

Publication

Six groups of ground-dwelling arthropods show different diversity responses along elevational gradients in the Swiss Alps

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Elevational gradients along mountain slopes offer opportunities to study key factors shaping species diversity patterns. Several environmental factors change over short distances along the elevational gradient in predictable ways. However, different taxa respond to these factors differently resulting in various proposed models for biodiversity patterns along elevational transects. Using a multi-taxa approach, we investigated the effects of elevation, area, habitat and soil characteristics on species richness, individual abundance and species composition of six groups of ground-dwelling arthropods along four transect lines in the Swiss National Park and its surroundings (Eastern Alps). Spiders, millipedes, centipedes, ants, ground beetles and rove beetles were sampled using standardized methods (pitfall traps, cardboard traps, visual search) in 65 sites spanning an elevational range from 1800 to 2750 m a.s.l.. A total of 14,782 individuals comprising 248 species were collected (86 spider, 74 rove beetle, 34 ground beetle, 21 millipede, 19 centipede and 14 ant species). Linear mixed model-analysis revealed that rarefied species richness in five out of the six arthropod groups was affected by elevation (the quadratic term of elevation provided the best fit in most cases). We found three different patterns (linear decrease in centipedes, low elevation plateau followed by a decrease in ants and rove beetles, and midpoint peak in spiders and millipedes). These patterns were only partially mirrored when considering individual abundance. Elevation influenced species composition in all groups examined. Overall, elevation was the most important factor explaining the diversity patterns, while most local habitat and soil characteristics have little influence on these patterns. Our study supports the importance of using multi-taxa approaches when examining effects of elevational gradients. Considering only a single group may result in misleading findings for overall biodiversity.

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