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Metagenomic and culturomic approachs for blueberry biofertilizer design

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Abstract: Some decade ago, the blueberry (*Vaccinium myrtillus*) crop has been introduced in Portugal, and nowadays is widespread along the North and Center of Portugal. It has a great relevance as exportation product, taking advantage of the climatic conditions they allow to produce when the market does not have entrances from the producing countries of Northern Europe. However, it is this climate condition that could create problems in the near future since, if climate change models are correct, an increase in temperature and a reduction in precipitation will happen. In this work, we study the rhizospheric and endophytic population of wild blueberry plants in three locations of mainland Portugal intending to determine the core bacterial populations of these plants in Portugal to design new biofertilizers to improve the adaptation of this crop. The metagenomic approach revealed that the rhizospheric populations are influenced by temperature and climate, but the endophytic populations of *Vaccinium* are modulated by the plant. From this plant s total of 318 bacterial strains were isolated and their Infraspecific diversity has been analysed using RAPD-M13, obtaining 66 different fingerprints, which were identified employing MALDI-TOF MS methodology and a comparison against the MALDI Biotyper 3.0 database. A 64% of the strains were identified at genus level and the remaining ones by 16S rRNA sequencing. *Bacillus*, *Rhizobium*, *Serratia*, *Steptomyces*, *Paenibacillus*, *Pantoea*, or *Pseudomonas* were some of the identified genera. Most strains were able to grow at pH 5.5, in presence of 2% NaCl and were psychoresistant. Plant growth promotion potential of these strains was analysed revealing that most of the isolates were capable of solubilizing dicalcium phosphate and only 17% of the isolates produced siderophores.

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