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Phylogenetics and Conservation Biology: Drawing a Path into the Diversity of Life

Roseli Pellens and Philippe Grandcolas

Abstract In the midst of a major extinction crisis, the scientific community is called to provide criteria, variables and standards for defining strategies of biodiversity conservation and monitoring their results. Phylogenetic diversity is one of the variables taken in account. Its consideration in biodiversity conservation stemmed from the idea that species are not equal in terms of evolutionary history and opened a completely new line of investigation. It has turned the focus to the need of protecting the Tree of Life, i.e. the diversity of features resulting from the evolution of Life on Earth. This approach is now recognized as a strategy for increasing options for future needs and values as well as for increasing the potential of biodiversity diversification in a future environment. Since its introduction in biodiversity conservation thinking much has been developed in order to compose our conceptual understanding of the importance of protecting the Tree of Life. The aim of this book is to contribute to the ongoing international construction of strategies for reducing biodiversity losses by exploring several approaches for the conservation of phylogenetic diversity. We hope that this concentrated effort will contribute to the emergence of new solutions and attitudes towards a more effective preservation of our evolutionary heritage. The chapters of this book are organized around three main themes: questions, methods and applications, providing a condensed updated picture of the state of the art and showing that either conceptually or methodologically phylogenetic diversity has everything to be on the global agenda of biodiversity conservation.

Keywords Tree-of-life • Sixth mass extinction • Evolutionary heritage • Biodiversity monitoring • Essential biodiversity variable

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During the last centuries and more dramatically in the last four decades, natural habitats were destroyed at rates much higher than ever observed in human history. All biomes were affected, but those located in tropical regions were more impacted, particularly because policies for the development and appropriation of these territories were emphasized during this period. Nonetheless, the massive transformation of these landscapes to give place to crops and towns multiplied species' losses and vulnerability at incredible rates (Millennium Ecosystem Assessment 2005), mostly due to the fact that most of world's biodiversity is concentrated around the tropics (Gaston 2000). In addition to habitat destruction and fragmentation, natural ecosystems were also submitted to high levels of pollution, overexploitation of forestry and fishery resources, invasive species, and to the effects of climate changes mainly provoked by man-induced greenhouse gas emissions. As a result, a high number of species were already extinct and others have suffered severe populations declines (Mace et al. 2005), with many advancing at high speed to higher categories of threat every year (e.g., Hoffmann et al. 2010). So, recent scenarios integrating main extinction drivers suggest that rates of extinction are likely to rise by at least a further order of magnitude over the next few centuries (Mace et al. 2005; Pereira et al. 2010; Barnosky et al. 2012; Proença and Pereira 2013).

This critical situation is now recognized as the “sixth mass extinction”, i.e. the sixth period in the history of life in which more than three-quarters of the living species is lost in a short geological interval (Barnosky et al. 2011). Compared to the first “big five”, this extinction period has the peculiarity of being caused mainly by the way of living of one single species, the humans. Counteracting this trend is perhaps the biggest ethic, political and scientific challenge of our times (Sarkar 2005), as the time for action is short, funds for biodiversity conservation are far from below the real needs (e.g., McCarthy et al. 2012), uncertainties are enormous (Forest et al. 2015), and the solution of conflicts with main-trend ways-of-living and main patterns of distribution and consumption (e.g., Lenzen et al. 2012) often takes much longer than habitat destruction.

In the race to combat extinctions, there is urgency for increasing conservation worldwide. The scientific community is pressed to provide criteria in order to define priorities, as well as for indicating variables and standards that allows for monitoring the evolution of biodiversity in the light of these strategies (Hoffmann et al. 2010; Pereira et al. 2010, 2013; Mace et al. 2010, 2014). Traditionally, biodiversity conservation was based on species counts, valuing sites in terms of species richness, number of endemics and number of threatened species (Myers et al. 2000; Myers 2003; Kier et al. 2009). However, in spite of its generalized use, this kind of data can be very heterogeneous making very difficult comparisons across taxonomic groups, along time and among sites, as species richness can be influenced by many factors, going from the species concept to the spatial scale and sampling effort (see Gaston 1996 for an overview on this subject). Similarly, in spite of the great interest of Red Lists of species' threats, such as that from IUCN (International Union for Conservation of Nature), to indicate imminent risks of extinction, concentrating conservation-limited resources on threatened species can be very risky and these limits must be considered (Possingham et al. 2002). Moreover, measures based on species counts also have the limitation of considering all species as equals, being

blind to particular functional roles in the ecosystem, to associations in communities, or to their evolutionary history.

The contribution of phylogenetic systematics to this debate stemmed from this idea that species are not equal and from the possibility of characterization in terms of evolutionary history (Vane-Wright et al. 1991; Faith 1992). Systematics addresses the interrelatedness of organisms in terms of shared inherited and original features (Hennig 1966; Eldredge and Cracraft 1980; Wiley 1981). This old but recently revived science moved from describing and classifying the living beings in the eighteenth century to macro-evolutionary biology in the twentieth century with modern phylogenetics (O'Hara 1992). Phylogenies are trees of history, showing both the species relationships and the evolution of sets of characters. They are the basis for organizing and retrieving all current knowledge about biodiversity, either structural or functional in an evolutionary context.

The consideration of phylogenetic systematics in biodiversity conservation opened a completely new line of investigation as it has turned the focus to the need of protecting the Tree of Life, i.e. the diversity of features resulting from the evolution of Life on Earth (Mace et al. 2003; Purvis et al. 2005; Mace and Purvis 2008; MacLaurin and Sterelny 2008; Forest et al. 2015). Since its introduction in biodiversity conservation thinking much has been developed in order to compose our present conceptual understanding of the importance of protecting the Tree of Life. Several methodological issues were developed and refined; the input of phylogenetic diversity in comparison with species richness was assessed in different ways; several studies attempting to prioritize species and areas for conservation were developed; the relationship between the losses of evolutionary history with extinctions was studied in different contexts; and different new concepts emerged (see Table 1).

Glossary

Biodiversity: is a very inclusive term formed by contraction of “biological diversity.” In this book, we use this term to express the variety of life, often willing to express the integrative definition of the Convention on Biological Diversity in which “Biological diversity” means “the variability among living organisms from all sources including, *inter alia*, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems”.

Evolutionary history: the chronicle of the process whereby the diversity of life is built.

Phylogenetic Systematics: the scientific discipline describing and naming the different organisms, assessing their relatedness in the Tree of Life and proposing subsequent classifications. Species phylogenetic relationships are assessed on the basis of originally shared characters modified during evolution.

Tree of life: an old metaphor to describe the interrelatedness of all organisms (living and extinct), based on their evolutionary history.

Table 1 Some examples of studies linking phylogenetic systematics and biodiversity conservation

Problems	Examples
Development of methods and measures to assess taxonomic or evolutionary distinctiveness or phylogenetic diversity	Vane-Wright et al. 1991; May 1990; Faith 1992; Posadas et al. 2001; Pavoine et al. 2005; Redding and Mooers 2006; Isaac et al. 2007; Steel et al. 2007; Hartmann and Steel 2007; Lozupone and Knight 2005; Rosauer et al. 2009; Cadotte and Davies 2010; Chao et al. 2010
Comparison of phylogenetic measures	Schweiger et al. 2008; Davies and Cadotte 2011; Pio et al. 2011
Comparison of phylogenetic diversity to traditional measures	Polasky et al. 2002; Rodrigues and Gaston 2002; Rodrigues et al. 2005, 2011; Hartmann and André 2013
Inclusion of phylogenetics in systematic conservation planning	Walker and Faith 1994; Arponen 2012
Prioritization of areas for the conservation of evolutionary history	Posadas et al. 2001; Lehman 2006; McGoogan et al. 2007; López-Osorio and Miranda-Esquivel 2010; Forest et al. 2007; Buerki et al. 2015; Pollock et al. 2015; Zupan et al. 2014
Prioritization of species	Weitzman 1998; Isaac et al. 2007; Kuntner et al. 2011; Redding et al. 2015
Relationship between extinctions and the loss of phylogenetic diversity	Nee and May 1997; Purvis 2008; Davies et al. 2008; Fritz et al. 2009; Fritz and Purvis 2010; Magnuson-Ford et al. 2010; Jono and Pavoine 2012; Yessoufou et al. 2012; Davies 2015; Faith 2015; Gudde et al. 2013; Huang and Roy 2015
Climate change and the loss of phylogenetic diversity	Faith and Richards 2012; Thuiller et al. 2011, 2015
Phylogenetic and functional diversity	Safi et al. 2011; Huang et al. 2012
Cost of conserving phylogenetic diversity	Weitzman 1998; Nunes et al. 2015
Development of key concepts related to biodiversity conservation that integrates phylogenetic diversity	Evolutionary heritage (Mooers et al. 2005) Phylogenetic diversity and option values (Faith 1992; Steel et al. 2007; Forest et al. 2007) Ecosystem services (Faith et al. 2010) Key biodiversity areas for conservation (Brooks et al. 2015) Phylogenetic planetary boundaries and tipping points (Faith et al. 2010)

Please note that these are leading marks: most of these researches approached more than one of these problems

The main aim of this book is to contribute to the ongoing international search for reducing biodiversity losses in this critical period for life on Earth by exploring several approaches for the conservation of phylogenetic diversity. As shown in Table 1, the universe of problems to be prospected in this subject is quite large and could not fit in a single volume. In spite of that, here we provide a condensed updated picture of the state of the art showing that either conceptually or methodologically phylogenetic diversity has everything to be on the global agenda of biodiversity conservation. This book is organized around three main themes: questions, methods and applications. We hope that this concentrated effort will contribute to

the emergence of new solutions and attitudes towards a more effective preservation of our evolutionary heritage.

Questions

This first section is composed of chapters addressing some central questions concerning the links between biodiversity conservation and phylogenetic systematics. The first, and perhaps the most important of these questions, concerns the nature of the role of phylogenetic systematics in conservation efforts. How do we value the Tree of Life? Why to use aspects of phylogeny in preference to other biodiversity variables? These questions are explored by Lean and Maclaurin in chapter “[The Value of Phylogenetic Diversity](#)”. They develop the idea that phylogenetic diversity plays a unique role in underpinning conservation endeavor and represents the foundation of a general measure of biodiversity. In a synthesis about the reasons and the types of values that should guide biodiversity conservation and qualify a general biodiversity measure, they propose that phylogeny is the only basis for large-scale conservation prioritization. They justify this argument by showing that phylogeny is the only guide for maximizing feature diversity (*sensu* Faith 1992) across many different taxa, and also is the best way to hedge our bets against uncertainties related to environmental changes and to human’s future needs and values.

Glossary

PD or Faith’s PD: is the measure of phylogenetic diversity created by Faith (1992). Specifically it is the sum of the lengths of all phylogenetic branches (from the root to the tip) spanned by a set of species. In this book, we refer to PD or Faith’s PD to indicate this measure.

Phylogenetic diversity: all over this book we use this term in very large sense, independently of the measure, willing to express the differences between organisms due to their evolutionary history, and so captured by a phylogeny. It can be used to express the uniqueness of one species or the representativeness of a set of organisms, according to several different measures.

Evolutionary distinctiveness (Isaac et al. 2007) **or Evolutionary distinctness:** is here used to indicate measures destined to assess the phylogenetic diversity of each species, independently if it is based on topology or branch length. Contrarily to PD, where the contribution of a species may vary from one set to another depending on the other species occurring in it, with measures of evolutionary distinctiveness each species has an invariable value.

Taxonomic distinctiveness (Vane-Wright et al. 1991): like in the case of Evolutionary distinctiveness, it is used to express measures designed to assess the phylogenetic diversity of species, but this definition is restricted to those measures based on tree topology.

If the way we value phylogenetic diversity is central for any justifications for including phylogeny in conservations efforts, an equally important consideration must be the choice of the measure that adequately captures the aspects of phylogenetic diversity that are important for conservation. Lean and MacLaurin propose that this measure should maximize feature diversity. However, there are very few studies comparing the performance of the measures under such criteria (Redding and Mooers 2006; Schweiger et al. 2008; Pio et al. 2011). Dan Faith (chapter “[The PD Phylogenetic Diversity Framework: Linking Evolutionary History to Feature Diversity for Biodiversity Conservation](#)”) addresses this question through the comparison of PD (Faith 1992), in relation to several measures of Evolutionary Distinctiveness (ED) in the context of priority setting for conservation. The core of Dan’s analysis is complementarity (marginal gains and losses of PD or feature diversity), an attribute intrinsic to PD’s algorithm, but lacking in ED measures. Here he shows that PD complementarity allows the identification of sets of species with maximum PD, whereas ED indices are unable to reliably identify such diverse sets.

The next contribution deals with the loss of phylogenetic diversity with extinction. Are there phylogenetic signals in extinctions? What is the role of extrinsic and intrinsic factors in extinctions, and what is the role of phylogeny in data exploration and analysis (Grandcolas et al. 2010)? Are extinction drivers similar to different groups of organisms? What is the role of evolutionary models in the patterns observed? These questions are here explored by Yessoufou and Davies (chapter “[Reconsidering the Loss of Evolutionary History: How Does Non-random Extinction Prune the Tree-of-Life?](#)”). They first review the main extinction drivers, showing that the most relevant might be quite different among vertebrates, invertebrates and plants. By exploring how non-random extinction prunes the Tree of Life under different models of evolution, they call our attention to the fact that the model of evolution is likely to be a key explanatory of the loss of evolutionary history. They also argue that more branches are likely to be lost from the Tree of Life under the speciation model of evolution.

Many of our considerations about the conservation of the Tree of Life are based on our knowledge of a micro-fraction of the living world, given that we often focus on organisms that are very close to human eyes, like vertebrates, vascular plants, and a few emblematic insects. Likewise, most of the phylogenies used to this purpose are based on molecular data, very often on very small sets of short gene sequences. An advantage of molecular data for phylogenetic inference is provision of a standardized set of characters, often reflecting the main patterns of relationship of the species in a group of organisms. However, the extent to which these genes portions evolve and reflect the evolution of other traits is seldom well studied. Such an issue is central to arguments that phylogenetic diversity links to general feature diversity. These problems are explored by Steve Trewick and Mary Morgan-Richards (chapter “[Phylogenetics and Conservation in New Zealand: The Long and the Short of It](#)”). With examples of the phylogenetic position (as assessed through molecular data) of some legendary organisms from New Zealand such as Kākāpō, takahē and tuatara, they shake some established views about the extent molecular branch length reflects other extraordinary ecological, morphological or behavioral

traits. Going further, they turn our lenses to the microscopic life that is much more deeply branched in the Tree of Life. Taking the example of marine sponges, they show that a single sponge provides an environment that can host several distinct microbial communities (microbiomes) and so preserve organisms from more than 40 phyla all branched much deeper than vertebrates and plants. At reading this chapter, we are guided to a more inclusive perspective of biodiversity and we can find more reasons for protecting Kākāpō, takahē, tuatara, marine sponges and... microbes.

Relict species are often presented as examples of important species for the conservation of phylogenetic diversity. Everyone has heard about Coelacanth and Platypus as examples of unique evolutionary histories. In spite of this, the concept of relict species is still plagued with misleading ideas and uses, potentially causing misunderstandings for the use of phylogenetic diversity in general. Philippe Grandcolas and Steve Trewick (chapter “[What Is the Meaning of Extreme Phylogenetic Diversity? The Case of Phylogenetic Relict Species](#)”) aim at freeing the concept from these problems, and use the extreme case of relict species to explore the nature and the use of phylogenetic diversity. The study of relicts helps understanding that early-branching species that make high values of phylogenetic diversity (the “unique PD” of Forest et al. 2015) are not necessarily evolutionarily “frozen”. Their conservation is not only aimed at retaining Life’s diversity but also at keeping evolutionary potential. It is also worth-mentioning that such species have often been empirically shown to have special extinction risks, highlighting again the important role of phylogenetic diversity in conservation biology.

Methods

In this section we introduce the set of contributions dealing with methodology *sensu stricto*. It starts with two papers dealing with different possibilities of applications and extensions of the PD framework in community assessments, area comparisons and long-term monitoring of biodiversity changes. In chapter “[Using Phylogenetic Dissimilarities Among Sites for Biodiversity Assessments and Conservation](#)”, Dan Faith details one possible extension of the PD family of measures, the Environmental Dissimilarity (*ED*) methods. While PD assumes that shared ancestry accounts for shared features among taxa, *ED* attempts to account for shared features through shared habitat/environment among taxa, thus including those shared features not explained by shared ancestry. With some graphical examples Dan shows how *ED* works. Further, he synthesizes a set of *ED*-based measures. These include *ED* complementarity measures designed with the similar aim of calculating and predicting features gains and losses as we gain or lose areas in conservation planning. He concludes by indicating that *ED* methods appear to offer a robust framework for global assessments and for long-term monitoring of biodiversity change.

In chapter “[Phylogenetic Diversity Measures and Their Decomposition: A Framework Based on Hill Numbers](#)”, Anne Chao, Chun-Huo Chiu and Lou Jost

develop a set of tools for integrating species abundances in PD calculations. This proposition enlarges the range of applications of the PD framework, making it a very useful tool for monitoring changes in biodiversity and warning about important changes in abundance before species become actually extinct. This framework is based on Hill numbers, describing the “effective number of species” found in a sample or region. Here Chao et al. provide a rich overview of abundance-based diversity measures and their phylogenetic generalizations, the framework of Hill numbers, phylogenetic Hill numbers and related phylogenetic diversity measures. They also review the diversity decomposition based on phylogenetic diversity measures and present the associated phylogenetic similarity and differentiation. With a real example, they illustrate how to use phylogenetic similarity (or differentiation) profiles to assess phylogenetic resemblance or difference among multiple assemblages either in space or time.

Phylogenetic reconstructions often result in different near-optimal alternative trees, particularly due to conflicting information among different characters. What do we do as conservation biologists when the phylogenetic reconstruction leads to multiple trees with conflicting signals? This problem is here addressed by a contribution by Olga Chernomor et al. (chapter “[Split Diversity: Measuring and Optimizing Biodiversity Using Phylogenetic Split Networks](#)”) with a proposition of combining the concepts of phylogenetic diversity and split networks in a single concept of phylogenetic split diversity. They show how split diversity works and design its application and the computation solution in biodiversity optimization for some well-known problems of taxon selection and reserve selection, exploring how to include taxon viability and budget in this kind of analysis.

The extent to which sampling effort might influence the rank of conservation priorities is long recognized as a central issue in selecting areas for conservation (Mace and Lande 1991; Mckinney 1999; Régnier et al. 2009), but has so far remained practically untouched in the study of conservation of phylogenetic diversity. Here we have the opportunity to present three different approaches to this problem. The convergence of these independent studies shows the importance of this subject and the recognition of the urgency of searching for solutions. In chapter “[The Rarefaction of Phylogenetic Diversity: Formulation, Extension and Application](#)”, David Nipperess deals with this question in the PD framework by further developing the rarefaction of PD first proposed by Nipperess and Matsen (2013). Here he provides a detailed formulation for the exact analytical solution for expected (mean) Phylogenetic Diversity for a given amount of sampling effort in which whole branch segments are selected under rarefaction. In addition, he extends this framework to show how the initial slope of the rarefaction curve (ΔPD) can be used as a flexible measure of phylogenetic evenness, phylogenetic beta-diversity or phylogenetic dispersion, depending on the unit of accumulation.

In chapters “[Support in Area Prioritization Using Phylogenetic Information](#)” and “[Assessing Hotspots of Evolutionary History with Data from Multiple Phylogenies: An Analysis of Endemic Clades from New Caledonia](#)”, the question of resampling and support of the dataset for defining priority areas is studied in the framework of evolutionary distinctiveness (ED). In chapter “[Support in Area Prioritization Using](#)

Phylogenetic Information”, Daniel Rafael Miranda-Esquivel develops one scheme to verify the support for area ranking using a jackknife resampling strategy. In this proposition, one can evaluate the more adequate index and the support of the area ranking with different probability values when deleting phylogenies, and/or areas and/or species. In chapter “**Assessing Hotspots of Evolutionary History with Data from Multiple Phylogenies: An Analysis of Endemic Clades from New Caledonia**”, we and our collaborators Antje Ahrends and Pete Hollingsworth, propose a scheme for solving the problem of sampling bias in datasets with phylogenies coming from independent and so, non-standardized, spatial sampling. We use the rarefaction of phylogenies to assess the role of the number of phylogenies, of species richness and of the influence of individual phylogenies on site’s scores. And then we design a resampling strategy using multiple phylogenies to verify the stability of the results. This method is applied to the case of New Caledonia, a megadiverse island with all locations equally rich in microendemic species and where phylogenetic diversity is especially helpful to determine conservation priorities among sites.

Applications

This last section is composed by contributions exploring the application of phylogenetic diversity methods in study cases. These studies are deliberately diverse in approaches of the use and applications of phylogenetic diversity, and of measures, spatial scales, geographic locations and taxonomic groups as well. It starts with two analyses integrating the conservation of evolutionary history in systematic conservation planning, a field of conservation biology that deals with conservation prioritization taking in account multiple factors, and in which we can define and revise pre-established criteria and goals (Margules and Pressey 2000; Ball et al. 2009; Moilanen et al. 2009; Kukkala and Moilanen 2013).

In chapter “**Representing Hotspots of Evolutionary History in Systematic Conservation Planning for European Mammals**” Arponen and Zupan use the Zonation software for spatial prioritization to prioritize areas for conservation of the evolutionary history of mammals in Europe. With an analysis at continental and at the scale of each European country, they show that: (a) a strategy focusing only on species richness would miss some areas with important levels of evolutionary history, mainly in regions with medium or low values of species richness; (b) the present system of protected areas performs worse than random selections for protecting the evolutionary history of mammals; and (c) a strategy to protect mammals at the continental scale would be much more effective than separated strategies for each country, although from a political point of view this last one is likely to be more feasible.

In the following contribution, Silvano et al. (chapter “**Priorities for Conservation of the Evolutionary History of Amphibians in the Cerrado**”) use a Gap Analysis to evaluate the protection status of 82 anuran species endemic from Brazilian Cerrado and to define priority areas for their conservation. Their results indicate an alarming

situation in which 39 (48 %) endemic and restricted range species are completely unprotected, among them species with very high ED values, and other 43 (52 %) are gap species with less than 20 % of their targets met. The priority areas for the conservation of these species mostly occupy the central portion of the biome, a region that already suffered major habitat destruction, and are forecast to undergo important habitat loss if economic scenario remains unchanged.

The following triad of studies explores the integration of species threat and phylogenetic diversity. It starts with the research of May-Collado, Zambrana-Torrel and Agnarsson (chapter “[Global Spatial Analyses of Phylogenetic Conservation Priorities for Aquatic Mammals](#)”) dealing with the prioritization of areas for conservation of 127 marine mammals worldwide. Here they use the EDGE (Isaac et al. 2007) and HEDGE (Steel et al. 2007) measures to provide the first spatial analysis for phylogenetic conservation priorities incorporating threat information at global scale. By assessing conservation under “pessimistic” and “optimistic” IUCN extinction scenarios they show how fragile is the world system of protected areas to conserve the evolutionary distinctiveness of marine mammals. They identified 22 Conservation Priority Areas all over the world and showed that only 11.5 % of them overlap with existing marine protected areas. Their results complete prior findings on conservation prioritization for marine mammals, providing a helpful tool for the Conservation of Biological Diversity plan to protect 10 % of world’s marine and coastal regions by 2020.

In the next contribution, Jessica Schnell and Kamran Safi (chapter “[Metapopulation Capacity Meets Evolutionary Distinctness: Spatial Fragmentation Complements Phylogenetic Rarity in Prioritization](#)”) design a framework to predict threat status of Data Deficient and Least Concern species. They propose to combine evolutionary distinctiveness with metapopulation capacity derived from habitat isolation. Here they apply this framework to terrestrial mammals endemic of oceanic islands worldwide, and show that balancing between extinction risks associated to island’s isolation and potential loss of evolutionarily unique species can be very useful to characterize conservation status of island endemic species. Based on it they show that islands such as Guadalcanal, Isle of Pines, Madagascar and Nggela Sule are very representative for reducing the extinction of mammals with high ED values.

In chapter “[Patterns of Species, Phylogenetic and Mimicry Diversity of Clearwing Butterflies in the Neotropics](#)”, Chazot et al. explore the patterns of distribution of several features of diversity of three genera of ithomiine butterflies in Neotropical Region. Ithomiine display Müllerian mimetism and numerically dominate many butterfly assemblages across the Neotropics, probably conditioning the distribution of other species that interact with them in positive or negative way. So, the loss of ithomiine species in local assemblages may strongly influence the vulnerability of butterfly assemblages. Here they show that, on the one hand, the pattern of distribution of phylogenetic diversity, species richness, and mimicry diversity are highly congruent within genera, and, in a lesser extent, across genera. On the other hand, the potential loss of species due to disruption of mimicry rings, as captured by a measure of vulnerability designed in this study, are not evenly distributed across genera presenting peaks in areas completely distinct of those observed to the other

features. This is a good example of the “agony of choice” of Vane-Wright et al. (1991) illustrating the difficulty of finding an optimal solution in situations in which several parameters account for the existing biodiversity.

We close this section with a note of optimism. The analysis of Soulebeau et al. (chapter “[Conservation of Phylogenetic Diversity in Madagascar’s Largest Endemic Plant Family, Sarcolaenaceae](#)”) shows that the system of protected areas of Madagascar is likely to protect all lineages and 97 % of the phylogenetic diversity of Sarcolaenaceae, the largest endemic plant family of this island. This result is particularly important because neither Sarcolaenaceae nor phylogenetic diversity were specifically considered in the conception or in the recent expansion of Madagascar’s network of protected area (Kremen et al. 2008), showing that a large system of protected area may capture much more biodiversity components and features than originally expected.

For concluding, in the last chapter we – Roseli Pellens, Dan Faith and Philippe Grandcolas – describe the recent transformations of phylogenetic systematics in the light of new facilities of molecular sequencing and data analysis, and discuss its impacts in biological conservation. We finish by exploring the possibility of defining “planetary boundaries” for biodiversity on the basis of phylogenetic diversity, and its important role in linking biodiversity into broader societal perspectives and needs.

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