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Meeting report

Using phylogenies in conservation: new perspectives

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The 2011 meeting of the European Ecological Federation took place in Ávila, Spain, from 26th September to 29th September. The French Ecological Society (SFE) and the Foundation for Research on Biodiversity (FRB) sponsored a session entitled 'Evolutionary history, ecosystem function and conservation biology: new perspectives'. We report on the main insights obtained from this symposium.

Keywords: conservation; phylogenies diversity; biodiversity; macroevolution

1. INTRODUCTION

The ongoing global biodiversity crisis requires that scientists develop ways to strategically allocate conservation efforts [1]. Among these is the proposal to directly integrate information on the evolutionary relationships between species (phylogenies) into the definition of biodiversity conservation priorities [2,3]. Over the past two decades, phylogenetic approaches have become increasingly prominent in the conservation literature [4,5]. Our symposium brought together a broad array of speakers from North America and Europe, who gave an overview of the challenges and perspectives of the use of phylogenies in conservation.

2. CONSERVING PHYLOGENETIC DIVERSITY

(a) *Phylogenetic diversity and ecosystem function*

Throughout the symposium, speakers reminded us why it may be critical to preserve phylogenetic diversity. Marc Cadotte (University of Toronto) and Nicolas Mouquet (CNRS, Montpellier) focused on the hypothesis that more phylogenetically diverse assemblages maintain higher function [6,7]. Cadotte summarized his 2008 meta-analysis of plant communities suggesting that phylogenetic diversity explains plant productivity better than other measures of diversity [6]. Furthermore, he presented new findings that suggest phylogenetic diversity can enhance ecosystem stability: using the long-term plant biodiversity experiments at Cedar Creek [8], he found that above-ground biomass production is more stable in communities composed of distantly related species. Matching results from plant communities, Mouquet and co-workers found that more phylogenetically diverse marine microbial assemblages are more productive [9]. However, when the same bacteria were allowed to evolve in a new environment [7], this relationship weakened, presumably as a result of adaptation. Mouquet concluded with a call for understanding evolutionary mechanisms that allow (or not) phylogenetic diversity to be used as a proxy for ecosystem functioning.

(b) *The tree of life facing global change*

If preserving phylogenetic diversity matters, measuring how much of the tree of life has been and will be affected by global change is crucial [10,11]. Sandrine Pavoine (National Museum of Natural History, Paris) presented an approach for evaluating how the phylogenetic composition of communities changes over time. Applying this method to rockfish communities in Southern California, Pavoine *et al.* [10] identified the particular rockfish lineages that were most affected by human activities.

To predict the extent to which phylogenetic diversity is at risk, researchers have contrasted scenarios of random species loss with predicted losses based on forecasts of extinctions [12–14], typically based on species extinction risk under the IUCN Red List (www.iucnredlist.org). Predicted losses are typically much higher than expected under random extinctions, because species at risk are clustered in the phylogeny [14]. Jonathan Davies (McGill University) illustrated this clustering for the flora of the South African Cape [15]. Wilfried Thuiller (CNRS, Grenoble), however, found only weak clustering for European birds, mammals and plants vulnerable to climate change, as predicted using species distribution models under various climate change scenarios [11]. These contrasting results suggest that current threat status as assessed by the IUCN Red List may provide a poor picture of extinction risk linked to forthcoming climatic changes. On the other hand, risk projections based on species distribution models currently omit other sources of vulnerability such as large body sizes or habitat degradation. Future research needs to combine both in order to obtain better predictions of extinction risk.

(c) *Phylogenetic diversity in conservation planning*

Phylogenetic diversity is arguably a better measure of biodiversity than species richness [3] and it can be

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targeted directly in conservation planning [16], but does it make a difference? Davies showed that, in the South African Cape flora, a focus on species classified as threatened according to IUCN criteria will preserve relatively little phylogenetic diversity, as these species are associated with short phylogenetic branches corresponding to recent diversification [15]. However, as Ana Rodrigues (CNRS, Montpellier) noted, conservation is usually not done on a species-by-species basis but rather using a site-based perspective. She found, using a global mammal dataset, that networks of the protection areas based on species distribution data, or on poorly resolved phylogenies, are nearly as efficient at representing overall phylogenetic diversity (estimated by the sum of branch lengths) as networks obtained by directly maximizing phylogenetic diversity itself [17]. These results, which confirmed earlier results on birds [16], suggest that when perfect phylogenetic information is lacking, poorly resolved phylogenies, or even taxonomic diversity, can be used as surrogates in conservation planning.

Phylogenetic trees have received much less attention in real-world conservation than in conservation research. In order to understand why phylogenetic diversity is not integrated in applied conservation, Marten Winter (Helmholtz Centre for Environmental Research, Halle) analysed 154 published papers that mentioned ‘phylogenetic diversity’ and ‘conservation’. He found that only very few of them really proposed concrete recommendations. However, Winter also noted that it had taken 20 years for global change knowledge to be integrated into policy, and that some recently applied programmes integrating phylogenetic diversity, such as Evolutionary Distinct and Globally Endangered (EDGE; [18]), are now emerging. Hence, the time for more concrete recommendations for the preservation of phylogenetic diversity may be ripe.

3. USING PHYLOGENIES TO HELP CONSERVATION

(a) *Making use of the mismatches between various facets of diversity*

The phylogenetic structure in species distributions is being increasingly used in community ecology to understand the processes driving community assembly [19,20], but such process based approaches have rarely been considered in conservation biology. Conservation biologists have rather mapped various facets of diversity with the goal of understanding where and what diversity is at risk [21], finding spatial mismatches between taxonomic, phylogenetic and functional diversity. This spatial mismatch was illustrated by Vincent Devictor (CNRS, Montpellier) for French birds [21], and by Laure Turcati (University Pierre et Marie Curie, Paris) for plants in the Île de France. Laure Zupan (University of Grenoble) described a mismatch in patterns of phylogenetic diversity for mammals, birds and amphibians in Europe, suggesting challenges in preserving the phylogenetic diversity of distinct groups simultaneously. Devictor emphasized that we must now go beyond describing these mismatches towards a better understanding of mechanisms, suggesting that analysing the spatial distribution of the temporal trends in various diversity measures could help us to understand what are the processes driving these trends.

(b) *Incorporating macroevolution into conservation research?*

Sébastien Lavergne (CNRS, Grenoble), Franck Jabot (Cemagref, Clermont-Ferrand) and Hélène Morlon (CNRS, Paris) brought a macroevolutionary perspective to the symposium. Presenting results of niche evolution in European birds, Lavergne suggested that models of trait evolution may be useful to assess the capacity of lineages to adapt to a changing environment, and thus to detect highly threatened clades. Lavergne and co-workers compared the rate of evolution of three different types of ecological niches: species climatic requirements, their habitat requirements and their food requirements. Deconstructing the niche in this way could shed light on the facets of species niches that are most evolutionarily labile or which tend to be conserved over time. In the future, rate estimates of trait evolution may also be incorporated into species distribution models, which currently ignore the potential capacity of species to adapt.

Jabot & Morlon [22] focused on methods for detecting lineages or areas of high evolutionary potential. Morlon presented approaches stemming from macroevolutionary models that provide estimates of present-day diversification rates and how these rates vary across lineages [23,24]. Such estimates could indicate which lineages or clades have the greatest chance of diversifying in the future, or conversely, which ones are the most prone to extinctions. Morlon suggested that character-dependent diversification models [25,26] could similarly be used to assess the evolutionary potential of lineages based on their traits. Finally, treating the geographical location of species as characters [27], these models could allow detection of areas with high evolutionary potential. Making use of phylogenies and species’ distributions to detect areas of high evolutionary potential has been proposed previously [28]. However, using simulations [29,30], Jabot showed that current methods for identifying such areas, which evaluate neo-endemism from species’ ranges and phylogenetic divergence, can be misleading. Maximum-likelihood methods, which use more of the information contained in molecular phylogenies in a model-based framework, should be much more powerful. This, however, remains to be tested.

Macroevolutionary models provide promising avenues. However, it is not at all yet clear whether the rates of trait evolution and diversification estimated over macroevolutionary time scales are relevant to present-day conservation. There was a consensus that a lot more tests are still needed to understand how much macroevolution can be useful for practical conservation.

4. CONCLUSION

When we organized the symposium, we wondered whether there was a future for phylogenies in conservation, and if yes, what it would look like. We were surprised by how positive many of the talks were about the promise of phylogenetic approaches in conservation, and by the diversity of methods and tests that have been recently developed. Although it is uncontestable that many more tests are needed to convince conservationists that phylogenetic diversity is of interest in conservation, and that more efforts need to be made by researchers to provide concrete recommendations to conservationists, we were able to identify some important avenues for future research.

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