Effects of species' similarity and dominance on the functional and phylogenetic structure of a plant meta-community

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Abstract (297 words): Studies of functional and phylogenetic diversity patterns have provided important insights into the assembly rules that govern the spatial structure of meta-communities. However they often rely on a single diversity measure and thus implicitly choose how they account for species relative abundances and how species similarities are linked to phylogenetic or functional distances, thus potentially failing to identify certain assembly rules.

Recent reviews[1,2] put back in the spotlight the family of Hill numbers[3] and its ability to gradually scale the importance of dominance in communities (i.e. the weight given to dominant vs. rare species) back in the spotlight. Some authors further generalized these indices to account for species similarities[4]. We are going a step further and combine this framework with the tree transformations proposed by Pagel[5] in order to gradually scale not only the importance of dominance but also species similarity (the weight given to small vs. large similarities). We applied this new flexible framework to study functional and phylogenetic diversity patterns in an alpine plant meta-community and tested them with a null model of random assembly and evaluated the contribution of environment and space on inter-community pairwise diversities[6].

Functional diversities were significantly high when the same weight was given to dominant vs. rare species and to large vs. small species' similarities and were random otherwise. In contrast, phylogenetic diversities were significantly low when greater weight was given to dominant species and were random otherwise. This suggested that the environmental gradients filtered species according to their functional traits, while, at the same time, competition prevented the co-dominance of too closely related species.

Our results highlighted the importance of an multi-indices framework (including our methodology) that, by utilizing the full extent of information provided by the structure of meta-communities, are able to disentangle patterns generated by multiple assembly rules.

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