Phylogenetic relatedness predicts priority effects in nectar yeast communities.

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Contingency is ubiquitous in community ecology and the common finding 'it depends...' can limit our ability to make broad predictions. Priority effects are one type of such contingency, in which the order in which species colonize affects the outcome of competition and which species ultimately becomes dominant. This paper finds that the strength of priority effects (i.e. the degree of contingency in the outcome of competition) increases with phylogenetic relatedness of the species involved, offering some hope for predicting when and where priority effects predominate and where competition has a more deterministic outcome.

Priority effects are known in diverse communities from land to sea, and their existence limits our ability to predict recovery after disturbance, community resilience and successional outcomes. This paper offers some hope for predicting the conditions under which priority effects are most likely by testing for priority effects across all pairwise combinations of six species of yeast that live in floral nectar. The paper finds that priority effects are strongest when competing species are closely related and virtually non-existent when species are distantly related. Phylogenetic distance is also related to ecological distance, suggesting a possible mechanism for this finding. Importantly, this is NOT to say that distantly related species don't affect each other or compete, only that the outcome of competition among distantly related taxa did not strongly depend on the order of colonization (i.e. the outcome is more deterministic). Of course, the paper does only use six species in laboratory microcosms but it still represents an important advance in that it suggests that we might predict which interactions are most subject to contingent outcomes. This twist on the application of phylogenetic approaches to a classic problem in community ecology provides an approach and framework for testing whether priority effects are similarly predictable across a broader range of taxa and communities.

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