

Measuring both functional and phylogenetic complexity: a new challenge for ecologists

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At the heart of ecology lies the notion of variability and even complexity. The term biodiversity has thus been imagined to encompass "the variety within and among living organisms, assemblages of living organisms, biotic communities, and biotic processes, whether naturally occurring or modified by humans [...]. It can be observed and measured at any spatial scale ranging from microsites and habitat patches to the entire biosphere" [1]. Biodiversity was first measured by taxonomic indices such as species richness and species evenness. Ecologists have then integrated the historical relationships among species through phylogenies [2]. There is now an upsurge in research on functional diversity [3].

Hotspots have been defined regarding the number of species (as a measure of diversity) and the number of endemic species (as a measure of rarity). However within a community, a species can be a unique or rare source of diversity. Two concepts have thus completed 'diversity': uniqueness and originality [4]. The uniqueness of a species will be said to be high if it displays a high amount of unique character states. The originality of a species is the average rarity of all its character states. Uniqueness and originality can be measured from phylogenies or from the functions of the species in ecosystems [5]. These components (diversity, uniqueness and originality) are parts of the biological complexity.

How do phylogenetic and functional complexity affect our understanding of biological complexity? Do we have to measure them separately or do we need to find connections between them? Comparative analyses have been used to test specific hypotheses regarding the origin and functional significance of traits and also the diversification among clades. This approach has also been used to partition the variation in a trait into phylogenetic and phylogeny-free components [6]. We will discuss the use of such methods in the context of understanding the links between functional and phylogenetic complexities and identified the factors that shape their patterns in communities.

References

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