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The Future of Phylogenetic Systematics in Conservation Biology: Linking Biodiversity and Society

Roseli Pellens, Daniel P. Faith, and Philippe Grandcolas

Given the rate at which sequence data in the public domain are accumulating, with initiatives to sequence the entire biota ... on the horizon, it seems likely that within a decade or two, phylogenetic data will cease to be the limiting factor: It could even be that an organism's place in the Tree of Life often will be one of the few things we know about it. Mace et al. (2003)

Abstract Phylogenetic diversity has become invaluable for conservation biology in the last decades, reflecting its link to option values and to evolutionary potential. We argue that its use will continue to grow rapidly in the next decades because of the transformation of systematics with new molecular techniques and especially metagenomics. In a near future, phylogenetic diversity typically will be the very first result at hand, and the great challenge of biodiversity sciences will be to preserve its link with natural history and the remainder of biological knowledge through species vouchers and names. The phylogeny availability and the very wide sampling allowed will facilitate obtaining detailed biodiversity information at local scale and considering the transition across scales – a fundamental need well highlighted in international conservation guidelines, and historically so difficult to achieve. All this suggests that phylogenetic diversity might be at the center of more explicit identification of conservation priorities and options. For concluding, we explore an emerging local-to-regional-to-global challenge: the possibility of defining “planetary boundaries” for biodiversity on the basis of phylogenetic diversity.

Keywords Species molecular characterization • Metagenomics • Knowledge databases • Option values • Planetary boundaries

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Phylogenetic diversity is now a core part of conservation biology, reflecting its link to option values and to evolutionary potential. Further, there is good overlap with related issues in broader ecology. These include community ecology's interest in productivity (e.g. Cadotte et al. 2012), resilience (e.g. Pugliesi and Rapini 2015) and the functioning of ecosystems (e.g. Srivastava et al. 2012) and microbial ecology's use of PD as a cornerstone for exploring diversity patterns at multiple scales (Lozupone and Knight 2005, 2008; Faith et al. 2009). As the chapters in this book demonstrate, the development of new methods and their applications are very much tuned into human impacts and sustainability issues. Thus, red listings, drivers of extinction, and changes in spatial and temporal distribution of phylogenetic diversity are common elements of these studies. All this promotes the incorporation of phylogenetic diversity in the international conservation agenda.

These prospects are magnified by the remarkable facilities for obtaining entire or large parts of genomes or other molecular sequences of any kind of organisms, and by the sheer magnitude of biological (gene sequences, trait databases, species occurrences, red lists) and environmental data (climate layers for past, present and future interpolated to very fine spatial scales; land-use layers, spatial data indicating particular important risks such as fires, floods, and so on) now available in the public domain. All these allow for rapid estimation of the phylogenetic relationships for a large number of organisms in association with potential distribution and threats for species and lineages. In addition, under the stimulus of modern phylogenetic and molecular methods, systematics is going through a significant transformation that will certainly influence biodiversity conservation (Mace et al. 2003; Pons et al. 2006; Vogler and Monaghan 2006; Faith et al. 2010; Yahara et al. 2010). For closing this book, we will briefly describe this transformation of systematics and then discuss some impacts of these changes 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.

In Phase with Modern Systematics and NGS Methods: The Tree First, Then the Species

Conventionally, species are first characterized, then described with morphological or molecular data, and only then analyzed for building a phylogenetic tree (Fig. 1). As the entire operation demanded a long time and effort of specialists, the extent to which the later stage of the process – calculations of phylogenetic diversity – provided additional information "worth waiting for" was a recurrent and important question. Stopping at the first step and using species richness was accepted as a good *proxy* of biodiversity and sometimes justified, as when phylogenetic trees were expected to be balanced, or when the species with higher values of phylogenetic diversity were widespread, so not bringing important additional information (Rodrigues et al. 2005; Hartmann and André 2013). This rationale involved an

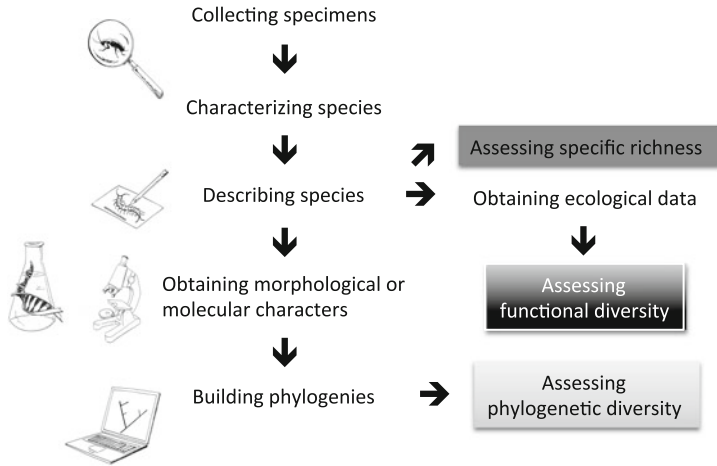


Fig. 1 The traditional data processing in systematics, beginning with the sampling of specimens and the characterization and description of species. Specimens were then specifically sampled for phylogenetic characters, allowing to build phylogenetic trees and to compute phylogenetic diversity. In parallel, other biological knowledge was obtained separately. Note that in this framework, the number of species is obtained at the early step of species characterization (the so-called “morphospecies” may be obtained before description if necessary) before the phylogenetic analysis (Drawings by Agathe Haevermans)

unfortunate circular reasoning in that it required the knowledge about the phylogeny of the group to be able to discard it.

This process now has been turned upside down. In the new paradigm, systematics proceeds in an all-in-one operation i.e. the result of the data processing makes that the species position on the tree is part of species delimitation and characterization (Fig. 2). A global sample of characters (e.g. DNA) x individuals can be partitioned into clusters – potentially species – through a tree-like guidance. The new rationale is simple: to define species, we need first to recognize and delimit different groups of individuals, by contrasting their characters (Goldstein et al. 2000; Pons et al. 2006; Vogler and Monaghan 2006; O’Meara 2010; Pante et al. 2015; but see DeSalle et al. 2005). This phylogenetic perspective is still certainly new for many, although it is inexorably implemented in the most recent molecular methods used for biodiversity exploration and characterization, such as molecular species delimitation or metagenomics.

Metagenomics recently went one step further by considering global amounts of DNA from environmental samples. In this approach there is no need to assemble the matrix ‘individuals x characters’ that is already all in the test tube. This technique is also remarkable by capturing all DNA at the same time and carrying out a very wide sampling including microbes and all organisms usually ignored by traditional taxonomic screening (Tringe and Rubin 2005; Yahara et al. 2010). Combined with proteomics, it can even provide functional information at the same time, by obtaining both DNA species and protein synthesis. At the point we are now, systematics is therefore able to offer a comprehensive picture of diversity, linking species, their

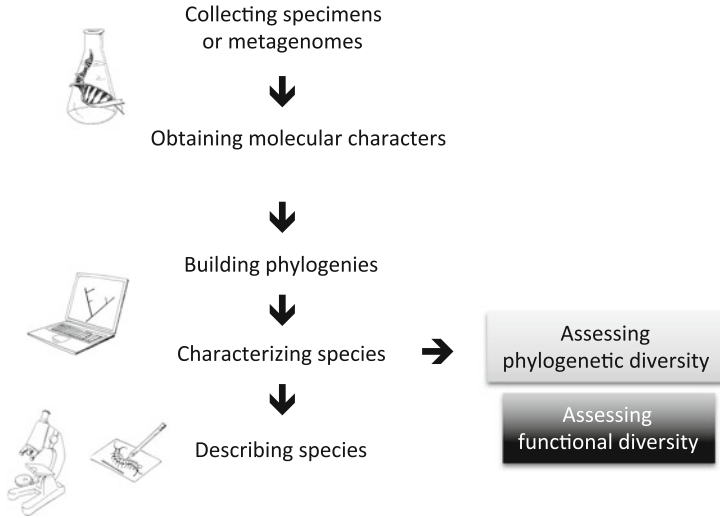


Fig. 2 The new and upcoming data processing in systematics, beginning with molecular characterization or even metagenomics, jointly allowing phylogenetic analysis and species characterization, and therefore computation of phylogenetic diversity. Note also that some assessments of phylogenetic diversity may proceed without the species characterization. The species description and name attribution is the last, but not the least, step to keep molecular data connected with biological knowledge. Note that in the same line, proteomics could provide – to some extent – the species functional characterization, with molecular analysis on its own (Drawings by Agathe Haevermans)

relationships and their characters to conservation biology (Funk et al. 2002; Wilson 2003; Faith et al. 2010; Lean and MacLaurin chapter “[The Value of Phylogenetic Diversity](#)”).

Obviously, this new framework enhanced by molecular biology and metagenomics will maintain biological significance and usefulness as long as molecular proxies will remain related to species concepts, taxon names and classifications linking to the wider biological knowledge (Mace 2004; German National Academy of Sciences Leopoldina 2014). The peril to invest only in an isolated and blind molecular database was already keenly emphasized by many taxonomists at the occasion of the rise of the barcoding initiative (e.g., Will et al. 2005). Building the network between names, biological knowledge and molecular data is from far the biggest challenge of present-day systematics and other sciences of diversity, much beyond the molecular technical tour de force (Grandcolas et al. 2013). We must keep in mind that this challenge takes place in a difficult moment when discovery rates of species new to science do not decline (Tancoigne and Dubois 2013) but in a context of rising rates of extinction (Régnier et al. 2015).

Impacts on Biodiversity Conservation

The first impact of these methodological breakthroughs in biodiversity conservation is the growing availability of phylogenies with adequate taxon and character sampling at fine scale. As a consequence, it will increase not only the possibility of identifying taxa and areas whose conservation will maximize phylogenetic diversity (Forest et al. 2007; Buerki et al. 2015; Soulebeau et al. chapter “[Conservation of Phylogenetic Diversity in Madagascar’s Largest Endemic Plant Family, Sarcolaenaceae](#)”) or whose loss would contribute to major losses of our evolutionary heritage (Faith and Richards 2012; Faith 2015). It will also facilitate the transition across scales, a fundamental need well highlighted in international conservation guidelines (e.g. the Convention on Biological Diversity, “CBD”), and historically so difficult to achieve. For example, some targets can be established at a global scale based on a general phylogeny (for example, a phylogeny with samples of all genera or families), and a more detailed phylogeny with the regional diversification of the group (including for example a large sample of the species occurring in this region) will allow for establishing the areas to be protected for attainment of the broader target. This, associated with modern methods of Systematic Conservation Planning (Moilanen and Arponen 2011; Kukkala and Moilanen 2013; Faith chapter “[Using Phylogenetic Dissimilarities Among Sites for Biodiversity Assessments and Conservation](#)”) in which biological variables, including phylogenetic diversity can be considered along with costs, risks and return to investment, will certainly contribute to more explicit identification of conservation priorities and options (Pollock et al. 2015; Arponen and Zupan chapter “[Representing Hotspots of Evolutionary History in Systematic Conservation Planning for European Mammals](#)”; Silvano et al. chapter “[Priorities for Conservation of the Evolutionary History of Amphibians in the Cerrado](#)”). With these developments in mind, we will close this book by exploring an emerging local-to-regional-to-global challenge: the possibility of defining “planetary boundaries” for biodiversity on the basis of phylogenetic diversity.

Phylogenetic Diversity as a Basis for Defining “Planetary Boundaries” for Biodiversity

The idea that we are approaching a state of shift in the planet’s environment, due to various human activities within the “Anthropocene” (Barnosky et al. 2012) is attracting attention in the scientific community. The definition and quantification of “planetary boundaries” is one approach to respond to this. “Planetary boundaries” (see Rockström et al. 2009; Steffen et al. 2015) refer to the idea of a “safe operating space” for humanity. The planetary boundaries framework considers processes relating to climate change, biodiversity loss, land-system change, biogeochemical flows, stratospheric ozone depletion, ocean acidification, freshwater use,

atmospheric aerosol loading, and chemical pollution. The rationale is that exceeding the identified boundaries means that thresholds and undesirable changes threaten human well-being.

There has been much debate about how to define a meaningful boundary related to biodiversity. The current rate of extinctions and the corresponding biodiversity crisis suggest a possible focus on global extinction rates. However, recent work has focused more on phylogenetic and functional diversity (Faith et al. 2010; Mace et al. 2014; Steffen et al. 2015). These aspects may have a good regional-to-global scope, and appealing links to current and future well-being. These two key aspects for a biodiversity boundary are now being investigated through a global change international program called “Future Earth”. The PD calculus may provide ways to describe boundaries related to phylogenetic diversity “tipping points” (Faith et al. 2010). Such phylogenetic tipping points correspond to the irreversible loss of deep branches of the tree of life, following successive losses over time of descendent taxa. The tipping points, and corresponding boundaries, then link naturally to concerns about the loss of evolutionary or ecosystem services, including option values (unanticipated future benefits for humans) and evolutionary potential. Such option values of biodiversity typically reflect global-scale benefits for future generations, and so they are a natural consideration for planetary boundaries. At the same time, phylogenetic diversity has local importance (e.g. for resilience and delivery of ecosystem services) and may be part of regional-scale planning. Early warnings with respect to a phylogenetic planetary boundary may focus on the changing status of Phylogenetic Key Biodiversity Areas – those places on the planet that are outstanding in their current contribution to retaining global phylogenetic diversity (Brooks et al. 2015; Faith chapter “[The Value of Phylogenetic Diversity](#)”).

The interest in Planetary Boundaries also reminds us that there are “boundaries” in the utility of phylogeny for conservation. The PD measure (Faith 1992; Faith chapter “[The Value of Phylogenetic Diversity](#)”) is useful, but does not tell us all we need to know about functional traits – one of the other possible foci for a biodiversity boundary. Functional traits, by their nature, are not always well accounted for by the PD assumption that shared ancestry explains shared features. This assumption could be especially hard to justify if these traits are defined too intrinsically and are therefore not heritable (Grandcolas et al. 2010; Weiher et al. 2011). Therefore, an alternative model assuming that shared *habitat* explains shared traits may be useful. Such companion models to phylogenetic diversity are in development (Faith chapter “[Using Phylogenetic Dissimilarities Among Sites for Biodiversity Assessments and Conservation](#)”). At the global scale, such approaches could provide, for multiple taxonomic groups, a running report card on risk of loss of functional trait diversity. This would nicely complement the emerging use of a PD report card to assess risks associated with resilience-loss, tipping points and planetary boundaries.

These issues highlight the broader need to integrate phylogenetic diversity – and its associated option values – into the broader perspectives on sustainability and multiple needs of society. This book demonstrates that effective development of the

measures – the toolbox – enables phylogenetic diversity to be “on the table” in these policy contexts.

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