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meeting summary

Discussing the latest advances in biogeography with young biogeographers

Advances in Biogeography: IBS Early Career Conference – Oxford, UK, 23-25 September 2011

Last September, the School of Geography and the Biodiversity Institute (University of Oxford) hosted the first International Biogeography Society (IBS) Early Career Conference, which brought together about one hundred biogeographers from sixteen different countries (Fig. 1). This conference offered young researchers the opportunity to present their work and exchange experiences, as well as to attend a workshop delivered by Robert Whittaker, Editor-in-Chief of the *Journal of Biogeography*, which provided an overview of the publication process. As this summary aims only to provide the main results of the conference rather than a comprehensive account of all sessions, those interested are referred to the full program¹.

Keynote talks were provided by four IBS board members. Kenneth Feeley discussed the impacts of climate change on tropical forests, identifying four possible responses of species to climate change: acclimation, adaptation, migration and extinction. Catherine Graham showed

how novel tools may help unravel the mechanisms influencing the diversity and structure of hummingbird assemblages on the Ecuadorian Andes. Michael Dawson described recent advances in marine biogeography, providing an overview of topics such as the relationship between gene flow and range size, and the pelagic larval duration (i.e. how long a species lives as a larva that dwells in the open sea). Lawrence Heaney described two paradigms in island biogeography, the equilibrium and vicariance models, and then identified challenges to island models and emerging questions regarding oceanic island biotas.

The junior participants presented cutting edge research in ten sessions that covered a broad range of non-exclusive and interrelated topics. Starting from a more local scale, in a study on the Bolivian lowland forest Stefan Abrahamczyk found that the relationship between hummingbirds and their food plants changes flexibly and idiosyncratically with climate. Leticia Ochoa-



Figure 1. Group picture of the participants in the first IBS Early Career Conference.

1. Available at <http://www.biogeography.org/html/Meetings/2011Oxford/>

Ochoa showed that the drivers of the diversity and structure of amphibian communities in Mexico could vary enormously between similar landscapes. Nina Curcic presented the first faunistic study of cave-dwelling fauna in Serbia to date. Jorge A. Noriega reported zones of high endemicity of dung beetles in the Amazonian region and the Sierra Nevada of Santa Marta in Colombia.

At a larger scale, William D. Pearse showed that community phylogenetic structure has different spatial and phylogenetic scales, and it is not consistent among plant clades. Fernando Monroy demonstrated that Collembola communities at the regional scale have fast species turnover, related to their functional adaptation to local environmental conditions. At the global scale, Jonathan Belmaker showed that functional diversity across a range of scales may be jointly determined by processes causing low functional turnover (e.g. ecological assembly rules), and processes causing high functional turnover (e.g. environmental filters). Rafael O. Wüest proposed that niche truncation, evolutionary canalization, and accelerated niche evolution influence the evolution of the species' geographic responses to climate. Using a different perspective, John D. O'Brien used Bayesian phylogeographic inference to study the worldwide migration patterns of the malaria causative agent. Finally, the global, cross-scale assessment presented by Dan F. Rosauer identified current climate, isolation and elevation as the best predictors of mammal phylogenetic endemism.

Many speakers used Species Distribution Modelling (SDM) to examine species distribution patterns and how these relate to biotic and abiotic factors, while also providing insights into different technical aspects of SDM. Patricio Plis-coff presented the advances of a project modelling past, present and future plant biodiversity in Chile. Regan Early showed that range shifts under climate change might be less severe than previously thought, but suggested a large degree of uncertainty in the predictions. Irina Laube showed that different niche dimensions have different dynamics and that climate niche tracking may not be the main driver of changes in species' distributions. Further, Juliano Sarmiento Cabral proposed

that species may occur in suboptimal conditions, producing biased predictions for correlative and single-species mechanistic approaches to SDM; he also highlighted that biogeographical patterns may emerge from range dynamics of interacting species. And Tomas Vaclavik concluded that if SDM are to be used effectively in conservation and management, invasion stages must be considered to avoid underestimating habitats at risk of future invasion spread. Cory Merow delved into the use of Maxent (a widely used SDM technique), exploring its assumptions and presenting new techniques to incorporate prior information into models. Rosa M. Chefaoui emphasised the importance of data quality for SDM and that extra care should be taken while modelling species inhabiting inconspicuous habitats or strongly affected by interactions at small spatial scales. Nicolas J. Matzke proposed a new technique called phylogenetic lineage distribution modelling, which tries to merge phylogenetic methods and SDM. Following a similar approach, Miquel Vila-Farré combined molecular techniques and SDM to describe the biogeography of the *Crenobia*, a turbellarian flatworm genus. Francisco Rodríguez-Sánchez also asked how good current climatic change predictions are and whether we can trust them. He illustrated the advantages of integrating all available data (fossils, biogeography, SDM, paleoclimate and ecology) into a single Bayesian statistical framework.

Furthermore, some talks linked past glaciation with current diversity patterns, with some being based on a diverse array of techniques and data that track environmental changes and human impacts during the last 21,000 years. Ricardo Dobrovolski showed that the nestedness component of beta diversity is more important in regions that were glaciated until recent times. Valentina Todisco presented the first comprehensive description of the mitochondrial genetic structure of a Holarctic alpine butterfly species complex, suggesting that these taxa may serve as a model for the effect of Pleistocene climate fluctuations on cold-adapted invertebrates of the Holarctic region. Findings by Serena Dool and colleagues on the lesser horseshoe bat add further evidence

that the Balkan region, in particular, has played a significant role in the postglacial recolonization of Europe compared to the two other Mediterranean peninsulas. Emma Boston questioned the traditional view of glacial refugia and postglacial recolonisation in Western Europe, showing that horseshoe bat populations from this region may have originated from two or more refugia. Alice C. Hughes modelled the past and present distribution of three Southeast Asia bat species, finding that genetic patterns fitted with geographic isolation during previous time periods. Alejandra Moreno-Letelier focused on three pine species that seem to have hybridized in Eastern Mexico during the Last Glacial Maximum. A study by Jesse L. Morris using preserved pollen and charcoal from lake sediments suggested that spruce beetle outbreaks recur at multi-centennial intervals and that the mean fire return intervals for significant fire episodes are similarly long, between 300-500 years. Sandra Nogué showed how the Canary Islands have been impacted by climate and human events during the Holocene, resulting in the loss of many plant and animal species. Working in Neotropical systems with different influence of glacial cycles, Kyle Dexter showed that tree species in Western Amazonia have very dynamic and disparate biogeographic histories. In contrast, after characterizing terrestrial planarians as good predictors of habitat stability, Marta Álvarez-Presas detected ancient stable areas in the Atlantic Forest of Brazil through analysis of nucleotide diversity of this taxon. Working on a wider geographic scale, Elizabeth Cooke described the occurrence of geographic structuring of genetic variation in *Cardamine hirsute*, a widespread weed.

On the subject of Evolutionary Biogeography, many presentations focused on the use of distributional, phylogenetic, molecular and fossil data to assess the historical processes behind current biotic patterns. Alex Pigot demonstrated that traditional explanations of the dynamics of range size during a species' life-time may be incorrect, suggesting that there can be a large component of randomness in geographic range sizes. Lynsey McInnes presented a large dataset enabling en-

quiry into whether monocot diversity is distributed unevenly across space and among lineages and whether long distance dispersal is associated with wind and ocean currents in this group. Christopher Beatty studied a dragonfly species with a very unique life history, and determined the boundaries of different populations using population genetic analysis. Alexander Gamisch investigated whether auto-pollinations (selfing) have negative long-term evolutionary consequences for orchids due to inbreeding depression. Paolo Gratton used Bayesian methods to explore the evolution of Mediterranean trout populations in Italy, allowing an explicit model for the evolution of these lineages to be set for the first time. Finally, Alexander N. Kirschel showed how some traits (song and morphology) of two African tinkerbirds vary among contact zones across sub-Saharan Africa, therefore finding evidence for character displacement.

Many speakers presented new advances on island biogeography, showing a large number of innovative results, from oceanic and continental islands to habitat-islands, using different taxa as case studies. Katy Jones suggested that gaps in taxonomic knowledge of the Azorean flora may help explain the differences in the patterns of endemic diversity shown by the Azores and Canary Islands. Anna Papadopoulou showed how diversity patterns in the Aegean islands are shaped by interactions between palaeogeography, contemporary geography, habitat stability and stochastic processes acting at population and community levels. Dirk Karger presented the initial results from a fern diversity study in Indonesia and the Philippines, which allowed a first insight into processes linking diversity levels with island conditions. Juan Carlos González used molecular phylogenetic techniques to demonstrate that Southeast Asian insular hornbill lineages radiated from Sundaland using different routes and arrived at Wallacea, the Philippines and Australasian islands at different times. Tiina Särkinen showed how comparative phylogenetic approaches can be used to explore large-scale patterns in macro-evolutionary studies in the Andean dry tropical forests. Finally, Ana M. Santos found that island

parasitoid community structure is mostly determined by the source pool but that on many islands functional diversity apparently is not assembled randomly from the source pool.

Aquatic environments were also present in this conference. For example, Cesc Múrria detected different slopes for the distance-decay of similarity of aquatic insects among regions and taxa, suggesting the influence of local disturbance and dispersal abilities. David Sánchez-Fernández found that at a continental scale, freshwater invertebrates have different degrees of equilibrium of the geographical distribution between lotic and lentic species. Further, Félix Picazo showed that species gradients in lotic fauna are related to large-scale deterministic factors, while current distributions of lentic species could be more related to physiological constraints. Reuben Shipway described a recent discovery of an invasive species of shipworm (Teredinidae) in the Mediterranean Sea that attacks submerged wooden structures, thus inflicting significant financial impacts. César Capinha provided a quantitative evaluation of two European invader crayfish species and showed that current distribution of the two species seemed to result from both human introductions and suitability of the abiotic environment. Luisa Borges described the distribution patterns of marine wood boring organisms, matching distribution with tolerance limits for salinity and temperature. Conservation Biogeography was also a popular subject, with different developments and challenges being presented. Seth Cunningham presented the rediscovery of a cryptic crocodile (*Crocodylus suchus*) population in Central and Western Africa. Using a different approach, Henry Cottee-Jones' demonstrated that the size of *Ficus* trees and the distance from the nearest protected area were important determinants of frugivorous bird occurrences in India. Working in France, Tonya A. Lander revealed that annual changes in

crops and management may impact the behaviour of wild cherry pollinators more than fragmentation.

After two and a half exhausting days, the first IBS Early Career Conference was a huge success, which allowed young researchers working on a wide range of topics and using very different methodological and conceptual approaches to gain a broader perspective on biogeographical research. In fact, in a later survey the participants stated that they learned a lot from their peers. We hope that this will be the first of many successful IBS young researcher conferences.

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You can find information about the **International Biogeography Society** at <http://www.biogeography.org/>, and contact with other biogeographers at the **IBS blog** (<http://biogeography.blogspot.com/>), the **IBS facebook group** (<http://www.facebook.com/group.php?gid=6908354463>) and the **IBS twitter channel** (<https://twitter.com/biogeography>).