



ABSTRACT BOOK

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Microbial Diversity as a Lever for Effective Biodiversity Conservation: Linking Hosts, Environments, and Health (Symposium)

Dr. Giulio Galla¹, Dr. Heidi Hauffe¹

¹*Research and Innovation Centre, Fondazione Edmund Mach, S. Michele All'adige, Italy*

Recent advances in high-throughput DNA and RNA sequencing have revolutionized our ability to characterize the taxonomic composition, diversity, and functional potential of complex host-associated microbial communities—including microeukaryotes, prokaryotes, and viruses. Among these, the prokaryotic component of the gut microbiota remains the most extensively studied. Established early in life, it plays fundamental roles in food assimilation, metabolism, immune system development, and pathogen defense, thereby shaping host health and survival (Koskella & Bergelson, 2020). Beyond physiological functions, animal microbiota may also enhance host adaptability to varying environments, diets, and pathogen pressures, and therefore, their conservation status (Hauffe & Barelli, 2018; Trevelline et al., 2019).

The composition and diversity of host-associated microbiota is influenced by a complex interplay of intrinsic (genetics, age, sex) and extrinsic (diet, lifestyle and environmental exposure) factors (Flores et al., 2025). However, the diversity and ecological roles of host-associated fungi and other microeukaryotes remain comparatively underexplored, underscoring the need for more integrative studies on their contributions to animal health and adaptive potential.

Moreover, within the framework of the One Health approach, recent research has revealed that environmental reservoirs such as soil and water, among the most microbially diverse ecosystems on Earth (Labouyrie et al., 2023), can act as sources of both beneficial and pathogenic microorganisms influencing animal microbiota across taxa (Banerjee & van der Heijden, 2023; Zanolletto et al., 2025).

This symposium aims to explore how our understanding of host-associated microbial diversity and function, under both controlled and natural conditions, is advancing, and how these results are essential for elucidating the intricate links between microbiomes and long-term animal conservation. We will encourage submission showing how multidisciplinary approaches integrating microbiology, ecology, and environmental sciences are critical to assessing the impacts of anthropogenic activities, habitat alteration, pollution, and climate change on host–microbe interactions and the resilience of animal populations.

Key references

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Soil microbes drive gut fungal assembly and immunity in a wild rodent model

Dr. Toni Jernfors¹, Dr. Esa Koskela¹, Dr. Giulio Galla², Dr. Matthias Scholz², Prof. Tapio Mappes¹, Dr. Eva Kallio¹, Dr. Heidi Hauffe², Prof. Phillip Watts¹

¹*University Of Jyväskylä, Jyväskylä, Finland*

²*Fondazione Edmund Mach, San Michele all'Adige, Italy*

Environmental microbial communities, particularly in soil, play an increasingly recognized role in wildlife health, yet their influence on host-associated fungi remains largely overlooked. Host associated microbiota, in turn, are tightly linked to immune function and disease resistance, meaning that environmental impacts on the gut microbiome can directly affect host health. Using a wild-derived bank vole model, we experimentally tested how exposure to forest soils from national parks versus urban greenspaces affects gut microbiome assembly and host immune function. Soil exposure substantially altered the gut mycobiota, increasing fungal diversity and incorporating environmentally sourced taxa that formed larger and more complex co occurrence networks than those of animals kept on sterile bedding. In contrast, bacterial communities showed weaker shifts, though soil exposure still reorganized bacterial network structure. Strikingly, only urban soil triggered an innate immune response in the colon, including strong upregulation of IFN γ -inducible and epithelial defense genes. These results indicate that anthropogenic alterations to soil can stimulate host immunity independently of pathogen transfer to the gut.

Our findings demonstrate that soil microbial diversity is a key ecological driver of gut fungal assembly, microbial network organization, and immune activation. These results highlight the value of integrating environmental microbiota, particularly soil fungi, into biodiversity monitoring, habitat management, and One Health-oriented conservation planning.