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Evoluzione

— 11th SIBE CONGRESS 2026



Book of Abstracts



Evaluating habitat health through species-level diet-microbiome interactions in an alpine specialist

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Understanding habitat health is fundamental for wildlife conservation. Fecal samples represent a non-invasive source of ecological information, yet their potential to simultaneously inform on diet, animal condition, and environmental quality remains largely unexplored. Here, we show how an advanced shotgun metagenomics framework overcomes the taxonomic limitations of standard methods, resolving dietary and microbial profiles at the species level. This allows us to explore how dietary-driven microbial taxa can serve as robust indicators for habitat health. Focusing on the Alpine rock ptarmigan (*Lagopus muta helvetica*), a boreal, cold-adapted glacial relict inhabiting high-altitude environments in the Italian Alps, we evaluated the performance of shotgun sequencing and Kraken2-based taxonomic annotation across diverse, quality-controlled databases of full genomes and marker sequences. Our co-occurrence network analysis reveals ecology-driven associations between plant and bacterial taxa, with specific gut bacteria emerging as indicators of habitat quality. *Pseudomonas putida*, a species associated with stressed soils, positively correlates with the habitat showing the lowest plant diversity, while *Methylobacterium bullatum* identifies habitats of high ecological quality. We also find that specific dietary taxa directly indicate animal health, as shown by the negative association between medicinal plants such as *Lavandula angustifolia* and potentially pathogenic bacteria. Additionally, the detection of plant pathogens like *Rhizobium tumorigenes* across sampling sites demonstrates that a single fecal sample simultaneously captures host condition, diet, and plant-ecosystem integrity. These findings demonstrate that integrated diet-microbiome analysis of fecal samples provides a multi-layered, non-invasive, and transferable tool for assessing habitat health, offering wildlife managers a new approach to monitoring ecosystem condition through host diet-microbiome interactions.