19 February 2018

Dear editors of *Journal of Tropical Ecology*,

We are pleased to submit our manuscript “Low functional and phylogenetic turnover of melastomes along a Costa Rican elevation gradient” for consideration as a Short Communication piece in your journal. We show that ubiquitous patterns of community-wide of trait turnover across gradients may not always be recovered within clades that span the gradient. These results will be of interest to anyone working on tropical forest functional and community ecology.

The turnover of functional traits at a community-wide scale across elevational gradients is a fundamental and well documented pattern in ecology: low-elevation communities tend to be dominated by resource-acquisitive species, which are replaced by resource-conservative species at high elevations (Read et al. 2014). Whether or not the functional traits of individual taxa turnover along the gradient in the same way is unclear, and there are compelling examples of intraspecific trait variation not matching community-wide turnover in sign or magnitude (Ackerly & Cornwell 2007). In our study, we tested whether functional traits turnover across a 2500m elevational gradient within the plant family Melastomataceae, which occurs from lowland forests to high elevation paramos. We measured 7 traits on ~100 melastome species at five sites along Volcan Barva in central Costa Rica. Additionally, we built a phylogeny of all species in our list using previously published sequences supplemented by sequences we generated for this study.

Overall, we show that there is little evidence for a functional or phylogenetic basis to the taxonomic turnover of melastomes along this gradient. This is in contrast to our expectation that the patterns of turnover within a clade would mirror the predicted shift in community-wide traits. These results caution against extending interpretations from one scale of study to another, and have important implications to the study of community assembly across environmental gradients.

Our questions regarding community assembly in tropical forests, database of functional traits, and phylogeny incorporating novel sequences generated for this study will be of great interest to the JTE readership. The manuscript contains ~1700 words, one figure, one table, and all data and analysis scripts will be freely available online.

Thank you for your consideration.

Sincerely,

Gaurav Kandlikar and Marcel Vaz, on behalf of my coauthors

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