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Analysis of the core microbiome of blueberry and blackberry plants as a first step in the design of efficient bacterial biofertilizers

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As humans, plants harbour a microbiome, and as human microbiome, plants microbiome is essential for their health and fitness. Several components of this microbiome are able to increase crop's yields and quality because of their ability to supply nutrients, phytohormones and protect them from pathogens. On the other hand, traditional farming usually uses chemicals to promote plant yields that are related to many negative effects to the environment and human's health. As an alternative to agrochemicals, we can select beneficial members of the plants' microbiome as plant probiotics, which can be applied in fields.
Blueberries and blackberries are forest fruits broadly consumed with high antioxidants content. Their production is increasing and the development of microbial probiotics for these crops is desirable. As a first step to select microbial probiotics for blueberry and blackberry plants, we analysed their microbiome using massive parallel sequencing. We collected DNA from the rhizosphere, roots and leaves of different plant samples from four different locations. Then, we analysed bacterial and fungal diversity through amplicon based metagenomics.

MATERIALS AND METHODS

Samples from rhizosphere, roots and leaves from blueberry and blackberry plants were taken from 4 different locations in Spain (Figure 1). We isolated the total DNA from each sample. In order to study their microbial communities, we performed 16S rRNA gene and ITS1 region amplicon metagenomics. 144 amplicon-based metagenomes were obtained in total. We processed the sequences of the microbiome with QIIME2[1]. All the necessary steps for sequence quality filtering and microbiome composition and diversity analysis were carried out with this program.

RESULTS AND DISSCUSION

While fungal communities are very (beta) diverse below the class taxonomic level, we found that blueberries and blackberries share common bacterial profiles at genus level (Figure 1b, 1c and Figure 2), mainly in their roots and rhizosphere. Both alpha and beta diversity metrics do not show big differences beween bacterial communities of same tissues for these 2 plants (Figure 1b, 1c).

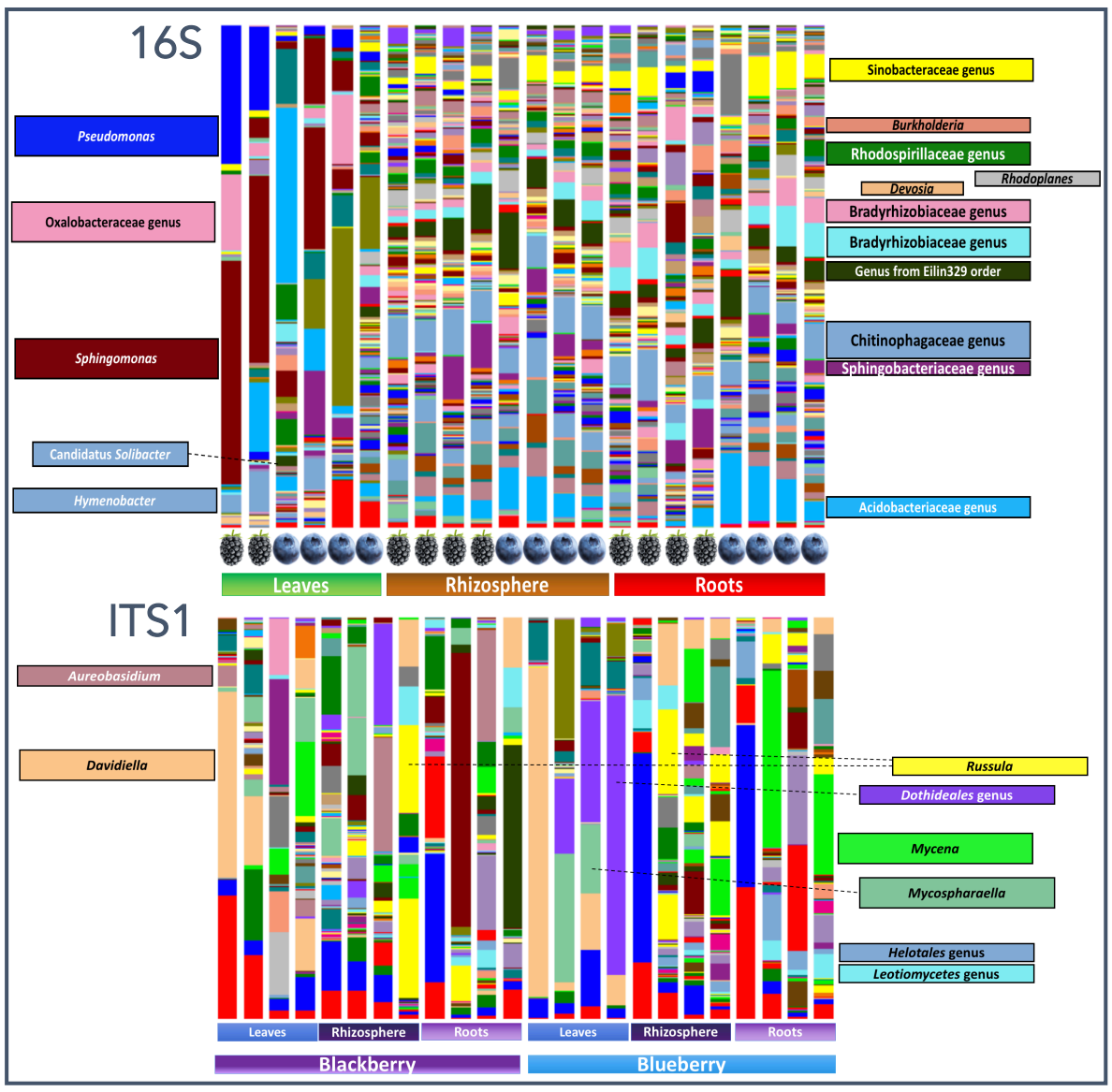

Figure 2. Taxonomic profiles of both 16S and ITS1 metabarcoding of blueberries and blackberries roots, leaves and rhizospheres. Each bar represents 3 replicates from each sampling site. Each color represent a taxa at genus level.

Since our aim is to design an effective biofertilizer based on a core microbe able to colonize inner plant tissues, we computed the core microbiome of both plant roots (Figure 1d).

Based on these data, we guided the isolation of core bacteria from the inner tissues of both plant roots. Once we have identified them, we are studying their ecological roles in the plants and will be tested in future works for their ability to enhance yields and quality of these crops.

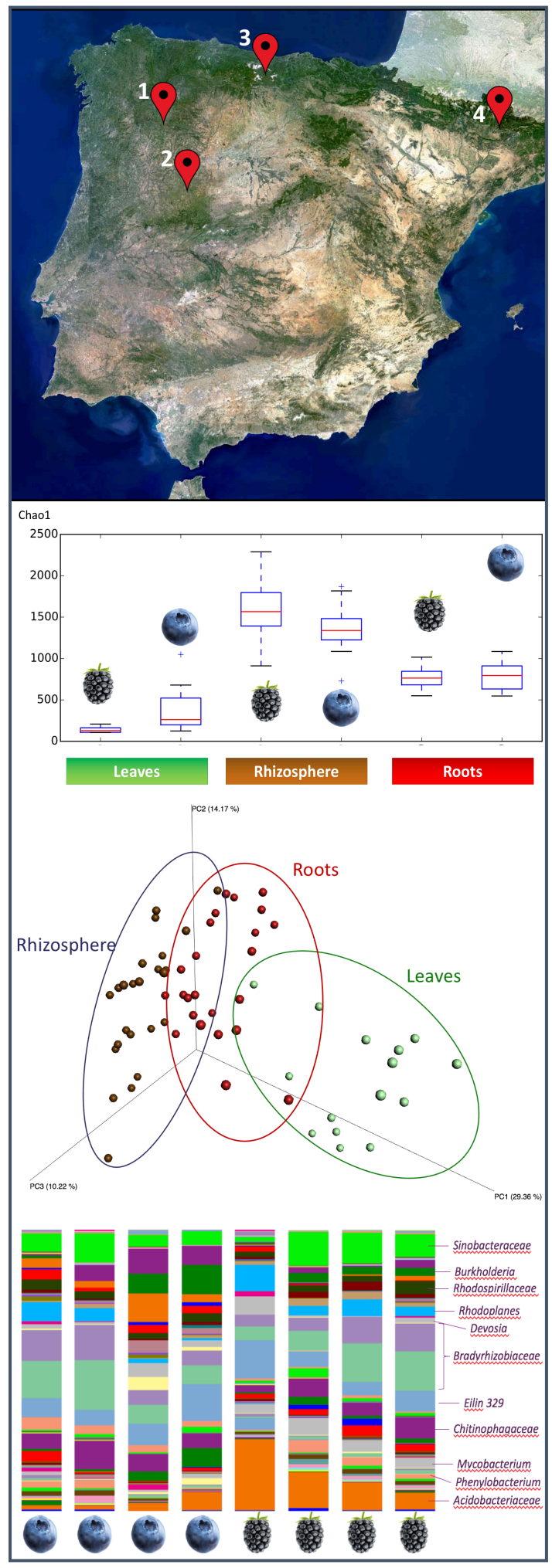

Figure 1. a) Representation of the 4 different sampling sites; **b)** comparison of alpha diversity (Chao index) of the bacterial communities of roots, rhizosphere and leaves from blackberries and blueberries; **c)** PCoA plot of the different bacterial communities from both plants; **d)** summary of the root core bacteriome

CONCLUSIONS

Despite fungal communities are very divergent among different samples, the bacterial communities for blackberry and blueberry plants are quite conserved in different locations. Once we have isolated members of their core microbiome, we will be able to design an efficient biofertilizer for both crops.

References:
[1]Bolyen et al., (2019). *Nature biotechnology*, *37*(8), 852-857.

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