meeting summary

Discussing the latest advances in biogeography with young biogeographers


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.

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. Wüst 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 Pliscoff 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 Sarmento 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 Todesco 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 tradi-
tional 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 distribu-
tion 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 out-
breaks 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 Is-
lands 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 spe-
cies in Western Amazonia have very dynamic and
disparate biogeographic histories. In contrast, af-
after characterizing terrestrial planarians as good
predictors of habitat stability, Marta Álvarez-
Presas detected ancient stable areas in the Atlan-
tic Forest of Brazil through analysis of nucleotide
diversity of this taxon. Working on a wider geo-
graphic scale, Elizabeth Cooke described the oc-
currence of geographic structuring of genetic
variation in Cardamine hirsute, a widespread
weed.

On the subject of Evolutionary Biogeogra-
phy, many presentations focused on the use of
distributional, phylogenetic, molecular and fossil
data to assess the historical processes behind cur-
rent 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 distrib-
uted unevenly across space and among lineages
and whether long distance dispersal is associated
with wind and ocean currents in this group. Chris-
topher Beatty studied a dragonfly species with a
very unique life history, and determined the
boundaries of different populations using popula-
tion genetic analysis. Alexander Gamisch investi-
gated whether auto-pollinations (selfing) have
negative long-term evolutionary consequences for
orchids due to inbreeding depression. Paolo Grat-
ton used Bayesian methods to explore the evolu-
tion 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 Af-
rica, therefore finding evidence for character dis-
placement.

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 en-
demic diversity shown by the Azores and Canary
Islands. Anna Papadopoulou showed how diversity
patterns in the Aegean islands are shaped by
interactions between palaeogeography, contem-
porary 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 proc-
esses linking diversity levels with island condi-
tions. Juan Carlos González used molecular phy-
logenetic techniques to demonstrate that South-
est 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 (*Crocodileus 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 fragmentiation.

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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