Dear editors,

We are excited to submit our manuscript entitled “Rates of biome shift predict diversification dynamics in flowering plants” for consideration at PNAS. It is the goal of many botanists and evolutionary biologists to understand and explain the remarkable diversity of angiosperms. Previous work has focused on discovering key traits and quantifying their subsequent effect on the species richness of a clade. Though this research line has proved fruitful for some clades, particularly those classified as “adaptive radiations”, recent work has shown that the key innovations of one clade are rarely the cause of diversification in another. In this paper we take a different perspective. Rather than searching for a key trait, we test whether the way traits evolve are related to diversification differences. Specifically, we examine the possibility that a lineage’s propensity to change their biome is a ubiquitous predictor of diversification dynamics across several clades of angiosperms. This hypothesis, first proposed by G. Ledyard Stebbins exactly 50 years ago, has not yet been tested using a large sample of clades and modern modeling tools.

When first proposed, Stebbins lacked the data and tools necessary to rigorously test his hypothesis. Nonetheless, the multitude of natural history examples he provided made a compelling argument. We parallel his approach of considering several angiosperm clades but using modern comparative tools. We compile a dataset of 49 angiosperms clades with over 18,000 species and use recently developed hidden Markov models to test whether lineages which more frequently shift their biome tend to have higher rates of speciation and extinction.

This topic can more broadly be framed as testing whether evolutionary lability, or the propensity to shift phenotypic values, is correlated with diversification rates. With this point of view, a wider body of literature can be considered as having tested this hypothesis. However, the modeling approach we take here includes a novelty that overcomes two important limitations of previous work. First, the use of State-dependent Speciation and Extinction (SSE) models allows us to overcome biases that are introduced when phenotypic evolution and diversification dynamics are treated independently. Second, the way we utilize the model estimates allows us to control for the variable ages of the clades used in this study. Without this latter issue being resolved, spurious correlations between rates of phenotypic evolution and diversification are possible as results are confounded by clade age.

Both the search for an universal driver of angiosperm speciation and extinction and understanding the frequency and directions of biome shifts in plants are topics that have received considerable attention in the last 10 years. Curiously, however, these topics have seldom been considered together. Because our work proposes a path to integrate these two relevant research venues, we are confident that this is a good fit for PNAS and is going to be a key reference for plant biogeographers and evolutionary biologists. Furthermore, we expect that the methodology introduced here will be used to test similar hypotheses in clades other than flowering plants and for other phenotypic traits. Finally, this work is timely not only because it addresses outstanding problems in the field, but also because it coincides with the 50th anniversary of Stebbins’ most important contribution to macroevolution “Flowering plants: evolution above the species level”, paying tribute to one of the greatest botanists to ever live by testing one of his most influential hypotheses.

Sincerely,  
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University of Michigan