

Assessing phylogenetic Alpha and Beta Diversity in a Papua New Guinea Forest

Tropical forests house a remarkable level of biodiversity - while they cover no more than 10% of the land on Earth, about 50% of the biodiversity on Earth is found in these ecosystems (Whitfeld et al. 2012). This arises because small tracts of land in temperate climates support a small number of species whereas a similar area in the tropics can house hundreds of species. For example, a 26 hectare plot of forest in Wisconsin houses only 36 species (Wang et al. 2011) whereas De Oliveira and Mori (1999) reported that one hectare of the Amazon rainforest houses >280 species. Very little is known about the immense amounts of tropical forest biodiversity, the evolutionary histories of tropical forest organisms, their interactions with each other and the abiotic environment, and the impact anthropogenic climate change may have on such ecosystems (Basset et al. 2004).

Until recently, ecologists' understanding of the tropical biodiversity was based on simple species diversity indices (eg. Fisher's Alpha, Shannon-Weiner Index); however, these measures ignore the evolutionary histories of the species (Ricklefs 1987, Swenson et al. 2012). To get a more comprehensive understanding of biodiversity, we must integrate data on local species diversity with information about the phylogenetic relatedness of the species and their functional attributes (Swenson 2011). Plant assemblages in tropical forests are remarkable in both the species diversity found within a sampled plot (alpha diversity) and the diversity of species between two sampled plots (beta diversity) (Whittaker 1972, Kessler et al. 2009). Whereas a lot of prior research has focused on using phylogenetic alpha diversity to understand community assemblages, the implementation of rigorous field data collection regimens and development of sophisticated analytical tools is spurring interest in both functional and phylogenetic beta diversity (Swenson et al. 2012).

Much of the data collected to date suggests that similar species are spatially clustered at larger spatial scales, whereas at a smaller scale, species are less similar to each other than expected by chance (e.g. because of negative density dependent mortality). These data support a hierarchical model of community assembly in which the species of a given community are the result of large scale historical processes, abiotic process on moderate spatial scales, and biotic interactions at the local (alpha diversity) scale (Swenson et al. 2012). Swenson et al. (2012) compared forests of Wisconsin, Virginia, China, Puerto Rico and Panama, representing various latitudinal regions, to suggest that abiotic factors play a strong role in determining plant community assemblages.

The island of New Guinea is home to the third largest continuous tropical forest behind those in the Amazon and Congo basins (Whitfeld et al. 2012). Dr. Weiblen, in collaboration with the Smithsonian Institute's Center for Tropical Forest Science, has set up a 50 ha plot near Wanang in the Madang Province of Papua New Guinea, from which vast amounts of functional and phylogenetic data of trees in the forest have been collected. This represents an independent forest system in which the predictions made by the hierarchical assemblage model described above can be tested. Whitfeld et al. (2012) recently reported a phylogeny of 349 species of the trees in the plot in the context of analyzing the change in community structure with forest succession and found significant phylogenetic clustering in younger forests, phylogenetic over dispersion in more mature forests. The authors suggest that this pattern may be described in relation to the ecological processes that drive forest assemblages.

In the proposed project, I will expand Whitfeld et al.'s phylogeny and conduct spatial analysis of trees in the Papua New Guinea plot. I will collect and analyze sequence data of the *rbcL* gene from 75 previously unsequenced species according to the protocols of Kress et al. (2009) and Whitfeld et al. (2012). The *rbcL* gene codes for the large subunit of RuBisCO and is

known to place land plants into appropriate orders and families (Whitfeld et al. 2012). To test the hierarchical assemblage model and the hypothesis that abiotic filtering drives species turnover in lowland rainforests of Papua New Guinea, I will synthesize phylogenetic and spatial data recorded at the 50 ha plot in Papua New Guinea. Analyses will mirror those shown in Swenson et al. (2012); more specifically, I will measure the relationship between alpha diversity of small subplots (as measured by the Net Relatedness Index, NRI) and pairwise beta diversity between those plots (as measured by a standardized version of the dissimilarity measure D'_{pw}). These two metrics will be calculated with the formulae

$$NRI = -1 * \left(\frac{MPD_{sample} - MPD_{random}}{\sigma_{MPD_{random}}} \right), \text{ where } MPD \text{ is the mean phylogenetic diversity,}$$

and

$$D'_{pw} = \frac{\sum_{i=1}^{nk1} f_i * \overline{\delta_{ik2}} + \sum_{j=1}^{nk2} f_j * \overline{\delta_{jk1}}}{2}, \text{ where } \overline{\delta_{ik2}} \text{ and } \overline{\delta_{jk1}} \text{ are mean pairwise phylogenetic}$$

distances, and f_i and f_j are the relative abundances of species i and j (Swenson et al. 2012).

This research will begin to test the hierarchical assemblage model of communities and the role abiotic factors play in community assemblages on forest plots from Papua New Guinea, which, being in the southern hemisphere and to the south of Wallace's Line, represents a unique biogeographical zone than those investigated in prior studies. New Guinea houses an immense tropical forest which has been disappearing at an alarming rate (Sodhi et al. 2004). Our understanding of the historical genesis of biodiversity lays the foundations to our efforts to attenuate biodiversity loss. The proposed research will add to our understanding the mechanisms contributing to production and maintenance of biodiversity in tropical forest ecosystems, which house a vast majority of Earth's biodiversity, and how these ecosystems may change with a changing climate.

References

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