

Abstract

The threats imposed on biodiversity by anthropogenic factors and climate change could cause major biodiversity loss that will have major detrimental effects on the livelihoods of humans and ecosystems. With time and resource constraints plaguing the conservation field it is of utmost importance that biodiversity assessments are prioritised and conducted effectively. Species richness and endemism have been used in biodiversity assessments for many years now but due to their shortcomings, phylogenetic metrics were developed. These phylogenetic metrics offer an advantage in that they include the evolutionary history and relatedness of taxa in the analysis of biodiversity, consequently providing in-depth information on the structure of a taxa and how it relates to other taxa.

Phylogenetic metrics also allow the differentiation between areas of neo- and palaeo-endemism, an important facet in the conservation field. Southern Africa is species diversity and endemism rich and conservation of the region is very important. Therefore, this study incorporated the use of phylogenetic metrics as well as a new metric for differentiating neo- and palaeo-endemism, CANAPE, with the aim of assessing the value of these phylogenetic metrics in identifying hotspots for biodiversity conservation in the biodiverse southern African region. The study also aimed to identify areas of neo- and palaeo-endemism in the region so as to maximise on their conservation. The widespread, everlasting daisy genus, *Helichrysum* (Asteraceae, Gnaphalieae) and the endemic dwarf chameleon genus, *Bradypodion* (Chamaeleonidae) were utilised for this study.

First, phylogenetic metrics and species metrics were calculated for both genera and hotspots were inferred. The hotspots revealed by phylogenetic metrics were then assessed for overlap with the hotspots revealed by species metrics. Next, the CANAPE analysis was run so as to identify the areas of neo- and palaeo- endemism in southern Africa. A phylogenetic diversity (PD) dissimilarity analysis was then conducted to analyse the clustering of the significantly high endemic areas on the phylogenetic tree. Lastly, all the hotspots identified were assessed for representation in the protected areas of southern Africa so as to check how well they are being conserved.

Phylogenetic metrics were largely congruent with the species metrics for both genera with the phylogenetic metrics revealing additional information about the taxa and its history. *Bradypodion* hotspots were mainly located in the Knysna area (South Africa), Walvis Bay

(Namibia) as well as in the Drakensberg region (South Africa) where it is likely that different niches have led to the proliferation of this genus. The results showed more *Helichrysum* hotspots distributed throughout the region with important areas being Sekhukhuneland, Wolkberg region, Drakensberg region, and the Maputaland-Pondoland centre of diversity in South Africa, as well as southern Namibia.

Some of the phylogenetic metrics did not reveal any useful information for *Bradypodion*, possibly due to the small genus size. However, using the large *Helichrysum* genus revealed more information about the hotspots of phylogenetic diversity and endemism in southern Africa. Protection of the hotspots of neo- and palaeo-endemism still requires attention since some of the major hotspots are not located in protected areas. Such areas where conservation is still lacking were identified by the study. Plans to include the hotspots not covered by protected areas need to be prioritised to avoid the loss of speciation hubs, valuable species, and the rich evolutionary history contained within them.

It can be concluded that phylogenetic metrics do reveal additional information that is important to conservation but care must be taken when making conclusions based on taxa of different sizes.

Keywords: *Bradypodion*, CANAPE, *Helichrysum*, neo- and palaeo-endemism, phylogenetic metrics, southern Africa