One of the main challenges following climate change is long, unpredictable periods of drought. In our search towards increased plant resilience against drought stress, we identified two leaf endophytic bacterial strains conferring such drought tolerance in maize. We also aim to study one commercially available fungal strain, that is currently used to improve maize growth under drought stress in Brazil.

In this project we aim to identify their mode of action (MoA) and elucidate the downstream signalling in the maize leaf. For the identification of the MoA, we have already sequenced, assembled, and annotated the bacterial genomes, which have subsequently been analysed for the potential production of secondary metabolites. We aim to do the same for the fungal strain. For all species, a kinematic analysis to determine the contribution of cell division and cell elongation has already been performed. This allows us to sample our material in a strategic manner, as the cell division zone and cell elongation zone are spatially separated along the maize leaf.

Concerning the bacterial strains, we have already performed some experiments with regard to the elucidation of downstream signalling *in planta*, showing reduced oxidative stress and enhanced polyamine levels, specifically in the growth zone of the maize leaf. Based on these results, we plan to do additional experiments regarding the localisation of the endophytes in the maize leaf and more in-depth analyses such as a transcriptomic analysis, metabolite and biochemical analyses, and enzyme activity measurements.

Concerning the fungal strain, a transcriptomics analysis of the maize leaf meristem has already been performed, so the aim is to, once a genomic sequence has been obtained, compare transcriptomic changes *in planta* with the genomic capacity of the fungal strain and verify our then formed hypotheses through in-depth analyses such as mentioned above for the bacterial endophytes.

Once elucidated, the MoAs of these bacteria and fungus will be verified by using plant lines that exhibit overexpression and/or knockout of a putative crosstalk mediating plant gene, by monitoring the identified downstream processes *in planta*.