
Patterns of endemism and species diversification in the Alps

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Abstract

Most of endemic plant diversity in the Alps is clustered in particular geographic areas. These hotspots of endemism have traditionally been explained in two ways: (i) those areas are glacial refugia, and current floristic patterns are linked to survival-recolonisation dynamics during the Quaternary, (ii) those areas are in high mountain ranges and endemism is caused by increased speciation rate on steep ecological gradients or in insular mountain biotopes.

Although both hypotheses can explain presence of endemic hotspots, they rely on contrasting evolutionary processes, and different types of hotspots should thus carry a different signature in phylogenetic structure. In particular, species linked to glacial refugia should be phylogenetically random or overdispersed, due to non-selective conservation and possible competition during glacial periods. Species in high mountain hotspots should be phylogenetically clustered, due to increased speciation rate and habitat filtering.

Using a formal spatially explicit model, we show that high endemism is indeed mostly occurring in quaternary refugia and in higher mountain ranges. To test our predictions concerning phylogenetic structure, we developed a bayesian method for accounting for phylogenetic uncertainty in community phylogenetic data. We found that glacial refugia show strong phylogenetic overdispersion – a signature of non-selective conservation forces and competition during ice ages. High mountain ranges show phylogenetic clustering – a signature of recent diversification and environmental filtering of certain plant clades.

Keywords: diversity, endemism, phylogenetic structure, Alps, phylogenetic uncertainty

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