

# Book of Abstracts



**Università  
degli Studi  
di Palermo**



Accademia  
Nazionale  
Italiana di  
Entomologia

**High inter-individual diversity of the gut microbiota in *Trypocoprís pyrenaicus* (Charpentier, 1825) (Coleoptera, Geotrupidae)**

Samuele Voyron<sup>1</sup>, Erica Lumini<sup>2</sup>, Gianluca Natta<sup>1</sup>, Alex Laini<sup>1</sup>, Alfredo Santovito<sup>1</sup>, Angela Roggero<sup>1</sup>, Antonio Rolando<sup>1</sup>, Claudia Palestrini<sup>1</sup>

<sup>1</sup> University of Turin, Italy;

<sup>2</sup> Institute for Sustainable Plant Protection (IPSP), Italy

Dung beetles contribute first and foremost to dung removal. Still, they also contribute to an impressive variety of other ecosystem services, and the gut microbiota (i.e., a heterogeneous group including bacteria, archaea and fungi) may be crucial in their role as ecosystem service providers. The taxonomic composition of gut microbiota is shaped by multiple factors including diet, developmental stage and gut morphology, host taxonomy, environment, and mechanism of transmission. These microorganisms play a crucial role in degrading otherwise unpalatable recalcitrant compounds such as cellulose and lignin. However, little is known about the taxonomic diversity and ecological functions these micro symbionts can provide. Moreover, until now, most of the studies focused on lab-reared species, whereas there is a need to study the microbiota of adult individuals in natural conditions.

Here, we describe and compare the taxonomic and functional diversity of bacteria, archaea, and fungi in the gut microbiota of ten wild adult individuals of *Trypocoprís pyrenaicus* – a dung beetle species widely distributed across Europe that feeds on faeces of several vertebrate species.

We found marked inter-individual variability in the taxonomic composition of the gut microbiota with multivariate ordination of individuals that changes depending on whether we consider bacteria or fungi. Shared OTUs and families (i.e., core microbiota) are very few. The individuals tested shared 0.25% of the bacterial-archaeal OTUs and 0.50% of the fungal OTUs. They also shared 0.91% and 2.35% of the bacterial-archaeal and fungal families respectively. Among bacteria and archaea, the most represented Phyla are Firmicutes, Proteobacteria, Bacteroidota, Actinobacteriota and Euryarchaeota, although the relative abundances varied between individuals. Among the fungal OTUs, the most abundant phylum is Ascomycota, followed by Basidiomycota.

The most frequently observed bacterial and archaeal functions relate to aerobic chemoheterotrophy, chemoheterotrophy and fermentation, while the fungal trophic categories most found in all individuals are pathotroph-saprotroph and pathotroph-saprotroph-symbiotroph.

The considerable inter-individual variability revealed by our results suggests that when studying the microbiota of dung beetles, many individuals should be considered per species to accurately describe the community and to identify a consistent core microbiota. Furthermore, since fungi or bacteria produce different inter-individual ordinations, we suggest considering both microorganisms in future microbiota studies.

**KEY WORDS:** dung beetles, gut microbiota, bacteria, archaea, fungi.

**POSTER**

**XXVII ITALIAN NATIONAL CONGRESS OF ENTOMOLOGY**  
12 - 16 JUNE 2023, PALERMO