



Pole for Doctoral Studies
Center for Doctoral Studies Sciences, Technologies, and Medical Sciences

ANNOUNCEMENT OF DOCTORAL THESIS DEFENSE



Ms. REMMAL Imane

**Will present their research work with the aim of earning a
Doctorate**

Doctoral program: Science and Technique Engineering
Discipline: Biological Sciences

Specialty: Molecular Genetics, Microbiology, and Bioinformatics

**On 14/02/2026 at 13H00 at the Conference Hall, “F” Building,
Faculty of Sciences and Techniques of Tangier, UAE
Under the Theme**

**Targeted Metagenomic Analysis Of Bacterial Communities In
Key Agricultural Insects: Mayetiola Hordei And Dactylopius
Opuntiae in Morocco**

Front of the jury composed of :

First Name & Last Name	Establishment	Designation
Pr. BOUAJAJ Adel	ENSA of Tangier, UAE	President
Pr. EL AMRANI Amal	FST of Tangier, UAE	Reviewer
Pr. EL GALIOU Ouïam	FST of Tangier, UAE	Reviewer
Pr. EL FAHIME Elmostafa	CM6RI of Benguerir, FM6SS	Reviewer
Pr. ELOUAAI Fatiha	FST of Tangier, UAE	Examiner
Pr. SEDQUI Abdelfettah	ENSA of Tangier, UAE	Examiner
Pr. TSIAMIS George	University of Patras, Greece	Co-Supervisor
Pr. MAURADY Amal	FST of Tangier, UAE	Supervisor

Host Research Structure: Laboratory of Innovative Technologies, National School of Applied Sciences of Tangier, Abdelmalek Essaadi University, Tetouan, Morocco.

Abstract



Insect-associated microbiomes significantly influence host biology, encompassing reproduction, immunity, and population dynamics, and serve as potential targets for sustainable pest management. This thesis presents a comparative analysis of the bacterial communities linked to two significant crop pests, *Mayetiola hordei* and *Dactylopius opuntiae*, utilizing targeted PCR Sanger sequencing, Next generation Sequencing (NGS), and Oxford Nanopore MinION 16S rRNA amplicon sequencing techniques.

Our analyses demonstrated distinct symbiont profiles between the two pests. *M. hordei* contained *Wolbachia* supergroup A, whereas *D. opuntiae* harbored *Wolbachia* supergroup B and *Spiroplasma* from the *poulsonii*–*citri* complex, with *Spiroplasma* infections identified solely in males. Low-abundance symbionts exhibit potential for reproductive manipulation, such as cytoplasmic incompatibility (*Wolbachia*) and male-killing (*Spiroplasma*), which may affect host sex ratios and population structure. Dominant taxa, exemplified by *Candidatus Dactylopiibacterium* in *D. opuntiae*, obscure rare taxa, underscoring the significance of methodological factors such as read depth, primer specificity, and taxonomic resolution. The removal of this dominant species highlighted a diverse microbial community, underscoring the importance of integrating both targeted and untargeted sequencing methods to fully capture bacterial diversity.

The results highlight the efficacy of microbiome-mediated pest control strategies, such as population suppression through symbiont-induced reproductive manipulation and their integration with traditional management practices. Tailoring approaches to specific species and contexts is crucial because the prevalence and function of symbionts vary depending on the host and environmental conditions. This thesis lays the groundwork for future functional and applied research, encompassing experimental validation, functional profiling, and microbiome manipulation studies, thereby facilitating the development of sustainable, microbiome-based strategies for agricultural pest management. These findings provide opportunities for further postdoctoral research on host–microbiome interactions, with implications for ecological and agricultural practices.

Keywords: *Mayetiola hordei*; *Dactylopius opuntiae*; *Candidatus Dactylopiibacterium* Biological control; full 16S rRNA gene; *Wolbachia*; *Spiroplasma*; pest management; NGS; MinION Nanopore sequencing