**ABRUPT GENOMIC BREAKS IN MYCOBIONT POPULATIONS ALONG ELEVATION, AND ASSOCIATED CHANGES IN GREEN ALGAL AND BACTERIAL COMMUNITIES**

Imke Schmitt1,2\*; Gregor Rolshausen1; Francesco Dal Grande1; Jürgen Otte1

1 Senckenberg Biodiversity and Climate Research Centre, Germany; 2 Goethe University Frankfurt, Germany; \*E-mail: imke.schmitt@senckenberg.de

Lichen holobionts can be regarded as dynamic ecosystems that respond to abiotic drivers. To better understand the collective response of “lichen microecosystems” to the environment, we uncover elevational diversity patterns in populations of *Umbilicaria pustulata* and *U. hispanica* along a gradient spanning 2100 altitudinal meters and covering three major biomes. Specifically, we assess genome-wide differentiation of fungal hosts, and associated taxonomic shifts in green algal symbionts, and the bacterial microbiome. Our study shows (i) discontinuous genomic variation in fungal hosts with one abrupt genetic break within each of the two host species, (ii) altitudinally structured bacterial microbiomes with pronounced community turnover within and between hosts, and (iii) altitude-specific presence of algal symbionts. Marked turnover in holobiont diversity occurred across two altitudinal belts: at 11-13°C average annual temperature (here: 800-1200m a.s.l.), and at 7-9°C average annual temperature (here: 1500-1800m a.s.l.). The two observed zones mark a clustering of distribution limits and community shifts. The three ensuing altitudinal classes, i.e. most frequent combinations of species, approximately correspond to the Mediterranean, cool-temperate, and alpine climate zones. We conclude that multitrophic microecosystems, such as lichen holobionts, respond with concerted compositional changes to similar climatic factors that also structure communities of macroorganisms, e.g. vascular plants.