

### Submitted Abstract

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## Abstract

High spatial heterogeneity of abiotic conditions and plant community composition are important and well-recognised features of alpine ecosystems, contributing to their status as hotspots of biodiversity. Topography and altitude interact with snow cover and meso-climate, leading to steep gradients and high spatial variability in abiotic conditions and the development of heterogeneous mosaics of plant communities. Heterogeneity is therefore an intrinsic and vital component for the functioning of alpine systems. However, most ecological importance attributed to heterogeneity is derived from above ground vegetation studies, with much less known regarding soil biodiversity distribution. Here, we report on the spatial congruence across six kingdoms of soil biodiversity associated with vegetation mosaics in an alpine ecosystem on Ben Avon in the eastern Highlands of Scotland, UK. Fifteen plots (9 in late snow beds) were sampled from each of seven distinct vegetation types for a range of environmental, chemical and biological parameters. We analysed soil communities beneath the vegetation mosaic using DNA metabarcoding approaches, using the 18S, 16S and ITS regions, which provided distribution data on the Animalia, Archaea, Chromista, Eubacteria, Fungi, and Plantae kingdoms. Data were also gained from the kingdom Protozoa, but diversity was too low to allow any spatial analyses.

A total of 13113172 reads were generated across the three barcodes, giving 773 Animalia, 98 Archaea, 741 Chromista, 16473 Eubacteria, 3415 Fungi, and 207 Plantae distinct entities. The Plantae were restricted to Chlorophyta (green algae). The 18S eukaryotic data also included 1524 unknowns which could not be assigned to any kingdom.

Ordination analyses of the community data from each of the six major kingdoms recovered by the metabarcoding demonstrated strong to very strong spatial segregation of communities, corresponding to the highly distinctive plant assemblages above ground. The challenge will now be to distinguish between the biological and abiotic drivers maintaining this remarkable congruity across the breadth of classified biodiversity.