



# Bacterial communities in soil, gut and casts of *Pontoscolex corethrus* under *Coffea arabica* and *Coffea canephora*



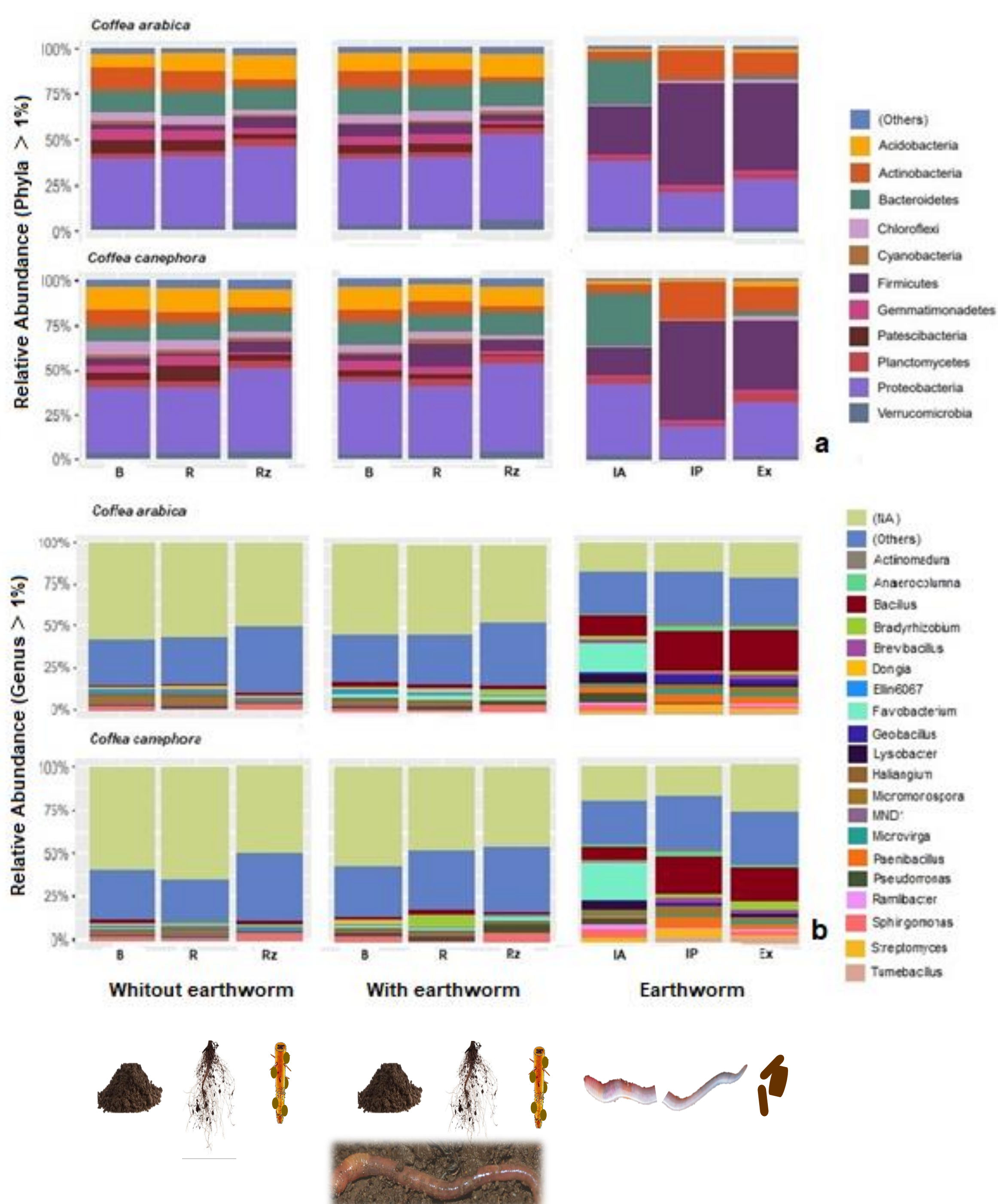
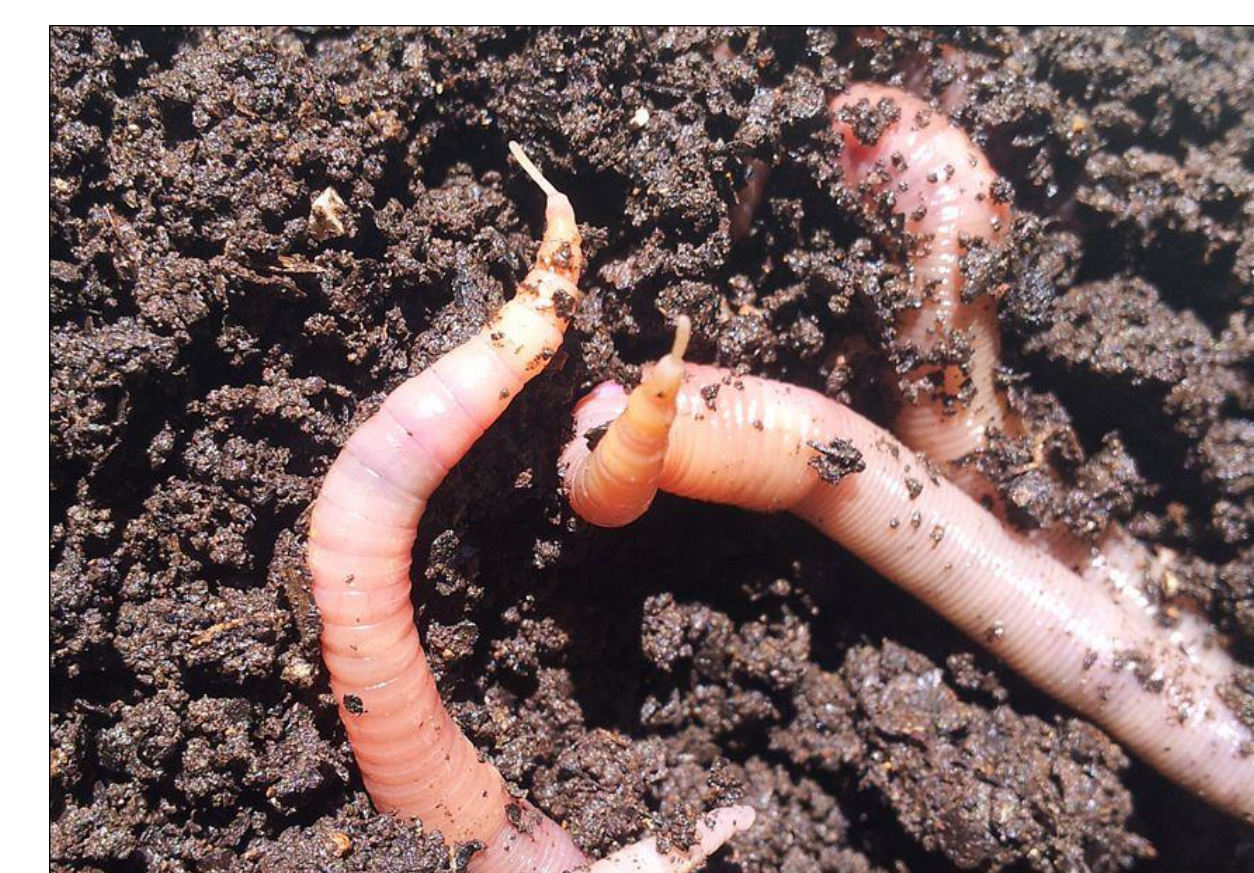
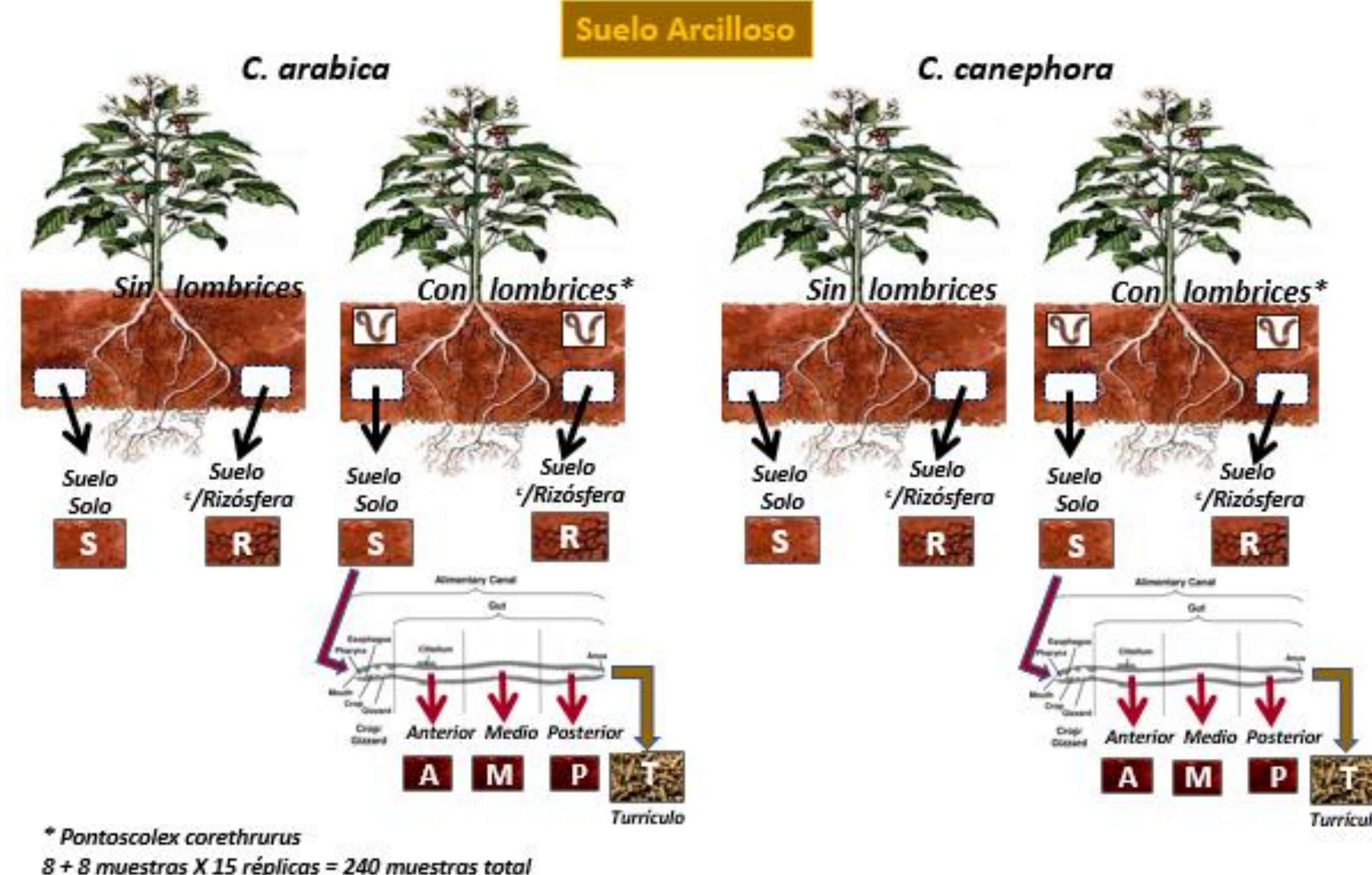
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**INTRODUCTION:** Earthworms stimulate microbial activity in their gut and surrounding soil, through the secretion of intestinal and cutaneous mucus that induces a priming effect on the soil and gut bacterial communities, potentially modifying their structure.

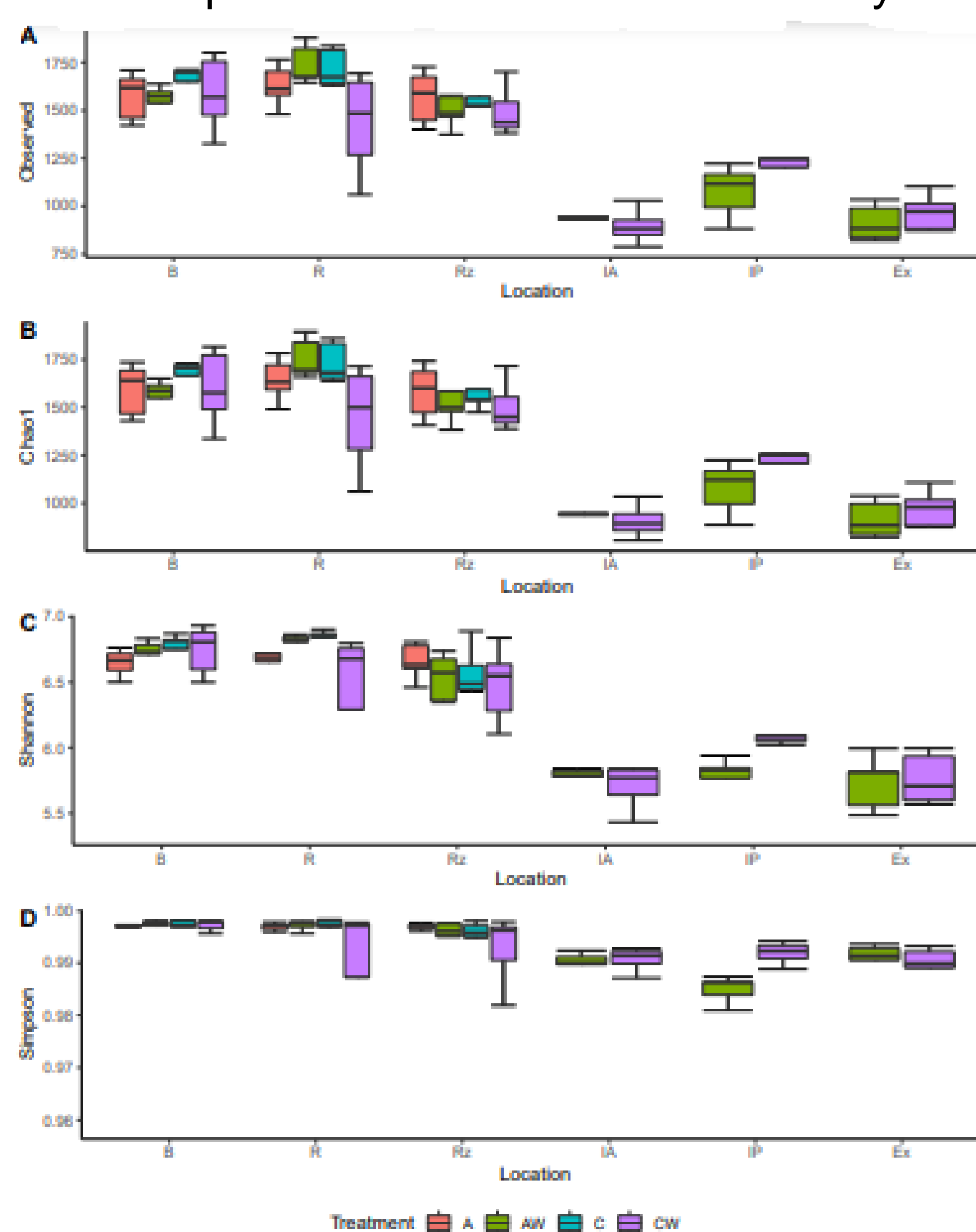
We look to determine that : 1) The earthworm *P. corethrus* modifies the taxonomic composition of the bacterial community in coffee soil, through the selection or enrichment of certain bacterial taxa in the soil and in their excreta; 2) The effect of the earthworm *P. corethrus* on the diversity and structure of the bacterial community in coffee soil varies depending on the studied compartment (bulk, rhizospheric soil, rhizoplane, gut or excreta) and 3) The intestinal microbiome of the earthworm comes from the soil or has its own microbiome.

## Finca Roma, Coatepec, Ver.

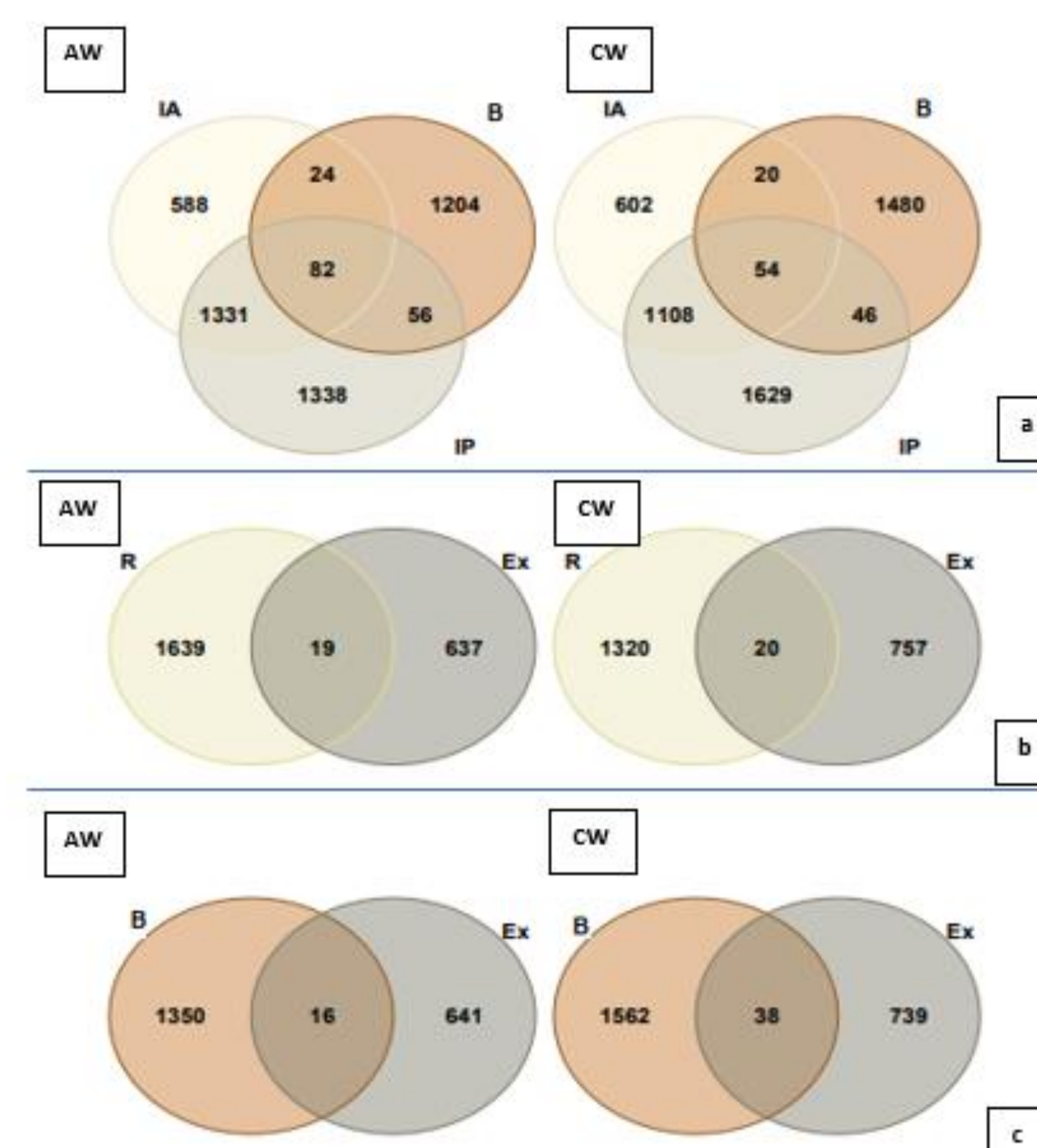


**Figure 1.** Bacterial community composition (phylum level) (a) and (Genus) (b) of bacterial communities from soil samples: *C. arabica* and *C. canephora* without earthworm, with earthworm; in soil location: bulk (B), rhizospheric soil (R) and rhizoplane (Rz); and earthworm samples: interior anterior (IA), interior posterior (IP) and excreta (Ex).

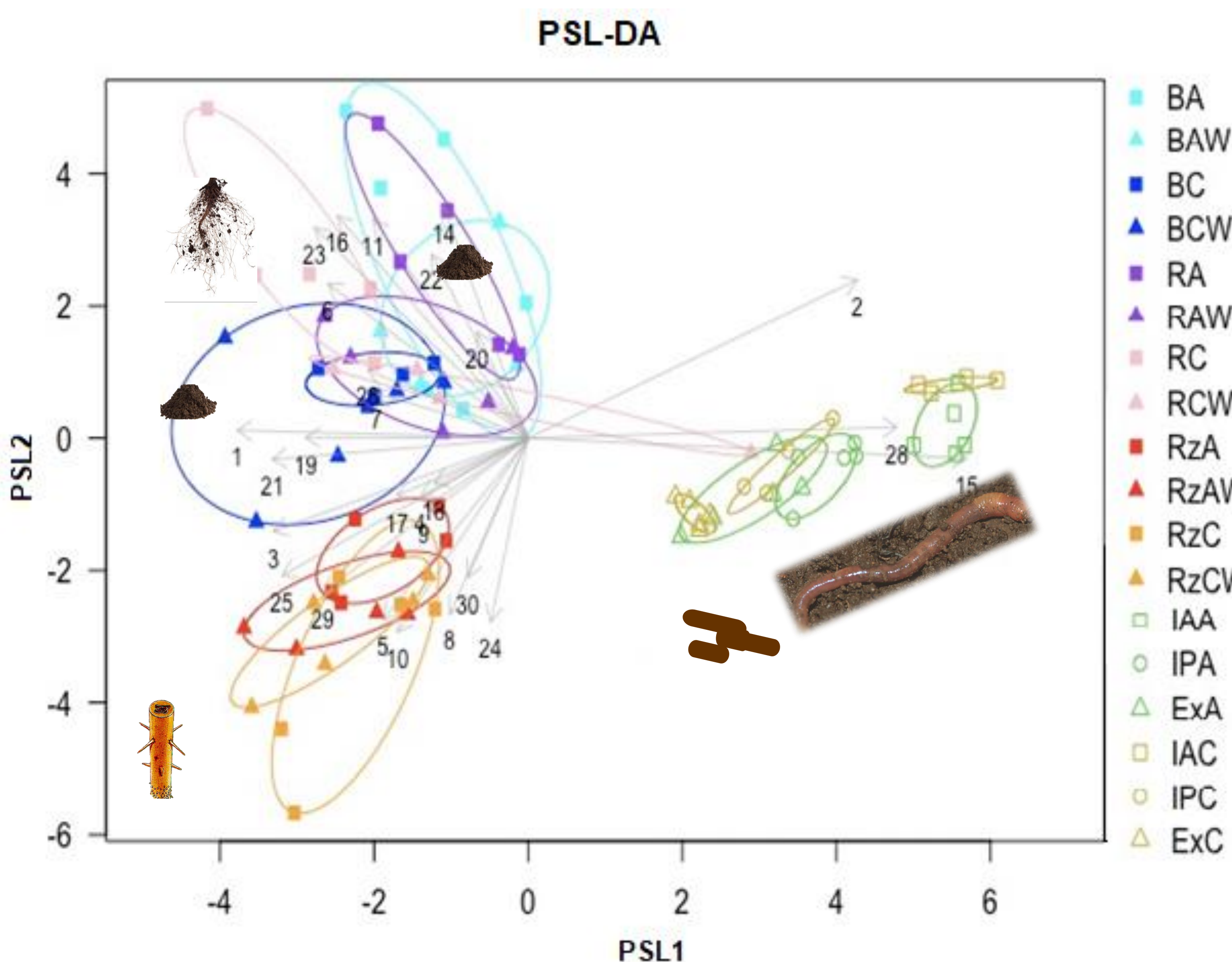
**MATERIAL & METHODS:** From the mesocosms, the bacterial communities of bulk soil, rhizosphere soil, and rhizoplane of *Coffea arabica* and *C. canephora*, with and without *P. corethrus*, as well as those present in the anterior and posterior sections of the earthworm gut and in excreta, were analyzed through 16S rDNA amplicon sequencing on a MiSeq Illumina platform. The bioinformatic analysis of sequences was performed in QIIME2.



**Figure 2.** Richness and alpha diversity of soil samples: bulk (B), rhizospheric soil (R) and rhizoplane (Rz); *C. arabica* (A) and *C. canephora* (C), with earthworm (W); and earthworm samples: anterior (IA), posterior (IP) gut content and excreta (Ex). N= 5.



**Figure 3.** ASV's shared between bulk (B), anterior (IA) and posterior (IP) gut content (a); rhizospheric soil (R) and excreta (Ex) (b); and bulk and excreta (c); *C. arabica* (A) and *C. canephora* (C); with earthworm (W).



**Figure 4.** Characteristics of bacterial communities of soil samples: Bulk (B), Rhizosphere soil (R), Rhizoplane (Rz) in *C. arabica* (A) and *C. canephora* (C); with earthworm (W); and earthworm samples: interior anterior (IA), interior posterior (IP) and excreta (Ex). 1 = Acidobacteria; 2 = Actinobacteria; 3 = Armatimonadetes; 4 = Bacteroidetes; 5 = Chlamydiae; 6 = Chloroflexi; 7 = Cyanobacteria; 8 = Dadaobacteria; 9 = Deinococcus. Thermus; 10 = Dependitiae; 11 = Elusimicrobia; 12 = Entotheonellaeota; 13 = Epsilonbacteraeota; 14 = Fibrobacteres; 15 = Firmicutes; 16 = Gemmatimonadetes; 17 = Hydrogenedentes; 18 = Kiritimatiellaeota; 19 = Latescibacteria; 20 = Margulisbacteria; 21 = Nitrospirae; 22 = Omnitrophicaeota; 23 = Patescibacteria; 24 = Planctomycetes; 25 = Proteobacteria; 26 = Rokubacteria; 27 = Spirochaetes; 28 = Tenericutes; 29 = Verrucomicrobia; 30 = Zixibacteria

## CONCLUSIONS:

- The soil taxonomic composition of bacterial communities is different from the gut content. There is a good estimation of the communities. The alpha diversity is highest in the soil.
- The diversity of rhizosphere bacterial community is greatest in the presence of earthworms, for both coffee species.
- The Earthworms modify the soil bacterial community and enrich its diversity in the rhizosphere.
- The taxonomic composition of bacterial communities in the anterior gut is markedly different than that of posterior gut and excreta both in *C. arabica* and *C. canephora*, with a dominance of Proteobacteria and Bacteroidetes.
- The earthworm select the soil and the bacteria.
- There is very few ASV's shared between the soil and the gut content (1- 7%).
- The gut content has its own microbiome

**ACKNOWLEDGEMENTS:** We thank CONACYT for its financial support : DILOBA Diversidad bacteriana del suelo de la rizosfera del café antes, durante y después su paso por el intestino de la lombriz de tierra *Pontoscolex corethrus*- proyecto 257819