Deciphering the ecological processes driving microbial inheritance from seeds to developing plants using synthetic community inoculation

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Résumé

Microbiota engineering through inoculation of synthetic communities (SynComs) is gaining attention as a potential way to improve basic knowledge on plant microbiota assembly and plant health. Seeds represent a vector of dissemination of plant-associated microorganisms. Hence, inoculation of SynComs on seeds could be a relevant way to modulate plant microbiota assembly from the very start of plant life using a limited amount of inoculum. However, many questions are to be answered to design efficient SynComs inoculated on seeds: What is the influence of SynCom composition (richness, phylogenetic diversity, strain identity, functional diversity) and concentration (mass effects) on its stability and ability to colonize seeds and seedlings? What are the impacts of SynCom inoculation on microbiota assembly during its entire life cycle (from seed to seed)?

To answer these questions, a collection of 1250 bacterial strains isolated from bean seeds and seedlings has been obtained. A total of 43 SynComs were designed to study the transmission and impact of SynCom inoculation on non-sterilized seeds that were sown in non-sterile potting soil. A metabarcoding approach was performed to track our bacterial strains in the inocula, seeds, seedlings and developing plants. We showed that SynCom concentration but neither richness nor phylogenetic diversity influence SynCom capacity to colonize seeds and seedlings. On average, SynComs are representing 97% of the relative abundance of the seed microbiota and 80% of the seedling microbiota, even in a coalescence context with the native seed and soil microbiota. We showed that strains identity and biotic interactions were the main drivers of strain and SynCom ability to colonize seeds and seedlings. In particular, some strains' transmission was strongly influenced (positively or negatively) by the phylogenetic or functional similarity they shared with the other SynCom strains. Despite a high SynCom colonization at the seedling stage, we showed that most inoculated strains were replaced by other taxa after 5 weeks of growth (vegetative stage) and that seed-to-seed transmission was a very rare event only detected for one strain (*Pantoea agglomerans*).

These results show that SynCom experiments permit to gain key knowledge on the ecological processes driving microbial inheritance between seeds and plants. In particular, we demonstrate that transmission of seed-borne taxa to the developing plant is mainly driven by mass effects and biotic interactions (phylogenetic/functional proximity between taxa), and that manipulation of seed taxa will have targeted effects only at early life stages.

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Mots-Clés: plant microbiota assembly, microbiota engineering, seed microbiota transmission, mass effects, phylogenetic diversity