

Unravelling the evolutionary origins of biogeographic assemblages

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Abstract

Aim: Floristic and faunal diversity fall within species assemblages that can be grouped into distinct biomes or ecoregions. Understanding the origins of such biogeographic assemblages helps illuminate the processes shaping present-day diversity patterns and identifies regions with unique or distinct histories. While the fossil record is often sparse, dated phylogenies can provide a window into the evolutionary past of these regions. Here, we present a novel phylogenetic approach to investigate the evolutionary origins of present-day biogeographic assemblages and highlight their conservation value.

Location: Southern Africa.

Methods: We evaluate the evolutionary turnover separating species clusters in space at different time slices to determine the phylogenetic depth at which the signal for their present-day structure emerges. We suggest present-day assemblages with distinct evolutionary histories might represent important units for conservation. We apply our method to the vegetation of southern Africa using a dated phylogeny of the woody flora of the region and explore how the evolutionary history of vegetation types compares to common conservation currencies, including species richness, endemism and threat.

Results: We show the differentiation of most present-day vegetation types can be traced back to evolutionary splits in the Miocene. The woody flora of the Fynbos is the most evolutionarily distinct, and thus has deeper evolutionary roots, whereas the Savanna and Miombo Woodland show close phylogenetic affinities and likely represent a more recent separation. However, evolutionarily distinct phyloregions do not necessarily capture the most unique phylogenetic diversity, nor are they the most species-rich or threatened.

Main conclusions: Our approach complements analyses of the fossil record and serves as a link to the history of diversification, migration and extinction of lineages within biogeographic assemblages that is separate from patterns of species richness and endemism. Our analysis reveals how phyloregions capture conservation value not represented by traditional biodiversity metrics.

KEYWORDS

Miocene, phylogenetic beta diversity, phyloregions, phytogeographic regions, Southern Africa

1 | INTRODUCTION

Biodiversity is under increasing anthropogenic pressure, and there is an urgent need to prioritize the protection of areas with high conservation value. Systematic conservation planning aims to optimize the use of limited resources for the conservation of biodiversity (James, Gaston, & Balmford, 2001; Margules & Pressey, 2000), with a common approach being the prioritization of biodiversity hotspots (i.e., geographic clusters of high conservation value; Myers, 1988; Myers, Mittermeier, Mittermeier, da Fonseca, & Kent, 2000). Hotspots may represent locations of important ecological and evolutionary processes, and they have proven useful for guiding effective allocation of limited conservation funds (Mittermeier, Myers, Gill, & Mittermeier, 2000; Myers et al., 2000). However, conservation efforts based on hotspots alone do not necessarily guarantee optimal conservation solutions. Hotspots are typically based upon only one or a few axes of diversity, most usually species richness, endemism and threat, and might not, therefore, capture other dimensions of biodiversity, such as phylogenetic diversity or latent risk (see Daru, Van der Bank, & Davies, 2015; Davies & Cadotte, 2011; Forest et al., 2007). In addition, conservation planners might wish to strive for representation of habitats, vegetation types or ecological communities as well as species within a protected area network (Margules & Pressey, 2000). Phylogenetic regionalization offers a relatively new approach for delineating landscapes or seascapes into geographic units that captures information on the evolutionary structure of the species assemblages within them (Daru, Holt, Lessard, Yessoufou, & Davies, 2017; Daru et al., 2016; Holt et al., 2013) and provides additional information for conservation planners beyond traditional hotspot approaches.

The association of species into distinct phylogenetically delimited biogeographic units (referred to as phyloregions by Daru et al., 2016) captures historical processes such as diversification, niche conservatism, dispersal and extinction that may have operated over several millions of years (Daru, Elliott, Park, & Davies, 2017; Davies & Buckley, 2012; Guo, Luo, Liu, & Wang, 2012; Wu, Chen, & Soong, 2016). For instance, dispersal limitation will tend to increase phylogenetic turnover among regions and, as a consequence, the evolutionary separation of phyloregions; whereas the phylogenetic composition of areas encompassing species with high dispersal abilities might be more homogeneous spatially. Dispersal limitation is one of several mechanisms that may be linked to the more general processes of niche conservatism—the tendency of species to retain their ancestral niche. The more phylogenetically conserved the niche, the greater the predicted phylogenetic structure in species assemblages. Speciation and extinction can also leave an imprint on the structure of phyloregions. Endemic radiations can increase the evolutionary separation of phyloregions by increasing clustering of closely related species, while vicariance speciation due to geographic isolation could reduce the evolutionary distinctiveness of phyloregions because sibling species may occur in neighbouring phyloregions. Extinction can structure phyloregions through its effect on both taxon richness and composition. For example, local extinction of old lineages (palaeoendemics) might decrease

the phylogenetic distance separating phyloregions. However, the loss of evolutionarily derived lineages (neoendemics) will have less impact on the phylogenetic structure of a region, at least initially (Daru, Elliott, et al., 2017).

The species composition of present-day assemblages can thus provide insights into the mechanistic processes that have shaped them (Pennington, Cronk, & Richardson, 2004), and more evolutionarily distinct phyloregions might deserve greater conservation priority because they may encompass co-occurring lineages with longer ecological histories. However, to fully understand their present-day structure, we must look backwards into their evolutionary past. Davies and Buckley (2011) examined the diversity of lineages present at different time slices through the phylogenetic tree to gain insight into the evolutionary past of present-day diversity of mammals. This framework opened a window into the historical processes by which present-day mammalian diversity arose. We present a related framework to explore the evolutionary origin of present-day biogeographic assemblages by successively removing phylogenetic structure in the tree linking regional species assemblages to identify the evolutionary depth at which they collapse into each other (Figure 1). We suggest that the phylogenetic depth at which biogeographic regions become indistinguishable may help inform estimates of the time at which they differentiated historically.

We illustrate our framework using a dated molecular phylogeny of woody species to investigate the evolutionary history of present-day vegetation types in southern Africa, an area covering Botswana, Lesotho, Mozambique south of the Zambezi river, Namibia, South Africa, Swaziland and Zimbabwe. On the African continent, southern Africa includes some of the most floristically diverse regions and is characterized by varied vegetation types including Savanna, Miombo Woodland (a type of woody savanna), Grassland, Forest, Desert and Fynbos (Mucina & Rutherford, 2006; Olson et al., 2001), which differ greatly in floristic composition. We show that some phyloregions have long evolutionary histories, whereas others represent relatively recent separations. We suggest that these patterns reflect the historical assembly of southern African vegetation into present-day biomes. We then contrast the evolutionary distinctiveness of phyloregions to alternative conservation indices and show how different indices capture distinct dimensions of diversity.

2 | METHODS

2.1 | Taxon sampling and phylogenetic reconstruction

Following Daru et al. (2016), we used a dated molecular phylogenetic tree for the woody flora of southern Africa from Maurin et al. (2014) to generate a classification of phyloregions representing the major vegetation types in southern Africa. Our definition of woody species follows previous studies (e.g., FitzJohn et al., 2014; O'Brien, 1993), as plant species with above-ground stems >0.5 m, including species that produce secondary xylem tissues such as some tree *Aloe* species, palms

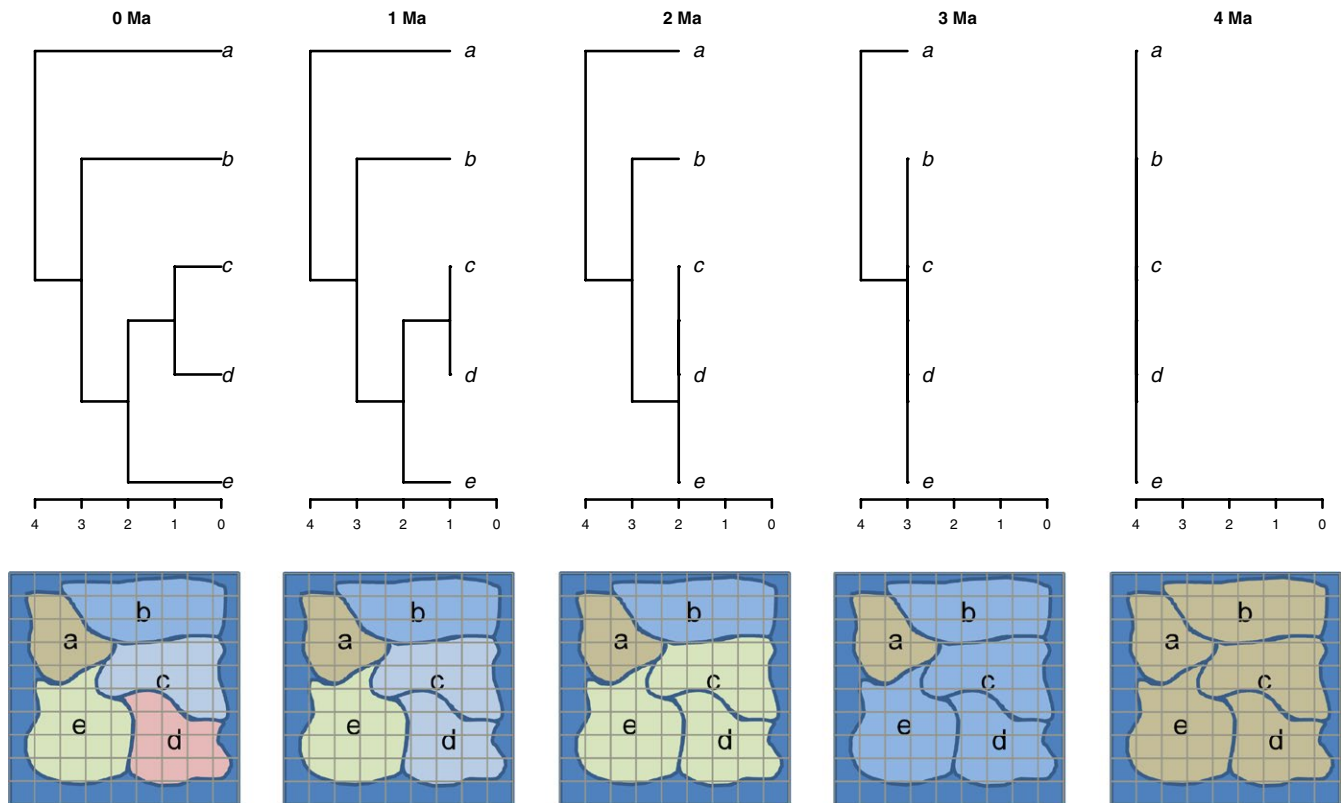


FIGURE 1 Cartoon demonstrating the successive removal of phylogenetic structure in a tree for five species (a–e) in five separate phyloreions, assuming each phyloreion is represented by one tip on the phylogeny. As the tree is deconstructed at 1-Myr intervals from 0 to 4 Ma, information on more recent branching patterns is sequentially lost, and only deeper splits in the tree are informative with respect to biogeographic groupings. For empirical data, phyloreions can be defined by multiple tips in the phylogeny. [Colour figure can be viewed at wileyonlinelibrary.com]

and bamboo. The total woody flora of southern Africa is estimated at ~2,200 species within 117 families representing 543 genera of angiosperms and gymnosperms (Boon, 2010; Palgrave, 2002; Schmidt, Lotter, & McClelland, 2007; Van Wyk, van der Berg, Coates Palgrave, & Jordaan, 2011), from which our analysis samples 1,400 species within 115 families representing 541 genera; sampling is thus almost complete for higher taxonomic levels (see Table S1). We used extent-of-occurrence maps for all 1,400 species from the literature (Palgrave, 2002; Van Wyk et al., 2011) and extracted species presences/absences within a matrix of 50 × 50 km grid cells (Behrmann equal-area cylindrical coordinate system) as described in Daru et al. (2015).

Full details of the phylogeny reconstruction are provided in Maurin et al. (2014) and Daru et al. (2016). The phylogenetic tree used here was estimated using Bayesian analysis of 1,400 species and 1,633 bp of chloroplast DNA sequences derived from a combination of *matK* and *rbcL*, assuming an uncorrelated relaxed molecular clock model, using the program BEAST v.1.7.5 (Drummond & Rambaut, 2007). Branch lengths were calibrated in millions of years using a Bayesian MCMC approach by enforcing topological constraints assuming APG III backbone from Phylomatic v.3 (Webb & Donoghue, 2005) and 18 fossil calibration points from Bell, Soltis, and Soltis (2010). A table with GenBank accession numbers is provided in the Supporting Information to Daru et al. (2016).

2.2 | Construction of phyloreions

Phyloreions were generated by combining the presence or absence of each species distributions within grid cells with branch length information from a dated phylogenetic tree to generate a pairwise distance matrix of phylogenetic beta diversity ($p\beta_{sim}$; Holt et al., 2013) between all pairs of grid cells using R (R Core Team, 2015). We tested the performance of eight clustering algorithms for the regionalization purpose including single linkage, complete linkage, unweighted pair-group method using arithmetic averages (UPGMA), unweighted pair-group method using centroids, weighted pair-group method using arithmetic averages, weighted pair-group method using centroids, Ward's minimum variance and DIANA's divisive hierarchical method. The best performing algorithm was identified using cophenetic correlation coefficient (Sokal & Rohlf, 1962) and Gower's distance (Gower, 1983).

In a second step, we used the "elbow" method of Salvador and Chan (2004) to "cut" the dendrogram and determined the optimal number of meaningful clusters (phyloreions) using the "elbow" function in the R package GMD (Zhao, Valen, Parker, & Sandelin, 2011). Last, we described the relationships among the resulting phylogenetically delimited clusters ("phyloreions"; Daru et al., 2016) using hierarchical dendrogram of dissimilarity and non-metric multidimensional scaling (NMDS) ordination, which represents the original distance

matrix in a few (usually 2 or 3) dimensions with a minimum loss of information. A full description of how phyloregions were delimited is included in Daru et al. (2016). For convenience, when present-day phyloregions correspond spatially to a recognized vegetation type, we refer to the phyloregion by this domain name (Daru et al., 2016); however, phyloregions do not represent a one-to-one match to the named vegetation type.

2.3 | Reconstructing the evolutionary history of phyloregions

First, we explored the phylogenetic signal in the distribution of species within phyloregions using a binary presence-absence matrix for each phyloregion. Phylogenetic signal was evaluated using the D-statistic from Fritz and Purvis (2010) implemented in the R package Caper (Orme et al., 2012). The D-statistic estimates phylogenetic conservatism by scaling the sum of sister-clade differences with those expected under a random model versus a Brownian motion model, and significance is assessed by shuffling the trait values (1,000 times) at the tips of the phylogeny. A D-value of 1 indicates a random distribution of traits at the tip of the phylogeny, whereas a D-value of 0 indicates a Brownian motion model (Fritz & Purvis, 2010).

The deeper branches of a phylogenetic tree (those towards the root of the tree) may capture the signature of past environments that might be different to their present-day descendants (Rosauer et al., 2014). To explore the phylogenetic depth at which the spatial signature of present-day biogeographic assemblages emerges, we successively removed phylogenetic structure in the tree from the tips to the root (i.e., collapse younger phylogenetic branches into older ones) and iterated the clustering algorithm at each time slice (see Figure 1). R-code for manipulating the phylogenetic tree and clustering using phylogenetic beta diversity is provided as Datas S1 and S2.

At each phylogenetic depth, we compare our newly generated phyloregions to the original clusters estimated using the fully resolved phylogeny and to the geographic distribution of currently recognized phytogeographic regions using a map of the vegetation zones of southern Africa (White, 1983 with modifications and additions from Low & Rebelo, 1996; Olson et al., 2001; Burgess et al., 2004; Mucina & Rutherford, 2006). We examined the phylogenetic depth of phyloregions at two temporal scales. First, we considered relatively coarse evolutionary intervals spanning from 260 Ma to present-day (0 Ma) in 20-million year (myr) time slices, and sequentially collapsed nodes and truncated branch lengths, such that the final phylogenetic topology had a total depth of zero. Second, we focus at a finer phylogenetic depth between 20 and 0 Ma (present-day), slicing the tree in 4-myr intervals. The latter time period corresponds to the Miocene-Pliocene (~20 to 3 Ma), which is hypothesized to represent a period of major biome reorganization in Earth's history (Edwards, Osborne, Strömberg, & Smith, 2010; Kürschner, Kvacek, & Dilcher, 2008; Osborne & Beerling, 2006).

Floristic relationships among phyloregions are represented using non-metric multidimensional scaling (NMDS) and a hierarchical dendrogram of dissimilarity.

2.4 | Dimensions of biodiversity

To evaluate how phyloregions captured different dimensions of diversity, we mapped five commonly used indices of biodiversity onto each phyloregion: species richness (SR), species endemism richness (SE), phylogenetic diversity endemism (PD-endemism), evolutionary distinctiveness (ED) and "evolutionary distinctiveness and global endangerment" (EDGE). SR is the total count of species in each phyloregion, SE was calculated as the richness of endemic species per phyloregion, PD-endemism measures the degree to which phylogenetic diversity is restricted to a phyloregion (Faith, Reid, & Hunter, 2004); and ED is the amount of unique evolutionary history represented by a species with few or no extant relatives and calculated based on the fair proportion metric (Isaac, Turvey, Collen, Waterman, & Baillie, 2007) and can be multiplied by each species global endangerment (GE) from IUCN conservation categories to form EDGE scores (species that are phylogenetically isolated and threatened with extinction). ED and EDGE were represented as the mean of the species values within each phyloregion. We tested the performance of phyloregions as a conservation decision-making tool by overlaying the top richest grid cells (i.e., hotspot cells) of five types of diversity metrics (SE, EDGE, ED, PD-endemism and SR) on the map of phyloregions to identify phyloregions that do not overlap any hotspots.

2.5 | Phyloregions at risk

Last, we examined the potential evolutionary future of present-day phyloregions by removing all currently threatened species (IUCN conservation categories VU, EN and CR), recalculating phylogenetic beta diversity metrics for the remaining extant species and then reconstructing a new set of phyloregions for this reduced taxon set following the methods described above.

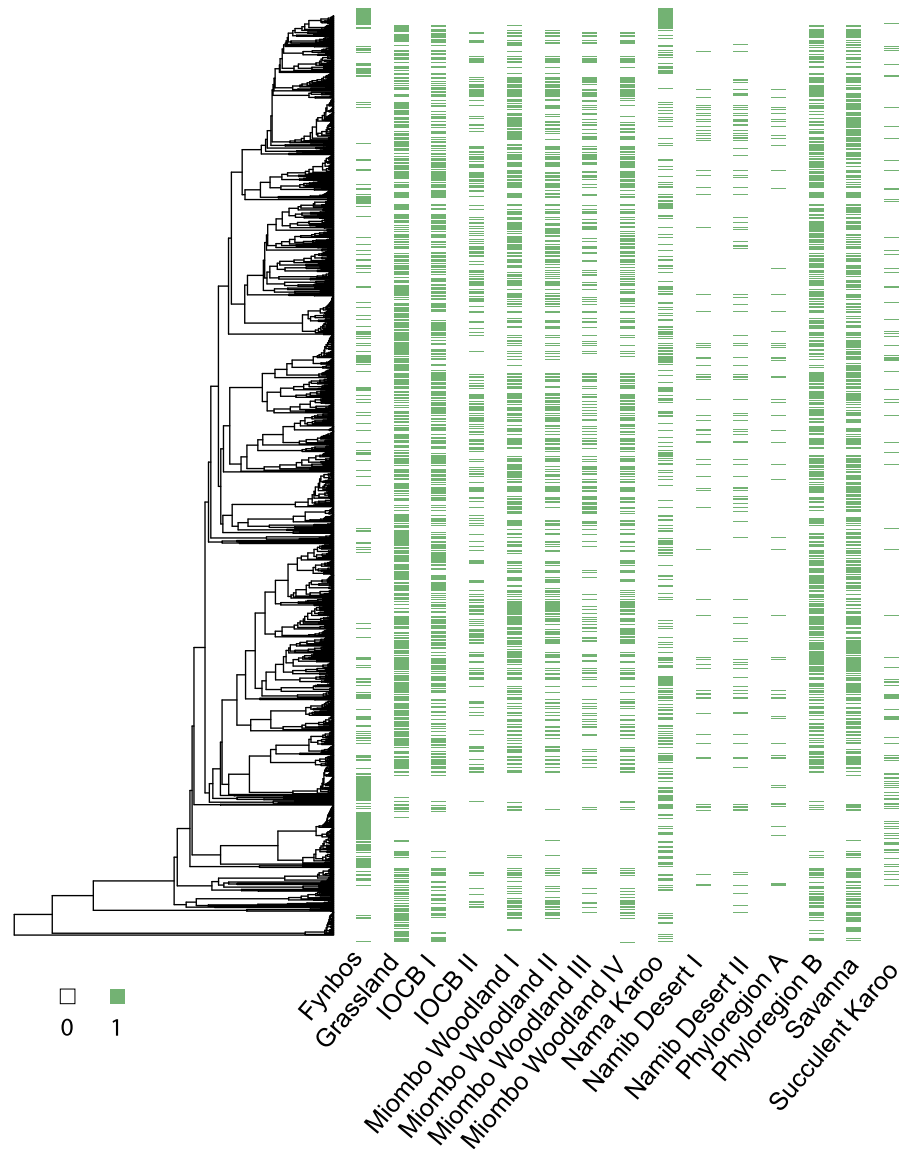
3 | RESULTS

Membership of a particular phyloregion appears to be a relatively labile trait and most phyloregions sample from clades across the phylogenetic tree (Figure 2). Although lineages show significant phylogenetic conservatism in phytogeographic affinity, phylogenetic signal is generally weak. However, there is some evidence for stronger phylogenetic signal in the Fynbos phyloregion and weaker signal in the Savanna and Grassland phyloregions ($D_{\text{Fynbos}} = 0.4$, $D_{\text{Savanna}} = 0.7$, $D_{\text{Grassland}} = 0.8$; all $p < .001$).

Phyloregions corresponding closely to present-day vegetation start to emerge with the inclusion of more recent evolutionary splits within the last ~60 myr. Between 40–20 Ma, the grassland phyloregion, encompassing present-day Grassland, Nama Karoo, Indian Ocean Coastal Belt and Albany thickets, becomes distinct (Figure 3), but it is only when we include evolutionary splits within the last 20 myr that we are able to fully differentiate among modern vegetation types.

To better characterize the emergence of vegetation types within the last 20 Ma, we explored this time window using finer phylogenetic

FIGURE 2 Distribution of lineages among present-day phyloreregions of southern Africa. The presence or absence of a species within a phyloreregion is indicated by the colour bars. The tree is a maximum clade credibility tree obtained from a Bayesian analysis of combined *matK* and *rbcl*a DNA regions of woody species of southern Africa and dated using 18 secondary calibration points (see Maurin et al., 2014). [Colour figure can be viewed at wileyonlinelibrary.com]



slices at 4-myr intervals. We found that the Miombo Woodland phyloreregion can be differentiated from the Savanna phyloreregion at a phylogenetic depth of ~12 Ma, indicating that present-day Savanna may have arisen during this period. The Grassland and Nama Karoo phyloreregions, which encompass parts of the Indian Ocean Coastal Belt and Albany thickets, differentiate ~8 Ma. It was also during this time period (~8 Ma) that we observe the emergence of a formerly unclassified vegetation type, which we previously referred to as “Gariep Karoo” (see Daru et al., 2016), located between the Succulent Karoo and the Namib Desert. Last, between ~4 Ma to the present, a second novel phyloreregion, which we refer to as the “Zambeian transition zone” (Daru et al., 2016), emerges at the border between South Africa, Zimbabwe and Mozambique (Figure 4). This is the youngest phyloreregion (i.e., is only differentiated by recent phylogenetic splits) and shows close phylogenetic affinity to the flora of the Indian Ocean Coastal Belt (Figure 4).

The order of differentiation of phyloreregions is supported by the NMDS ordination and hierarchical dendrogram of dissimilarity

(Fig. S1 in Appendix S1). As we step back through time, adjacent phyloreregions collapse into each other sequentially. Notably, around 20 Ma, the NMDS ordination plots support a major split separating a northern group encompassing Savanna, Miombo Woodland, Indian Ocean Coastal Belt and Desert, and a southern group encompassing Fynbos, Nama Karoo, Grassland and Albany thickets (Fig. S1 in Appendix S1). This split is also reflected in the hierarchical dendrogram of dissimilarity and indicates that the differentiation of the present-day vegetation types may have initially progressed along a north–south axis.

Present-day phyloreregions differ in relative rank depending on the biodiversity index evaluated. For example, Fynbos emerged as the most evolutionarily distinct phyloreregion (mean $p\beta_{sim} = 0.447$; Figure 5), whereas the Grassland phyloreregion that overlaps parts of the Eastern Cape to Drakensberg in KwaZulu-Natal and Gauteng captured the most unshared phylogenetic diversity (PD-endemism = 2,480.36). In contrast, the Indian Ocean Coastal Belt and Miombo Woodland phyloreregion in Mozambique had the highest proportion of phylogenetic

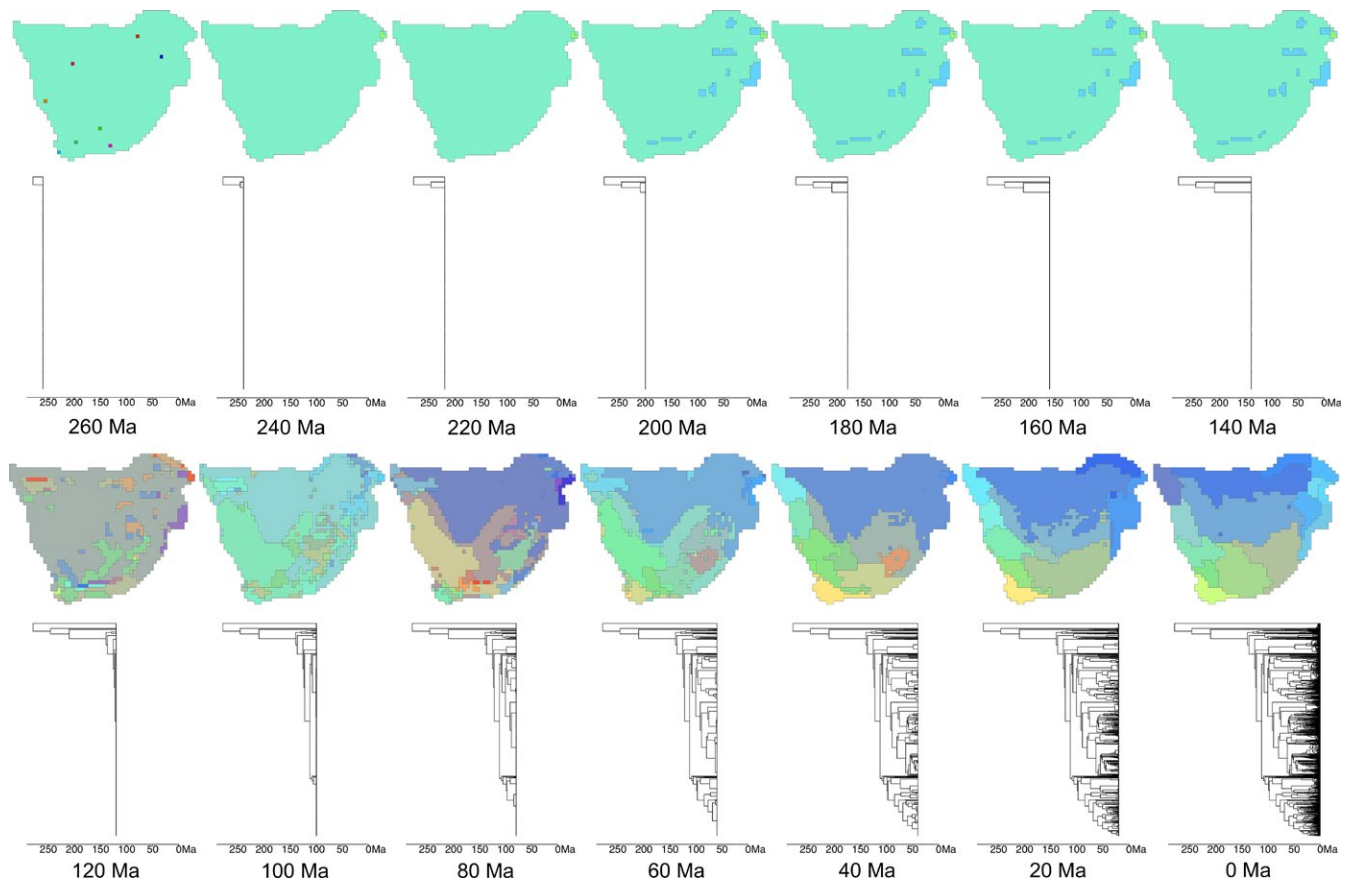


FIGURE 3 Temporal window into the evolutionary past of the present-day phyloregions of southern Africa at successive phylogenetic depths over the last 260 myr. The phylogenetic tree is cut at 20-my intervals (below), and the corresponding geographic clustering is illustrated above. The map is plotted in Behrmann (equal-area) projection using 50×50 km grid cells. The time slice at which phyloregions become indistinguishable may be indicative of the time at which they differentiated historically. The spatial representation of aggregated phyloregions as we step back in time should not be interpreted as representative of their true historical distribution as past climates likely differed from the present day, but is simply provided to illustrate spatially the phylogenetic linkages between present-day phyloregions. Colours are in NMDS space and indicate levels of differentiation of the flora in different phyloregions. Phyloregions with similar colours have similar clades and those with different colours differ in the plant clades they enclose. [Colour figure can be viewed at wileyonlinelibrary.com]

diversity under threat (mean EDGE; Figure 5c). We also found that hotspots based on grid cells capture only 13 of 15 phyloregions, and any one single conservation metric prioritizes a smaller set of phyloregions (see Table S2).

With the removal of currently threatened species, present-day phyloregions became less distinct, and with this increasing homogeneity, we are no longer able to distinguish some phyloregions (Figure 5f). For instance, we lose the newly defined “Zambezian transition zone” (Daru et al., 2016) that overlaps south-western Mozambique at the border between Zimbabwe and South Africa (Figure 5f), and we are also unable to differentiate the Namib Desert I and Nama Karoo phyloregions, which now collapse into the Grassland and Namib Desert, respectively (Figure 5f).

4 | DISCUSSION

Here, we have presented a novel approach for exploring the evolutionary history and geographic organization of biotic diversity using

information from a dated phylogenetic tree of extant taxa. By exploring phylogenetic affinities at successive phylogenetic depths, we are able to make inferences on the historical sequence of the formation of biogeographic assemblages and gain insights into the history of dispersal, extinction and speciation of lineages between and within them. In the flora of southern Africa, we show that the emergence of modern vegetation types was recent, and probably within the last 40–20 myr, suggesting that the present-day species distributions may retain some signature of the earlier migration and habitat filtering of lineages across Africa. By looking backwards in time, we identify phyloregions with long evolutionary histories and those that represent relatively recent separations. We suggest not only that phyloregions represent important conservation units, but just as species with long evolutionary histories might deserve more conservation attention (Vane-Wright, Humphries, & Williams, 1991), so too might equivalent phyloregions. Such phyloregions encompass lineages that have co-evolved over many millions of years and capture the biogeographic processes that have shaped modern diversity patterns (Holt et al., 2013).

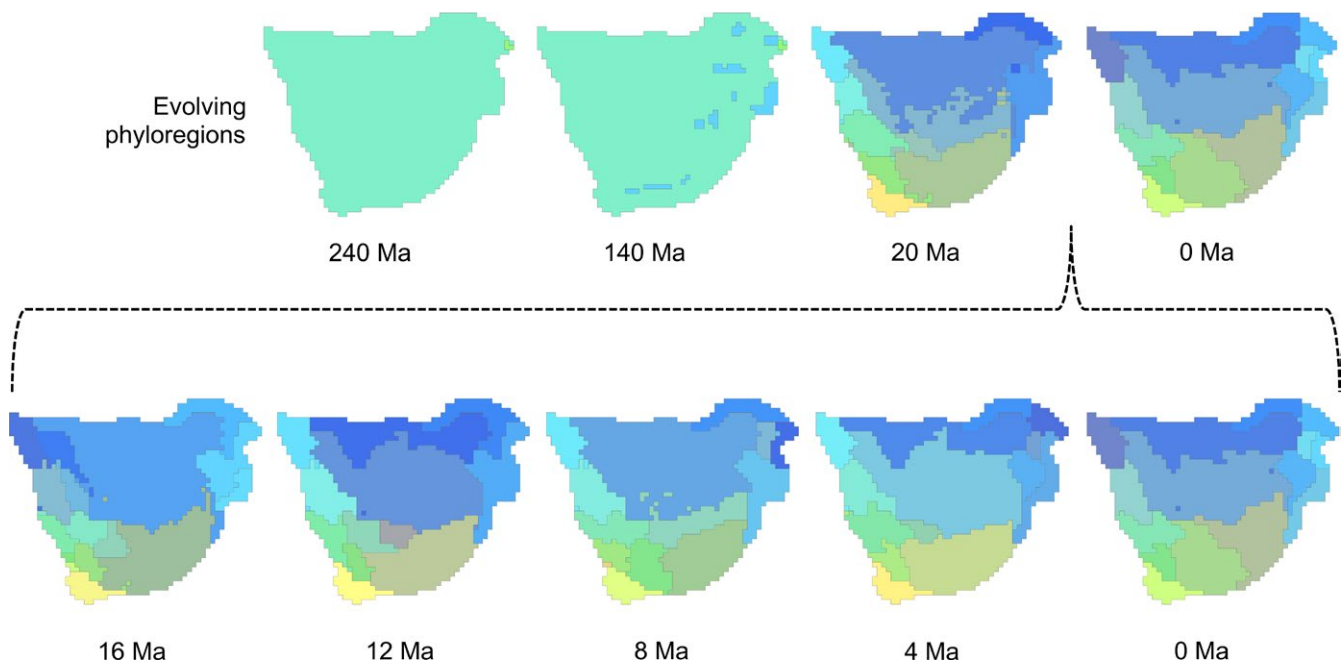


FIGURE 4 Equivalent representation of the evolution of modern phyloregions to that shown in Figure 3, but focusing on 20 Ma to present. Five maps resulting from the phylogenetic beta diversity ($p\beta_{sim}$) values for species assemblages in 50×50 km grid cells, cut at phylogenetic depths of 16, 12, 8, 4 and 0 Ma, are illustrated. Colours are in NMDS space and indicate levels of differentiation of the flora in different phyloregions. Phyloregions with similar colours have similar clades and those with different colours differ in the plant clades they enclose. The colour gradient in the shading of the maps depicts northern regions in darker colours and southern regions in lighter colours. The map is plotted using Behrmann (equal-area) projection. [Colour figure can be viewed at wileyonlinelibrary.com]

Undoubtedly, there have been major floral and faunal shifts over the past several million years, and the geographic distribution of extant species we observe today obviously does not necessarily reflect the geography of the past. Our depiction of the spatial aggregation of vegetation types as we step back in time is only provided to illustrate spatially the phylogenetic linkages among them and should not be interpreted as representative of historical distributions. Nonetheless, present-day vegetation types tend to be characterized by a phylogenetically distinct set of lineages, and using a dated phylogenetic tree of the woody flora, we show how phylogeny provides a window into their evolutionary history that complements approaches using fossil data and climate reconstructions.

4.1 | Phyloregions and the origins of the vegetation types of southern Africa

Our results indicating a relatively recent origin of present-day vegetation types in southern Africa match to previous studies focused on particular taxa (e.g., Linder & Hardy, 2004; Richardson et al., 2001) and changes in atmospheric CO_2 (Kürschner et al., 2008). The evolution of the Fynbos of the Cape floristic region (CFR) has attracted perhaps the most attention and has been linked to the upwelling of cold waters—the Benguela upwelling system (BUS)—along the Atlantic seaboard of southern Africa during late Miocene about 10–8 Ma (Siesser, 1980). Varying dates for the development of the Fynbos biome have been proposed, depending on the lineages examined. Some studies have inferred younger dates, <5 Ma (Cowling & Pressey,

2001), whereas others suggest much older dates within the Oligocene or early Miocene (Goldblatt et al., 2002; Linder & Hardy, 2004). Our study supports a Miocene origin; however, the Fynbos vegetation type might only have become more widespread later, explaining the relative sparsity of Fynbos vegetation in the fossil record. The strong phylogenetic signal in membership of the Fynbos and Karoo vegetation types likely reflects recent in situ radiation of particular clades, such as *Protea* and *Leucadendron*, in these phyloregions (Linder, 2003), further emphasizing their evolutionary distinctiveness.

Our analysis also sheds light on the differentiation of modern-day Savanna and Miombo Woodland around the mid-Miocene ~12–8 Ma. The Miocene was a period characterized by extreme climatic fluctuations and followed a major cooling event at the Oligocene-Miocene boundary that has been suggested to coincide with the origin of many modern terrestrial biomes worldwide (Kürschner et al., 2008). The spread of Savanna in Africa during the Miocene coincides with the rise to dominance of flammable C_4 grasses and shifts in atmospheric CO_2 concentrations (Kürschner et al., 2008; Osborne & Beerling, 2006). The Miombo Woodland, which covers much of Zimbabwe, Mozambique and stretches across the continent to Angola (Campbell, Frost, & Byron, 1996), has been variously categorized as Savanna (Huntley, 1982), Woodland (White, 1983) and Forest (Freson, Goffinet, & Malaisse, 1974; Malaisse, 1978), although it differs from these formations by the dominance of three Fabaceae genera: *Brachystegia*, *Julbernardia* and *Isoberlinia* (Campbell et al., 1996). Geological records indicate that Miombo Woodland also arose during the Miocene ~25–7 Ma, corresponding to the formation of the Central

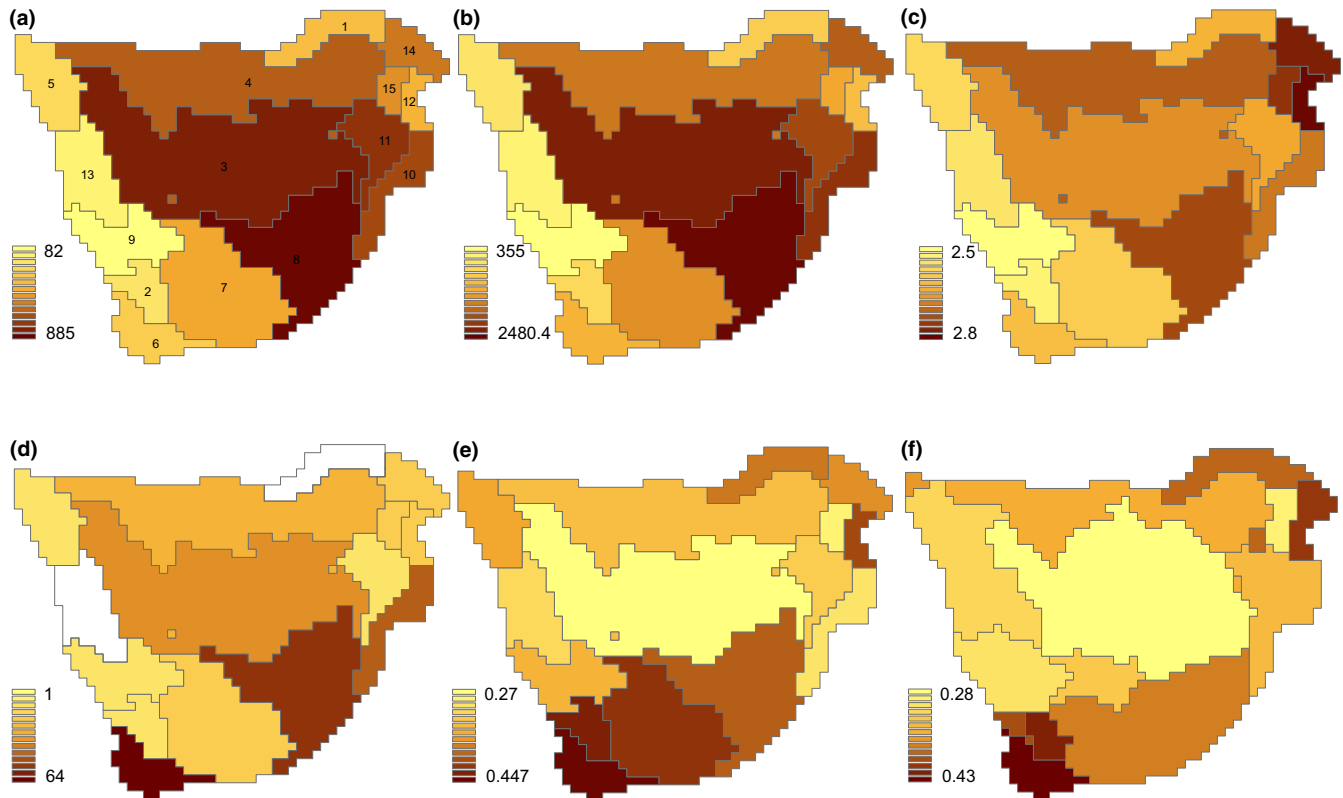


FIGURE 5 Diversity metrics for the woody plants of southern Africa within phyloregions. (a) species richness, (b) PD-endemism, (c) average EDGE, (d) species endemism, (e) evolutionary distinctiveness and (f) evolutionary distinctiveness of a subset of non-threatened taxa, assuming currently threatened species go extinct. 1 = Miombo Woodland III, 2 = Succulent Karoo, 3 = Savanna, 4 = Miombo Woodland I, 5 = Namib Desert II, 6 = Fynbos, 7 = Nama Karoo, 8 = Grassland, 9 = Gariep Karoo, 10 = Indian Ocean Coastal Belt I, 11 = Zambezian transition zone, 12 = Indian Ocean Coastal Belt II, 13 = Namib Desert I, 14 = Miombo Woodland IV, 15 = Miombo Woodland II (see Daru et al., 2016). [Colour figure can be viewed at wileyonlinelibrary.com]

African plateau (Lister, 1987). Our results highlight the close phylogenetic affinities between Savanna and Miombo Woodland, which are also reflected in the weaker phylogenetic conservatism observed in the Savanna vegetation, and favours the younger date for the differentiation between the two vegetation types.

Another feature of interest that emerges from our results is the differentiation of the Grassland vegetation. The present-day Grassland in southern Africa is dominated by C_4 grasses of the Poaceae family and occurs inland in the summer rainfall areas of South Africa covering the highveld areas, eastern seaboard and the high mountains along the east coast (Mucina & Rutherford, 2006). However, plants other than grasses such as herbaceous elements (forbs) and woody species constitute an important part of the native grassy biomes. These woody lineages are adapted to the unique ecological and abiotic features of the grassland biome, which include particular rainfall regimes, nutrient availability and generally low competition for light (Parr, Lehmann, Bond, Hoffmann, & Andersen, 2014), and they thus allow us to define the biome even though they do not represent the dominant life-forms within it. Palaeoecological evidence indicates that grasses evolved ~70–55 Ma (Kellogg, 2001) and gradually extended their distribution into tropical woodland (Bredenkamp, Spada, & Kazmierczak, 2002), but that the rapid spread of grasses came only later ~45–30 Ma triggered by increases in global aridity (Zachos, Pagani, Sloan, Thomas,

& Billups, 2001) and mediated by frequent disturbances such as fire and animal grazing (Bond, Midgley, & Woodward, 2003; Woodward, Lomas, & Kelly, 2004). Flammable C_4 grasses appeared ~30–25 Ma in the tropical and arid regions of Africa when atmospheric CO_2 was low, and climatic conditions were hot and dry (Kellogg, 2001), and are then thought to have spread rapidly into other plant biomes ~8–4 Ma (Woodward et al., 2004). Once again, the concordance with our results is striking. We find phyloregions corresponding to present-day Grassland and encompassing parts of the Nama Karoo, Indian Ocean Coastal Belt and Albany thickets appear between 40 and 20 Ma, whereas the differentiation of the Grassland from the Nama Karoo occurs ~8 Ma.

The time-scales of the past and future changes are very different (current species extinctions and climate change are occurring on scales of decades, but historical events rolled over 10's or 100's of thousands of years). Secondly, we suggest that, while past climate change likely influenced species distributions, it is possible that co-adapted species shifted in synchrony. For example, the Fynbos phyloregion may have shifted and expanded southwards as the climate became drier, but the composition of lineages within it may have remained relatively stable. Thus, we can still draw inference on the timing of the evolutionary origins of the Fynbos and Savanna biomes, and we show that our age estimates fit well with current theory. Indeed, we show that lineages

dated to 20 Ma form distinct phylogroups that resemble the signature of present-day phylogroups.

4.2 | Phylogroups as units for conservation

The phylogroups presented here represent evolutionary coherent units, a product of species assembly processes and co-evolutionary dynamics that have taken place over many millions of years. While we do not mean to suggest that phylogroups are better conservation units than more standard measures of species richness or endemism, phylogroups can help identify floras overlooked by traditional floristic studies, such as the newly defined Gariep Karoo and Zambezi transition zone in southern Africa (Daru et al., 2016).

We identified phylogroups that are the most evolutionarily distinct; here, the Fynbos stands out, enclosing lineages that tend to be conserved in their ancestral areas of origin (Pennington, Richardson, & Lavin, 2006). Phylogroups with high evolutionary distinctness might represent geographic regions that harbour species with rare features not found elsewhere (i.e., locally restricted radiations), and thus rank highly for conservation purposes (Daru et al., 2016; Daru, Holt, et al., 2017; Holt et al., 2013). However, evolutionarily distinct phylogroups do not necessarily capture the greatest taxonomic richness or unique phylogenetic diversity. Nonetheless, it is possible to integrate more traditional conservation metrics, such as richness, and threat within a phylogroups framework.

We indexed phylogroups using common conservation currencies, and show that while the Fynbos is the most evolutionarily distinct, phylogroups of the Eastern Cape, Drakensberg and Gauteng capture greater species and unique phylogenetic diversity (i.e., PD-endemism). While high evolutionary distinctness of the Fynbos might reflect its history as a centre of speciation (e.g., Forest et al., 2007), the Grassland phylogroup, with high PD-endemism, is a likely centre of neo- and palaeo-endemism (Mishler et al., 2014). The Grassland phylogroup thus ranks highly with respect to irreplaceability. However, we are losing some parts of the phylogenetic tree more rapidly than other parts (Davies, 2015; Vane-Wright et al., 1991; Veron, Davies, Cadotte, Clergeau, & Pavoine, 2017). If we wish to minimize the loss of evolutionary history, we may therefore want to focus conservation efforts on those areas where evolutionary history is currently most at risk, for this our priority shifts to Mozambique where the phylogroups of the Indian Ocean Coastal Belt and Miombo Woodland enclose a high proportion of species which are both threatened and evolutionarily distinct.

4.3 | Missing taxa and phylogenetic error

Although our study focused on woody plants, we predict that analyses of non-woody taxa such as grasses, herbs, forbs might show similar patterns to those revealed here, but currently, the data are not available to explore this further. We recognize that incomplete sampling (i.e., missing taxa) or misplaced taxa on the phylogeny could potentially influence reconstructed phylogroups, especially when such biases are geographically non-random (Daru, Park, et al., 2017). We did not explicitly evaluate the impact of phylogenetic error in our analyses; however,

we have reason to believe that any effect might be relatively small, and certainly less biased than when estimating diversification rates from phylogenies, where exact branch lengths are critical. First, our sampling includes all the major woody lineages, so missing taxa will contribute relatively little additional unique phylogenetic diversity. Second, phylogroups are generated by analyzing multiple pairwise distances between many taxa. One or a few misplaced taxa would thus have only small leverage. Third, phylogroups represent information on both species composition and phylogenetic distance, and similar clusters can be generated considering only species composition (although all data on evolutionary distinctness, age of assemblages and their phylogenetic relationships are obviously lost). Last, phylogenetic errors will tend to homogenize phylogroups, reducing the apparent separation between them, rather than generate spurious structure. At the extreme, if species were distributed at random across space, we would only return a single homogeneous phylogroup. Nonetheless, it is still possible that omitting an endemic radiation within a particular phylogroup could add error to our estimates. However, our phylogroups demonstrate a remarkable congruence with currently recognized vegetation types both in distribution and age, giving us confidence in our findings.

4.4 | The evolutionary future

If currently at-risk species become extinct, the vegetation of the African flora might be very different in the future, and the evolutionary coherence of phylogroups may be lost. For instance, we would no longer be able to distinguish the newly defined “Zambezi transition zone” (Daru et al., 2016) overlapping south-western Mozambique, Zimbabwe and South Africa. This region has been characterized as a “mixing zone” for long-separated African flora migrating from the Cape or the Drakensberg in the south to South Central Africa in the north (Galley, Byteler, Bellstedt, & Linder, 2007; Van Wyk & Smith, 2001; Weimarck, 1941). However, part of this phylogroup in Mozambique is already experiencing high degree of threat from timber logging (Fath, 2001), and we risk losing many of the evolutionarily distinct and globally endangered species that are found within it (Daru et al., 2015). The loss of distinct phylogroups might suggest greater phylogenetic homogenization, potentially destabilizing centres of diversification and endemism.

It is possible that climate change could shift the spatial distribution of species, and thus phylogroups, perhaps over shorter periods of time. However, phylogroup responses may tend to lag behind individual species responses (i.e., phylogroups will tend to be more stable over time than individual species distributions).

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BIOSKETCHES

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SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

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