



Phylodiversity to inform conservation policy: An Australian example



Tania Laity^{a,*}, Shawn W. Laffan^b, Carlos E. González-Orozco^c, Daniel P. Faith^d, Dan F. Rosauer^{e,f}, Margaret Byrne^g, Joseph T. Miller^{h,1}, Darren Crayn^{i,j}, Craig Costion^{j,k}, Craig C. Moritz^{e,f}, Karl Newport^a

^a Science Division, Department of Environment, GPO Box 787, Canberra, ACT 2601, Australia

^b Centre for Ecosystem Science, School of Biological, Earth and Environmental Science, University of New South Wales, Sydney 2052, Australia

^c Institute for Applied Ecology and Collaborative Research for Murray-Darling Basin Futures, University of Canberra, Canberra, ACT 2601, Australia

^d The Australian Museum Research Institute, Australian Museum, 6 College St, Sydney, NSW 2000, Australia

^e Division of Evolution, Ecology and Genetics, Research School of Biology, The Australian National University, ACT 2601, Australia

^f Centre for Biodiversity Analysis, The Australian National University, ACT 2601, Australia

^g Science and Conservation Division, Department of Parks and Wildlife, Locked Bag 104, Bentley Delivery Centre, WA 6983, Australia

^h Centre for Australian National Biodiversity Research, CSIRO, GPO Box 1600, Canberra, ACT, Australia

ⁱ Australian Tropical Herbarium, James Cook University, Cairns Campus, PO Box 6811, Smithfield, QLD 4878, Australia

^j Centre for Tropical Environmental Sustainability Science, James Cook University, Cairns Campus, PO Box 6811, Smithfield, QLD 4878, Australia

^k Botany Department, National Museum of Natural History, MRC 166, Smithsonian Institution, P.O. Box 37012, Washington, DC 20013-7012, USA

HIGHLIGHTS

- We demonstrate tangible advantages of phylodiversity to conservation
- Study regions have a higher proportion of phylodiversity than species richness.
- Low regional phylogenetic endemism was found despite high numbers of endemics.
- High congruency found between PD and SR and between PE and WE within taxa
- Biotic responses to evolutionary processes are strongly influenced by life history

ARTICLE INFO

Article history:

Received 8 October 2014

Received in revised form 28 April 2015

Accepted 29 April 2015

Available online 12 May 2015

Keywords:

Phylogeny

Species

Conservation planning

Policy

Diversity

Phylogenetic diversity

Phylogenetic endemism

ABSTRACT

Phylodiversity measures summarise the phylogenetic diversity patterns of groups of organisms. By using branches of the tree of life, rather than its tips (e.g., species), phylodiversity measures provide important additional information about biodiversity that can improve conservation policy and outcomes. As a biodiverse nation with a strong legislative and policy framework, Australia provides an opportunity to use phylogenetic information to inform conservation decision-making.

We explored the application of phylodiversity measures across Australia with a focus on two highly biodiverse regions, the south west of Western Australia (SWWA) and the South East Queensland bioregion (SEQ). We analysed seven diverse groups of organisms spanning five separate phyla on the evolutionary tree of life, the plant genera *Acacia* and *Daviesia*, mammals, hylid frogs, myobatrachid frogs, passerine birds, and camaenid land snails. We measured species richness, weighted species endemism (WE) and two phylodiversity measures, phylogenetic diversity (PD) and phylogenetic endemism (PE), as well as their respective complementarity scores (a measure of gains and losses) at 20 km resolution.

Higher PD was identified within SEQ for all fauna groups, whereas more PD was found in SWWA for both plant groups. PD and PE complementarity were strongly correlated with species richness and species complementarity for most groups but less so for plants. PD and PE were found to complement traditional species-based measures for all groups studied: PD and PE follow similar spatial patterns to richness and WE, but highlighted different areas that would not be identified by conventional species-based biodiversity analyses alone.

The application of phylodiversity measures, particularly the novel weighted complementary measures considered here, in conservation can enhance protection of the evolutionary history that contributes to present day biodiversity values of areas. Phylogenetic measures in conservation can include important elements of biodiversity in conservation planning, such as evolutionary potential and feature diversity that will improve decision-making and lead to better biodiversity conservation outcomes.

Crown Copyright © 2015 Published by Elsevier B.V. All rights reserved.

* Corresponding author.

¹ Current address: Division of Environmental Biology, National Science Foundation, Arlington, VA 22230, USA.

1. Introduction

Australia is one of 17 countries identified as biologically ‘megadiverse’ (Mittermeier et al., 1997). This reflects not only its sheer number of species, but the high degree of endemism (uniqueness) of its biodiversity – approximately 92% of higher plant species, 87% of mammal species, 93% of reptiles, 94% of frogs and 45% of bird species are found nowhere else (Chapman, 2009). This extraordinary biodiversity has evolved over many millions of years partly as a consequence of Australia’s geographical isolation from other continents.

Biodiversity refers to the variety of life, spanning genetic, species and ecosystem levels (Convention on Biological Diversity, 2006). However, for conservation evaluation and prioritisation, biodiversity is typically described and quantified using species level measures such as species richness, which is the count of the number of different species in a given area or region. Implicit in the application of such measures is the assumption that the species category as a unit of measurement is an appropriate surrogate for other facets of biodiversity (Soutullo et al., 2005) such as those represented by genes, traits and ecosystems.

Measures based on evolutionary history capture aspects of biodiversity missed by species level measures. Evolutionary history is usually represented by a phylogenetic tree (see Fig. 1), which depicts not only ancestor–descendent relationships among lineages of organisms but also the amount of evolutionary difference among those lineages. Phylogenetic diversity (PD) is a measure of the representation of evolutionary history (Fig. 1), and extends to a family of “phylodiversity” measures based upon the PD framework.

Importantly, calculating species richness alone does not identify areas where few species represent a significant amount of evolutionary history or phylogenetic diversity (Faith, 1992; Mooers and Atkins, 2003; Soutullo et al., 2005; Yek et al., 2009). This is because different sets of species can

differ greatly in the amounts of evolutionary history they represent (Faith, 1992; Mace et al., 2003; Isaac et al., 2007; Faith, 2008) as can geographic areas (Sechrest et al., 2002; Rosauer et al., 2009; Mishler et al., 2014). For example, the extinction of a species that does not have any close living relatives, such as the Wollemi pine (*Wollemia nobilis*), which is the sole living descendent of a 150 million year old lineage, would result in a greater loss of phylogenetic diversity than the extinction of a young species with many close relatives (May, 1990; Mace et al., 2003; Faith, 2008). A further advantage of phylodiversity is that, by shifting the measure of diversity from species to features or characters (i.e., units of phylogenetic variation), assessments of biodiversity/conservation value become relatively robust to taxonomic uncertainty and changes (Mace et al., 2003).

Explicitly considering evolutionary processes to address adequacy of conservation actions is frequently suggested but rarely undertaken in conservation planning (Klein et al., 2009; Winter et al., 2012). The paucity of work in this area is probably due to the challenges associated with understanding evolutionary processes and identifying spatial data to represent them (Possingham et al., 2005). The necessary phylogenetic trees and data have, until recently, been available for too few taxa to enable effective conservation planning. These factors (particularly data adequacy and coverage) are magnified when considering a large jurisdiction such as Australia. However, over the past 20 years there has been an exponential growth in the availability of phylogenetic trees for major taxon groups (Lyubetsky et al., 2014), and therefore methods that use them are increasingly relevant for conservation planning. In addition, the availability of comprehensive species data has improved in recent times. In the context of the current global extinction crisis, it is critical that conservation planning maximizes the capacity of biota to respond adaptively to environmental change, and it has been argued [e.g., Faith (1992), Moritz (2002)] that conserving phylogenetic diversity is the best way to achieve this.

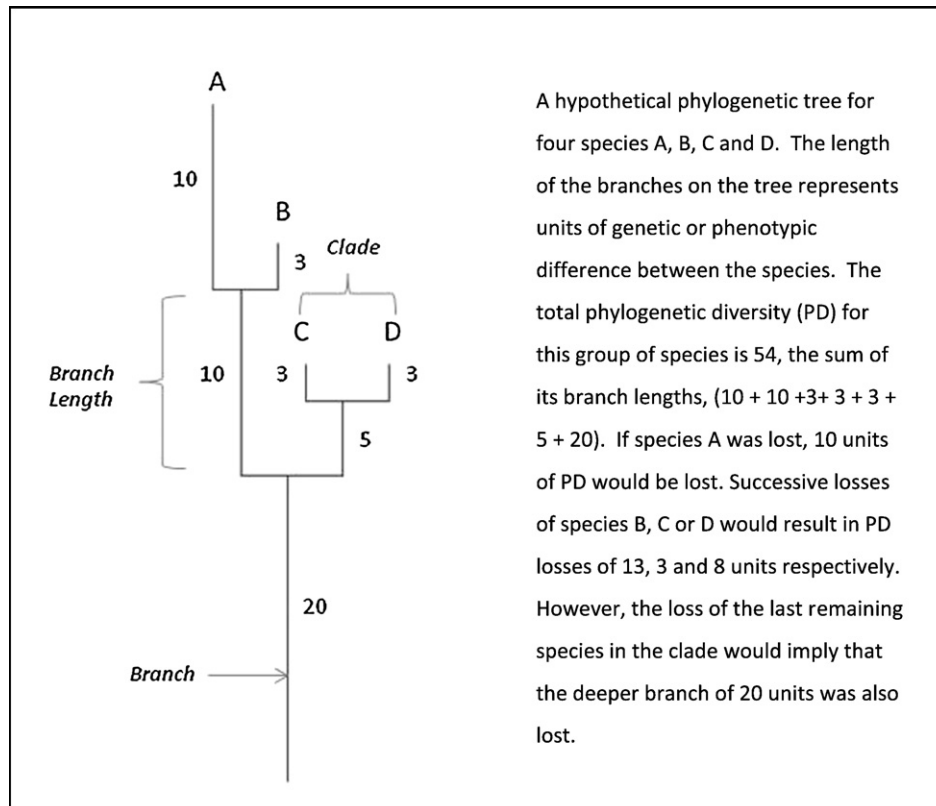


Fig. 1. A hypothetical example of phylogenetic diversity. Adapted from Faith and Richards, 2012.

Download English Version:

<https://daneshyari.com/en/article/4428341>

Download Persian Version:

<https://daneshyari.com/article/4428341>

[Daneshyari.com](https://daneshyari.com)