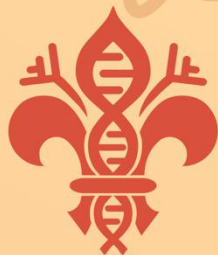




I think

B



Evoluzione

— 11th SIBE CONGRESS 2026



Book of Abstracts



They are what they eat - effects of diet on the gut microbiota of the gray wolf (*Canis lupus*)

Giulio GALLA^{1*}, Matthias SCHOLZ¹, Naomi FLUX^{1,2}, Elena SGARABOTTO¹, Stefano CASARI¹, Chiara ROSSI¹, Luca PEDROTTI³, Martha HIRBER⁴, Roberto GUADAGNINI⁴, Andrea MARCOLLA⁴, Heidi C. HAUFFE^{1,6}

¹ Research and Innovation Centre, Fondazione Edmund Mach, Italy

² School of Biosciences, Cardiff University, UK

³ Consorzio Parco Nazionale dello Stelvio, Italy

⁴ Belpark – Parco Faunistico Spormaggiore, Italy

⁶ National Biodiversity Future Center, Italy

* Corresponding author: giulio.galla@fmach.it

The grey wolf (*Canis lupus* L.) is undergoing a notable increase in population size and range across Europe, and the recolonization of peri-urban and agricultural areas may lead to dietary changes due to increased predation on livestock. While well-studied in humans, the effect of dietary changes on the gut microbiota of wildlife in human-impacted environments remains largely unknown. Here, we investigated dietary impacts on wolf gut microbiota by analysing faecal samples collected with non-invasive methods from a pack of nine healthy wolves hosted by the Belpark – Parco Faunistico Spormaggiore (Italy). Over a three-month period, wolves were sequentially fed a diet based on either whole sheep (*Ovis aries*) or roadkill red deer (*Cervus elephas*) before returning to a conventional mixed diet. Prokaryotic and fungal communities the entire pack throughout the experiment were characterized using metataxonomy (16S rRNA V3-V4 and ITS2 gene regions). To link taxonomic changes to changes in gut function, the gut microbial transcriptional profile of a subset of 20 samples was investigated using metatranscriptomics. Longitudinal comparisons revealed a small core microbiota of dominant bacteria and fungi shared by all animals, numerous low-abundance or individual-specific microorganisms. Shifting to a wildlife-based diet elicited contrasting responses: bacterial richness increased rapidly but transiently, whereas fungal communities exhibited a continuous increase in richness and greater inter-individual variability. Fungal community composition was strongly associated with diet, while bacterial composition was only marginally linked. Our results clarify the temporal natural variation of the gut microbiota in captive, related animals sharing a controlled home range. These findings have direct implications for wildlife health, contributing to dietary regimes that preserve microbial diversity and functional potential, thereby supporting animal welfare in wildlife parks.