



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

ANNOUNCEMENT OF DOCTORAL THESIS DEFENSE



M. EL YAMLAHI Youssef

**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 02/02/2026 at 10H00 at the Conference Hall Pr. OTMAN
FILALI MEKNASSI, the National School of Applied Sciences of
Tangier, UAE**

Under the Theme

**Genotypic Characterization of the Bacteriome of Tsetse Flies
(Glossina spp.) in Tanzania and Olive Fruit Fly (Bactrocera
oleae) in Morocco**

Front of the jury composed of :

First Name & Last Name	Establishment	Designation
Pr. BRITEL Mohammed Réda	ENSA of Tangier, UAE	President
Pr. EL AMRANI Amal	FST of Tangier, UAE	Reviewer
Pr. AANNIZ Tarik	FMP of Rabat, UM5	Reviewer
Pr. MAROUI Itto	FMD of Rabat, UM5	Reviewer
Pr. ZEROUK Hassani Mounir	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 pests, including tsetse flies (*Glossina* spp.) and the olive fruit fly (*Bactrocera oleae*), pose significant threats to public health and agricultural productivity due to their roles in pathogen transmission and crop damage. Recent advances in bacteriome research underscore the critical influence of symbiotic bacteria on insect physiology, development, reproduction, and ecological adaptation, offering potential for innovative pest control strategies.

This thesis investigates the bacterial communities associated with these two ecologically and economically important pests through distinct studies. The work culminates in a synthesis of findings that inform sustainable management strategies. The first study focuses on *Glossina* spp., the exclusive vectors of African trypanosomiasis in sub-Saharan Africa, comparing the microbiota of natural and laboratory populations in Tanzania. Using 16S rRNA gene sequencing, the analyses reveal a stable core bacteriome dominated by *Wigglesworthia glossinidia*, with variability influenced by habitat conditions, species, and developmental stages. Facultative symbionts such as *Sodalis glossinidius* and *Wolbachia* are detected, with *Wolbachia* showing species-specific prevalence (e.g., in *G. morsitans*), suggesting potential applications in vector control. The second study examines wild populations of *Bactrocera oleae*, the principal pest of olive cultivation, across multiple agroecological regions in Morocco.

Employing full-length 16S rRNA gene sequencing, the research identifies a dominant bacterial community led by *Candidatus Erwinia dacicola*, an obligate symbiont essential for larval survival on phenolic-rich olives. Additional taxa, including *Erwinia persicina* and *Asaia bogorensis*, exhibit regional variability, which indicates their roles in host adaptation to local environments. In synthesizing these studies, the thesis highlights the structured yet dynamic nature of insect microbiomes, with core symbionts providing essential functions and facultative taxa responding to environmental cues.

These findings contribute to a deeper understanding of host-microbe interactions and open new avenues for targeted, environmentally friendly pest management strategies, such as symbiont manipulation for sterile insect technique (SIT) and integrated pest management (IPM). Future research is recommended to explore the functional roles of *Wolbachia* and *Asaia bogorensis* in biological control programs.

Keywords: Insect microbiome, symbiotic bacteria, *Glossina*, *Bactrocera oleae*, microbial ecology, pest insects, 16S rRNA gene, biological control, sustainable management