Soil Microbiome analysis to improve drought resilience in maize

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Water availability may be the most important environmental factor limiting crop growth and productivity. Climate change will likely make drought events more frequent in many regions, including Portugal, and increasing the demand on freshwater resources and creating major challenges for sustainable agriculture. Maize (*Zea mays*) is an extremely important crop cultivated worldwide, being used for food for both humans and livestock, as well as biofuel, and as a crude material in industry. However, it demands high amounts of water, and is even considered a "thirsty" crop.

Microbiomes support plant health and adaptation to environmental transitions, exhibiting increased phenotypic plasticity comparing to plants with lesser dynamic genomes. This Master thesis aims to contribute to sustainable production of maize by identifying the putative functional microbiome that can improve resilience of *Zea mays* to drought stress.

The work plan is proposed as follows:

1- Extraction of Metagenomic DNA from soil associated with two cultivars, one resilient and one susceptible to drought, and growing under different water regimes (full irrigation, deficit irrigation).

2- Identification of microbiome composition by bioinformatic analysis of 16S rRNA gene metabarcoding.

3- Measurements of plants' optical signals to infer physiological responses to drought in both resilient and susceptible genotypes.