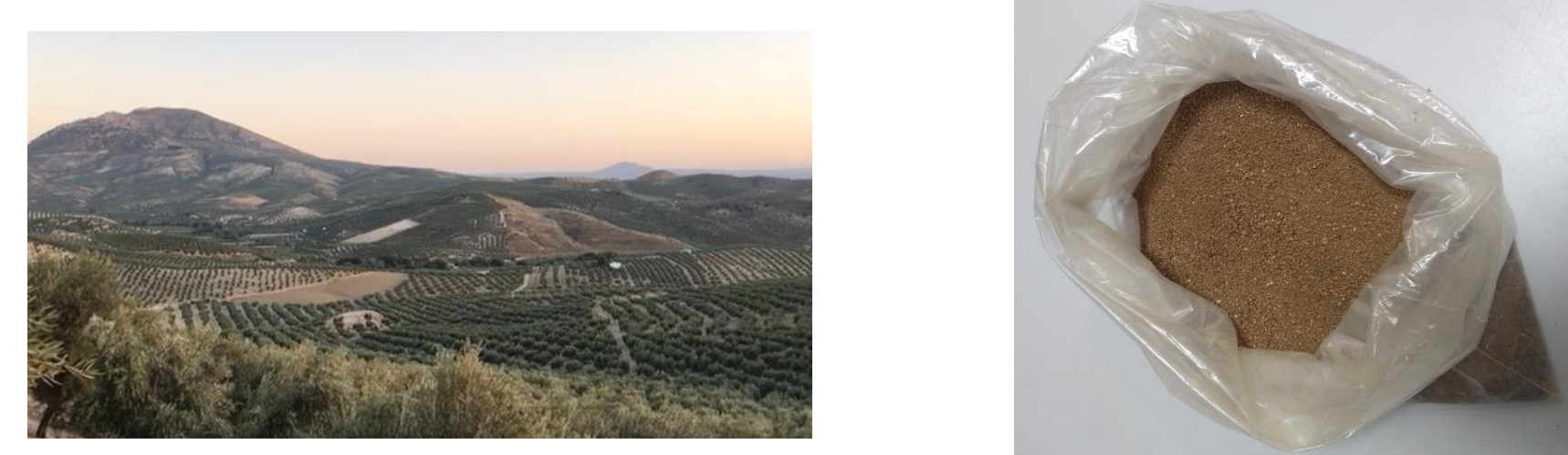


SOIL MICROBIAL COMMUNITIES FROM OLIVE CULTIVARS ARE SHAPED BY SEASONALITY AND GEOGRAPHICAL SCALES

INTRODUCTION

Soil biodiversity is essential to sustain healthy ecosystems supporting the maintenance of the environment and agricultural practices. Soils provide vital habitat for microorganisms which play determinant roles through organic matter transformation and nutrient cycling having a high impact in agriculture and food production and climate regulation. Unravelling the function and structure of microbial communities prevailing in soils is essential for a better understanding of plant development. However, the vast majority of soil microorganisms remain unknown and their variability at regional and temporal seasonal scale is still an unexplored field.

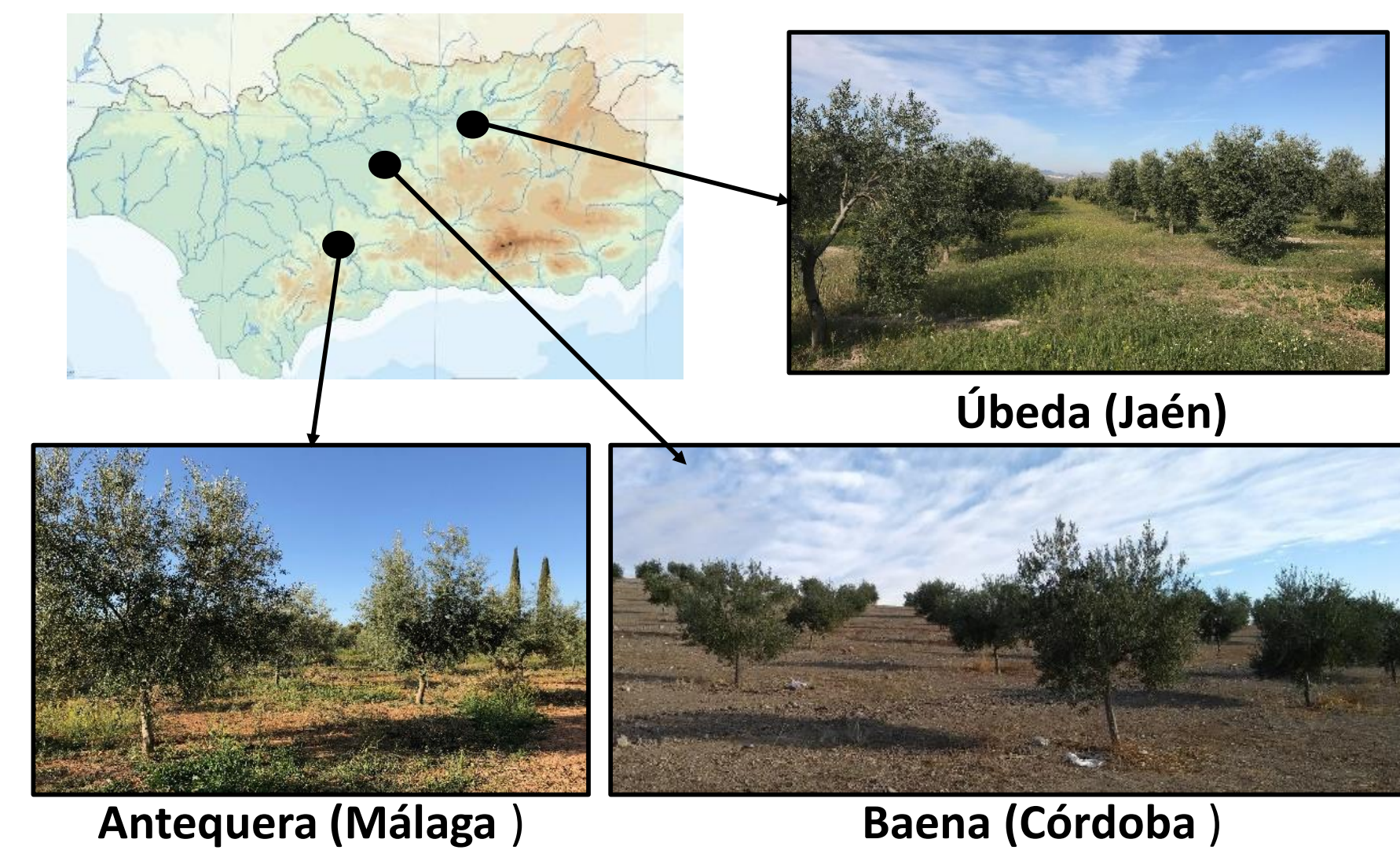


MATERIAL AND METHODS

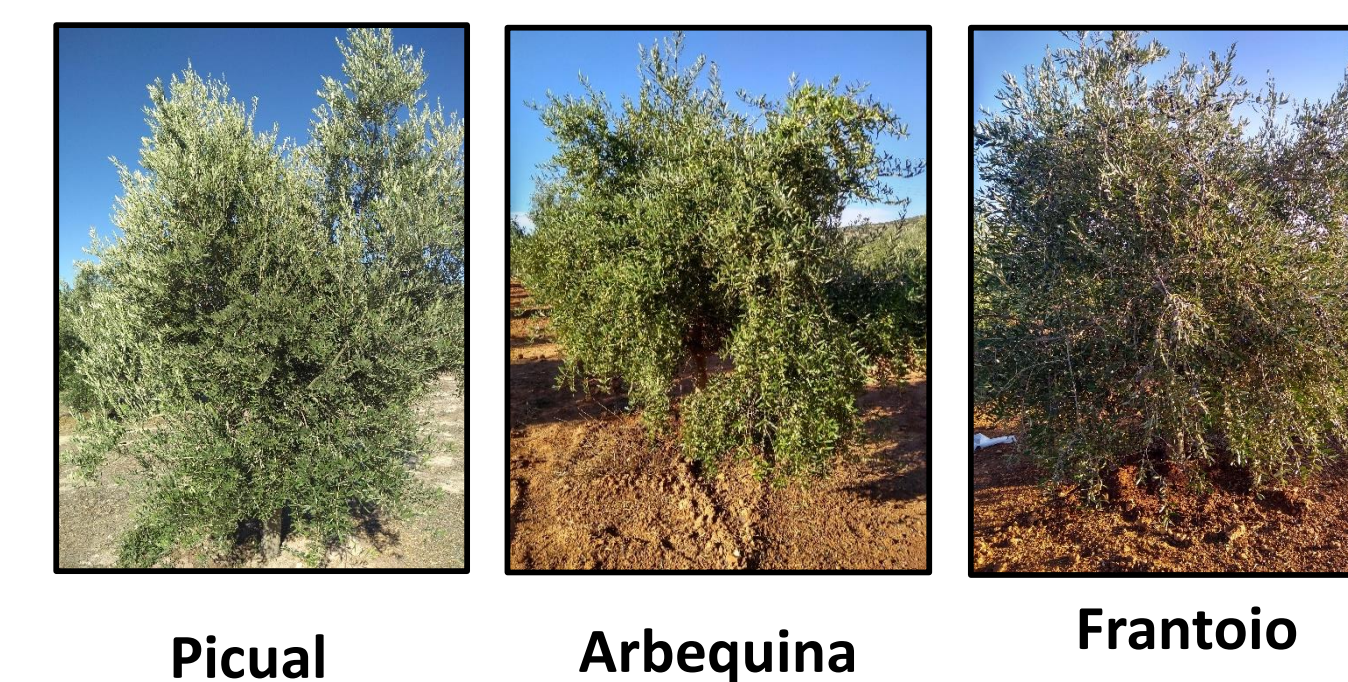
Study area, collection samples and experimental analysis

In this study, soils associated to the rhizosphere of three olive genotypes were sampled during autumn 2018 and spring 2019 in three olive orchards with differences in physicochemical soil characteristics and climate, located in the provinces of Jaén, Córdoba and Málaga, in Andalusia, Southern Spain. Bacterial and fungal populations were analysed using Illumina MiSeq platform to determine the structure and diversity of soil microbial communities.

Field locations in Andalusia (South of Spain)



Olive plant genotypes



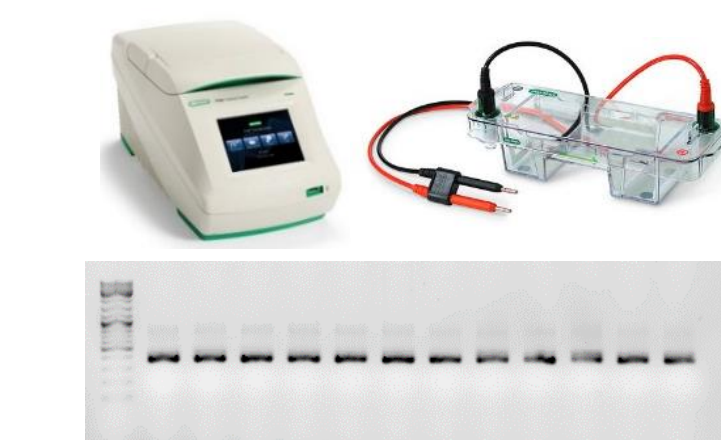
DNA extraction



Bioinformatic analysis

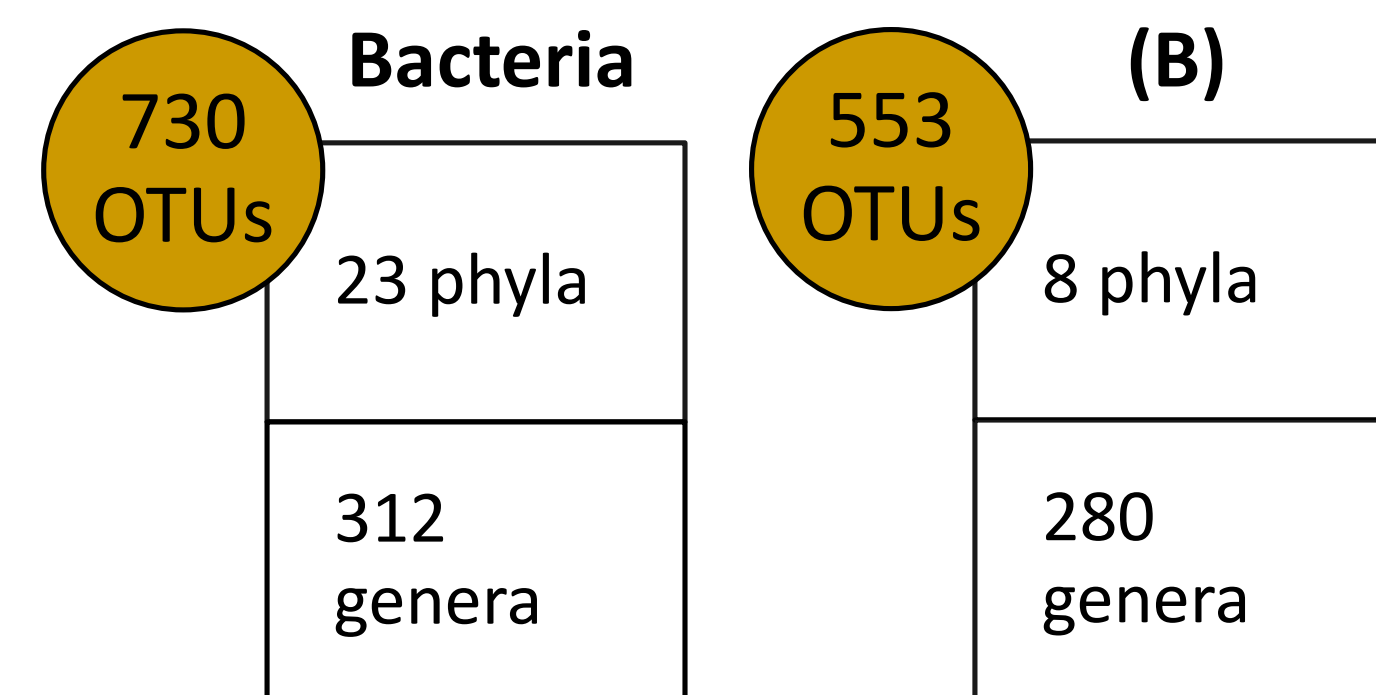


PCR library

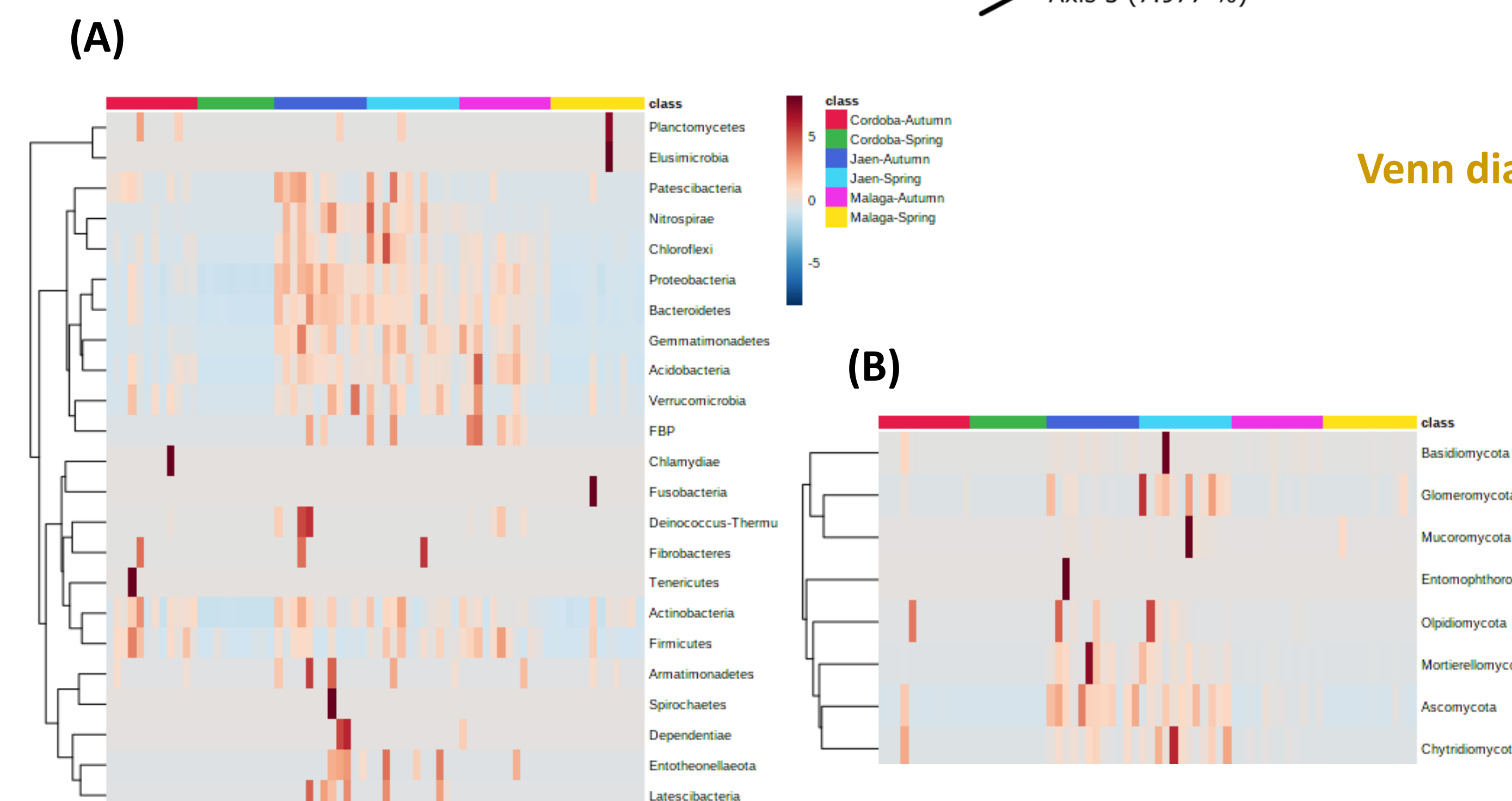


RESULTS

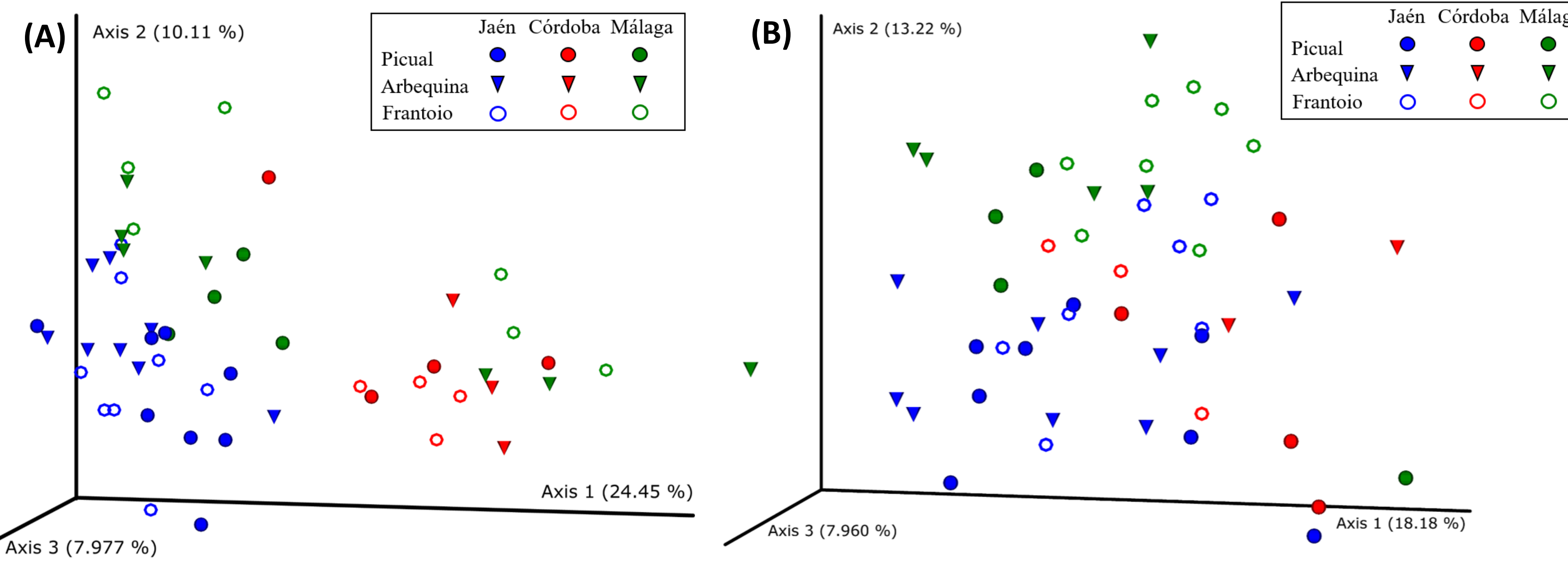
Main taxonomy overview from bacterial (A) and fungal (B) communities



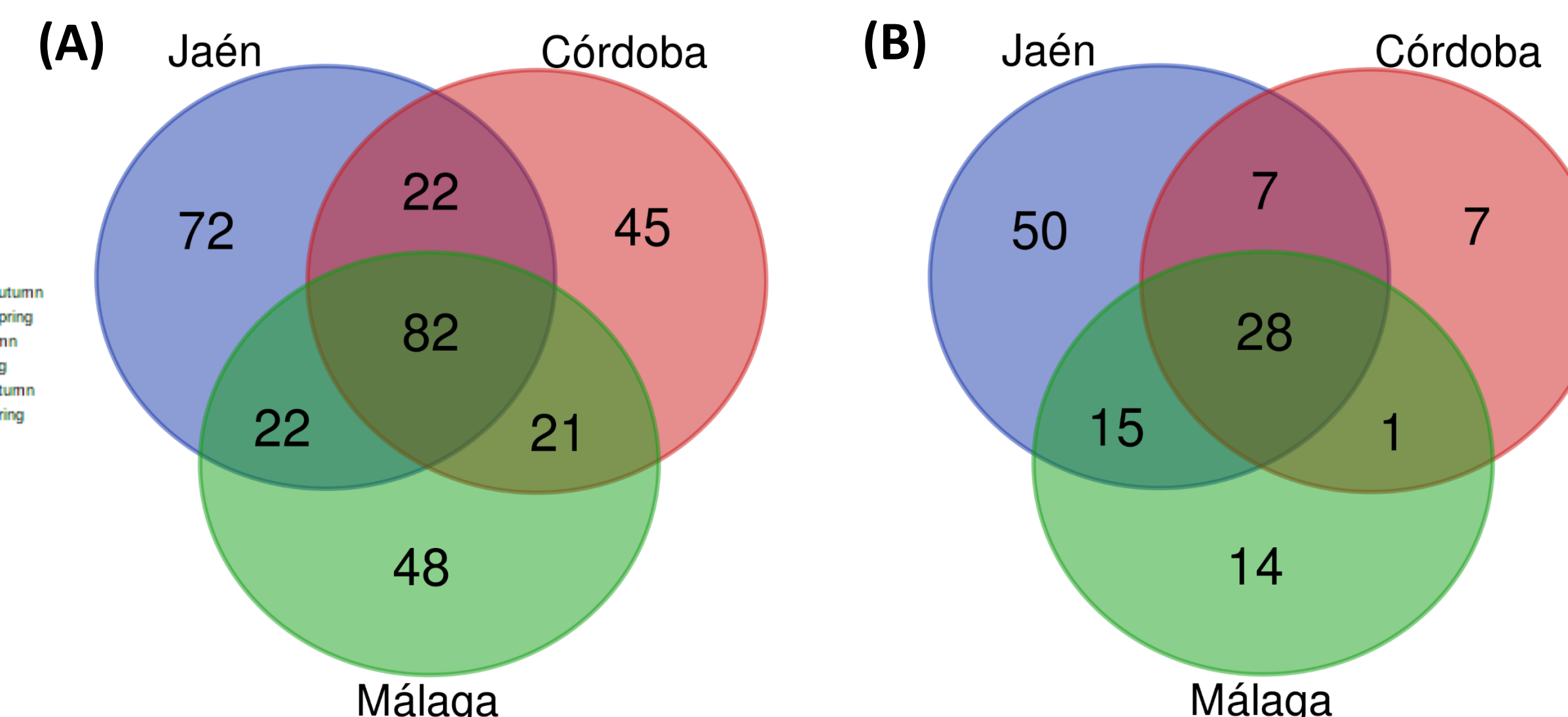
Heatmap of bacterial (A) and fungal (B) phyla variation according to field locations and season



PCoA of Weighted UniFrac distances in bacterial (A) and fungal (B) communities according to olive genotypes and geographical scales



Venn diagram of unique and shared bacterial (A) and fungal (B) genera among field locations



16S – Bacterial community

Proteobacteria was the most abundant bacterial phylum across olive orchard locations (30.37%-5.52%) followed by *Actinobacteria* (10.72%-5.49%) and *Bacteroidetes* (7.73%-0.89%). There was circa 50% abundance reduction of these phyla on samples taken in autumn compared to that sampled in the spring. Unique bacterial genera differed according to field location in Jaén (72), Córdoba (45) and Málaga (48) while the shared bacteria genera among plots was 82. Principal coordinate analysis of weighted UniFrac distances indicated that main differences among bacterial communities (measured as phylogenetic distances) were due to the environment where the plants grow (field locations) with minor effect of olive cultivar (Picual, Arbequina and Frantoio) or season (Autumn vs. Spring).

ITS – Fungal community

Ascomycota (49.13%-3.13%) and *Basidiomycota* (25.64%-2.79%) were the two most abundant phyla in all olive orchards. A reduction on the abundance of *Ascomycota* was noticed on samples from Autumn to Spring (37.84% and 20.42%, respectively), while *Basidiomycota* displayed a distinct behavior (11.89% and 20.27%, respectively). Exclusive fungal genera varied from Jaén (50), Córdoba (7) and Málaga (14), whereas the core fungal genera among fields was 28. PCoA indicated that main differences among fungal communities were due to geographical scales (field locations) with minor effect of olive cultivar (Picual, Arbequina and Frantoio) or season (Autumn vs. Spring).

CONCLUSIONS

Our results suggest that main differences in bacterial and fungal communities in olive orchard soils are mainly due to geographical scales and environmental conditions and depend to a lesser extent on plant genotype or season. This information can contribute to generate new knowledge regarding the effect of temporal and spatial scale on soil microbiome associated to olive crop which may be of interest to increase or maintain soil microbial diversity and olive health.