

An Evolutionary Case for Plant Rarity

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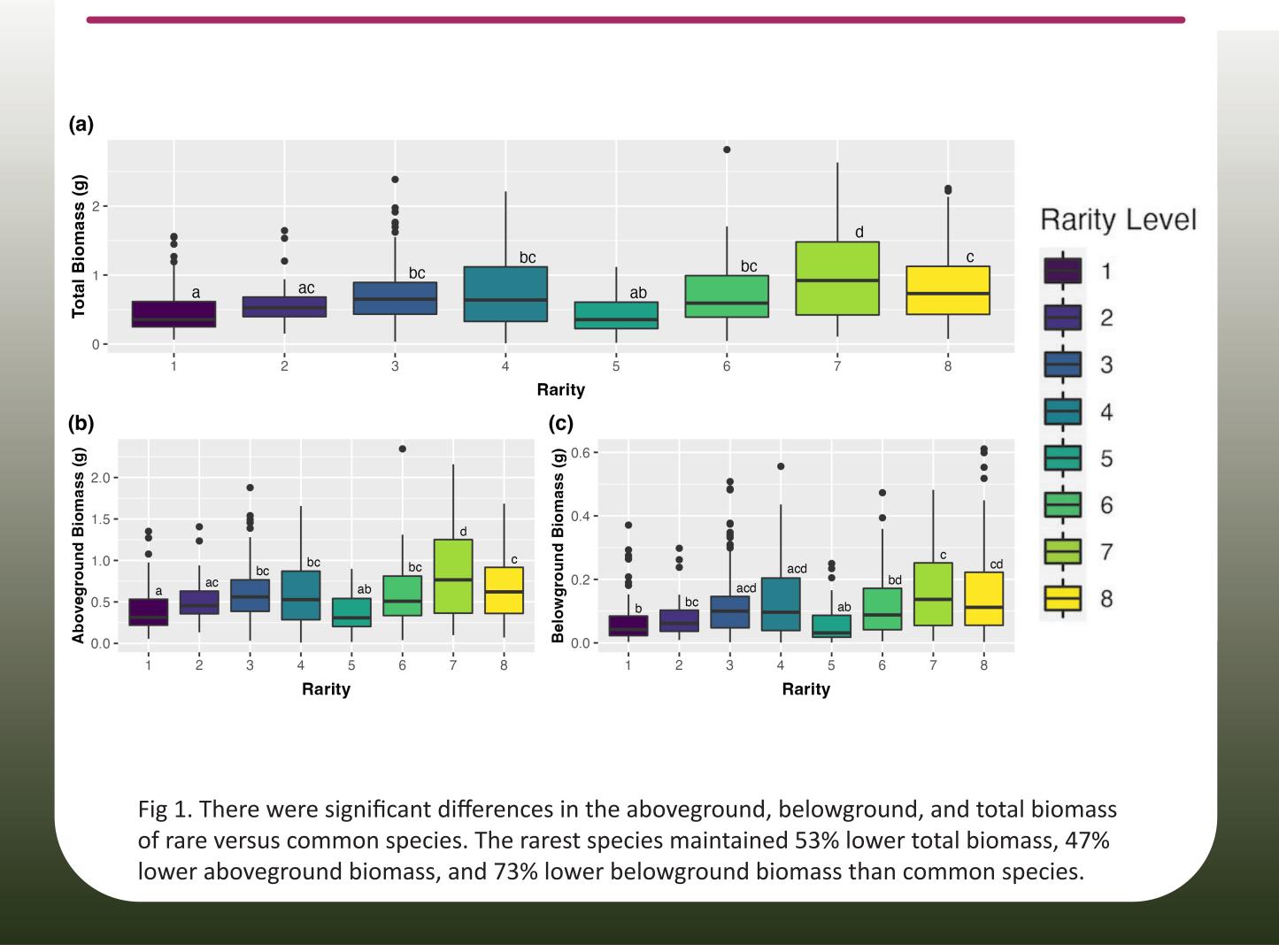


Species Rarity is Common

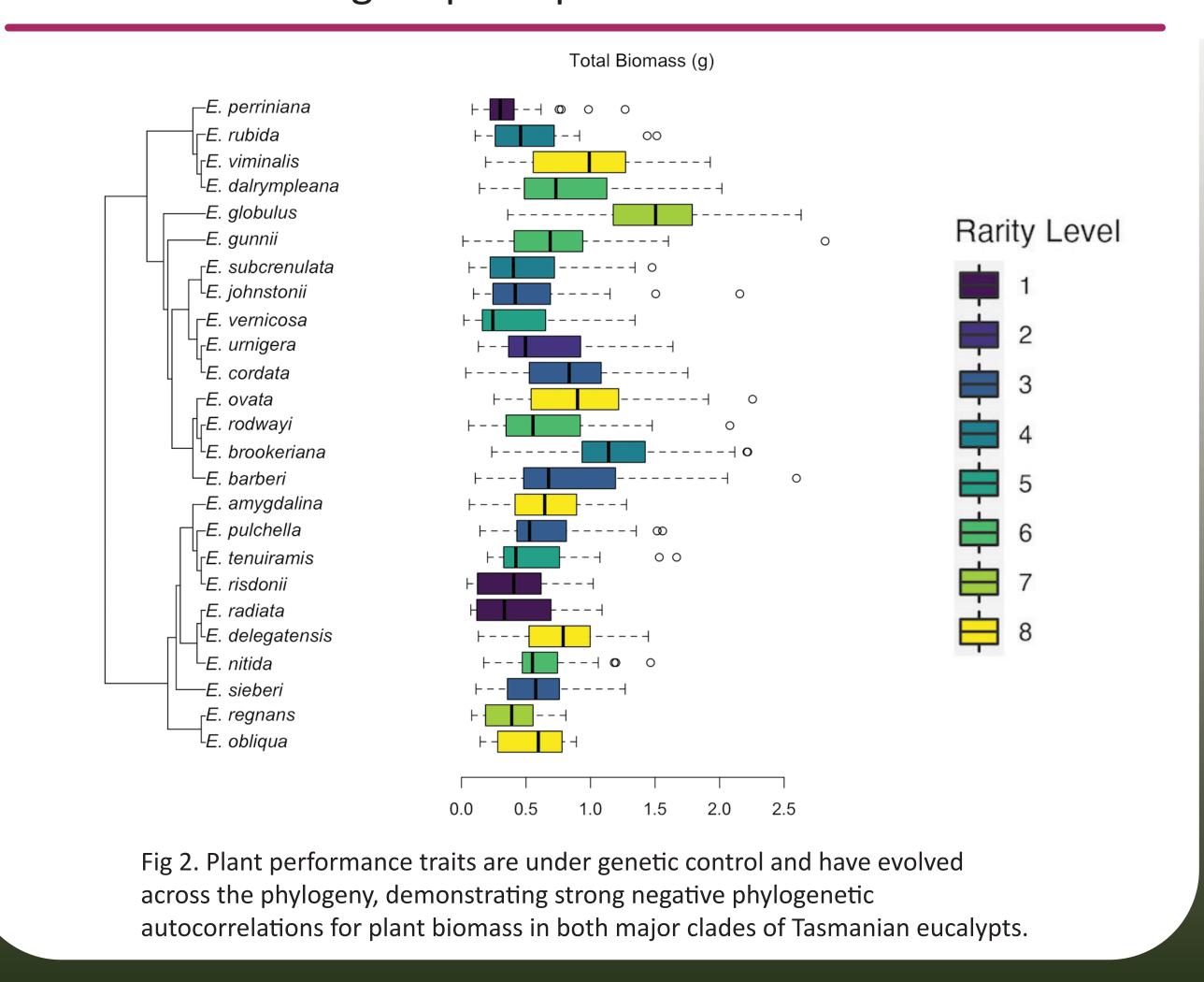
Most species are rare, have high conservation value, and contribute disproportionately to ecosystem function.^{1,2} As anthropogenic change increases in prevalence, species rarity is expected to increase across global landscapes.³ While rare species are often characterized spatially using geographic axes such as range size, habitat specificity, and local population size, factors such as functional traits, many under genetic control, are not accounted for when classifying rare species.⁴ Consequently, many rarity studies lack an eco-evolutionary perspective to understanding and predicting the future persistence of rare species.

Although rarity is commonly thought to be a culmination of unfavorable random ecological processes and environmental factors leading to poor survival outcomes, studies suggest that performance traits, such as biomass, are positively related to geographic aspects of rarity.^{2,5} Identifying a suite of evolved traits associated with geographic rarity is critical in connecting genes to ecosystems to demonstrate the trait-mediated evolution of range size, habitat specificity, and population size. Furthermore, if an endemic suite of traits is correlated with the evolution of rarity, as rarity increases, there are likely to be significant impacts on biodiversity and ecosystem function critical for climate change mitigation.

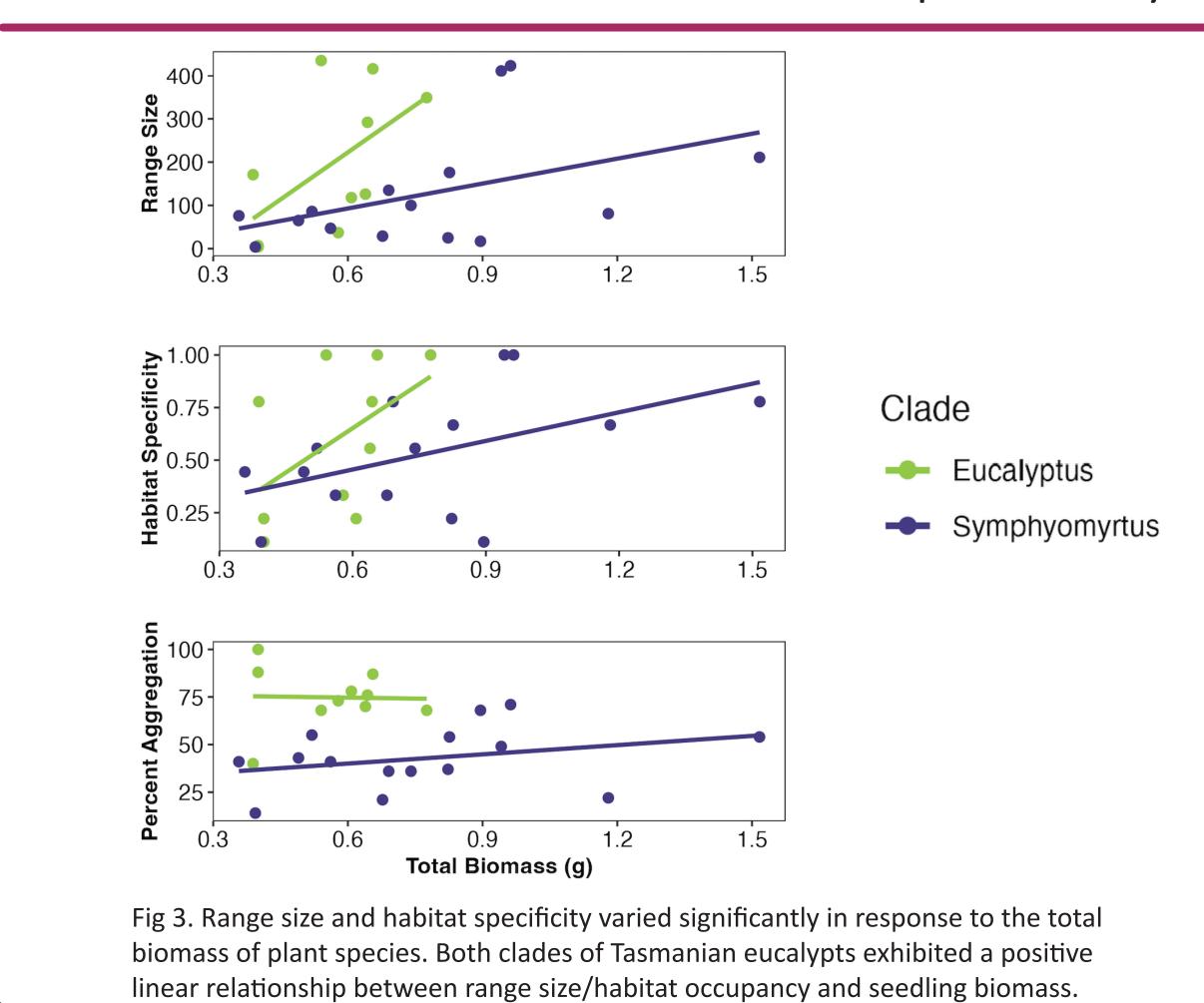
There are specific performance traits associated with plant rarity that may determine if and how a species is rare



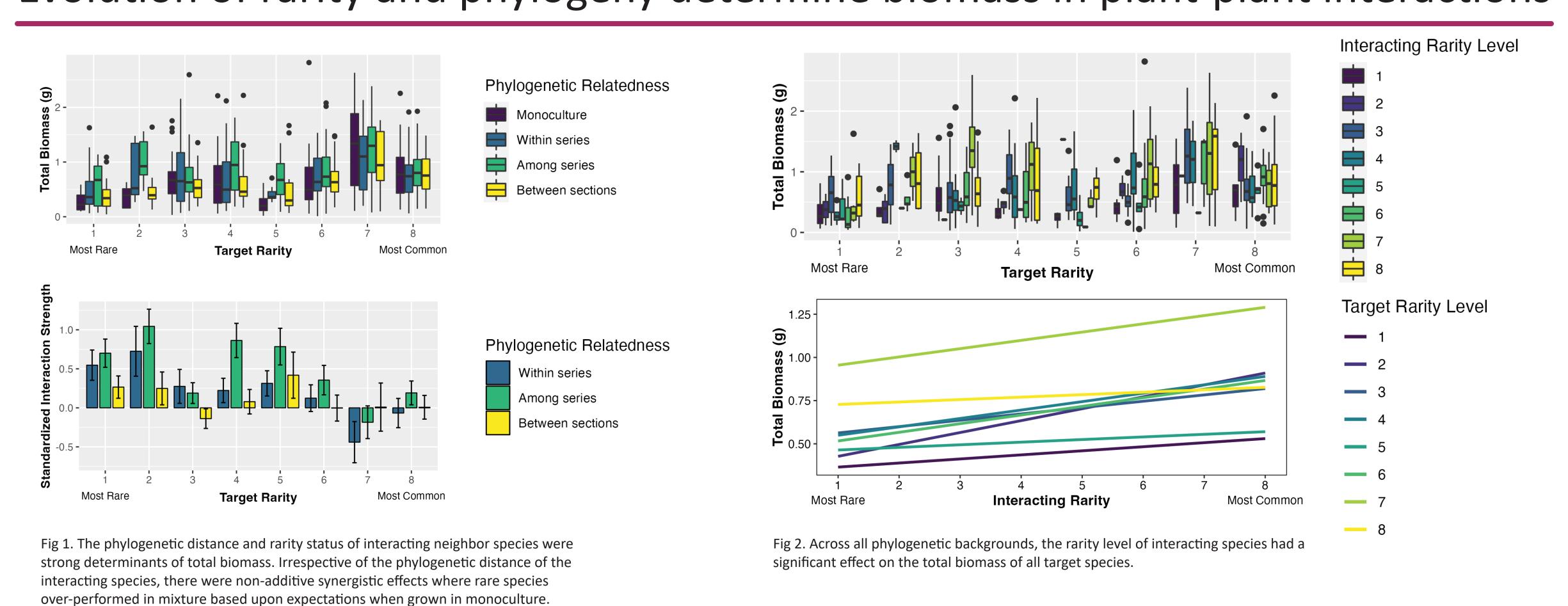
Rarity may be a consequence of evolutionary processes acting on plant performance traits



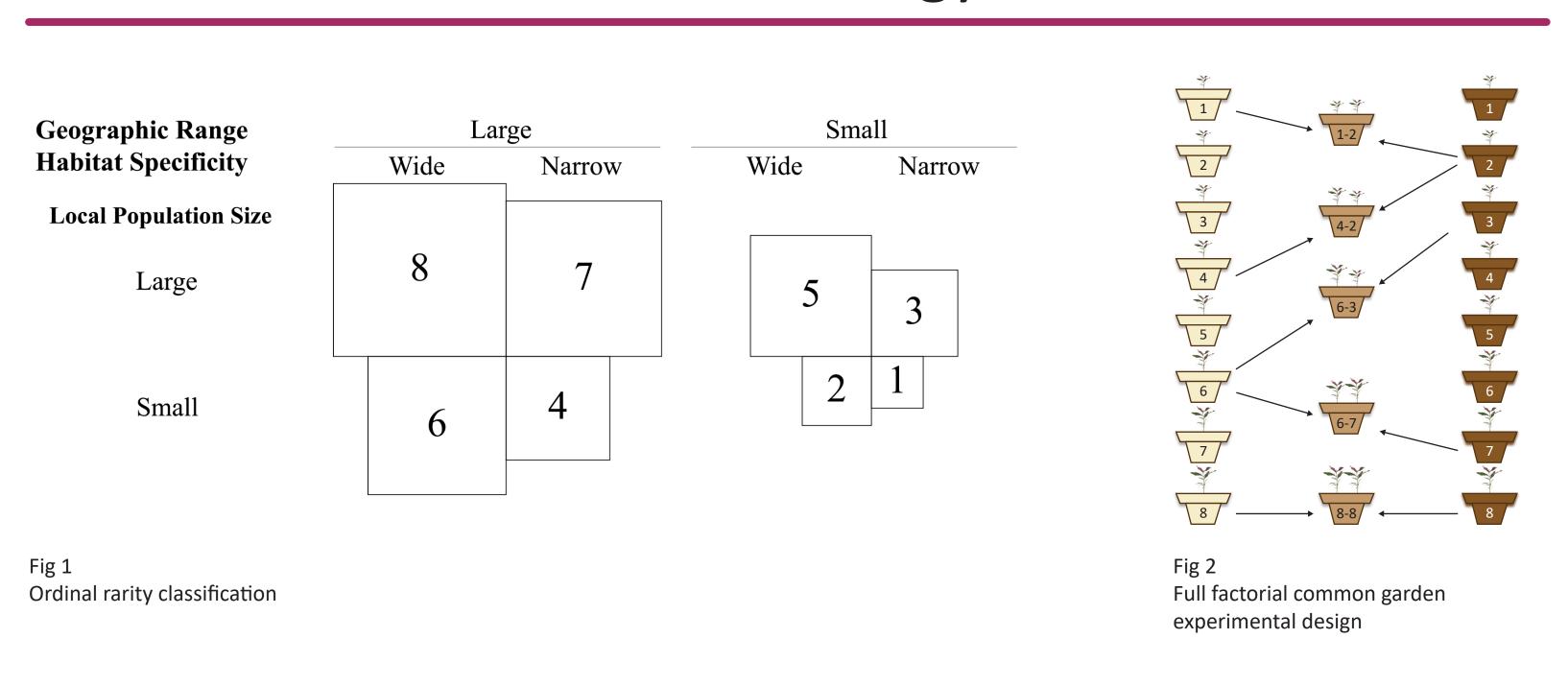
Convergent evolutionary patterns of biomass production can affect fundamental determinants of species rarity



Evolution of rarity and phylogeny determine biomass in plant-plant interactions



Methodology



- Linear mixed models (LMM) were first used to demonstrate a lack of interactive effects between rarity and other variables.
- Phylogenetic generalized least squares (PGLS) models were used to determine statistical differences in the above- and belowground biomass of rare versus common species as well as analyze the effects of biomass and clade on range size, habitat, specificity, and local population aggregation.
- Phylogenetic signals of total, above, and belowground biomass were analyzed using Blomberg's K.