Variability in phylogenetic diversity (PD) estimates illustrated with plant data for the high Andes of South America

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Phylogenetic diversity (PD) is commonly calculated by adding together the branch lengths or ages of a subset of taxa present in an area, using a single phylogeny as a backbone. However, a phylogenetic hypothesis is the consensus of a range of equally likely trees, inherently variable in branch lengths and sometimes in topology. This study incorporates confidence intervals into PD calculations in order to account for such variability. Using the genera of Fabaceae and Solanaceae present in the high Andes, we calculated PD for three macro-zones (Puna, Paramo and Southern Andean Steppe) and studied its correlation with generic richness for these areas. We found a similar pattern between PD and richness in the Fabaceae, but not in the Solanaceae. Variability proved useful in interpreting the results, especially in the Solanaceae which showed alternative topologies. Further studies are needed to address the possible effects of this variability on the PD index.