

# Including distantly related taxa can bias phylogenetic tests

Park and Potter (1) examine patterns of relatedness between invasive and native thistles (Cardueae, Asteraceae) in California and found evidence that invasive species were more closely related to natives than expected by chance. This is an intriguing finding, with important ecological and management implications (2). Park and Potter rightly argue that examining patterns across anciently diverged clades make inferences about ecological mechanisms difficult and thus advocated for a clade-level approach. I fully agree that a highly resolved, clade analysis can provide important insights into potential ecological mechanisms.

However, Park and Potter's results are brought into question because of two potentially problematic issues. The first is an important unrecognized assumption. In their phylogeny of the 202 sequenced species in the Cardueae (figure 1 in ref. 1), only a handful were classified as native, introduced, or invasive, and most were not present in California. The assumption is that all species have had a chance to enter the region and that the successful invaders are those that fit local conditions best. The concern is that the introductions were phylogenetically nonrandom (3). Some groups of thistles may be associated with agriculture or certain dispersal pathways, and had other groups been introduced, they may also have invaded California successfully. Phylogenetically nonrandom introductions could produce the

same pattern that Park and Potter observed, but the mechanism would be very different, as would any resulting management recommendations.

The second issue results from the potentially problematic species pool outlined above and may alter inferences. Again, looking at their figure 1, the natives are almost all clustered in a single monophyletic clade, whereas the successful invaders are found in several other clades. Meanwhile, there are a few very distantly related clades lacking both natives and invasives, including the Carlininae and Echinopsidinae subtribes, and the most distantly related group within the Carduinae. Including these groups in the null model would bias the results toward detecting clustering. The mean pairwise phylogenetic distances will always be larger when very distantly related taxa that do not include the groups being analyzed are included. Had the analyses included only the subtribes that included native or invasive species, the result would most likely have been no significant pattern or perhaps overdispersion. Other work has shown the influence that phylogenetic scale can have on results (4).

Park and Potter's argument that analyzing relatedness patterns within a carefully selected clade is best is a valid one, but I would argue that including very distantly related subclades that do not house species pertinent to the analysis does not necessarily improve ecological inference. Without evidence that

species from those groups have been introduced and failed, their inclusion creates a bias in the null distances, which may be responsible for the statistically significant clustering. Analyses such as in Park and Potter's paper are very important for understanding and managing invasions, but we need to ensure that they are robust if we are to provide managers and policy makers with the tools needed to maintain or restore native ecosystems.

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