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commentary

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Phylogeography and ecological niche modelling are two key approaches advancing biogeography. A special issue of *Folia Zoologica* (64: 2015) considers these advances in eight articles, including two reviews—on Next Generation Sequencing (NGS) and Ecological Niche Modelling (ENM)—and six research articles, plus two book reviews. The reviews on NGS and ENM stand out as the main interests of the issue. The six research articles provide different biogeographical case studies in which phylogeography and ENM are used together, representing a timely comparison of the current most common practices and the advances highlighted by the reviews.

First, Edwards et al. (2015) present an outstanding review of the parallel evolution of molecular techniques and the domain of phylogeography, including a complete view of current NGS approaches applied in this discipline. Consistent with other recent publications (e.g. McCormack et al. 2013, Rocha et al. 2013), Edwards and colleagues emphasize that genome subsampling methods, such as RAD-seq, outperform all previous techniques for the core topics of phylogeography: reconstruction of phylogenetic lineages and neutral demography within species. The increased potential of these new approaches to classical questions of phylogeography is due to the increased resolution provided by the vast number of loci available per specimen; such high resolution could be difficult to improve even by whole-genome resequencing. Interestingly, this review also points out the weaknesses of these genome subsampling methods to simultaneously infer the genomic targets of selection (a growing praxis in phylogeography studies), and highlights that whole-genome resequencing rather than subsampling is essential to advance this expanding edge of phylogeography. Overall, the review offers a mostly comprehensive up-to-date overview of the ways that NGS has solved previous impediments in phylogeography, and it promotes understanding of present and future perspectives of the field. However, a topic lost from this review is the potential of performing and integrating multiple phylogeographic results for regional biogeographic inference, that should be favoured by the cost-efficiency and the more comparable results of the NGS techniques (Lexer et al. 2013). NGS provides the opportunity to greatly scale up the numbers of loci, individuals, populations but also species sampled, potentially merging intraspecific and interspecific approaches. This integrated approach, despite still being poorly applied, is clearly an expanding domain of biogeography mediated by the application of NGS, and will allow for a multi-hierarchical understanding of the general principles underlying community assembly and the distribution of biodiversity (Emerson and Hewitt 2005, Emerson et al. 2011).

In the second review, Peterson and Anamza (2015) provide an interesting overview on the use of ENM and how it could be a relevant complement to phylogeographical studies. The authors aim to guide potential users of these tools toward these applications while at the same time avoiding common mistakes and pitfalls. The section regarding caveats is especially interesting, as ENM approaches have been subjects of considerable abuse and misuse. These tools have become (perhaps too) easy to use, have been applied in situations in which they are not applicable, and their outputs have consequently been misinterpreted (see Peterson et al. 2011). Beyond typical methodological considerations, such as how to deal with uneven sampling, the authors highlight the importance of exploring the distribution of occurrences on the environmental space of the areas accessible to species. In absence of physiological parameters to define the fundamental niche, this exercise could be needed if we aim to know how far we can get with the interpretation of the results. This is especially useful in the case of model transfers in space and time, as very often we extrapolate beyond the currently available environment. However, considering these caveats, ENM, by offering spatial and environmental dimensions as key parameters, can provide exciting and testable hypotheses for phylogeography about where distinct lineages may be found, and about the timing of key historical events.

Finally, the set of six research articles illustrate how ENM can be used to evaluate or develop phylogeographic hypotheses about the spatial or historical processes generating patterns of genetic variation in disparate taxa and geographic regions (see also Richards et al. 2007, Alvarado-Serrano and Knowles 2014). Savit and Bates (2015) and Smyth et al. (2015) address one of the most common applications of ENMs in phylogeography: interpreting genetic patterns based on their post hoc concordance with projections of the species distribution. Savit and Bates (2015) examine the competing hypotheses of vicariant refugia versus long-distance dispersal in the burnished-buff tanager in South America; Smyth et al. (2015) study species formation in a ring of song sparrow subspecies that surround the Sierra Nevada in North America, showing how ENM can incorporate ecological factors in the test of different phylogeographic models. Two other articles (Galbreath and Hoberg 2015, Perktaş et al. 2015) use ENM to infer geographic corridors of highest dispersal probability under current and past environmental conditions to better understand species-specific demographic histories, another common application of ENM in phylogeography and landscape genetics. Notably, Galbreath and Hoberg (2015) focus on the phylogeography of host-parasite co-speciation in the North American pika/parasite assemblage, while Perktaş et al. (2015) use Bayesian coalescent simulations to discuss glacial refugia hypotheses in Europe for the Eurasian green woodpecker. In addition, ENM can be used to identify regions of environmental stability where a species may have persisted overtime, as shown by Ornelas et al. (2015), who examine the effects of Quaternary habitat and climate stability on the genetic diversity of eight widespread or range restricted hummingbird species in Mesoamerica. Finally, the article by Fahey et al. (2015) is the only purely phylogeographic study included in this issue, as it does not incorporate ENM. They examine the historical demography of 16 Hispaniola birds and illustrate how reliance on a single molecular marker for reconstruction of demographic history may be a concern.

In sum, this special issue provides a timely and interesting overview of the advances in phylogeography and ENM, showing how these could overcome traditional obstacles and promote further advances in biogeography. However, we feel that the two reviews are conceptually a step ahead of the six case studies. NGS has not been used to generate the phylogeographic datasets in any of these articles, and in that sense they do not reflect the recent revolution in DNA sequencing technologies that is transforming the field of phylogeography. In the same way, although the use of ENMs in the articles is interesting and complements the information obtained with genetic data, most of them have not considered the methodological recommendations highlighted in the review of Peterson and Anamza (2015), resulting in hazardous conclusions in some cases. In general, this special issue is a good illustration of how the combination of these disciplines provides valuable insights that can improve our understanding of the spatial patterns of biodiversity in the past and present. The challenge now is to implement the recommendations and methodologies provided in the two reviews in future specific study cases.

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