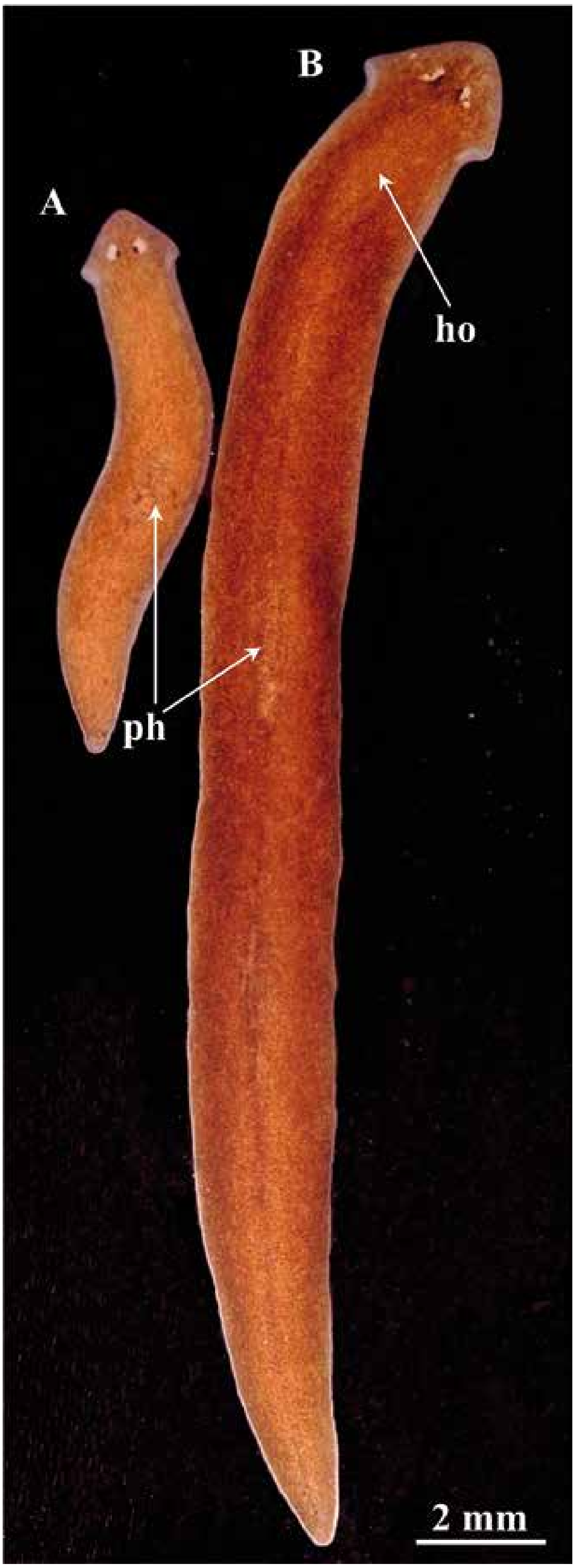
12. ***Cordylocrinus rugobrachialis*** (Ramsbottom MS) Donovan, Widdison, Lewis & Fearnhead, 2012
    Donovan, S.K., R.E. Widdison, D.N. Lewis & F.E. Fearnhead, 2012. The British Silurian Crinoidea. Part 3, Addendum to parts 1 and 2, Camerata and columnals, with Title-page, Contents and Index. Part 3. *Monograph of the Palaeontographical Society* London 166: 135-259, pls 37-62.



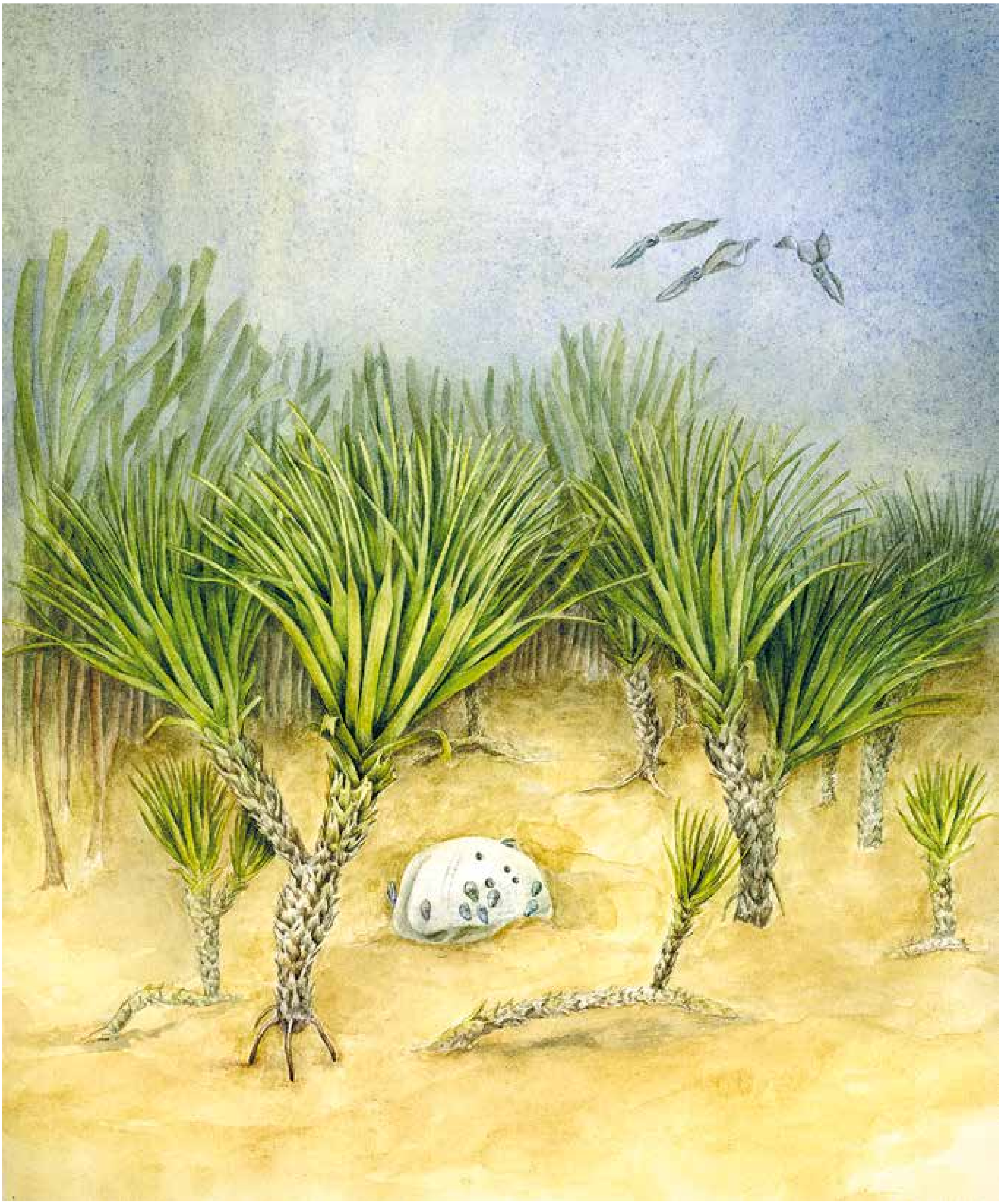
13. ***Metacrangonyx dhofarensis*** Jaume & Vonk, 2012
    Jaume, D. & Vonk, R. 2012. Discovery of *Metacrangonyx* in inland groundwaters of Oman (Amphipoda: Gammaridea: Metacrangonyctidae). *Zootaxa* 3335: 54-68.



14. ***Dugesia afromontana*** Stocchino & Sluys, 2012
Stocchino, G.A., Sluys, R., Manconi, R. 2012. A new species of *Dugesia* (Platyhelminthes, Tricladida, Dugesiidae) from the Afromontane forest in South Africa, with an overview of freshwater planarians from the African continent. *Zootaxa* 3551: 43-58.
Ph: pharynx; ho: hyperplasic ovaries.



15. ***Mosacaulis spinifer*** Van der Ham &
Van Konijnenburg-Van Cittert
Van der Ham, R.W.J.M., Van Konijnenburg-van Cittert, J.H.A., Kieft, B.N. & Walsmit Sachs, A. 2011. *Mosacaulis spinifer* gen. et sp. nov.: an enigmatic Maastrichtian plant. *Review of Palaeobotany and Palynology* 168: 51-67.
Watercolor: A. Walsmit Sachs.



Staff, projects, and Naturalis publications

Research staff

Sector management

Prof. dr. Erik F. Smets	Scientific director. Director Nationaal Herbarium Nederland. Chair of Systematic Botany, Leiden University
Dr. Jan van Tol	Associate director for Research and Education

Naturalis Department of Geology

Research staff

Dr. Leo M. Kriegsman	Head of department, petrology
Dr. Martin D. Brazeau	Devonian fishes (from 1 January 2011)
Dr. Stephen K. Donovan	Palaeozoic and Mesozoic invertebrates
Dr. Lars W. van den Hoek Ostende	Fossil microvertebrates
Prof. dr. Han (J.H.A.) van Konijnenburg-van Cittert	Palaeobotany, fossil Pteridophyta, fossil Gymnosperms
Dr. Hanneke J.M. Meijer	Postdoc (20 May-19 September 2009)
Dr. Willem Renema	Fossil Foraminifera
Dr. Kenneth F. Rijsdijk	Dodo research project (until 30 June 2011)
Dr. John de Vos	Fossil macrovertebrates / Dubois collection (until 1 November 2012)
Dr. Isabel M. van Waveren	Palaeobotany
Dr. Frank P. Wesselingh	Fossil mollusca
Dr. Hanco (J.C.) Zwaan	Mineralogy, Gemmology

PhD candidates

Drs. Menno Booi	Gymnosperms from the Early Permian of Jambi (Sumatra, Indonesia) and their implications for palaeoecology and palaeogeography. – Until 28 February 2009. Promotor J.H.A. van Konijnenburg-van Cittert. Daily supervisor I. van Waveren
Drs. Hylke Bosma	Late Cretaceous conifers from Western and Central Europe. – Private funding. Promotor J.H.A. van Konijnenburg-van Cittert
Dr. drs. Alexandra van der Geer	The evolution of Hoplitomeryx (Gargano, Italy, Late Miocene): the island rule applied. – 1 January–31 December 2012. Promotor J. Reumer. Daily supervisor J. de Vos
Pepijn Kamminga MSc	Ecomorphology in sharks. – From 8 November 2011. Promotor M. Richardson. Daily supervisor M. Brazeau
Anneke Madern MSc	The rise and fall of a Miocene hotspot: palaeobiogeography of the early Vallesian mammals of the Vallès-Penedès (Catalonia, Spain). – From 1 January 2012. Promotor P.C. van Welzen. Daily supervisor L. van den Hoek Ostende
Vibor Novak MSc	Larger benthic foraminiferal assemblages in Miocene mixed carbonate-siliciclastic systems of Indonesia. – EU-ITN grant. From 4 November 2010. Promotor L.J. Lourens. Daily supervisor W. Renema
Sonja Reich MSc	Miocene diversification of Indo-Pacific molluscan communities associated to seagrass meadows. – EU-ITN grant. From 1 July 2010. Promotor L.J. Lourens. Daily supervisor F.P. Wesselingh

Other

Marianne van Abbe MSc	Projectassistant (from 1 March 2012)
Esther M. Dondorp MSc	Project assistant (1 October 2010 - 31 July 2011)
Renate A. Holwerda MSc	Project assistant (July 2011)
Drs. Jacob Leloux	Project assistant (20 September - 19 December 2012)
Elisa Locatelli MSc	Project assistant (1 June - 1 July 2011)

Naturalis Department of Terrestrial Zoology

Research staff

Dr. Jan van Tol	Head of department ad interim, Odonata Phylogeny and biogeography of the Platystictidae (Odonata). – Promotor E. Gittenberger. Co-promotor J.P. Duffels. PhD defence 26 February 2009, Leiden University
Dr. ing. C. (Kees) van Achterberg	Hymenoptera
Dr. J.W. (Pim) Arntzen	Reptilia and Amphibia
Prof. dr. J.C. (Koos) Biesmeijer	Research fellow, pollination biology (from 18 October 2010)
Dr. Luisa Carvalheiro	Postdoc. EU-FP7 STEP project (from October 2010)
Dr. Heike Kappes	Postdoc. Determinants of species diversity at 14 spatial scales in tropical microsnails from endangered limestone habitats – NWO ALW Open programme. From 1 October 2011
Drs. Roy M.J.C. Kleukers	Head, Bureau EIS-Nederland
Drs. André J. van Loon	Data editor EIS-Nederland
Dr. Thibaut de Meulemeester	Postdoc. Automatic identification of bees. (from September 2012)
Dr. Jeremy A. Miller	Arachnida
Dr. Erik J. van Nieukerken	Lepidoptera
Prof. dr. Menno Schilthuizen	Coleoptera, Mollusca, Evolutionary biology
Dr. Freek Vonk	From 1 October 2012
Dr. A.J. (Ton) de Winter	Mollusca

PhD candidates

Jesus Aguirre Gutierrez MSc	Pollinator distribution across time and spatial scales in the Netherlands. – From 18 July 2011. Promotor J.C. Biesmeijer. Daily supervisor E.E. van Loon
Drs. Camiel Doorenweerd	Evolution and diversification of leafmining Lepidoptera and northern hardwood forest trees. – From 1 June 2012. Promotor S.B.J. Menken. Daily supervisor E.J. van Nieukerken
Vincent Kalkman	The impact of the Australian monsoon climate on the exchange of freshwater faunas between Australia and New Guinea as demonstrated by Megapodagrionidae (Odonata). – 9 months 2012-2013. Promotor P.C. van Welzen. Daily supervisor J. van Tol
Philippe Roger Kok	Islands in the sky: species diversity, evolutionary history and patterns of endemism of Pantepui herpetofauna. – Private funding. Promotors E. Gittenberger & E.F. Smets. Daily supervisor M.S. Hoogmoed
Thor Seng Liew MSc	Morphospace in tropical microgastropods driven by Red Queen evolution. – NWO ALW open programme. From 1 April 2010. Promotors M. Schilthuizen & P. Brakefield
Kim Meijer MSc	Evolutionaire veranderingen in de biodiversiteit van Nederlandse insecten in respons op invasieve planten en insecten. – Uyttenboogaart-Eliasen Stichting / Rijksuniversiteit Groningen / Naturalis. 2008-2012. Promotors M. Schilthuizen & L.W. Beukeboom
Dr. Menno Reemer	Unravelling a hotchpotch. Phylogeny and classification if the Microdontinae (Diptera: Syrphidae). – 2011/2012. Promotor E. Gittenberger. Co-promotor G. Stahls. PhD defence 13 March 2012, Leiden University
Dr. Ben Wielstra	Tracing Triturus through time. Phylogeography and spatial ecology. – 2009-2012. Promotor A.K. Skidmore. Co-promotors J.W. Arntzen & A.G. Toxopeus. PhD defence 3 October 2012, University of Twente

Other

Dr. Dirk Gassmann	Project assistant (1 September – 12 October 2009)
Drs. Rik Rievers	Project assistant (various contracts)

Naturalis Department of Marine Zoology

Research staff

Dr. Bert W. Hoeksema	Head of department, stony corals
Dr. Charles H.J.M. Fransen	Shrimps
Dr. Dick S.J. Groenenberg	Molecular biology Molecular taxonomy and natural history collections. – Promotor E. Gittenberger. Co-promotor M. Schilthuizen. PhD defence 12 December 2012, Leiden University
Dr. Leen P. van Ofwegen	Soft corals
Dr. Martien J.P. van Oijen	Fish
Dr. Katja T.C.A. Peijnenburg	Research fellow Marine zoology (since 1 January 2012)
Dr. Nicole J. de Voogd	Sponges

PhD candidates

Dr. Lisa E. Becking	Marine lakes of Indonesia. – NWO ALW grant, until 30 September 2011. Promotor E. Gittenberger. Co-promotor N.J. de Voogd. PhD defence 4 December 2012, Leiden University
Alice K. Burridge MSc	Evolution in marine planktonic gastropods. – Naturalis and University of Amsterdam. From 1 September 2012. Promotor S.B.J. Menken & J. Huisman. Daily supervisor K.T.C.A. Peijnenburg
Drs. Sancia E.T. van der Meij	The evolutionary history of parasitic coral gall crabs and their coral hosts. – From 1 January 2012. Promotor E. Gittenberger. Daily supervisors B.W. Hoeksema and C.H.J.M. Fransen
Drs. Bastian T. Reijnen	Evolution of parasite-host interactions in the sea. – From 1 January 2012. Promotor E. Gittenberger. Daily supervisors L.P. van Ofwegen and B.W. Hoeksema
Zarinah Waheed MSc	The position of Malaysia in the world's centre of maximum marine biodiversity: Exploring the boundaries of the Coral Triangle. – From 1 July 2010. Promotor E. Gittenberger. Daily supervisor B.W. Hoeksema

Zoological Museum of the University of Amsterdam

Research staff

Drs. Tom Hakbijl	Archaeo-entomology and economic entomology
Dr. Herman de Jong	Diptera
Dr. Ronald Sluys	Platyhelminthes (IBED)
Dr. Rob W.M. van Soest	Sponges, until 1 May 2011
Dr. Sandrine A. Ulenberg	Hymenoptera
Dr. Ronald Vonk	Fish, Crustacea

Nationaal Herbarium Nederland, Leiden Branch

Director

Prof. dr. Erik F. Smets	Director Nationaal Herbarium Nederland, chair of Systematic Botany, Leiden University

Research staff

Dr. Marco C. Roos	Group leader PITA, Flora Malesiana, Coordinator of academic teaching
Dr. Machiel E. Noordeloos	Group leader PCNE, fungi (0.5 fte, until 31 July 2011)
Dr. Tinde R. van Andel	Plant use of the motherland. Linking West African and Afro-Caribbean ethnobotany. – NWO VIDI. From 1 February 2010
Ir. Edu Boer	Various projects for Voedsel- en Warenautoriteit. – 0.5 fte, 1 February 2010 – 31 March 2010; 0.8 fte, 1 April 2010 – 30 September 2010; 0.6 fte, 1 October 2010 – 31 October 2011; 0.5 fte, 1 November 2011 – 31 December 2011; 0.44 fte, from 1 March 2012
Dr. Hugo de Boer	DNA barcoding of Tanzanian world-harvested medicinal plants to identify and monitor trade and commercialization. – Postdoctoral position, NWO-WOTRO and TASENE, from 1 September 2012

Dr. Stefano G.A. Draisma	Algae (until 30 November 2009)
Dr. Leni Duistermaat	Flora of the Netherlands, including some projects
Dr. Barbara Gravendeel	Orchidaceae, molecular biology
Dr. Raymond W.J.M. van der Ham	Palynology, fossil plants
Dr. Jozsef Geml	Fungi. – Kits van Waveren Fund, 1 August 2009 – 31 July 2011. Tenure track from 1 August 2011
Dr. Peter H. Hovenkamp	Pteridophyta (0.7 fte); project funding 1 February 2011 – 31 July 2011, 0.3 fte; 1 July 2012 – 31 December 2012, 0.2 fte
Dr. Paul J.A. Keßler	Vascular plants SE Asia (0.2 fte). Until 28 February 2012
Dr. Frederic P. Lens	Wood anatomy (from 1 November 2010)
Dr. Vincent S.F.T. Merckx	Mycoheterotrophic plants (1 March 2011 until 31 March 2012); Does specialization lead to rarity? The distribution of mycoheterotrophic plants in relation to their mycorrhizal fungi. – NWO VENI, from 1 April 2012
Dr. Michael Stech	Bryophyta
Dr. Hans ter Steege	Diversity of Amazonia (from 1 January 2012)
Dr. D. Thomas	Flora Malesiana, Annonaceae (from 1 September 2012)
Dr. T. van der Niet	Evolution of pollinator-plant interaction (from 1 May 2012)
Dr. Jaap J. Vermeulen	Orchidaceae (until 31 December 2010)

Extra-ordinary professors

Prof. J.H.A. van Konijnenburg-van Cittert	Pre-Quarternary Palaeobotany, Leiden University
Prof. D.J. Mabberley	Systematic Plant Anatomy, Leiden University
Prof. L.J. Slikkerveer	Ethnobotanical Knowledge Systems, Leiden University
Prof. dr. P.C. van Welzen	Tropical Plant Biogeography, Leiden University, on behalf of Treub Foundation

Other

Dr. Silvia Mota de Oliveira	Flora of the Guianas (editor), Alberta Mennega Stichting (from 14 March 2011)
Dr. Niels Raes	Plant diversity assessment of Malesia deduced from collection databases. – Promotor P. Baas. Co-promotors M.C. Roos & H. ter Steege. PhD defence 11 February 2009, Leiden University Back to the future? Biodiversity gradients revisited (Postdoc), NWO ALW-Open programme. From 1 May 2010
Dr. Herre Stegenga	Algae of the Netherlands, GiMaris (0.2 fte, 1 March 2010 – 31 May 2010, 1 January 2011 – 30 June 2011)

PhD candidates

Dr. Nanet P. Ambaretnani	Iber Kesehatan in Tatar Sunda, Indonesia: Utilisation of Traditional and Modern Health Information and Communication Systems in Sukamiskin, Bandung. – Promotor L.J. Slikkerveer. PhD defence 1 February 2012, Leiden University
Dr. Johann Angerler	Bius, parbaringen und paniaran : über Demokratie und Religion bei den Tobabatak Nordsumatras. – Promotor L.J. Slikkerveer. PhD defence 18 June 2009, Leiden University
Dr. Marc S. Appelhans	Phylogeny and biogeography of Spathelioideae (Rutaceae). – Until 31 January 2012. Promotor E.F. Smets. Co-promotor P.J.A. Keßler (joint Hortus botanicus & NHN project). PhD defence 15 November 2011, Leiden University
Mega Atria MSc	Biogeography and evolution of the rattan Calamus javensis Bl. (Arecaceae, Calamoideae) complex. – DIKTI Indonesia. From 1 December 2012. Promotor P.C. van Welzen
Dr. Christian Bödeker	Phylogenetic, taxonomic and biogeographical studies in the Pithophoraceae (Cladophorales, Chlorophyta). – Until 31 December 2009 0.2 fte. Promotor E.F. Smets. Co-promotor F. Leliaert, daily supervisor S.G.A. Draisma. PhD defence 21 December 2010, Leiden University
Bhanumas Chantarasuwan MSc	Taxonomy and systematics of Ficus subsection Urostigma (Moraceae). – Fellowship Royal Thai Government. From 1 September 2009. Promotor P.C. van Welzen

Tanawat Chaowasku MSc	Systematics of Miliusa (Annonaceae) and its closest relatives. – Fellowship Royal Thai Government. Until 30 November 2012. Promotor E.F. Smets. Daily supervisors L.W. Chatrou & D. Thomas
Nicolas Davin MSc	Evolution of secondary woodiness: driver of island plant radiations? – From 1 September 2011. Promotor E.F. Smets. Daily supervisor F. Lens
Dr. Poppy S.C. Djen Amar	Gunem Catur In the Sunda Region of West Java: Indigenous communication on the MAC plant knowledge and practice within the Arisan in Lembang, Indonesia. – Promotor L.J. Slikkerveer. PhD defence 19 October 2010, Leiden University
Renato Gama Dias Neto MSc	Phylogeographical patterns between the rain forest and the amazon forest: An approach with the family Dicranaceae s.l. (Bryophyta) and other haplolepideous mosses. – CAPES. From 1 September 2011. Promotor E.F. Smets. Daily supervisor M. Stech
Nor Hidayah Binti Yahaya MSc	Morphological, cytological and phylogenetic studies of Nephrolepis cordifolia complex (Pteridophyta, Nephrolepidaceae). – Fellowship Malaysian Government. From 1 April 2009. Promotor E.F. Smets. Daily supervisors P. Hovenkamp & M. Stech.
Dr. Sam V.S. Hoang	Uses and conservation of plant diversity in Ben En National Park Vietnam. – Fellowship Ministry of Education and Training Vietnam. Until 1 March 2009. Promotor P. Baas. Co-promotor P.J.A. Ke&ler. PhD defence 8 April 2009, Leiden University
Dr. Kevin van den Hof	Evolution of Viola stagnina and its sisterspecies by hybridization and polyplioidization. – Promotor E.F. Smets. Co-promotors B. Gravendeel & R.G. van den Berg. PhD defence 9 June 2010, Leiden University
Adam Karremans MSc	Niche differentiation in the epiphytic orchid genus Specklinia and close relatives in Pleurothallidinae. – Fellowship Universidad de Costa Rica. From 1 September 2011. Promotor E.F. Smets. Daily supervisor B. Gravendeel
Annick S. Lang MSc	Morphological variability and phylogeography of the Dicranum scoparium Hedw. species complex. – From 1 November 2009. Promotor E.F. Smets. Daily supervisor M. Stech
Dr. Liesbeth Leurs	Medicinal, aromatic and cosmetic (MAC) plants for community health and bio-cultural diversity conservation in Bali, Indonesia. – Promotor L.J. Slikkerveer. PhD defence 13 January 2010, Leiden University
Svenja Meinke MSc	Evolutionary studies on the liana habit within Annonaceae. – Until 30 November 2012. Promotor E.F. Smets. Daily supervisors P.J.A. Ke&ler, L.W. Chatrou & M. Stech (joint Hortus botanicus & NHN project)
Constantijn B. Mennes MSc	Diversification of mycoheterotrophic angiosperms. – From 1 October 2011. Promotor E.F. Smets. Daily supervisor V.S.F.T. Merckx
Luis M. das Neves Morgado MSc	Biodiversity and habitat partitioning of arctic ectomycorrhizal fungi and their role in vegetation change due to climatic changes. – From 1 September 2011. Promotor E.F. Smets. Daily supervisors J. Geml and M.E. Noordeloos
Drs. Marijke M. Nauta	Taxonomy of the Agaricales. – Until 31 August 2010 (0.8 fte). Promotor P. Crous, CBS Utrecht
Edwin Pos MSc	Unraveling Amazon tree diversity: The importance of dispersal in maintaining species richness in Amazonian forests. – From 1 September 2012. Promotor W.F. Laurance. Daily supervisor H. ter Steege
Dr. Kanchana Pruesapan	The rise and fall of Sauropus (Phyllantaceae): a molecular phylogenetic analysis of Sauropus and allies. – Fellowship Agricultural Research Development Agency Thailand. Until 30 November 2010. Promotors E.F. Smets & P.C. van Welzen. PhD defence 23 November 2010, Leiden University
Yotsewate Sirichamorn MSc	Revision, classification, phylogeny and biogeography of the Asian species of the genus Derris sensu lato (Fabaceae). – Fellowship Commission on Higher Education Thailand. Promotor P.C. van Welzen
Rachel Schwallier MSc	Niche differentiation of tropical pitcher plants. – Private funding. From 1 November 2011. Promotor E.F. Smets. Daily supervisors B. Gravendeel & N. Raes
Tatyana Semenova MSc	Biodiversity and habitat partitioning of root-associated fungi and their role in vegetation change due to climatic changes. – NWO ALW open programme. From 22 September 2012. Promotor E.F. Smets. Supervisor J. Geml

Dr. Abishkar Subedi	New species, pollinator interactions and pharmaceutical potential of Himalayan orchids. – Private funding. Until 31 August 2010. Promotors E.F. Smets & R.P. Chaudhary. Co-promotor B. Gravendeel. PhD defence 13 October 2011, Leiden University
Alexandra Towns MSc	Plants used for women's health and child care in Benin and Gabon. – NWO VIDI project to T.R. van Andel. From 22 December 2010. Promotor E.F. Smets. Daily supervisor T.R. van Andel
Tamara J.J. Vernimmen MSc	Impact of man and climate on a unique tropical ecosystem. – NWO ALW Open programme. From 1 October 2009 (0.8 fte). Promotors E.F. Smets & P. Baas

Other

Chequita R. Bhikhi	Supporting the Saramacan Ethnobotanical Knowledge centre Tonka-Island, The Twinning Facility Surinam - The Netherlands (UTSN) (15 November 2010 – 14 November 2011)
Bardo A. Cornelder	Teaching Leiden University (14 November 2011 – 19 November 2011; 1 June 2012 – 30 June 2012)
Thomas D. Hamann MSc	e-Taxomony, EU KP7 EDIT (14 June 2010 – 13 August 2010, 1 September 2010 – 31 October 2010, 15 May 2011 – 14 May 2012), mark-up Floras (from 1 September 2012)
Wout Holverda	Flora of the Netherlands
René C.M.J. van Moorsel	Invasive plants of the Netherlands. – LNV Voedsel- en Warenautoriteit Until 31 January 2010 (o.5 fte); 1 February 2010 – 31 December 2010 (0.8 fte)
Dr. Soraya E.C. Sierra	Project manager EU FP7 EDIT Workpackage 3.5. – EU funding. From 1 August 2009 – 30 November 2010 (0.5 fte), 1 December 2010 – 28 February 2011, 1 fte. E-taxonomy project 1 October 2011 until 31 August 2012 (0.89 fte). Project manager EU FP7 pro-iBiosphere. – EU FP7 funding. From 1 September 2012

Nationaal Herbarium Nederland, Wageningen Branch

Research staff

Prof. dr. Marc Sosef	Flora of Africa
Dr. Christina Flann	Global Compositae Checklist and 4D4Life project. – NWO Veni grant and EU FP7 program. Until December 2010 (0.8 fte).
Dr. ir. Jan J. Wieringa	Flora of Africa (0.4 fte)

PhD candidates

Dr. Maria C. Banaticla-Hilario	An ecogeographic analysis of Oryza series Sativae in Asia and the Pacific. – IRRI the Philippines. Promotor M.S.M. Sosef. Co-promotors R.G. van den Berg & K.L. McNally. PhD defence 24 October 2012, Wageningen University
Ms Pulchérie Bissiengou MSc	Systematics and evolutionary history of the African genus Campylospermum Teigh. (Ochnaceae). – WUR Sandwich Scholarship & FORENET. From 1 May 2009. Promotor M.S.M. Sosef. Daily supervisors J.J. Wieringa & L.W. Chatrou
Ximena Cadima MSc	Comparative assessment of genetic diversity conservation of ex situ and in situ Bolivian wild potatoes. – Nuffic. (0.7 fte). Promotor M.S.M. Sosef. Daily supervisors R.G. van den Berg & R. van Treuren
Dr. Robert Chakanda	Rice genetic resources in post-war Sierra Leone. – Wageningen University Sandwich Scholarship. Promotor M.S.M. Sosef. Co-promotors R.G. van den Berg & dr. ir. B. Visser. PhD defence 15 September 2009, Wageningen University
Dr. Corneille Ewango	The liana assemblage of a Congolian rainforest – Diversity, structure and dynamics. – Wageningen University Sandwich Scholarship. Promotor M.S.M. Sosef. Daily supervisors F.J.J.M. Bongers & L. Poorter. PhD defence 29 November 2010, Wageningen University
Dr. Stef de Haan	Potato diversity at height: multiple dimensions of farmer-driven in-situ conservation in the Andes. – CIP (Peru) and INIA (Spain). Promotor

	L.J.G. van der Maesen. Co-promotors C.J.M. Almekinders, M. Bonierbale & G. Thiele. PhD defence 16 March 2009, Wageningen University
Paul Hoekstra MSc	Living apart together - on niche evolution in African lianas. – Wageningen University & Naturalis. From 1 November 2012. Promotor M.S.M. Sosef. Daily supervisors L.W. Chatrou & J.J. Wieringa
Dr. A. Maroyi	The genus Gloriosa (Colchicaceae) – ethnobotany, phylogeny and taxonomy. – NUFFIC. Promotor L.J.G. van der Maesen. Co-promotor L.W. Chatrou. PhD defence 29 May 2012, Wageningen University
Berhane Kidane Mengesha MSc	Ethnobotany and ecology of wild edible and medicinal plants in South Omo Zone. – Nuffic. From 1 January 2010. Promotors M.S.M. Sosef & L.J.G. van der Maesen. Daily supervisor T. van Andel
André van Proosdij MSc	What determines species diversity in Central African plants? – Wageningen University. From 1 June 2010. Promotor M.S.M. Sosef. Daily supervisors J.J. Wieringa & N. Raes
Diana Quiroz MSc	Sacred and ritual plants of Benin and Gabon. – NWO VIDI to T.R. van Andel. From 1 September 2010. Promotor M.S.M. Sosef. Daily supervisor T.R. van Andel
Robin van Velzen MSc	Host tracking by Cymothoe (Nymphalidae) feeding on Rinorea (Violaceae): evolution and mechanisms of association. – Wageningen University. Until 30 April 2012. Promotor M.S.M. Sosef. Daily supervisor F.J. Bakker
Dr. Romaric Vihotogbé	Characterization of African Bush Mango trees with emphasis on the differences between sweet and bitter trees in the Dahomey Gap (West Africa). – NUFFIC. Promotor M.S.M. Sosef & B. Sinsin. Co-promotor R.G. van den Berg. PhD defence 1 November 2012, Wageningen University

Nationaal Herbarium Nederland, Utrecht Branch

PhD candidates

Dr. Olaf S. Bánki	Does neutral theory explain community composition in the community composition in the Guiana Shield forests? – WOTRO grant. Promotor M.J.A. Werger. Co-promotor H. ter Steege. PhD defence 19 April 2010, Utrecht University
Dr. Paddy P. Haripersaud	Collecting biodiversity. – WOTRO grant. Promotor M.J.A. Werger. Co-promotor H. ter Steege. PhD defence 21 September 2009, Utrecht University
Dr. Sylvia Mota de Oliveira	Bryophyte diversity in the Amazon. A neutral model with zero dispersal limitation? – CAPES grant. Promotor M.J.A. Werger. Co-promotor H. ter Steege. PhD defence 26 April 2010, Utrecht University
Dr. Juliana Stropp Carneiro	Tree diversity and habitat specificity in white sands of the upper Rio Negro and Guyana – National Council of Scientific and Technological Development Brazil grant. Promotor M.J.A. Werger. Co-promotor H. ter Steege. PhD defence 21 March 2011, Utrecht University

Supra-departmental programmes and projects

Drs. Minke van Det	SYNTHESYS project manager (until 1 July 2009)
Dr. Tom J.M. van Dooren	Bioinformatics (1 August 2010 – 1 February 2013)
Drs. Berry van der Hoorn	Programme manager Nature of the Netherlands (from 1 June 2012)
Ing. Youri Lammers	Project assistant (since August 2011)
Dr. Christiane Quaisser	Programme manager EDIT (until 30 September 2009)
Dr. Rutger Vos	Research fellow Bioinformatics (from 1 February 2012)
Maarten van 't Zelfde	GIS laboratory (from 1 July 2011)

Laboratories

Vacant position	Head of department
Dr. Kwaku Aduse-Poku	Molecular laboratory (24 January - 22 April 2011)
Els Baalbergen	Molecular laboratory (from 1 March 2011)
Kevin Beentjes MSc	Molecular laboratory (from 20 December 2010)

J.E. Breugel	Molecular laboratory (28 February - 17 August 2011)
Roland P.T. Butôt	Molecular laboratory (from 1 June 2012)
Drs. Camiel Doorenweerd	Molecular laboratory (1 November 2009 – 31 May 2012)
Dr. Rory A. Dow	Molecular laboratory (various contracts)
René Glas	Molecular laboratory (until 31 December 2011)
Constantijn B. Mennes MSc	Molecular laboratory (9 May - 1 October 2011)
Aline M. Nieman MSc	Molecular laboratory (from 1 March 2011)
Rense Schelfhorst	Molecular laboratory (1 July - 31 December 2010)
Drs. Frank R. Stokvis	Molecular laboratory (from 1 April 2010)
Dr. Oscar F.J. Vorst	Molecular laboratory (from 1 August 2010)

Awards 2009-2012

Naam	Award
Dr. Hugo de Boer	Richard E. Schultes Award, Society for Economic Botany, 2012. French-Swedish Prize for Young Researchers: Biodiversity and Human Health, 2010.
Dr. Martin Brazeau	Taylor & Francis Award for Best Student Article in the Journal of Vertebrate Paleontology for: Friedman, M. & Brazeau, M.D. (2010) “A reappraisal of the origin and basal radiation of the Osteichthyes”, 2010.
Dr. Masaki Hoso	Young Scientist Initiative Award from the Society of Evolutionary Studies, Japan, 2011.
MSc Adam Karremans	Best scientific poster at the 4th Andean Orchids Conference. Guayaquil, Ecuador, 2012.
Dr. Frederic Lens	New Phytologist Tansley Medal for Excellence in Plant Science for the paper Lens et al. (2011) Testing hypotheses that link wood anatomy to cavitation resistance and hydraulic conductivity in the genus Acer (New Phytologist 190: 709-723). Comment of the Editor-in-Chief: New Phytologist 190: 509, 2010.
MSc Constantijn Mennes	Honorable citation, Professor Lam Student prize, 2010.
Dr. Niels Raes	Professor Lam Student prize, 2009.
MSc Sonja Reich	Student poster prize at the Jahrestagung der Paläontologischen Gesellschaft, Vienna, Austria, 2011.
MSc Bastian Reijnen	Keith Sutherland Award, Malacological Society of Australasia, 2009.
MSc Natia Santadomingo	JanJoost ter Pelkwijk student price, 2010.
MSc Yotsawate Sirichamorn	Second prize of oral presentation during Flora of Thailand meeting, 2011.
Dr. Daniel Thomas	BioSyst EU 2009, Systematics 2009. Best student talk: 3rd prize. NHN, Leiden, The Netherlands, 2009.
Dr. Freek Vonk	NWO Eureka Price for science communication, 2012.
Dr. Hanco Zwaan	Dr. J. Gübelin Most Valuable Article Award - first prize’, as voted by the readers of the American journal Gems and Gemology, with the article ‘Copper-bearing (Paraíba-type) Tourmaline from Mozambique’, 2008.

Lipke Bijdeley Holthuis
In memoriam of a Dutch carcinologist

Charles H.J.M Fransen[1], Sammy De Grave[2] & Peter K.L. Ng[3]

[1] *Naturalis Biodiversity Center, Leiden*
[2] *Oxford University Museum of Natural History, UK*
[3] *Raffles Museum, National University of Singapore*

Dutch carcinologist Lipke Bijdeley Holthuis (1921-2008, Fig. 1) dedicated his life to the taxonomy and systematics of Crustacea. His scientific career started in Leiden at 's Rijksmuseum van Natuurlijke Historie in 1941 with his first publications and continued for 69 years at the Leiden Museum presently known as the Naturalis Biodiversity Center. In this period of time he produced 617 publications totalling 12,795 pages (Fig. 2).
This included papers in which he erected 2 new families, 5 new subfamilies, 83 new genera, and 338 new species of mostly crustaceans, though 7 plant taxa are included as well. We devoted a special volume of Crustaceana Monographs to the memory of this most prominent carcinologist of the XXth century (Fig. 3).
The first chapter of the volume entitled 'In Memoriam Lipke Bijdeley Holthuis' (Fransen et al., 2010) is a comprehensive obituary including an overview of his travels (Appendix I), a complete list of his publications, an enumeration of the 66 taxa that are named after him (not including the 48 named in this volume) (Appendix II), and listing all taxa described or erected by him (Appendix III).
The second chapter entitled 'Personal recollections' (Vervoort et al., 2010) by his close friends and colleagues tells stories about the harsh working conditions during World War II, and about his dedication towards his work. From these memories rises an image of a reserved but warm human being who was always there to share his time and knowledge.
Following these two chapters, his friends and colleagues pay tribute to his legacy in 54 papers of high quality. These contributions mainly deal with systematic and taxonomic issues, which emanate from his knowledge and inspiration.

About this volume

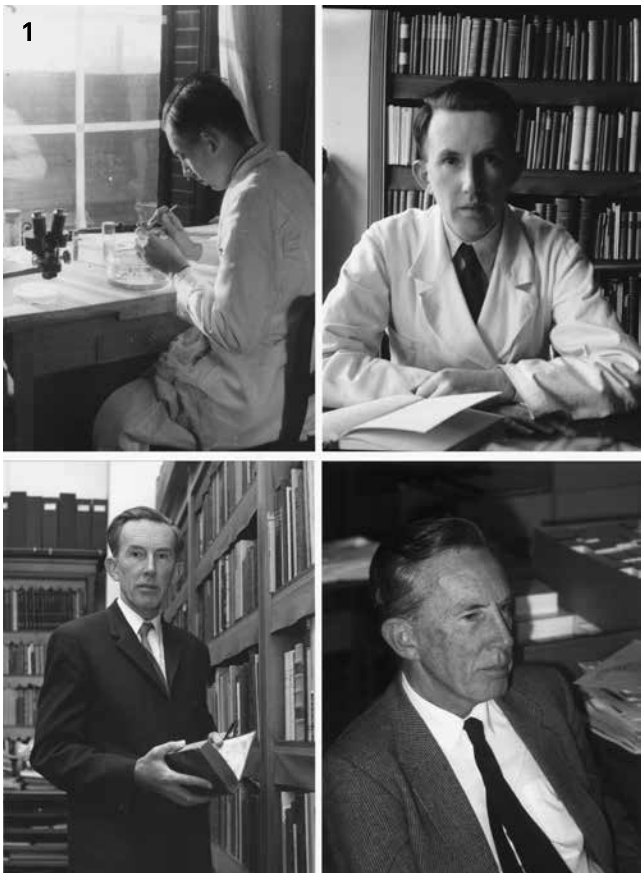
From a review by Luis A. Soto, 2011 (Crustaceana, 84 (12-13): 1662-1663)

'This is an exceptional compendium of crustacean knowledge to honour the memory of an also exceptional scientist, Lipke B. Holthuis, undoubtedly the most prominent carcinologist of the XXth century. The Preface offers the reader an excellent personal profile of this famous Dutch scholar, who pursued with intuition and great passion the study of Nature, focusing his interest on the taxonomy of Crustacea. This volume was edited by his close friends and colleagues, as a celebration of Lipke's many scientific achievements. His legacy stands up there amongst the Greatest of Systematics. For specialists, and also for those who had the privilege of receiving Lipke's wise counsel, it will be a delightful experience to open the pages of this volume and reminisce on the fond memories of a gifted carcinologist.'

From a review by Frederick R. Schram, 2011 (Journal of Crustacean Biology, 31(3): 576-576)

'Of course, it is the nature of such memorials of a taxonomist that a fair number of patronyms be created: to wit 7 new genera of which 4 honor Holthuis, and 49 new species of which 44 commemorate Lipke. There are of course more than enough examples of "*Xus*" *holthuisi* and "*Yus*" *lipkei*, but some names are rather ingenious, e.g., *Eosamon nominathuis*, or *Parasesarma liho*. Some might view this name spinning as over the top, and I suspect Lipke Holthuis himself would have been embarrassed by it all (we are told he forbad such a mass commemoration of his 1986 retirement and his 2001 80th birthday while he was alive). Nonetheless, it's nice; it is what taxonomical colleagues do on these occasions. The papers are of uniformly high quality.'

1



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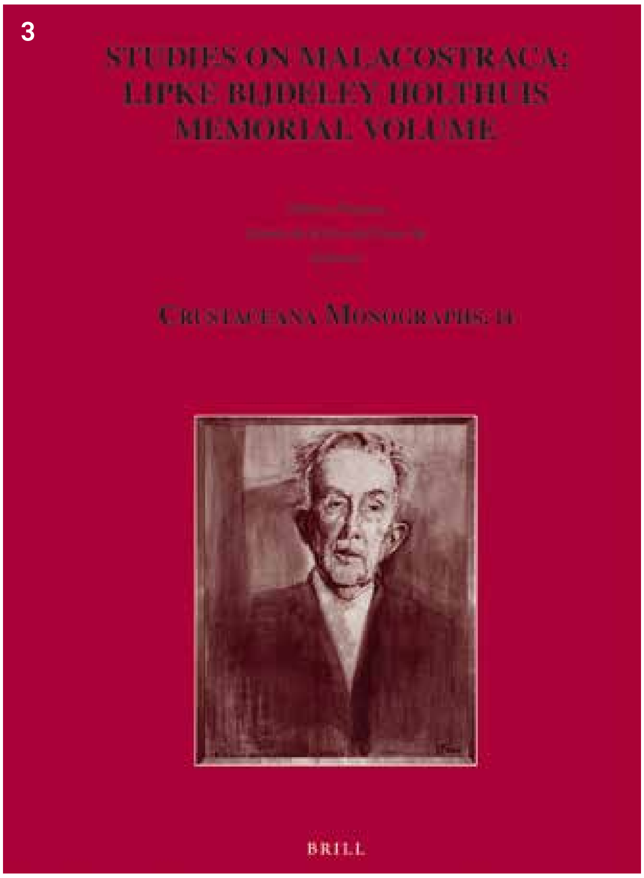

STUDIES ON MALACOSTRACA:
LIPKE BIJDELEY HOLTHUIS
MEMORIAL VOLUME

CRUSTACEANA MONOGRAPHS: 14

BRILL

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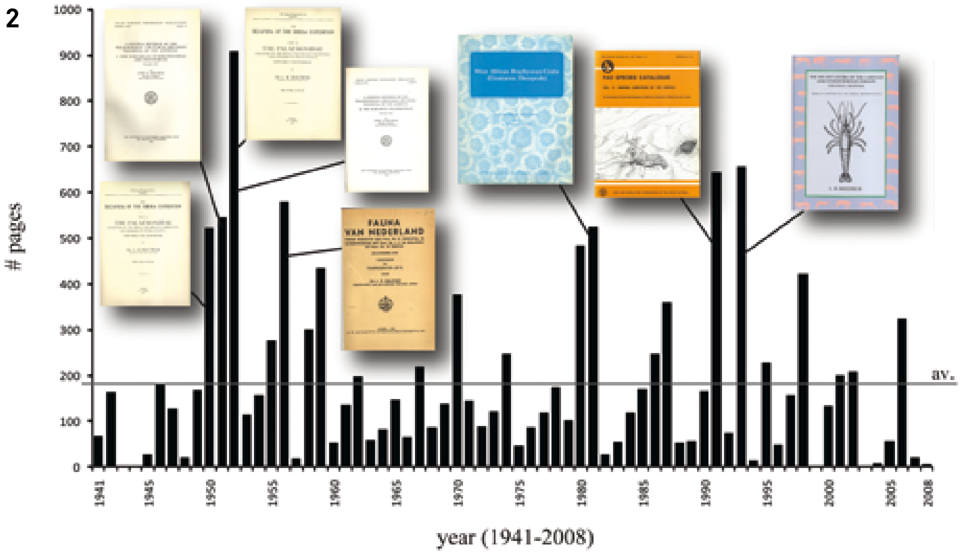

Fig. 1. Portrets of Lipke Bijdeley Holthuis.
Fig. 2. Productivity of Holthuis in average pages per year.
Fig. 3. Cover of the special volume of *Crustaceana Monographs* to the memory of Lipke Bijdeley Holthuis

References

Fransen, C.H.J.M., S. De Grave & P.K.L. Ng, 2010. In Memorial Lipke Bijdeley Holthuis. In: C.H.J.M. Fransen, S. De Grave & P.K.L. Ng (eds.), Studies on Malacostraca: Lipke Bijdeley Holthuis Memorial Volume. *Crustaceana Monographs* 14: 1-75.

Fransen, C.H.J.M., S. De Grave & P.K.L. Ng (eds.), 2010. Studies on Malacostraca: Lipke Bijdeley Holthuis Memorial Volume. *Crustaceana Monographs* 14: i-xii, 1-754. (BRILL, Leiden).

Vervoort, W., C. Smeenk, C.H.J.M. Fransen & P.K.L. Ng, 2010. Personal recollections of Lipke Bijdeley Holthuis. In: C.H.J.M. Fransen, S. De Grave & P.K.L. Ng (eds.), Studies on Malacostraca: Lipke Bijdeley Holthuis Memorial Volume. *Crustaceana Monographs* 14: 77-99.

Education

Staff of Naturalis is involved in the BSc- and MSc-curriculum of the partner universities, the Hogeschool Leiden and a few other institutions. The volume of the present activities in academic education amount per year to:

- University of Leiden – 4 extraordinary chairs and substantial input of staff with responsibility for and/or significant contribution to 60 EC cursory BSc/MSc-education and ca 500-750 EC internships; this involves all aspects of the Tree of Life; taxonomical, palaeontological and morphological expertise; methodological skills for (molecular) character analyses and phylogeny reconstruction; historical biogeography, spatial patern analyses and ecological modelling; evo-devo; evolution and speciation.
- Hogeschool Leiden – 0.4 fte Lectureship dedicated to provide courses and internships in the TopLab; this involves the application of diverse molecular techniques and the bioinformatics for analysis and processing of results.
- University of Wageningen – 1 chair and the responsibility for 12 EC BSc-and MSc-education and ca. 100 EC internships; this involves Dutch and SW European flora and fauna and biosystematics.
- University of Amsterdam – 1 chair and substantial involvement in 16 EC cursory BSc-education + 200-300 EC internships; this involves especially zoological, ecological and evolutionary courses and diverse excursions.
- University of Utrecht – 0.6 fte UD appointment with responsibility for 24 EC cursory BSc-education + 250-300 EC internships; this involves biodiversity, ecology and evolution, including a field course.
- The Netherlands Gemmological Laboratory organises three successful gemmological courses, one on HBO-level on contract basis, one at HBO-Zadkine and at the UvA (total 16 EC). Furthermore, individual staff members contribute more or less incidentaly to ca 5 EC education, e.g. at University of Groningen, University of Cologne, Museum für Naturkunde in Berlin and the Free University of Brussels.

Professor Lam Student Prize

Since 1963 the *"Stichting Rijksherbariumfonds Professor Lam"* aims to promote plant systematic research in its broadest sense.
To implement this aim, the Board of the foundation decided in 2008 to re-install the Professor Lam Student Prize. Each year the board of the *"Stichting Rijksherbariumfonds Professor Lam"* will award this Prize to one student (BSc, MSc or PhD) affiliated to then the National Herbarium of The Netherlands and now Naturalis for an outstanding article or book dealing with a Naturalis research related topic published in the preceding year. From 2010 onwards a special honors was given to the best paper by a BSc or MSc student, when the Professor Lam Student prize was awarded to a PhD.

The laureates are:
2008: ***Mr. Kevin van den Hof*** for the paper 'Chalcone Synthase Gene Lineage Diversification confirms allopolyploid evolutionary relationships of European rostrate Violets, *Molecular Biology and Evolution* 25 (10): 2099-2108. 2008. K. van den Hof, R.G. van den Berg & B. Gravendeel.
2009: ***Mr. Niels Raes (PhD student)*** for the paper 'Botanical richness and endemicity patterns of Borneo derived from species distribution models', *Ecography* 32: 180-192, 2009. N. Raes, M.C. Roos, J.W.F. Slik & E.E. van Loon & H. ter Steege.
2010: ***Mr. Christian Bödeker (PhD student)*** for the paper 'Global decline of and threats to *aegagropila linnaei*, with special reference to the Lake Ball habit', *BioScience* 60 (3): 187-198, 2010. C. Bödeker, A. Eggert, A. Immers & E. Smets.
Special honors:
Mr. Constantijn Mennes (MSc student) for the paper 'Pollen Morphology' in W.J.J.O. de Wilde & B.E.E. Duyfjes, Cucurbitaceae, *Flora Malesiana* I, 19: 10-15, 2010. C. Mennes & R.W.J.M. van der Ham.
2011: ***Mr. Marc Appelhans (PhD student)*** for the paper 'Phylogeny, evolutionary trends and classification of the *Spathelia-Ptaeroxylon* clade: morphological and molecular insights', *Annals of Botany* 107: 1259-1277, 2011. M.S. Appelhans, E. Smets, S.G. Razafimandimbison, T. Haevermans, E.J. van Marle, A. Couloux, H. Rabarison, M. Randrianarivelojosia & P.J.A. Kessler.
Special honors:
Mrs. Jasmijn van der Weide (MSc student) for the paper 'Pollen Morphology and Phylogeny of the Tribe Tabernaemontanae (Apoycynaceae, subfamily Rauvolfioideae)', *Taxon* 61: 131-145, 2012. J.C. van der Weide & R.W.J.M. van der Ham.
2012: The student prizes for 2012 will be awarded later this year.

Extramural functions

T.R. van Andel	Hortus Botanicus Amsterdam (member of board, since 2009) Treub Foundation for Tropical Research (member of board, since 2010) Van Eeden Fund for Botanical Research in Suriname and the Dutch Antilles (member of board, since 2009)
J.C. Biesmeijer	Apimondia, Standing Commission for Bee-flora and pollination (president)
H. de Boer	Center for Sustainable Development, Uppsala University (member of board, 2011) Elias Fries Scholarship Fund (member of board, since 2007) Faculty of Technical and Natural Sciences' Scholarships Board Uppsala University (member of board, 2009-2012) K.V. Ossian Dahlgrens Scholarship Fund (member of board, since 2009) Uppsala University's Board for Stipends and Scholarships (member of board, until 2012) PhytoKeys (associate editor)
S.K. Donovan	Palaeontographical Society (secretary, from 2011) Palaeontological Association (council member, 2008-2010) Geological Journal (UK) (member of editorial board, since 2007, book review editor since 2009
H. Duistermaat	Koninklijke Nederlandse Botanische Vereniging (excursion coordinator, 2007-2009) Nationale Database Flora en Fauna (member validation team, since 2010)
C.H.J.M. Fransen	World Register of Marine Species (WoRMS) (editor) Crustaceana (member of editorial board) Crustaceana Monographs series (editor) Arquipélago (Bulletin of the University of the Azores, Life and Marine Sciences) (member of advisory board)
B. Gravendeel	University of Applied Science, Leiden (Biodiversity Chair, since 2012) Taxon (assistant editor)
R.W.J.M. van der Ham	Grana (editor)
B.W. Hoeksema	Marine Biodiversity (associate editor) ZooKeys (editor) World Register of Marine Species (WoRMS) (editor, and member of steering committee) Treub Foundation for Tropical Research (member of board, since 2010) Scientific Committee for Oceanographic Research (SCOR) (member for the Netherlands, since 2004) Netherlands Organisation for Scientific Research: Earth and Life Sciences. Research programme Netherlands Caribbean (member, Committee for Programme Development) AcroporaNet (board member)
P. Hovenkamp	Varen-Varia (editor)

H. Kappes	Member of the “Akademie für ökologische Landesforschung” (Münster), since 2007.
A. Karremans	Lankesteriana (managing editor)
	Icones Orchidacearum (editor)
R.M.J.C. Kleukers	Entomologische Tabellen (editor-in-chief)
L.M. Kriegsman	National Research Programme on Plant Health (member fof steering group, until 2009)
	EU-FP6 programme SYNTHESYS-1 (member of steering group, until 2009)
	EU-FP6 Network of Excellence EDIT (member of steering group, until 2011)
	OECD Global Science Forum on Scientific Collections (member of steering group, until 2009)
	Consortium of European Taxonomic Facilities (member of steering group, until 2009)
	EU-FP7 Programme SYNTHESYS-2 (member of steering group, until 2011)
	Dutch Biodiversity Platform (member, until 2009)
	Geotectonic Research (associate editor, since 2003)
	Museologia Scientifica (member of editorial board, since 2007)
F.P. Lens	International Association of Wood Anatomists (executive secretary)
	International Association of Wood Anatomists Journal (associate editor, since 2009)
J. Miller	Zootaxa (editor, since 2008)
	Biodiversity Data Journal (deputy editor-in-chief, since 2012)
J.B. Mols	Professor Lam Fund (secretary and treasurer, since 2007)
	“Leidse Bibliotheekstichting” Collectanea Botanica (treasurer, since 2007)
	Dutch node of Global Biodiversity Information Facility (NL-BIF) (member of board, since 2009)
	Martha Tilaar Foundation (treasurer, since 2009)
S. Mota de Oliveira	Flora of the Guianas (editor-in-chief)
E.J. van Nieukerken	Tijdschrift voor Entomologie (editor-in-chief)
	ZooKeys (editor)
	Nota Lepidopterologica (editor)
	Societas Europaea Lepidopterologica (general secretary, since 2011)
	Fauna Europaea project (group coordinator Lepidoptera)
	Society for Management of Electronic Biodiversity Data (member of council)
	Werkgroep Vlinderfaunistiek (chair)
	Scratchpads, Vibrant project (ambassador, since 2011)
L.P. van Ofwegen	Zookeys (editor)
W. Renema	Palaeontological Association (member of council)
	Frontiers of Biogeography (editor)
M.C. Roos	Newsletter Treub Foundation for Tropical Research (editor, since 1993)

	Foundation for International Nature Conservation (Van Tienhoven Stichting) (member of board, since 2005)
	Foundation Flora Malesiana (secretary, since 1991)
M. Schilthuizen	Royal Society's Southeast Asia Rainforest Programme (member, since 2001)
	Biodiversity thinktank for the Ministry of Agriculture, Nature and Food Quality (member, until 2010)
	Heimans & Thijsse Foundation (member of board, since 2007)
	Treub Foundation for Tropical Research (member of board, since 2008)
	Stichting Bargerveen (member of board, since 2009)
	Research School Biodiversity (chair, 2010-2012)
	Netherlands Prize for Zoology (member selection committee, since 2012)
	Journal of Tropical Biology and Conservation (managing editor, until 2009)
R. Sluys	GenBank (taxonomic consultant)
	National Geographic Television (biological consultant)
	Committee Systematiek Nederlandse Avifauna (member)
	Commissie Genetische Modificatie (COGEM) (consultant)
E.F. Smets	European Journal of Taxonomy (member of the Advisory Editorial Board, since 2012)
	Natural History Museum Stuttgart and the Natural History Museum Karlsruhe (member of the Scientific Advisory Board, since 2012)
	National Authority for Data concerning Nature (member of the Committee of Scientific Advisors, since 2012)
	ETI Bioinformatics (member of board, until 2012)
	Research School Biodiversity (member of board, until 2012)
	International Organisation for Systematic and Evolutionary Biology (council member, since 2011)
	Fungal Biodiversity Centre, CBS-KNAW (member of the Scientific Advisory Board, since 2011)
	Taxon (Associate Editor, 2010-2011)
	European Distributed Institute of Taxonomy (member of the board of directors, until 2011)
	Leopold III-Fund for Nature Research and Nature Conservation, Belgium (member of board, since 2009)
	Feddes Repertorium (member of Advisory Board, since 2009)
	Research Foundation Flanders (member and chair of the expert panel biodiversity and ecology, until 2009)
	Alberta Mennega Foundation (member of board, since 2007)
	Professor Lam Fund (chair of board, since 2007)
	"Leidse Bibliotheekstichting" Collectanea Botanica (chair of the board, since 2007)

	Flora Malesiana Foundation (vice-chair of board, since 2006)
	National Geographic Nederland – België (member of the advisory board, since 2006)
	Dr. E. Kits van Waveren Foundation (chair of board, since 2005)
	Consortium of European Taxonomic Facilities (member of board of directors, since 2005
	National Botanic Garden of Belgium (member of the scientific advisory board, since 1997)
	Alumni Society PDL, Belgium (member of board, since 1991)
M. S.M. Sosef	Moabi Foundation (member of board, since 2004)
	ETI Bioinformatics (member of board, since 2004)
	Research School Biodiversity (scientific director, since 2005)
	Alberta Mennega Foundation (member of board, since 2005)
	Treub Foundation for Tropical Research (member of board, since 2005)
	Global Taxonomy Initiative (Convention on Biological Diversity (national focal point, since 2006)
M. Stech	Tropical Biology (editor, since 2011)
J. van Tol	International Commission on Zoological Nomenclature (commissioner since 2001, president since 2009)
	Dutch node of Global Biodiversity Information Facility (NL-BIF) (treasurer)
	Tijdschrift voor Entomologie (editor)
	Deutsche Entomologische Zeitschrift (editor)
	International Journal of Odonatology (editor)
	ZooKeys (editor)
	Encyclopedia of Life (council member)
N.J. de Voogd	World Register of Marine Species (WoRMS) (editor)
	Journal of the Marine Biological Association of the United Kingdom (editor)
R.A. Vos	PhyloInformatics Research Foundation (member of board, since 2010)
	Frontiers in Bioinformatics and Computational Biology (review editor)
I.M. van Waveren	IGCP 575 UNESCO project (treasurer, since 2010)
P.C. van Welzen	Flora of Thailand (editor, since 2005)
	Thai Forest Bulletin (editor, since 2009)
	Flora Malesiana (editor-in-chief, since 2011)
J.C. Zwaan	World Jewellery Confederation (CIBJO): Gemmological Commission (vice-president 2009-2011, president since 2011)

The following staff were member of one or more Evaluation Committees of the Netherlands Organisation for Scientific Research, Earth and Life Sciences Open Competition: M.C. Roos and M. Schilthuizen.

Naturalis publications

Naturalis Biodiversity Center is involved in the publishing of several scientific journals and book series. This chapter is an overview of these activities and the volumes published in the years 2009-2012.

Journals

Blumea – Biodiversity, Evolution and Biogeography of Plants

Blumea is an international journal on the biodiversity, evolution and biogeography of plants, including topics on systematics, floristics, phylogeny, morphology and anatomy. For floristic studies, the focus is on tropical Africa south of the Sahara, tropical Southeast Asia with a strong emphasis on Malesia, and South America with emphasis on the Guianas. Papers in *Blumea* are subjected to peer review and are in English. *Blumea* is published three times a year, comprising c. 300 pages in total, in A4 format. *Blumea* is online via open access available through Ingenta: www.ingentaconnect.com/content/nhn/blumea.

Editor-in-Chief: Dr. P.H. Hovenkamp.

	2009	2010	2011	2012
Scient. papers	48	45	35	28
Total pages	299	300	299	302
SCI	0.243	0.500	0.699	0.266

Contributions to Zoology

Contributions to Zoology solicits high-quality papers in all systematics-related branches of zoology and paleontology. Preference will be given to manuscripts dealing with conceptual issues and to integrative papers (e.g., palaeobiology *and* biodiversity, morphology *and* phylogeny *and* character state evolution, phylogeny *and* historical biogeography, systematics *and* bioinformatics, bioinformatics *and* biodiversity, habitat disturbance *and* biogeoghraphy, etc. etc.). Reviews and alpha-taxonomic contributions may be considered for publication, but acceptance will depend on their high quality and exceptional nature.

Editor-in-Chief: Dr. J.W. Arntzen.

	2009	2010	2011	2012
Scient. papers	13	13	19	18
Total pages	160	191	284	251
SCI	1.244	1.118	1.231	2.452

Gorteria

Gorteria is dedicated to research on the wild Flora of the Netherlands. The taxa treated must occur in The Netherlands, but the issues dealt with need not be limited to the Netherlands only. The journal aims to be useful for a broad scientific audience and botanical research arena (systematics, floristics, ecology, vegetation biology). Especially papers on the identification or distinction of critical or taxonomical challenging plant taxa are welcome.
The journal is published in Dutch, with an abstract in Englis, and each volume consists of 6 fascicles. More information can be found on: www.nhn.leidenuniv.nl/index.php/publications/gorteria

Editor-in-Chief: Dr. M.C. Roos.

	2009	2010	2011	2012
Scient. papers	13	11	5	7
Total pages	176	113	205	53
SCI	0.400	0.200	0.167	0.133

Nederlandse Faunistische Mededelingen

The journal *Nederlandse Faunistische Mededelingen* publishes original papers and short communications on the invertebrates of the Netherlands.
It is especially targetting the working groups of the European Invertebrate Survey and related researchers with the aim to enhance the knowledge of Dutch biodiversity. The journal is published twice a year as a cooperation between the European Invertebrate Survey and Naturalis. Additionally, supplements are published dealing with a specific topic. Most papers are in Dutch with an English summary.

Editor-in-chief: Mr. R.M.J. Kleukers.

	2009	2010	2011	2012
Scient. papers	21	14	24	21
Total pages	431	148	210	229

Persoonia – Molecular Phylogeny and Evolution of Fungi

Persoonia aims to publish papers dealing with molecular phylogeny and evolution of fungi. A further aim is to promote fungal taxonomy by employing a polythetic approach to clarify the true phylogeny and relationships within the kingdom Fungi.
The journal publishes high-quality papers elucidating known and novel fungal taxa at the DNA level, and also strives to present novel insights into evolutionary processes and relationships. Papers to be considered include research articles, topical and book reviews. Papers are published using a Fast Track system. This implies that the papers are immediately published online and freely available through the internet via this website. Hard copy volumes are published twice a year, in A format and full colour, when the online published papers are bound. *Persoonia* is a journal published jointly by the Nationaal Herbarium Nederland and the Centraalbureau voor Schimmelcultures. Online papers in *Persoonia* can be found through www.ingentaconnect.com/content/nhn/pimj/pre-prints and www.persoonia.org.
Editors-in-Chief: Dr. J. Geml and Prof. dr. P.W. Crous.

	2009	**2010**	**2011**	**2012**
Scient. papers	25	19	9	22
Total pages	380	298	163	388
SCI	-	-	4.136	3.486

Scripta Geologica

Scripta Geologica publishes original papers and monographs dealing with the various branches of vertebrate and invertebrate palaeontology, palaeobotany/palynology, stratigraphy, petrology and mineralogy, including gemmology. The journal appears twice per calendar year, although it may be supplemented by special (thematic) issues. Each issue has its own serial number. The focus of the journal is systematics, although papers on all aspects of the subjects listed above are welcomed. Only original papers that have not been submitted or published elsewhere will be considered for publication. The electronic version of *Scripta Geologica* is available at www.scriptageologica.nl. Back articles of *Scripta Geologica* are available through www.repository.naturalis.nl.
Editor-in-Chief: Dr. S.K. Donovan.

	2009	**2010**	**2011**	**2012**
Scient. papers	6	11	19	7
Total pages	207	544	112	142

Zoologische Mededelingen

Zoologische Mededelingen publishes original papers and monographs dealing with various branches of vertebrate and invertebrate biology. The focus of the journal is systematics. The majority of the publications in *Zoologische Medelingen* are the result of research projects of Naturalis, or are based mainly or entirely on specimens in the collections of Naturalis. Only original papers that have not been submitted or published elsewhere will be considered for publication. The journal is accessible through: http://www.zoologischemededelingen.nl/. Back articles of *Zoologische Mededelingen* are available through www.repository.naturalis.nl.
Editor-in-chief: Dr. L.P. van Ofwegen.

	2009	**2010**	**2011**	**2012**
Scient. papers	34	10	16	7
Total pages	1081	575	956	604

Series

Entomologische Tabellen

Entomologische Tabellen publishes identification keys on the invertebrates of the Netherlands. It is a joined publication of the Nederlandse Entomologische Vereniging, the European Invertebrate Survey and Naturalis. *Entomologische Tabellen* is published on an irregular basis.
Editors-in-chief: Dr. O. Vorst, Mr. R.M.J. Kleukers & Dr. M. Reemer.

	2009	2010	2011	2012
Volumes	2	1	1	0
Total pages	277	159	108	0

2009: Volume 3: De Nederlandse hooiwagens (Opiliones)
2009: Volume 4: De Nederlandse prachtkevers (Buprestidae)
2010: Volume 5: De Nederlandse boorvliegen (Tephritidae)
2011: Volume 6: De Nederlandse rivierkreeften (Astacoidea & Parastacoidea)

Flora Agaricina Neerlandica

The *Flora Agaricina Neerlandica* is a critical mycological flora, which covers the agarics and boleti occurring in the Netherlands and adjacent regions. It provides identification keys, extensive descriptions and illustrations of all taxa. In addition data on ecology and distribution patters are included. The flora is essentially based upon own observations of the authors on fresh material and herbarium specimens collected by Dutch mycologists over more than 50 years. Presently 6 volumes have been published for Naturalis by CRS press. No issues were published between 2009-2012.
Editors-in-chief: Dr. M.E. Noordeloos, Prof.dr. Th.W. Kuijper and Dr. E.C. Vellinga.

Flora Malesiana

Flora Malesiana is a systematic treatment of the tropical plant species (flowering plants and ferns) in the Malay Archipelago (Malaysia, Singapore, Brunei, Indonesia, Philippines, Timor Este, Papua New Guinea), estimated at 40,000 species. It is the first flora for the region. Therefore a monographic approach is used to describe the species including long detailed descriptions and full synonymy, and literature references.
Up to now 20 volumes have been published in series

I (no. 2 and 3, intended for vegetation descriptions and ecology have never been written) and 4 volumes in series II (so far covering c. 20% of the flora). Treatments are made by internationally renowned taxonomists.

The instalments contain family treatments, single when concerning a large family (or at most 2 instalments as with Moraceae), several together when small families are involved. Every family has introductory chapters about morphology, anatomy, pollen, and other topics when of interest, followed by a key to the genera, keys per genus and species descriptions.

The reader can, in conjunction with the digital family key produced by Kew and Leiden, use *Flora Malesiana* to identify species, to get information about plants, uses, references, anatomy, vernacular names, pollen, pollination, etc. Quite often *Flora Malesiana* contains the first drawings of species.

A Flora Malesiana Dataportal is under construction: dev.e-taxonomy.eu/dataportal/flora-malesiana/

Editors-in-Chief: Prof. dr. P.W. van Welzen and Dr H.P. Nooteboom.

	2009	2010	2011	2012
Volumes	0	1	1	1
Total pages	0	342	66	156

2010: Series I, Volume 19: Cucurbitceae.

2011: Series I, Volume 20: Acoraceae, Pandaceae & Picrodendraceae

2012: Series II, Volume 4: Blechnaceae, Hypodematiaceae, Monachosoraceae, Nephrolepidaceae, Oleandraceae, Pteridaceae subfam. Parkerioideae & Arthropteris.

Flora of the Guianas

The *Flora of the Guianas* is a critical treatment of the plant taxa occurring in the Guianas (the political territories of Guyana, Suriname and French Guiana) and deals, in principle, with phanerogams as well as cryptogams. It is based on studies of herbarium collections, including types, living plants, and of all relevant literature. The Flora is designed not only for use by taxonomists, but also for practical use. Whenever possible, it will contain data on the economic value and use of the plant taxa, such as chapters on wood and bark anatomy in timber-supplying families, potential for cultivation, and also information on the need for conservation of taxa and/or habitats. The Flora is expected to stimulate research in many other fields, especially with regard to the natural resources of the area and their conservation and development.

Publication takes place in fascicles, each treating a single family, or a group of related families, in the following series: A. Phanerogams; B. Ferns and Fern allies; C. Bryophytes; D. Algae; and E. Fungi and Lichens. A list of numbered families in taxonomic order has been established for the Phanerogams. Publication of fascicles will take place when available and are published by Kew Publishing for the *Flora of the Guianas* consortium (of which Naturalis is part).

Executive editor: Dr. S. Mota de Oliveira.

	2009	2010	2011	2012
Volumes	1	0	2	1
Total pages	212	0	820	196

2009: Series A, Phanerogams Fascicle 27: Cyrillaceae, Theophrastaceae, Rhabdodendraceae, Proteaceae, Combretaceae, Dichapetalaceae, Limnocharitaceae & Alismataceae.

2011: Series A, Phanerogams Fasicle 28: Leguminosae subfamily Mimosoideae.

2011: Series C Bryophytes Fascicle 2: Musci IV.

2012: Series A, Phanerogams Fasicle 28: Sapindaceae.

Flore du Gabon

The *Flore du Gabon* series provides access to the information on the botanical wealth of this central African country, reputedly harbouring the richest lowland rain forest in Africa. The series was started in 1961 by the Muséum national d'Histoire naturelle (MNHN) in Paris. In 2009, a new editorial team was formed including Naturalis. They developed a new and more concise format and rendered the goal to finish the series within 10 years. From now on, 2 or 3 volumes are expected to be published each year, in order to keep up a steady and high pace of production. With 11% of all plant species being endemic to the country and some 80% of its surface being covered with a highly diverse lowland rain forest, Gabon is a botanical paradise and biodiversity hotspot. The *Flore du Gabon* provides the essential tools for reliable identification, stressing the need for simple and straightforward identification keys, diagnostic descriptions and clarifying illustrations. As such, it hopes to assist researchers, foresters and conservationists alike and to contribute to the survival of Gabon's unique biodiversity. *Flore du Gabon* is published for Naturalis by Margraf Pubishers.

Editors-in-chief: Prof.dr. Marc S.M. Sosef, Dr. Jacques Florence, Dr. Ludovic Ngok Banak and Dr. Henri-Paul Bourobou Bourobou.

	2009	2010	2011	2012
Volumes	2	2	1	2
Total pages	171	148	110	337

2009: Volume 38: Alismataceae, Apiaceae, Goodeniaceae, Hernandiaceae, Huaceae, Iridaceae, Oxalidaceae, Smilacaceae, Sphenocleaceae, Taccaceae.

2009: Volume 39: Begoniaceae.

2010: Volume 40: Apodanthaceae, Balanophoraceae, Campanulaceae, Caricaceae, Hyacinthaceae,Hydroleaceae, Lobeliaceae, Menyanthaceae, Nymphaeaceae, Pontederiaceae, Typhaceae.

2010: Volume 41: Anthericaceae, Burmanniaceae, Colchicaceae, Crassulaceae, Dipterocarpaceae, Lemnaceae, Pittosporaceae, Rosaceae, Ternstroemiaceae, Thismiaceae, Triuridaceae.

2011: Volume 42: Aizoaceae, Aristolochiaceae, Gnetaceae, Hypericaceae, Lecythidaceae, Pedaliaceae, Polygalaceae, Turneraceae, Xyridaceae.

2012: Volume 43: Phyllanthaceae.

2012: Volume 44: Cyperaceae.

Natuur van Nederland

The *Natuur van Nederland* series is a continuation of the *Nederlandse Fauna* series. It is published by Naturalis in cooperation with KNNV Publishers and the European Invertebrate Survey. Each volume offers an overview of a particular species group of the Dutch flora or fauna. The subjects tackled are taxonomy, distribution, status, identification keys, ecology and aspects of their biology. Presently, 11 volumes have been published. Website: science.naturalis.nl/research/publications/nederlandse-fauna.

Editors-in-chief: A.J. van Loon & G.O. Keijl.

	2009	**2010**	**2011**	**2012**
Volumes	1	1	0	1
Total pages	476	510	0	544

2009: Volume 9: De amfibieën en reptielen van Nederland

2010: Volume 10: De Nederlandse biodiversiteit

2012: Volume 11: De Nederlandse bijen.

EDIT
European Distributed Institute of Taxonomy

Leo M. Kriegsman & Soraya Sierra

Naturalis Biodiversity Center, Leiden

One of the tasks of taxonomists is to describe and classify life. Hence, the Countdown 2010 initiative of the IUCN to halt the decline of biodiversity in Europe also needed to address the global reduction in the number of professional taxonomists. In 2006 a 5-year, 10.9 M€ project was funded by the European Commission under its 6th Framework Programme (FP6) to build a European infrastructure for taxonomy that should change both the way taxonomists work and publish, and how the related natural history collections are curated and used in Europe. The project consisted of 8 workpackages, one of which was led by staff of Naturalis “avant la lettre” (1st year ZMA: Wouter Los; then NNM/Naturalis: Leo Kriegsman). Dutch tasks and successes in EDIT include:

- maintenance and expansion of the Fauna Europaea database and expert system; this was successfully done through the project Pan-European Species directories infrastructure (PESI), an EDIT spin-off;
- coordination of the interaction between EDIT and other EU and global infrastructures, leading to joint proposals, with the new e-Biosphere project as a key spin-off;
- coordination of DNA-barcoding efforts (led by CBS Utrecht), both at European level (European Consortium for the Barcoding of Life; European Barcoding of Life Database; see www.ecbol.org) and at national level (DNA-barcoding component funded through a FES grant to Naturalis and CBS);
- co-leadership (with MNHN Paris) of the efforts to give more power to the Consortium of European Taxonomic Facilities (CETAF; see Kriegsman 2010, 2011) to ensure more contact between the directors of institutions and to give more impetus to common action and lobbying efforts through an operational CETAF office;
- coordination of efforts to streamline collections policies of European natural history museums, in relation with the SYNTHESYS-1 & -2 projects (see Kriegsman & Quaisser 2011); this successful component is now continued in the Collections Policy Board, chaired by NCB’s Director of Collections René Dekker; topics included loans policy, collection digitisation to expand the user base, and contribution to global efforts, under the umbrella of the OECD, to foster collaboration and exchange of expertise on scientific collections and to promote their use as a scientific infrastructure through SciColl, a global organisation that is still being initiated.

Other activities and successes at EU level include:

- the EDIT Scratchpads and EDIT Cybertaxonomy Platform are transforming the way that taxonomists collaborate and publish; these elements of web-based taxonomy will speed up species discovery and description.
  To share taxonomic information and facilitate discussion about a specific taxonomic group, Naturalis has performed various pilots using Scratchpads, among them:
  - The Cholevidae Scratchpad (http://cholevidae.myspecies.info/).
  - The Nepticuloidea Scratchpad on leaf- and stem-mining moths (http://nepticuloidea.info/).
  - The Sponge Scratchpad for increasing access to the Naturalis sponge collection (link not yet available).
  - The Early Conifers Scratchpad on fossil taxa (http://earlyconifers.myspecies.info/).

- To facilitate access and usability of plant species legacy data and information, Naturalis has performed three pilots using the EDIT Platform for Cybertaxonomy:
  - Flore du Gabon (http://dev.e-taxonomy.eu/dataportal/flore-gabon/).
  - Flora of the Guianas (http://160.45.63.201/dataportal/preview/flora-guianas/).
  - Flora Malesiana (http://dev.e-taxonomy.eu/dataportal/flora-malesiana/).
- many taxonomists, including some from Naturalis Biodiversity Center, actively participated in All Taxon Biodiversity Inventories (ATBIs) in various European countries and elsewhere; based on the experience, a manual was produced on best practices in ATBIs that will facilitate future

species surveys; some ATBIs were combined with DNA barcoding of all species encountered;
- the Distributed European School of Taxonomy (DEST) organised many short courses and summer schools related to the ATBIs; it now continues under Belgian finances;
- establishment of European Journal of Taxonomy (EJT) to replace several older, local taxonomy journals and raise them to a higher level; EJT has a global scope, is fully electronic, and open access.
- a plethora of outreach activities on biodiversity, linked to Countdown 2010, culminating in the Biodiversity Year Special Events (BYSE 2010);
- some EDIT projects led to successful follow-up programmes funded by the EC (e.g., EDIT Scratchpads led to the FP7 ViBRANT infrastructure project (coordinated by the NHML) ;international infrastructure collaboration between Naturalis and global projects/initiatives led to the FP7 CSA infrastructure project “pro-iBiosphere” (coordinated by Naturalis).

The final review of this complex project by the EC was very positive. EDIT has significantly modified the landscape of global taxonomy. In addition, large European natural history institutions have grown closer, have learned to see the benefits of common strategies and shared policies, and have seen the merits of joint action at a profound level. If the new CETAF office housed in Brussels, at an arm’s length from the EC, manages to coordinate both the EC funded and the national initiatives, the EDIT legacy will continue to inspire.

Economic Structure Enhancement Fund (FES)

New research infrastructures

Naturalis substantially improved its research infrastructure between 2009 and 2012. The most important impulse of 30 million euro was received from the *Fonds Economische Structuurversterking* or Economic Structure Enhancement Fund. This sum was provided for merging and digitizing the collections of Naturalis, Zoological Museum Amsterdam and the National Herbarium of the Netherlands, and to set up an improved research infrastructure. The ministry of education also provided an additional grant for this goal, so that a total of 15.3 million euro became available.

First we set up a DNA barcoding lab, in collaboration with CBS-KNAW. DNA barcodes have proved an important tool for the identification of fungi, plants and animals. Based on morphological characters, identification of immature stages is often difficult or impossible, while there is, of course, no difference between immature and adult stages based on DNA sequences. Establishing a reference system for automated identification is, however, a task that can only be accomplished by institutions with taxonomic expertise. This task is co-ordinated by the Consortium for the Barcode of Life, and Naturalis contributes to this with a set of at least 27 000 barcodes. After interviews with stakeholders like the food safety or CITES authorities, we made a selection of preferred taxa. We also established co-operation with amateur organizations, such as the Netherlands Malacological Society, to collect fresh material for this reference system. However, also hypothesis driven research projects are implemented in the DNA Barcoding laboratory, such as the 2012 Kinabalu Expedition focusing on the evolution of species on this highest mountain of Borneo.

Apart from the DNA Barcoding lab we enlarged the existing DNA Markerpoint, which was established some years ago as a co-operation with the Institute Biology Leiden of the Leiden University. Apart from an upgrade and development of this laboratory, we also introduced next generation sequencing with an Ion Torrent Personal Genome Machine of Life Technologies.

The huge amount of data, especially from NGS projects, asks for bioinformaticians. Naturalis appointed a researcher and a technical expert in this field, which is rapidly evolving and in which we wish to acquire a leading position. These experts have also assisted in the specifications of the work stations and networks needed for these tasks.

Also our morphological laboratories were significantly upgraded. We purchased a JEOL FEG-SEM 7600F, which was installed in the Van Steenis building. Both stereomicroscopes and compound microscopes were upgraded to new high-end models, including some microscopes with automated focusing and camera. A SatScan Micro-CT-scanner appeared to be one of the most successful additions to our research infrastructure. It is used seven days a week, and appears to be very attractive for visitors on Sythesys grants. Finally we changed the existing microtomes for new models. Installation of phytotrons was postponed until 2013.

The digitized data of the collection are an important basis for studies on the dynamics of flora and fauna. We set up a specialized GIS-laboratory (Global Information Systems) with high-end workstations and software. A specialist was appointed for maintenance and instruction.

Finally, te preparation of the purchase of an electron microprobe, as foreseen in the original proposal, took significantly more time than anticipated, and the tender only started in 2013. This microprobe will be placed, together with an ion microprobe, in a central facility at the University of Utrecht.

As explained before, this equipment is not only used by our own permanent staff, but also by researchers from other institutions, and by newly appointed postdocs and PhD candidates.

Publications 2009-2012

This list includes the publications of permanent staff, students and honorary staff (names in **bold**) of the National Herbarium (Leiden, Wageningen), the Zoological Museum Amsterdam (2010-2012 only), and Netherlands Centre for Biodiversity Naturalis (Leiden). These institutes are now merged into Naturalis Biodiversity Center, Leiden). Abstracts and reviews have been omitted.

2009

Abdulsamad, E.O. & **Tmalla, A.F.** 2009. A stratigraphic review of the Al Bayda Formation, NE Libya: calcareous nannofossils versus Foraminifera. *Petroleum Research Journal* 21: 57-66, (2008/2009).

Abdulsamad, E.O., Bu-Argoub, F.M. & **Tmalla, A.F.** 2009. A stratigraphic review the Eocene to Miocene rock units in the al Jabal al Akhdar, NE Libya. *Marine and Petroleum Geology* 26: 1228-1239.

Albers, P.C.H. & **de Vos, J.** 2009. *Through Eugène Dubois' eyes. Stills of a turbulent life*. 186 pp. Brill, Leiden

Anderson, R.J., Bolton, J.J. & **Stegenga, H.** 2009. Using the biogeographical distribution and diversity of seaweed species to test the efficacy of marine protected areas in the warm-temperate Agulhas Marine Province, South Africa. *Diversity and Distributions* 15: 1017-1027.

Aratake, S, Trianto, A., Hanif, N., **de Voogd, N.J.** & Tanaka, J. 2009. A new polyunsaturated brominated fatty acid from a *Haliclona* sponge. *Marine Drugs* 7: 523-527.

Arntzen, J.W. & Smit, G. 2009. *Triturus cristatus* (Laurenti 1768) - noordelijke kamsalamander. In: Creemers, R. & J. Van Delft (eds.). De amfibieën en reptielen van Nederland. *Nederlandse Fauna* 9: 105-113. Nationaal Natuurhistorisch Museum Naturalis, Leiden.

Arntzen, J.W., Jehle, R., Bardakci, F., Burke, T. & **Wallis, G.P.** 2009. Asymmetric viability of reciprocal-cross hybrids between crested and marbled newts (*Triturus cristatus* and *T. marmoratus*). *Evolution* 63: 1191-1202.

Baas, P. 2009. Biofuels and tropical forests. Guest Editorial. *Journal of Tropical Forest Science* 21: v-vii.

Babik, W., Pabijan, M., **Arntzen, J.W.**, Cogalniceanu, D., Durka, W. & Radwan, J. 2009. Long-term survival of a urodele amphibian despite depleted MHC variation. *Molecular Ecology* 18: 769-781.

Baird, A.B., Hillis, D.M., Patton, J.C. & Bickham, J.W. 2009. Speciation by monobrachial centric fusions: A test of the model using nuclear DNA sequences from the bat genus *Rhogeessa*. *Molecular Phylogenetics and Evolution* 50: 256-267.

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