

REPORTS FROM SYSTEMATICS RESEARCH FUND GRANTS AWARDED IN 2013

Twenty eight awards were made in 2013. We have received reports from all except the following five which, for a variety of reasons (ill health, delays with permits etc) have yet to be completed. I have granted all extensions and will request a report from the awardees in September (hopefully received in time for the LS and SA October Council meetings):

- Timothy Colston, University of Mississippi, Disentangling Species Boundaries in the Brazilian Lancehead (*Bothrops moojeni*) (£1140)
- Zoe Goodwin, University of Oxford, Completing the global inventory of plants – Species discovery and diversity (£600)
- Nicholas Mason, Cornell University, Phylogeographic patterns, local adaptation, and species limits in the Horned Lark (£965)
- Henrik Sundberg, Uppsala University, *Orectogyrus specularis* revisited: Testing Thaxter's sixteen species. (£1500)
- Martin Thompson, University of Cambridge, A RAD phylogeny of the diverse butterfly genus *Acraea* (£1200)

Report format

The 2013 guidelines requested reports of no more than 100 words (as you will see, some authors exceeded this) and an accompanying photo if possible. I also asked authors to confirm that the funds were used for the purpose awarded since we do not request a statement of accounts.

In some cases, the covering email included additional comments or information that I considered relevant. I have included these in the reports below in italics.

*Mark Carine
Grants and Awards Secretary
Systematics Association
5th June 2014*

Mary Aime, Purdue University (£1260)

Macrofungal Diversity on the Guiana Shield: Year 14 of a long-term expeditionary field study

The Fund was applied to defray costs for the Dec. 2013-Jan. 2014 expedition to Mabura, Region 10, Guyana as part of a continuing long term study of the macrofungi that occur in extremely remote tropical forests of the Guiana Shield. A bush camp was erected and a total of 72 fully documented collections were made, including new species, extremely rare new taxa, and several that, despite 14 years of field work in the region, had never been previously encountered. Additionally, new populations of a newly described endemic genus and species, will be used in studies seeking to understand the drivers of adaptive evolution in sequestrate fungi.

Thank you so much for your email and for my Systematics Research Fund Award from the Society. I did, indeed, use these funds for field research in Guyana for Dec. 2013-Jan. 2014 expedition.



The Dec. 2013-Jan. 2014 team: Dillon Husbands, Francino Edmond, Peter Joseph, Cathie Aime, Christopher Andrew, Rachel Koch, and Luciano Edmond.



Olaoluwa P. Akinwale, Molecular Parasitology Research Laboratory, Public Health Division, Nigerian Institute of Medical Research, Lagos, Nigeria (£980)

Molecular systematics of snail intermediate hosts of *Schistosoma haematobium* in Nigeria

Despite the importance of freshwater snails of the genus *Bulinus* as intermediate hosts of schistosomes, unambiguous identification and differentiation remain challenging. This study funded by Systematics Research Fund (SRF) award applied molecular approaches to characterize 149 *Bulinus* snails in order to achieve a better understanding of schistosomiasis epidemiology in an endemic region Southwest Nigeria. They were PCR screened for schistosome infection and characterized by PCR-RFLP/sequencing of amplicons of their entire *Its* regions including the 5.8S rRNA gene. About 31% were infected, while *B. globosus* (*Bulinus africanus* species complex), *B. forskalii*, *B. camerunensis* and *B. senegalensis* (*B. forskalii* species complex) were identified. All the sequences have been submitted to GenBank database and have accession numbers [GenBank: KF989347 - KF989359, KJ184520, KJ361799 - KJ361814].

I also confirm that the funds were used for the purpose awarded.



Picture showing a member of the team using a standard snail scoop net to search for snails from a human-water contact point within Yewa River Southwest Nigeria.

Manuscript submitted for publication

Olaoluwa P. Akinwale, Opeyemi G. Oso, Oyetunde T. Salawu, Alexander B. Odaibo, and Pam V. Gyang. Molecular characterization of *Bulinus* snail intermediate hosts of schistosomes in Ogun state, Southwest Nigeria. *Parasites and Vectors*.

Enhancing the zoological collection of the National University of Laos

Zoological Collection, NUoL

The Faculty of Environmental Sciences, National University of Laos has provided a room with air conditioning for the zoological collection. With the Systematic Association funding, we obtained:

- three steel cabinets for the storage of wet specimens and dry skins and skulls,
- alcohol for preserving wet specimens,
- an external hard drive for the storage of digital images of specimens, echolocation calls of bats and pdf literature.

A highlight of the collection to date is the holotype of the Laotian giant flying squirrel, *Biswamoyopterus laoensis* Sanamxay *et al.* 2013 (see extract from title page above). Paratypes are held in the UK and Thailand. This new species is a member of one of the world's rarest genus of flying squirrels, previously only known from one specimen collected in North-east India in 1981.



Wet specimens of bats (above) and dry skin of squirrels (below) in the zoological collection in the National

Research and Publications

The Systematics Association's grant is acknowledged in two published papers. The grant will be acknowledged in a further two papers which have been submitted/ accepted for publication respectively.

On behalf of all the staff and students of the National University of Laos, I would like to thank the Systematics Association for their financial support.

Through such support, I am certain that the zoological collection will expand considerably over the coming years and will provide an essential foundation for an expansion of biodiversity research by university-based, in-country taxonomists in the future.

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Article

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Rediscovery of *Biswamoyopterus* (Mammalia: Rodentia: Sciuridae: Pteromyini) in Asia, with the description of a new species from Lao PDR

DAOSAVANH SANAMXAY^{1,2,*}, BOUNSAVANE DOUANGBOUPH^{1,2}, SARA BUMRUNGSR¹,
SYSOUPHANH XAYAVONG¹, VILAKHAN XAYAPHET¹, CHUTAMAS SATASOOK^{2,3} & PAUL J.J. BATES⁴
¹Faculty of Environmental Sciences, National University of Laos, Dong Dok Campus, P.O. Box: 7322, Xaythany District, Vientiane Capital, LAO PDR

²Department of Biology, Faculty of Science, Prince of Songkla University, Hat Yai, Songkhla 90112, THAILAND

³Princess Maha Chakri Sirindhorn Natural History Museum, Prince of Songkla University, Hat Yai, Songkhla 90112, Thailand

⁴Harrison Institute, Centre for Systematics and Biodiversity Research, Bowerwood House, St. Botolph's Road, Sevenoaks, Kent, TN13 3AQ, GREAT BRITAIN

*Corresponding author. E-mail: daosavanhx@gmail.com

Abstract

A new species of the flying squirrel genus *Biswamoyopterus* is described from Lao PDR. It is based on a single specimen collected from a local food market at Ban Thongnami, Pak Kading District, Bolikhamxai Province. The new taxon shows close affinities to *Biswamoyopterus biswani*, which is only known from the holotype collected in 1981, 1250 km from the current locality, in Arunachal Pradesh, Northeast India. However, it differs substantially in pelage colour, most particularly on the ventral surfaces of the body, patagia, tail membrane, and tail. The single specimen was found in an area of central Lao PDR, which is characterised by its extensive limestone karst formations and which is home to other rare endemic rodents, including the Khayou (Lomomys oenigmus) and the Lao limestone rat (Saxatilomys paulinae).

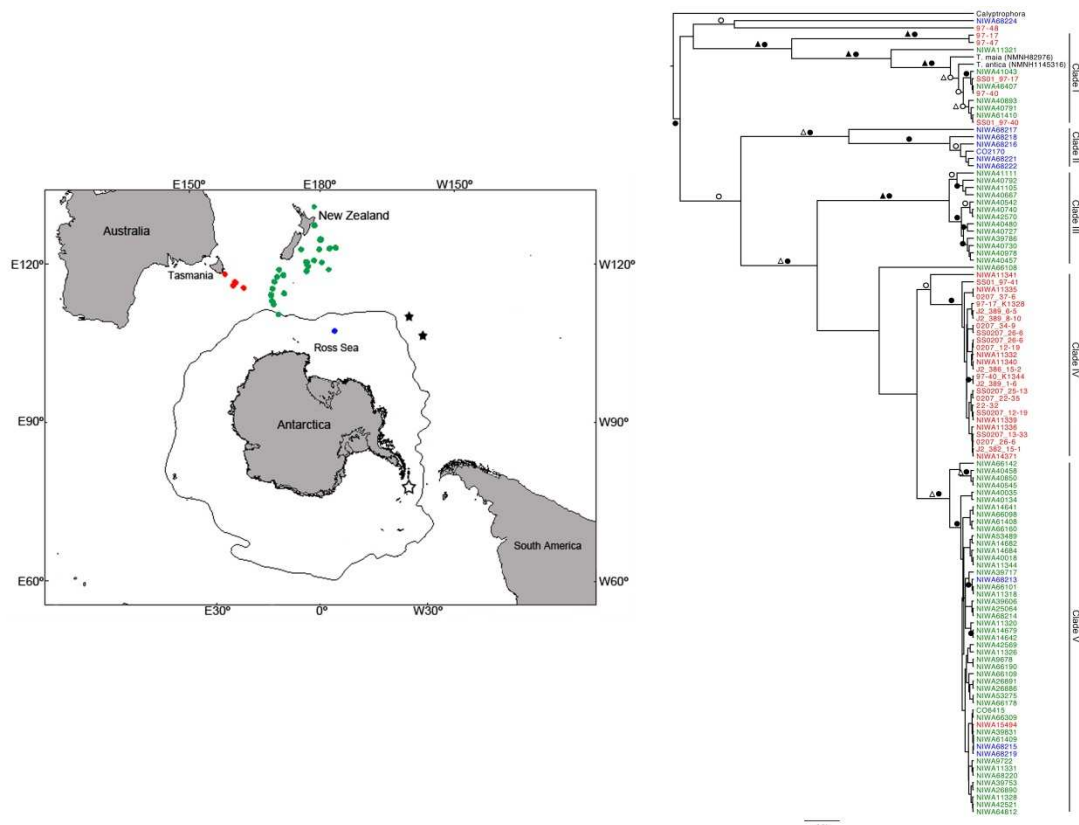
Key words: Southeast Asia, flying squirrel, taxonomy, bush meat

Luisa F. Dueñas, Laboratorio de Biología Molecular Marina -BIOMMAR-, Universidad de los Andes, Bogotá, Colombia (£1000)

Diversification of the deep-sea octocoral *Tokoprymno maia* across the Antarctic Circumpolar Current

Despite the unquestionable importance of Antarctica to various global processes, the distribution of deep-sea populations across the Southern Ocean remains poorly known. Antarctica is surrounded by the Antarctic Circumpolar Current (ACC), which is the largest and strongest in the world, which is thought to be a permeable barrier allowing for widespread distributional patterns. The deep-sea octocoral *Tokoprymno maia* is a brooder species widely distributed on the sub-Antarctic and Antarctic regions. Given the potential for population structure due to limited dispersal we want to determine the role of the ACC as a barrier for dispersal. We used sequences from one nuclear region, ITS2, to evaluate gene flux between populations from Tasmania, New Zealand and Antarctica. Our preliminary results show high population structure between the three localities. From a morphological and molecular perspective, we found cryptic species distributed in New Zealand (Clade III), Tasmania (Clade IV), and Antarctica (Clade II). With our preliminary results it is not possible to discard the hypothesis of the ACC acting as a barrier against genetic flux between northern and southern populations. The use of additional genetic markers and correlations with oceanographic data could aid in the proposal of a phylogeographic hypothesis for *T. maia*.

The funds that were granted to me by the Systematics Research Fund were used for sequencing services for the ITS2 gene, as stated in the application budget.



Anahí Espíndola, University of Idaho, Moscow, ID, USA (£1164)

Disentangling the evolutionary, biogeographic and ecological evolution of *Chalepogenus* Holmberg (Apidae: Tapinotaspidini)

The South American bee genus *Chalepogenus* (Apidae: Tapinotaspidini) has been proposed to contain 26 species included into two subgenera: *Chalepogenus* (*Chalepogenus*) and *Chalepogenus* (*Lanthanomelissa*). Although previous studies have tried to use morphological data to disentangle the relationships in the group, much discussion exists on the taxonomic accuracy of the different taxa.

Here, I used six molecular markers to infer a molecular phylogeny for the genus, and thus advance in the understanding of its taxonomy, biogeography and patterns of plant exploitation. My results indicate that the genus *Chalepogenus* s.l., as well as many of its species are supported by molecular data. However, subgenera do not always appear to be supported by the molecular data and future work should further investigate this.

Besides stating that the funds have been used for the purposed award, I wanted to take advantage of this email to thank the Systematics Association for giving me the opportunity to perform this work.

Antonia G Ford, University College London (£1032)

***Oreochromis* phylogeny and the colonisation of soda waters**

A SRF 2013 award has enabled the generation of a robust *Oreochromis* phylogeny in which to investigate the colonisation of soda lake and freshwater habitats by these cichlid fishes. The grant award has been used to support sequencing of nuclear markers in a dataset including 5 nuclear markers and 3 mtDNA markers of 45 samples. These data are currently being analysed using Bayesian inference of the concatenated data as well as coalescent approaches of the nuclear dataset. BEAST software is being used to estimate divergences based on fossil calibrations. Species delimitation and origination of adaptation will be further tested using BPP and BayesTraits software programs.

I can confirm that the funds were used for the purpose awarded - sequencing of nuclear markers for the project

Elliot Gardner, Chicago Botanic Garden / Northwestern University (£970)

Population genetics and species limits of *Artocarpus odoratissimus* Blanco (Moraceae)

The genus *Artocarpus* J.R. Forst. and G. Forst. (Moraceae) contains about 70 species of monoecious trees, with a center of diversity in the lowland tropical forests of Malesia. In addition to well-known species such as *A. altilis* (Parkinson) Fosberg (breadfruit) and *A. heterophyllus* Lam. (jackfruit), the genus contains numerous other underutilized crops including *Artocarpus odoratissimus* Blanco, native to the lowland dipterocarp forests of Borneo. Fieldwork and microsatellite analysis supported by the Systematics Research Fund have focused on a putative wild form (the *barbtus* form) characterized by smaller syncarps, less frequent flowering, and different vegetative characters. Initial results suggest that the genetic diversity of the cultivated form comprises a subset of that found in *barbatus*, supporting a hypothesis that the *barbatus* form is the wild progenitor of a domesticated cultivated type.

Mark van der Giezen, Biosciences, University of Exeter & Chris G. Bryan, Environment and Sustainability Institute & Camborne School of Mines, University of Exeter (£1500)

Assessing the rare biosphere of an acid mine drainage site.

Acid mine drainage (AMD) samples were isolated from Wheal Jane in Cornwall.

Sample collection was initially hindered by extreme rainfall in South West England which led to very high water levels (sample dilution) and site access issues.

Cultures established to assess metal tolerance under various conditions.

A final year Applied Geology student worked with us to determine basic physiological data of these cultures. Basic rates of iron removal have been determined.

Environmental DNA has been isolated from initial AMD samples.

New promising method for microbial profiling is being trialled (Faith et al (2013) DOI: 10.1126/science.1237439) which delivers high depth and high precision but at reduced cost.

We started collaborating with Dr. David Bass from the Natural History Museum because of his experience in microbial profiling of microbial eukaryotes and we believe our joint expertise will be a fruitful collaboration in this exciting field.

We expect to get publishable results early summer and our plan is to produce a manuscript by late summer/early autumn acknowledging the Systematics Research Fund.

All funds, plus own additional contributions, have been spent as indicated in original application.

This grant, plus a few other small ones we have secured recently, have allowed us to make momentum and we have been invited to take part in a multi-million EU grant related to the topic of our SRF proposal. So, it are truly great times for us and we are thankful for the support of the Systematics Association and the Linnean Society.

**Gareth Wyn Griffith, Institute of Biological. Environmental and Rural Sciences,
Aberystwyth University (£1486)**

**Does (Bacterial) Taxonomy Matter? The curious case of *Polaromonas* and the
*Betaproteobacteria***

The project's aim was to compare phylogenomic and 16S rRNA phylogenetic insights into the taxonomy of the *Betaproteobacteria*, and specifically the genus *Polaromonas*, which is thought to be cosmopolitan within glacial environments on the basis of 16S rRNA gene analyses. Consequently we isolated bacteria from snow and slush samples from Arctic and alpine glaciers (Fig. 1) using low--- nutrient agar and sequenced 16S rRNA genes to identify the taxonomic affiliations of the isolates. *Betaproteobacteria* were highly dominant, followed by *Alphaproteobacteria* and a small number of actinobacterial isolates. Of the *Betaproteobacteria*, most isolates were affiliated to *Janthinobacterium* and *Polaromonas*. A subset of these isolates were analysed by whole genome sequencing using Ion Torrent PGM. Analysis of assembled and annotated genomes is ongoing, but an early insight is the presence of a 2Mbp dispensable genome within cryospheric *Polaromonas* isolates. The rRNA gene operons in the sequenced genomes are present at low copy number, thus presenting a putative explanation for the apparent ubiquity of ribotypes against a background of genomic diversity. Our analyses continue, with the intent of preparing a manuscript for publication.



Fig1: Sampling glacier surfaces for bacteria (credit: S Jennings)

Traci Grzymala, Department of Environmental Science, University of California, Berkeley (£945)

Utilizing Confocal Laser Scanning Microscopy to Elucidate the Systematics of the Aderidae

This project resulted in the acquisition of Confocal Laser Scanning Microscopy (CLSM) images for the male and female genitalia of all currently described genera of the Aderidae (Coleoptera). Image detail and quality were found to be comparable to Scanning Electron Microscopy (SEM) images, but with the added benefit of specimens being fully recoverable after imaging. This is essential for many groups in which taxa are only known from type series. Numerous morphological characters relating to the size and shape of the genitalia have now been scored and will be analyzed with additional characters of the integument for this understudied beetle family. Results from phylogenetic analyses using these morphological character data will be published within the next year. The success of this project indicates that CLSM is a currently under-utilized microscopy technique for systematists and should be employed in future studies.

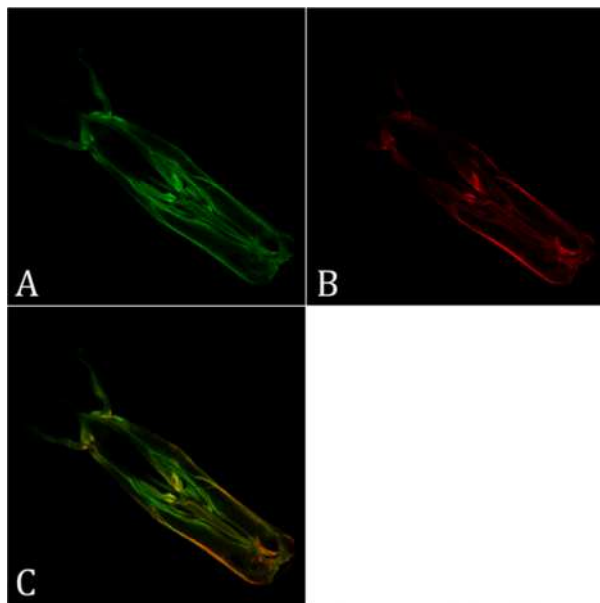


Figure 1. CLSM images of male genitalia of *Zarcosia troglodytes*. (A) Emission from Argon laser, (B) Emission from HeNe1 laser, and (C) composite image from these two laser sources.

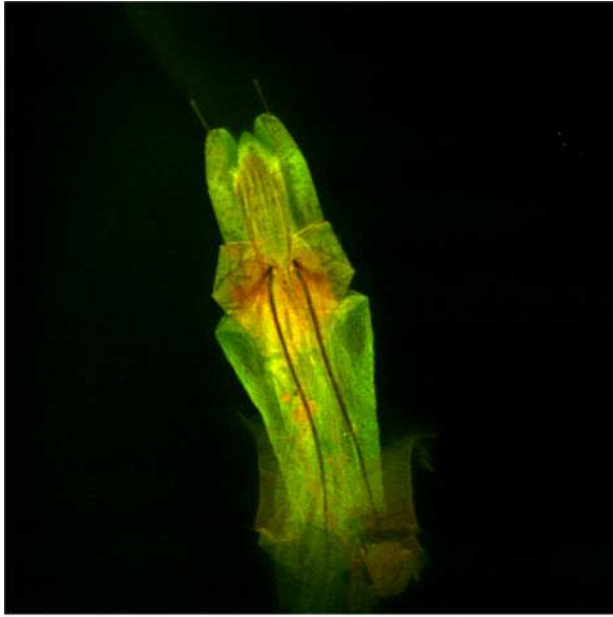


Figure 2. Composite CLSM images of female genitalia for *Ganascus ventricosus*.

Zeehan Jaafar, National Museum of Natural History, Smithsonian Institution, USA (£1300)

A Review of Mudskippers & Allies – Implications for Broader Studies

The proposed study aimed to carry out a systematic review of the mudskippers and allies, a group of cryptic fishes belonging to the subfamily Oxudercinae, family Gobiidae. The funds I received facilitated a critical portion of this study, the examination of type and non-type specimens at the Muséum National d'Histoire Naturelle in Paris, France, and Museum Naturalis in Leiden, The Netherlands. These, together with other non-type material I examined, allowed me to solve long-standing uncertainties of the *Periophthalmus argentilineatus* and *Periophthalmus minutus* species complexes. These findings will directly culminate in two papers, one of a revision of the genus *Periophthalmus* and another a revision of the genus *Apocryptodon*. The data will also be used in two other indirectly related papers, on the phylogenetic and biogeographic studies of the subfamily Oxudercinae. All papers are currently being prepared for publication.



Periophthalmus minutus, Cleared and double-stained, blue for cartilage and red for ossified bone.

Enhancing the systematics and recording of British ascidians with improved field characteristics

Short summary: During the summer of 2013 Seasearch volunteer divers undertook fieldwork around Anglesey and the Llyn Peninsula, targeting known ascidian-rich reefs. A substantial number of species were photographed *in situ* and then sampled to generate voucher specimens for archive at the National Museum of Wales. The highlight of the work was finding four current undescribed *Aplidium* species that do not fit existing keys. These are distinctive and readily visible, often covering 10-20% of the reef surface. To find so many undescribed species close to shore and within recreational diving depths (< 20m) is a stark reminder of how little we know regarding the biodiversity of our own coastal waters.

Full summary: Ascidians are soft-bodied suspension feeders that contract strongly upon disturbance. For British ascidians, the key reference materials (Berrill's *The Tunicata*, Millar's Linnean Synopsis) are 40-60 years old, and predominantly use internal anatomical features. Descriptions of the appearance of expanded animals *in situ* are very limited, reflecting the lack of underwater photography at that time and the predominant examination of dredge or intertidal samples, often post-preservation. Very little formal taxonomic work has been undertaken on British ascidians since 1970, at which point extensive lumping of taxa had been imposed. Since then scuba diving has become widespread amongst amateur and professional naturalists, and recently there has been an explosion in the use of digital underwater cameras. A photograph can show a range of anatomical and morphological features (including distinctive colour patterns), many of which can only be seen properly when the animal is alive and actively pumping water. Divers can also access specimens under-represented in grab/dredge samples. This has led to reports of several undescribed species (eg the "strawberry" seasquirt present around Skomer and several other species that do not fit existing keys).

The purpose of this project was to use volunteer divers to take *in situ* digital photographs of ascidians and to take matched samples for preservation as voucher specimens, thus allowing dissection-based verification of the identification at a later point. A group of Seasearch volunteer divers undertook a total of 24 person-dives around Anglesey and the Llyn Peninsula during the summer of 2013, with each buddy pair taking photographs and collecting samples that were relaxed and fixed later the same day.

A good range of species were recorded, photographed and sampled. Seasearch survey forms were completed for each dive and submitted to Marine Recorder and the voucher specimen collection will be maintained in the National Museum of Wales. Although this core aim of the project was fulfilled, what became quickly evident was that these sites were densely covered with several species of compound ascidians in British waters that are visually very distinctive and appear undescribed. All four appear to be *Aplidium* species based on zooid morphology, and examination of specimens taken during this project by both Bernard Picton (NMNI) and John Bishop (MBA) confirms them to be not only new to the UK species but also apparently undescribed in the literature (although with the caveat that there are some 300+ known *Aplidium* species worldwide), with all four species being very visually distinct from any known British or NE Atlantic species.

It should be noted that these species are far from cryptic; at some dive sites they were a dominant component of the sessile fauna, forming large patches covering 10-20% of the reef surface, and once identified most of the volunteer divers could readily find specimens for photography. Why then have these species not been recorded or described before? The answer is undoubtedly our partial ability to sample the ocean fauna around our shores. These dive sites are all readily accessible recreational dive sites within a few hundred metres of the shore, in depths of less than 20m. Yet the ascidian researchers from the mid 20th century were not divers able to record these species *in situ*, but instead were dependent upon grab or dredge samples. These four are all soft, low-growing encrusting species that are found on solid bedrock substratum, meaning that grab samples would be highly unlikely to contain them in an intact state. The widespread take up of inexpensive underwater digital cameras over the last decade has transformed the ability of amateur and professional divers to record species and morphological appearances that are simply not possible using surface-based sampling techniques. That a small group of volunteer divers can spend a weekend in a readily-accessible area of the British coastline and dive on reefs where much of the sessile life are species new to science is a sobering reminder about how very little we

know about the waters around the United Kingdom. For other taxa it may be necessary to mount complex expeditions into remote areas of tropical rainforest in order to discover new species; for ascidians you just have to swim off the Welsh coast.

Diver-based recording is non-trivial, and expensive activity especially when boats are required (as was here, in order to reach the tide-swept ascidian-rich reefs). To undertake 24 person-dives at full economic cost would have been prohibitive were it not for the willingness of Seasearch volunteer divers to give their own time, together with their own diving and photography equipment, to the project. The project would also not have been possible without the extensive preparation that had been undertaken by the North Wales Seasearch community who spent many dives over the previous 18 months scouting out potential ascidian-rich reefs to be targeted in this fieldtrip. The result was that all four dives were on extremely diverse and ascidian-rich reefs, generating a high species count and a substantial specimen collection. Funding from the SRF was instrumental in releasing this added value from the volunteer base and demonstrates how the Seasearch citizen science community can act as a very cost-effective research resource.

Again thanks for the SRF funds - it was amazing how a small amount of money unlocked so much additional benefit by using 'citizen scientists'!



Krzysztof M. Kozak, Department of Zoology, University of Cambridge (£800)

Phylogenomics demonstrates the non-hybrid origin of a hybrid phenotype in a *Heliconius* butterfly

Heliconius hermathena (Hewitson 1854) is a Neotropical butterfly with a uniquely non-mimetic aposematic wing pattern, which resembles a combination of the red band of *H. erato* and the white stripes of *H. charithonia*. I tested the tempting idea that this unique morphology resulted from a homoploid hybridisation event. I collaborated with Dr Owen McMillan at the Smithsonian in Panama and generated whole exome data (17 million base pairs) for 17 species of *Heliconius* by mapping Illumina reads to a reference genome. Phylogenies and population genetic tests with thousands of genes demonstrate that the supposedly hybrid *H. hermathena* is essentially a sister species of its putative parent *H. erato* and does not have a mosaic genome. Sliding window analysis across the wing pattern loci shows no evidence of adaptive introgression of the white locus from *H. charithonia*. However, coalescent analyses intriguingly suggest that another species in the group may be a cryptic hybrid, and I am now extending the study to the entire tribe Heliconiini.

I can confirm that the funds were used towards the designated purpose (relevant molecular work and travel to visit the project supervisor in Panama). The project had some surprising results and I am now writing it up with an intent of submitting to a major journal. My final PhD chapter is a continuation of this project, trying to test some of our ideas on Heliconius hybridisation and phylogeography more broadly. In addition, the trip to Panama was a great opportunity to give a Heliconius systematics talk at the Smithsonian Tropical Research Institute, and to launch a workshop on Genomics for Ecologists.

Jim Labisko, Durrell Institute of Conservation and Ecology (£1466)

Amphibians on the EDGE: Evolutionary relationships and conservation ecology of sooglossid frogs

The generous support of the SRF provided me with the opportunity to significantly extend the scope of my phylogenetic work on an endemic, threatened, globally significant family of frogs; the Sooglossidae. Focussing my research on a newly discovered population, results thus far have indicated significant genetic differentiation between these and related frogs on other islands; results supported by observable differences in their respective vocalisations. In addition, and as a direct result of my SRF award, additional analyses incorporating all four sooglossid species have revealed further divergence between separate island populations, the final analyses of which are ongoing and due to be published in 2014.

I confirm that the sum awarded was used for molecular work as stated in my original application.



Jesús E. Maldonado, Center for Conservation and Evolutionary Genetics , National Zoological Park , National Museum of Natural History , Smithsonian Institution, USA (£695)

Systematics of New World deer, with emphasis on neglected Neotropical species

I was awarded with £695 from the Systematics Research Fund (SRF; 2012/13 round) to carry out molecular work for the project “Systematics of New World deer, with emphasis on neglected Neotropical species”, in which I am working in collaboration with Dr. Kristofer Helgen and Dr. Eliécer Gutiérrez at the Smithsonian Institution. The funds were used to cover the costs of one pyrosequencing run in an Illumina Miseq platform for obtaining mitochondrial genomes of Americas’ deer.

During this last year, we have accomplished the isolation of DNA from ca. 300 museum specimens; the preparation of corresponding DNA libraries (using Nextera protocols); and the design and use of an array for capturing mitochondrial genomes from these libraries. We used the total amount awarded by the SRF to cover the costs of the aforementioned pyrosequencing run, by which we successfully obtained 78 mitochondrial genomes. These mitochondrial genomes represent the most comprehensively dataset available for phylogenetic inference of Americas’ deer of the tribe Rangiferini, and include data for all genera and species of currently recognized for this group. We are working in order to obtain both nuclear sequence data and numerous additional mitochondrial genomes (to allow dense geographic sampling of widely distributed species) using the DNA libraries already prepared. We expect to complete laboratory work in late 2014, and have the first manuscript to report our results in early 2015.

My collaborators and I thank the Systematics Association and the Linnean Society of London for the support they have provided us with. The funds received were critical to obtain the first mitochondrial genomes of our project; the latter allowed us to detect deep intraspecific divergences for taxa in which we are now making emphasis with regard to geographic sampling.

Nigel Marley, Marine Biology & Ecology Research Centre, and the Marine Institute, Plymouth University Drake Circus, Plymouth (£1000)

Tardigrades of the South Shetland Islands, Antarctica, and Chile

In January-February 2014 I took part in an expedition to South Shetland Islands, Antarctica, organised by INACH. Project funding was awarded to Dr. Matthew R. Lee, Universidad de Los Lagos, Chile, and my SRF award enabled me to reach the expedition start in Punta Arenas, Chile.

I spent 37 days in Chile and Antarctica collecting samples of mosses, lichens and sediments in which to search for tardigrades. Expedition time in Antarctica was curtailed due to weather and logistics reasons. Sample processing is expected to take 18 months. Specimens of other taxa collected will be sent to other researchers.

Could I also express my sincere thanks to both societies for awarding me the grant, without which I would not have been able to join the expedition. It was a fantastic experience and I am looking forward to publishing the results in papers and articles over the next couple of years. I've already given three presentations since returning to work in March.



Collecting lichen samples on the beach at Snow Island, South Shetlands Islands (photo: Dr. Matthew R. Lee)

Sarah Pene, South Pacific Regional Herbarium, University of the South Pacific, Fiji (£542)

Taxonomy, phylogeography and evolutionary history of Fiji's native *Peperomia* Ruiz & Pav. (Piperaceae)

This project aims to expand and consolidate the collections of Fijian *Peperomia* species, to investigate more closely their distributions across the archipelago, to review their taxonomic classification and to determine their phylogenetic and evolutionary history.

So far specimens of 9 *Peperomia* species have been collected from sites in the interior of the two largest islands: Viti Levu and Vanua Levu, including areas of cloud forest at elevations over 900m. In Viti Levu, specimens were also collected in the Wainavadu catchment, a region from which there have been no *Peperomia* collections previously.

Fieldwork will continue throughout 2014, with expeditions currently planned for the island of Rotuma and its surrounding islets, which lie 600km north of the main Fiji archipelago, as well as the island of Taveuni, Fiji's 3rd largest island.

Navigation and location recording in the field was greatly assisted by the use of the GPS receiver purchased with funding from the Systematics Association.



The Wainavadu River, Viti Levu, Fiji (photo: S. Pene)

David Penney, Faculty of Life Sciences, University of Manchester (£1200)

Fossil Insects: An introduction to palaeoentomology (book)

Summary: Funds were sought to cover the purchase of images and to part subsidise publication costs of a new book on fossil insects by Drs D. Penney & J.E. Jepson to be published by Siri Scientific Press, a publisher specializing in this area, whose books consistently receive excellent reviews in professional newsletters and journals. The funds have been used for the intended purposes and this work is now in the very final stages of preparation. We are aiming for a formal release date of 31 July, 2014, with an initial print run of 1000 copies. A copy of the book will be sent to the Library of the Linnean Society when available.

About the book: ISBN 978-0-9574530-6-7 (this number has not yet been formally registered, but will be within the next few weeks). 224 pages, 240 x 165 mm (printed and bound in the UK by Henry Ling). 240 colour photographs (representing 44 insect orders from 54 deposits dating from Carboniferous to Recent) Softcover, expected RRP £24.99

From the back cover: *Palaeoentomology represents the interface between two huge scientific disciplines: palaeontology – the study of fossils, and entomology – the study of insects. However, fossils rarely feature extensively in books on insects, and likewise, insects rarely feature in books about fossils. Similarly, college or university palaeontology courses rarely have an entomological component and entomology courses do not usually consider the fossil record of insects in any detail. This is not due to a lack of insect fossils. The fossil record of insects is incredibly diverse in terms of taxonomic scope, age range (Devonian to Recent), mode of preservation (amber and rock) and geographical distribution (fossil insects have been recorded from all continents, including Antarctica). In this book the authors aim to help bridge the palaeontology–entomology gap by providing a broadly accessible introduction to some of the best preserved fossil insects from a wide range of deposits from around the globe, many of which are beautifully illustrated by colour photographs. Also covered are insect behaviour and ecology in the fossil record, sub-fossil insects, trace fossils and insect species longevity.*

Just as insects are useful as ecological indicators today, the same can be expected to be true of the past. Such applications of the insect fossil record are briefly discussed. It is hoped that this book will encourage a few future researchers to enter the fascinating realm of palaeoentomology and to this end there is a section on how to become a palaeoentomologist. However, it is aimed at a much broader audience – those with an interest in fossils and/or insects in general, who will no doubt marvel at the diversity and excellent preservation of the fossils illustrated.

David Penney is an Honorary Lecturer in the Faculty of Life Sciences at the University of Manchester, UK, a Fellow of the Linnean Society of London and has a PhD and two decades of research experience on fossils preserved in amber. James E. Jepson is a Humboldt Research Fellow at the Museum für Naturkunde in Berlin, Germany and has a PhD and one decade of research experience studying fossil insects in rock. Both are Fellows of the Royal Entomological Society.

There is a statement at the end of the acknowledgements as follows: *Special thanks also go to the Linnean Society of London and the Systematics Association for a grant to DP to part support production of this work.*

Thank you again for supporting this important project!

Cover image: Ground beetle (Coleoptera: Carabidae) from Enspel, Westerwald, Germany. An Upper Oligocene (24.7 Ma) oil shale deposit with abundant and diverse fossils insects.

For further details about Siri Scientific Press see here:
<http://www.siriscientificpress.co.uk/Pages/default.aspx>



Ana Perera, CIBIO-Universidade do Porto, Portugal (£1372)

Phylogeography and taxonomic revision of the Moroccan Rock Lizard, *Scelarcis perspicillata*

During this proposal, genetic samples from all the distribution range of *S. perspicillata* were analysed using multiple mitochondrial and nuclear markers. The results confirmed the non-validity of the three existing subspecies, described on basis to external morphology and distribution. The mitochondrial data confirmed the existence of two main lineages, one distributed across northeast Morocco, Habiba islands and Minorca (Balearic Islands), and the other in the rest of Morocco. Structure within the lineages followed a geographic pattern, with different morphotypes sharing the same lineage. Nuclear markers support these results, and confirm the lack of gene flow between morphotypes when in sympatry. A taxonomic revision including genetic, morphological and environmental data is currently under preparation.

Funds received were used for the purpose awarded. The outcome will be shortly submitted to an indexed scientific journal, and the Systematic Research Fund acknowledged due to its valuable contribution.



Scelarcis perspicillata

Photo: Ana Perera

Unravelling the divergence mechanisms in *Tarentola mauritanica* geckos: a complex species complex

Since the first phylogeographical study on *T. mauritanica*, it was recognized that this species was, in fact, a complex (or species---complex) comprised by several cryptic forms, characterized by extremely high levels of mitochondrial DNA divergence between them, but with a corresponding lack of morphological diversity. In this project and using distinct morphological characters and molecular markers (7 nDNA, and 2 mtDNA), I was able to:

- Confirm that the five cryptic taxa correspond to distinct species of *Tarentola*;
- To make a taxonomic revision of the genus.

For all 60 individuals of *T. mauritanica* we obtained 857bp for the mitochondrial DNA (12S and 16S) and 3,417bp for the concatenated nuclear dataset (ACM4+bzw1+lfabp+lztf1+MC1R+PDC+ Rag2).

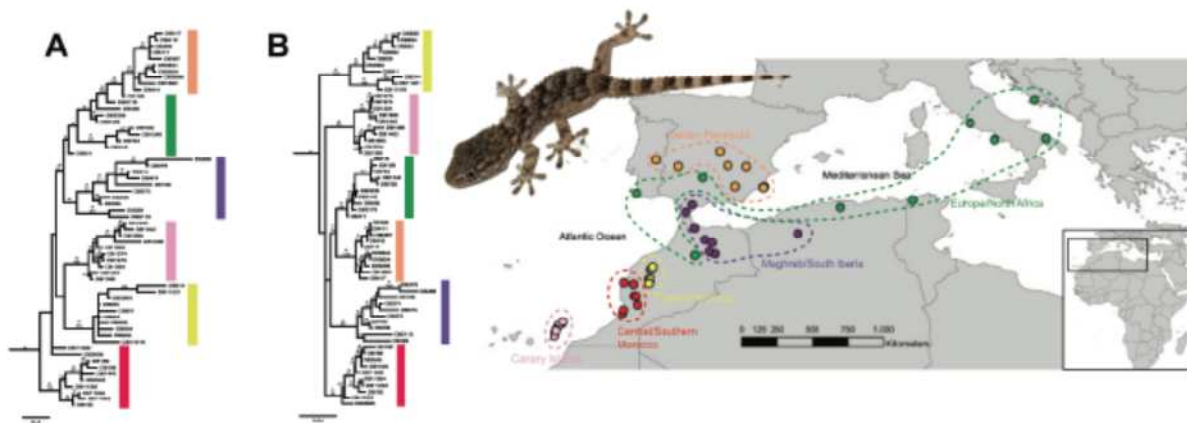


Figure 1. Phylogenetic trees for the concatenated nDNA (A) and all the combined markers (mtDNA+nDNA) (B). Values above the branches are ML bootstrap scores and the asterisks indicate the nodes with Bayesian posterior probabilities $\geq 95\%$. The colours of each lineage are the same as in the map where the geographic distribution of the specimens used in the study is represented.

The phylogeny based on nuclear DNA fragments (Fig.1A), supports as monophyletic groups the Maghreb/South Iberia, Canary Islands and Central Morocco clades. The European/North African Clade renders the Iberian Clade as paraphyletic and also the Central/Southern Morocco group is not monophyletic. On the contrary, the genealogy obtained when all markers are concatenated (Fig.1B) supports all candidate species as monophyletic lineages, with high scores of bootstrap and posterior probabilities. Nevertheless, the phylogenetic relationships between both genealogies are roughly identical, although not highly supported. The results obtained from the Bayesian cluster analyses (Fig.2) support the six candidate species as independent groups.

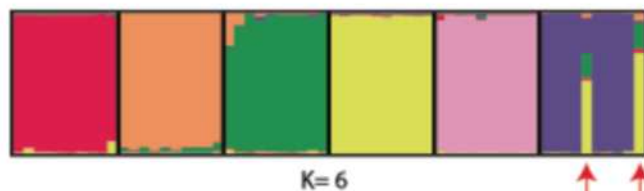


Figure 2. Population structure estimation with $K=6$, considering an admixture model with allele frequencies correlated. Each individual is represented by a thin vertical line, which is partitioned into K coloured segments that represent the individual's estimated membership fractions in K clusters. The black vertical divisions separate individuals from different populations.

The results from STRUCTURE with $K=6$ were used to define the “species” for the species tree analysis in *BEAST. The tree inferred with information from both mitochondrial and phased nuclear markers (Fig.3) recovered a similar topology as observed in Fig. 1B, with higher posterior probabilities and no polytomies.

The cladogenesis between the Canary Islands and Central/Southern Morocco was poorly supported (60%) and also the split between these two groups and the Central Morocco has a low posterior probability (73%). Bayesian species delimitation supports all six candidate species within the *T. mauritanica* species-complex as “putative” species.

The morphological analyses are still an ongoing task and once they are finished, I will proceed to the description of each lineage of the *Tarentola mauritanica* complex as a full species.

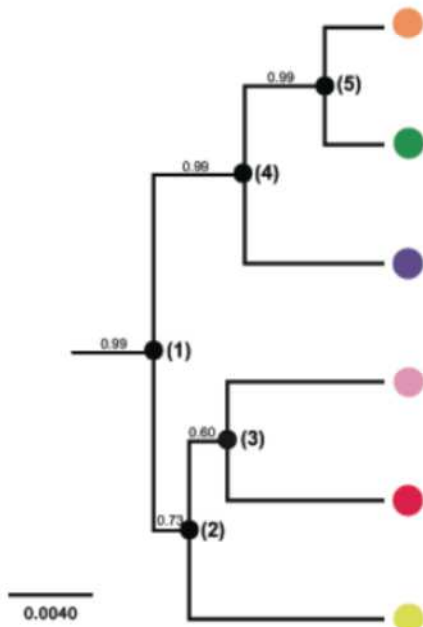


Figure 3. The six candidate species models for the *T. mauritanica* species-complex inferred with *BEAST using the combined mitochondrial and nuclear DNA markers. Values above the branches are posterior probabilities. Bayesian species delimitation infers a speciation event at nodes marked by a solid circle; numbers in parentheses refer to node number. The colors used are the same as in Figure 1.

**Marie-Stéphanie Samain, Instituto de Ecología, A.C., Centro Regional del Bajío, Mexico*
(£1500)**

Botanical “Lonesome Georges” of the Andes: systematics of climbing Hydrangeas in Peru

On one day in Peru you can take breakfast on the beach, lunch in the high Andes, and dinner in rainforest. It needs no further explanation that these spectacular landscape changes may challenge field work, especially in the rainy season! Amidst extreme rains, resulting amongst others in fallen bridges and muddy roads, we have observed and documented fourteen *Hydrangea* species, many of them new to science. And thanks to these rains, most plants were flowering! We have confirmed that some of these indeed are botanical “Lonesome Georges”, known from only one locality, and discovered that caterpillars of a yet undefined night moth family seem to have a specific relation with these lianous hortensias.

Please find in attachment the report about the expedition we organised in Peru from 21 November to 16 December 2013, partially funded by the Systematics Research Fund in the framework of the project "Botanical "Lonesome Georges" of the Andes: systematics of climbing Hydrangeas in Peru", for which we are very grateful. For your information, the collection permit granted to us by the Dirección de Gestión Forestal has as number 0395-2013-MINAGRI-DGFFS/DGEFFS.



The inflorescence of a male plant of a new *Hydrangea* species, from a locality near Huancabamba in the so-called “Selva Central” in the department of Pasco, one of the diversity hotspots of this plant group.

*In cooperation with Esteban MARTÍNEZ SALAS, National Herbarium of Mexico, Guillermo PINO INFANTE, Museo de Historia Natural, Lima, Peru, Rocío ROJAS, Jardín Botánico de Missouri, Oxapampa, Pasco, Peru, and local instances for collection permits .

Michelle Taylor & Catherine Head, Department of Zoology, University of Oxford (£1160)

Hidden Biodiversity of Madagascan Coral Reefs: are humans impacting the unseen?

In July 2013 we embarked on fieldwork in Nosy Be, Northwest Madagascar, to quantify coral reef cryptofauna biodiversity and study how this unseen community is affected by human impact. Cryptofauna includes small vertebrates and invertebrates such as crabs, brittlestars etc. that live hidden within reef framework. With assistance from local dive shop Sakatia Lodge, we surveyed 37 dead coral colonies on inshore (varying degrees of human impact) and offshore (relatively unimpacted) reefs, whilst concurrently collecting fish diversity and benthic cover data to quantify reef health. We are presently identifying decapod and mollusc cryptofauna species using morphological and molecular techniques, and analysing associated reef health data.



An 'unimpacted' reef at Nosy Be

Alpha taxonomy of *Squalus* in the eastern Atlantic, Mediterranean and Black seas

Our project aims to clarify the alpha taxonomy of the highly diverse, worldwide-distributed shark genus *Squalus*. We used genetic markers, morphology and biological data to compare the diversity of the genus in the eastern Atlantic, Mediterranean and Black seas to that found worldwide. We collected tissue samples from 122 specimens from the eastern Atlantic (Portugal to South Africa) and 35 from the Mediterranean Sea (Cyprus to eastern Spain), and generated 106 and 98 sequences of the mtDNA COI and ND2 genes, respectively. We also added publicly available sequences for each gene region totaling 736 COI sequences and 180 ND2 sequences, representing 17 of the 28 *Squalus* species currently recognized. Over 30 specimens from several eastern Atlantic and Mediterranean locations from 3-4 putative species have been deposited as vouchers at the MUHNAC (Lisbon) and MNHN (Paris & Concarneau).

Our results show many inconsistencies in species identification in the target region, particularly for *S. blainville* and *S. megalops* (Figure 1). Our data also confirms the presence of five distinct lineages of *Squalus* in the target region, although species designations for each lineage (aside from *S. acanthias*) needs to be discussed further. Our molecular, morphological and biological data suggest that previous reports of *S. megalops* in the eastern Atlantic and Mediterranean need to be revised, as it may comprise a closely related but distinctive taxonomic entity. In addition, our results reinforce the need to revise the status of *S. mitsukurii* as it appears to refer to several distinct species around the globe.

The funds granted to our project were used for the purpose awarded, namely to purchase fresh *Squalus* specimens from fish markets (e.g. n=15, off Portugal), and to cover for shipping costs of specimens from South Africa to Portugal (~40 kg of specimens).

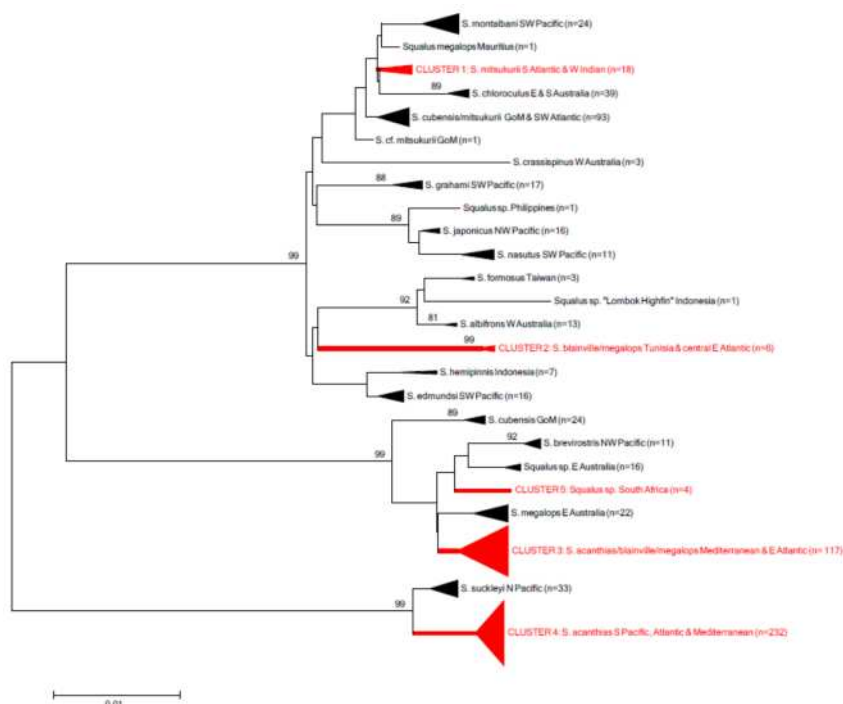


Figure 1 legend – Neighbor-joining tree of Kimura-2 parameter genetic distances among mtDNA COI haplotypes. Numbers above branches are bootstrap support values >80% (based on 1000 replicates). Species designations in front of each cluster are based on the original species identification of each individual sampled. Clusters highlighted in red include specimens sampled from the Mediterranean Sea and eastern Atlantic locations. The number of samples grouped in each cluster is indicated in the brackets.