

INTERLABS - IBIS



Oussama Yahmi

Étudiant au doctorat

Sous la direction de Jean-Baptiste Leducq et co-direction d'Edel Pérez-López

Integrating Metagenomics and Bacterial Isolation to Investigate the Canola Clubroot Microbiome

Jeudi, 5 novembre à 12 h 30

Pavillon Charles-Eugène-Marchand, salle Hydro-Québec (1210)

Abstract :

Clubroot, caused by *Plasmodiophora brassicae*, remains a major threat to canola production, particularly given the emergence of pathotypes capable of overcoming cultivar resistance. Although the plant microbiome offers a promising avenue for sustainable disease management, our understanding of canola–*P. brassicae*–microbiome interactions remains limited, largely because most studies rely on metabarcoding approaches, which provide limited insight into microbiome functional diversity. This study therefore aimed to better understand these interactions by combining metagenomic approaches with microbial isolation to identify pathobiome-associated taxa and potential antagonists whose complementary functions could be combined to develop synthetic microbial communities (SynComs). Hybrid sequencing of more than 40 gall samples enabled the construction of a nonredundant catalog of 10 million microbial genes and the reconstruction of approximately 150 bacterial genomes. Microbiome analyses revealed complex microbial networks with presence of potential secondary phytopathogens, including *Fusarium*, *Ralstonia*, and *Pectobacterium*, that may contribute to disease development through the degradation of plant defense metabolites and cell wall components. To move beyond descriptive characterization toward identifying microbiome functions, 250 bacterial strains were isolated from infected and uninfected canola tissues and evaluated *in vitro* and *in planta*. Several strains, primarily belonging to *Bacillus* sensu lato, exhibited strong inhibition of pathogens such as *Sclerotinia* and *Fusarium*, as well as plant growth-promoting traits. These preliminary findings provide a foundation for the next phase of the project, which will involve testing these strains in combination to design synthetic microbial communities tailored to control clubroot in canola under field conditions.