

# Technologies

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# Abstract 57

## Oral Presentation

## The role of microbial diversity in conservation: insights from ecosystem metataxonomics

Giulio Galla<sup>1</sup>, Nadine Praeg<sup>2</sup>, Theresa Rzehak<sup>2</sup>, Paul Illmer<sup>2</sup>, Julia Seeber<sup>2,3</sup> & **Heidi C. Hauffe<sup>1</sup>**

<sup>1</sup> Fondazione E. Mach, Italy

<sup>2</sup> Universität Innsbruck, Austria

<sup>3</sup> EURAC Research, Italy

As microbial communities hosted in various body niches (microbiota) are of recognized importance to individual health, the maintenance of such microbial diversity in natural ecosystems could impact the conservation status of animal species. Metataxonomy using amplicon sequencing has become the standard for characterizing the diversity and composition of microbial communities associated with multicellular organisms and their environment, and numerous studies have now shown that human- and climate-mediated behavioural and dietary changes in wild animal populations are associated with changes in microbiota richness and composition. However, identifying the interactions between the microbiotas within the same ecosystem (i.e. those of water, soil, plants and animals) is essential for fully understanding the role of microorganisms in evolutionary and ecological processes. Comparative studies across such diverse biological samples are rare, due to potential biases during sample processing. Here we discuss the technical adjustments that can be applied to support direct comparisons of microbiota composition, using a terrestrial alpine ecosystem as a case study. We also show how microbial communities from 900 samples (1900 libraries) of wild vertebrates and invertebrates vary with those of domestic breeds and environmental microbiotas (soil and rhizosphere) across an altitudinal gradient, with implications for microdiversity conservation in light of climate and land use changes.