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## Frontiers of Biogeography

### Title

symposium summary: New perspectives on comparative phylogeography: novel integrative approaches and challenges

### Permalink

<https://escholarship.org/uc/item/71v614tf>

### Journal

Frontiers of Biogeography, 3(1)

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### Publication Date

2011

### DOI

10.21425/F5FBG12378

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a similarly high heterogeneity in the research approaches to Mediterranean biogeography. In addition to the lectures described above, more than 35 poster contributions addressed various aspects of both marine and terrestrial Mediterranean biogeography, ranging from phylogeographic analyses to studies of fossil faunas and floras. Thus, one take home-message from this Symposium is that the Mediterranean can be also designated as a 'hotspot of biogeographic research'.

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Edited by Joaquín Hortal

## symposium summary

# New perspectives on comparative phylogeography: novel integrative approaches and challenges

A symposium at the 5th International Biogeography Society Conference – Heraklion, Greece, 7–11 January 2011

Phylogeographic inference reveals that many species, as recognized by current taxonomy, are comprised of multiple genetically divergent lineages that are morphologically cryptic yet represent terminal branches on the tree of life and are relevant to understanding evolutionary processes in relation to environmental change (Avice 2000, 2008). Comparative phylogeography endeavors to reveal how whole communities or assemblages become structured into co-distributed sets of divergent lineages by shared responses to past environmental changes as well as histories that are unique to specific species. In so doing, comparative phylogeography makes the link between traditionally separate ecological and evolutionary processes thereby leading to ecosystem-level understanding about how climate change and geography interact with aspects of species ecology and natural history to drive geographic patterns in biodiversity, community assembly and natural selection. The symposium “New perspectives on comparative phylogeography: Novel integrative ap-

proaches and challenges” brought together researchers who are using multi-taxa phylogeographic data sets to answer these questions while allowing the idiosyncrasies of particular systems to guide specific questions, hypotheses being tested and level of detail at which inference can be made.

Highlighting that conservation is one of the most pressing applications for comparative phylogeography, Moritz et al. demonstrated how divergent lineages within species can inform land resource management strategies. Spatial bioclimatic modeling and phylogeographic inference across wide assemblages in tropical Australia and coastal Brazil strongly demonstrate that non-adaptive and allopatric divergence can drive species diversification and that narrow-range phylogeographic lineages will be concentrated in climatically stable landscapes (Schneider et al. 1998; Carnaval et al. 2009). This result aligns with emerging consensus on the need to protect present climatic refugia in the context of rapid global

warming. Thus, not only do we now have the means to predict these areas that harbor narrow range endemics, we can then protect this prevalent component of biological diversity (Moritz 2002).

In the context of island biogeography across major Pacific archipelagoes, Gillespie et al. used multiple lineages of animals and plants from remote Pacific islands to test hypotheses about determinates of island colonization. Wind and storm patterns, ocean currents, and migratory routes provide sufficient information to formulate, comparative phylogeographic hypotheses of island colonization by (1) rafting over water, (2) attachment to migratory birds, or (3) aerial dispersal. Differentiable predictions based on these three dispersal mechanisms are that (1) rafting will lead to sequential stepping stone colonization, (2) bird vector dispersal will lead to colonization along migratory routes, and (3) wind dispersal will lead to colonization of remote sites directly from a mainland source if there is a good match between the mainland and island habitats. Generally speaking all three mechanisms of long distance dispersal, (ocean currents, winds and bird vectors) interact with the biotic forces of selection and competition in the islands which then lead to observed patterns of island biodiversity.

In a similar vein, Riginos demonstrated that the magnitude of egg dispersal potential in benthic fishes globally predicts population subdivision and taxonomic diversity at the family level (Riginos et al. 2011). In this case, the tools from landscape genetics are used to statistically evaluate how coastline features, geographic distance and transitions between biogeographic regions can potentially drive population subdivision and ultimately biodiversity. While landscape genetics makes use of space explicitly, doing so within a model-based coalescent framework has not been possible beyond spatial approximations. In this light, Baird describes a method of connecting the spatial ecological parameter 'effective density' with 'effective population size', an important population genetic parameter used in standard coalescent population genetic inference (Baird and Santos 2010). To illustrate, a coalescent

model based on Kimura's stepping stone model was presented and applied to recent range expansion of the cane toad (Estoup et al. 2010). As spatial coalescent methods become mature technology, applications to make inferences across spatially co-distributed species using multi-taxa models will drive comparative phylogeography to a new level.

Moving beyond well-studied biogeographic regions and groups, Reynolds et al. focused on the biogeographic inference of ectomycorrhizal truffles while Ramakrishnan et al. were interested in the biogeographic drivers of regional diversity in the Indian subcontinent. Using phylogenetic data, Reynolds et al. demonstrated, contrary to expectations for low dispersing taxa (truffles are dispersed only by mammalian mycophagists attracted to their scent), that frequent long-distance dispersal expands the known geographic ranges of common Northern Hemisphere species. Ramakrishnan et al. demonstrated that, unlike many other regions, strong physical barriers are absent within the Indian subcontinent, and with its relatively small area, most mammalian groups are present due to recent colonization. Given these factors, phylogeographic patterns are hypothesized to be driven by species' ecology, as shown in seven mammal taxa that include cats and primates (Mukherjee et al. 2010; Robin et al. 2010). Following this general prediction, Ramakrishnan et al. found that habitat preference drives phylogeographic patterns as does body size and differences in sex-biased dispersal for some groups. Although the Indian subcontinent is tropical, like temperate zones it was heavily impacted by Pleistocene glaciations due to the surrounding Himalayas, and expectedly, the authors do find genetic signatures of post-Pleistocene population expansions in some groups.

In conclusion, we look forward to expansion of the novel and traditional approaches presented in this Symposium. As this field matures and becomes fully integrated with ecological fields that make use of GIS technologies and rapidly improving global databases, comparative phylogeography will become a major tool for identifying climatic refugia for conservation in the context of

rapid global warming. In so doing, comparative phylogeographic inference will increasingly be able to predict and identify climatically stable landscapes that harbor divergent lineages below the species level.

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Edited by Michael N Dawson

## symposium summary

# Analytical advancements in macroecology and biogeography

A symposium at the 5th International Biogeography Society Conference – Heraklion, Greece, 7–11 January 2011

Macroecology analyzes patterns and processes of biological diversity at broad scales, both in space and time, based on an integration of distinct fields of ecology, physiology, behavioural sciences, evolution and biogeography. Common definitions of macroecology (e.g., Brown 1995, Gaston & Blackburn 2000) emphasize two sets of contrasting issues: “patterns and processes” and “scale”. In that context, we can ask not only how ecological and evolutionary processes at local scales—such as selection, drift, dispersal and competition—affect individuals and populations, but also how they may lead to geographic range dynamics

(extinction, contraction and fragmentation) at the species level. We can then contemplate how the patterns derived from ecological and evolutionary processes may shape broad-scale patterns of diversity, and also how other emergent processes or properties contribute to diversity patterns.

To achieve this synthetic, integrative view, and understand the roles of different processes and emergent properties at distinct scales, it is important to think about which methods could be used. The continuous development of computing capacity and increasing data generation allow ever more sophisticated analyses, enabling novel in-