**Climate drives genome‐wide divergence within mycobiont species along elevational gradients**

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Many species of lichenized fungi have wide geographic distributions and broad ecological niches. To better understand local adaptation, a critical evolutionary process shaping mycobiont populations, we here identify genomic variation associated with climate in two mycobiont species across an elevational gradient. *Umbilicaria pustulata* and *U. hispanica* have broad elevational distributions – thus inhabiting strongly contrasting environments within small spatial scales – making them ideal systems for investigating local climate adaptation. We employed genomic data (Pool-Seq) to test for signals of selection across a gradient in Sierra de Gredos (Spain) spanning 1400 altitudinal meters. We examined single-nucleotide polymorphisms in 600 individuals from 6 locations in each species. Our analyses indicate the presence of two genetic clusters (a high altitude and a low altitude cluster) in each mycobiont species. Within *U. pustulata* there is an abrupt genetic break at 900-1000 m (12-13°C annual average temperature), which corresponds to the transition between the Mediterranean and the cool temperate biome. In *U. hispanica* a genetic turnover occurs at 1500-1800 m (7-8°C annual average temperature), marking roughly the transition between the cool temperate and the alpine biomes. Environmental correlation analysis showed species-specific variation in functional genes. Overall, our study highlights the presence of strong environment-associated genetic structure in populations of lichen mycobionts. This suggests that demographic shifts in lichen populations can be expected in regions projected to become hotter and more arid, or less frost-prone in the future.