

Composition, structure et héritabilité des communautés de microorganismes racinaires et rhizosphériques associées à *Pisum spp.* au cours de son développement - GeHoPi

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Plants interact with a multitude of microorganisms, including bacteria, some of which play a role in ecological functions that impact their host. Symbiotic associations between plants and microorganisms are the most well-known and documented, the most famous being the Rhizobia genus associated with legumes, enabling them to fix atmospheric nitrogen and illustrating a long co-evolutionary history. Beyond these associations, numerous bacteria in non-symbiotic interaction with plants also impact their host. Significant gaps persist in understanding these complex microbial communities, requiring holistic approaches at different temporal and spatial scales.

We conducted a greenhouse experiment to investigate the dynamics of bacterial communities associated with *Pisum* throughout its developmental cycle, in various microhabitats provided by the host. These microbiomes were analyzed using full-length 16S rRNA gene PACBIO sequencing with ecological and phylogenetical approaches.

Results revealed that plant microhabitats act as ecological filters, shaping the composition and structure of bacterial communities. Shifts in bacterial communities were observed across plant growth stages, with these effects increasing with spatial proximity to the plant. Finally, spatial and temporal patterns in associated bacterial community dynamics were linked to bacterial phylogenetic relatedness. These findings enhance our understanding of the dynamics of plant-associated bacterial community recruitment.