Mixed synthetic communities "bacteria - fungi" for seed protection against the pathogenic fungus Alternaria brassicicola

The seed microbiome constitutes the primitive microbial inoculum at the starting point of the assembly of the adult plant microbiome. The composition and diversity of this primitive inoculum could have a crucial role in plant fitness and protection against plant pathogens. We aim to develop an alternative disease control strategy against the seed-borne fungal pathogen Alternaria brassicicola. This strategy is based on the use of Synthetic Communities (SynComs) consisting of bacterial and fungal isolates that will be applied as bio priming seed treatment in order to limit plant infection by A. brassicicola.

In order to find the good candidates to build our SynComs, we will focus on 15 bacterial and 31 fungal taxa recently identified as «core microbiota» of radish seeds. We will select typical isolates among our collection (500 bacterial and 150 fungal strain isolated from radish seed Raphanus sativus var. Flamboyant 5). To date, molecular typing of our fungal strain collection (ITS1) reveals that nine taxa were successfully isolated. To increase this diversity, we will re-isolate fungal strains using an alternative dilution-to-extinction culturing method.

The isolates will be tested for their antibiosis and fungistasis capacity against A. brassicicola. Their metabolic and growth profiles will be analyzed. All these data will be used to select the most promoting isolates. We will reconstruct mixed bacteria-fungi SynComs and assess their influence on the transmission of A. brassicicola from radish seed to seedling. The meta-barcoding analysis (gyrB for bacteria, ITS1 for fungi) will reveal the dynamics of each bacterial and fungal isolate present in the SynComs and identify which taxa have negative interactions with A. brassicicola within a microbiota. Finally, these identified SynComs will helped us to study the mechanisms of microbiota assembly during its transmission from seed to seedling and to develop microbiota management approaches to limit the transmission of pathogens.

1. What is your pathogen? Multiple options possible (e.g. if working on coinfections)
   
   **Fungi** : Alternaria brassicicola

2. On a scale of 1-5 is your work mostly eco/epidemiological or evolutionary? 1 (100% eco/epidemiological)

3. On a scale of 1-5 is your work mostly theoretical or experimental/empirical? 3