
To conserve biodiversity, we must first measure it: but how? Patterns of diversity vary with time, space and the tools we use to examine them, making the question of which metric to use a nontrivial one. Of the many diversity indicators, species richness is perhaps the simplest metric available for measuring diversity and is often emphasized in conservation planning (Gotelli & Colwell, 2001; Llorente-Bousquets & Luis-Martinez, 1993; Myers et al., 2000). While richness accounts for the number of species present in an area, other metrics take into account additional aspects of diversity. Measures of endemism shift the focus of diversity assessment to organisms that are restricted geographically to a specific area and are therefore more vulnerable to extirpation than widespread species (Gaston, 1998; Kruckeberg & Rabinowitz, 1985). Phylogenetic diversity (PD) measures the sum evolutionary history of an area (total branch length on a phylogenetic tree) for a selected assemblage. The PD concept was developed more recently, first suggested as a metric of diversity in the early 1990’s (Faith, 1992). While each is useful in describing the biodiversity of an area, measures of species richness, endemism and phylogenetic diversity can suggest very different sets of conservation priorities. The authors of this paper explore the consequences that favoring each of these measures could have on conservation planning in the immensely diverse freshwater habitats of Madagascar.

To tease apart the relationship between levels of endemism and phylogenetic diversity, the authors of this paper conducted a large-scale biological inventory of the diverse yet understudied Adephagan water beetle assemblage of Madagascar’s freshwater systems. One hundred fifty-three localities spanning all 7 ecoregions (as defined by the WWF) and located in or around ten pre-existing protected areas of Madagascar were sampled. The beetles were preserved and identified, when possible, to the species or morphospecies level. Mitochondrial (coxI) and nuclear markers (16S rRNA, 28S rRNA), in conjunction with a Generalized Mixed Yule-Coalescent approach (GMYC), were used to construct a three gene phylogeny and recover estimates of PD. Additionally, species diversity, endemism, and percent of PD represented by endemic taxa were calculated for each of the 10 protected areas.

The GMYC approach generated 169 species groupings, 91% of which were congruent with identified Linnaean species. About 20 undescribed species were identified using this approach, indicating that Adephagan beetle diversity is still in need of further taxonomic investigation. When the 10 protected areas sampled in this study were ranked by PD, the top three were Zombitse (greatest PD), Andringitra and Andasibe. The top three areas for species richness were Andasibe, Isalo and Zombitse. Levels of endemism were greatest in Zahamena, followed by Montagne d’Ambre and Marojejy. Percent PD represented by endemic species only was greatest in Andasibe (40%), followed by Isalo and Zahamena. PD and endemism were only negatively correlated in situations where endemism exceeded 46% and were positively correlated otherwise.
I think the authors overemphasize the contradiction between species richness, endemism, and PD – the real conflict seems to lie in the differing units of measurement and not in the actual composite levels of diversity. Species richness estimates can be calculated using known taxonomic units, or via a phylogenetic approach, as demonstrated in this study; our lack of taxonomic knowledge (and alpha taxonomists) hinders the first approach (Agnarsson & Kuntner, 2007; Crozier, 1997). Calculating species richness by counting species is often considered the simplest method of quantifying diversity (Hellmann & Fowler, 1999). I would argue that a phylogenetic approach is equally simple. With the same amount of effort in the field, estimates of species richness can be derived from phylogenetic analyses in addition to information about evolutionary history and rates of endemism.

Not only can PD potentially be used to recover rates of endemism, it can be used to distinguish between types of endemism (Faith & Reid, 2004; Nipperess et al., 2010). Adolph Engler proposed a distinction between endemics originating from a recent adaptive radiation and those that represent a mostly extinct ancient radiation in 1882 (Cronk, 1992; Kruckeberg & Rabinowitz, 1985). The scientific community has been debating these distinctions and creating new definitions ever since (Cronk, 1992), with the categories of neoendemic and paleoendemic emerging as the contemporary classifications (Anacker, 2007; Bates, 2002; Ferreira & Boldrini, 2011; Kruckeberg & Rabinowitz, 1985; Waller, 2007; Yoder & Nowak, 2006). Using PD to estimate endemism levels as proposed by Faith (2004) – by calculating the proportion unique branch length contributed to total PD of an area – could be the integrated framework needed to make optimized conservation decisions.

Using a phylogenetic framework requires little to no extra effort in the field, allowing for continued utilization of parataxonomists, and only a slight addition of effort in the form of computation-heavy analysis. It should be noted that most of the effort in phylogenetic analysis is exerted by computer programs guided by experienced bioinformatics specialists. Additionally, with the advent of new sequencing techniques, the scale of phylogenetic data that can be acquired in a short amount of time is continually increasing (Horner et al., 2010; Mardis, 2008; Metzker, 2010; Schuster, 2008).

Overall, this paper is a step in the right direction for conservation planning protocols. Consideration of multiple metrics and a thorough understanding of which aspect of biodiversity those measures are representing are both necessary if we are going to correctly identify (to the best of our ability) conservation priority areas. The authors demonstrate how additional estimations of diversity such as PD and endemism can be obtained using virtually the same collection protocols that once yielded only richness estimates. The use of genetic analysis to make a hypothesis about species richness via the GMYC is a creative ‘quick and dirty’ approach to a large scale inventory that, at 91% congruence with identified Linnaean species, seems like a viable approach to estimating both richness and PD. The statement about negative correlation between PD and endemism only occurring at high rates of endemism seems to indicate that in general (in places with low to average rates of endemism), PD is a good metric for indicating species diversity (although I still think a standardized PD framework would
eliminate the incongruence between the two measures of diversity by assessing them using the same base unit: branch length).

Literature Cited:


