INTERNSHIP PROPOSAL M2 RESEARCH 2025-2026

TITLE: What is the role of plant cell wall composition in the adaptation of a pathogenic fungus to its hosts?

Supervisors: Thierry MARCEL (BIOGER)

Address, phone, e-mail: INRAE BIOGER, Campus Agro Paris-Saclay, 22 Place de l'Agronomie - CS80022, 91120 Palaiseau – France, Tél. : +33 1 89 10 13 35, thierry.marcel@inrae.fr

INTRODUCTION, SCIENTIFIC CONTEXT:

Zymoseptoria tritici is a pathogenic fungus responsible for the Septoria tritici blotch (STB) disease observed on the leaves of bread wheat, durum wheat, and triticale. STB occurs in all wheat-growing regions and causes particularly severe damage in temperate areas. While *Z. tritici* is capable of infecting both bread wheat (*Triticum aestivum*) and durum wheat (*T. turgidum* var. *durum*), individuals of this pathogen are generally specialized toward one or the other of these two host species. However, the genetic determinants and molecular mechanisms underlying this specialization remain unknown. Several lines of evidence indicate that the composition of the plant cell wall and the ability of *Z. tritici* isolates to degrade cell wall polysaccharides may contribute to their specialization toward one or the other wheat species.

The plant cell wall (PCW) is indeed one of the first lines of defense of the plant against pathogens such as *Z. tritici* (Munzert & Engelsdorf, 2025). It is composed of different classes of polysaccharides, which in turn are built from 22 different monosaccharides. These monosaccharides are linked together by various glycosidic bonds that may potentially serve as substrates for the glycosyl hydrolases (GHs) secreted by pathogens (Rebaque *et al.*, 2024). To degrade a single polysaccharide, numerous GH activities may be required. GHs are classified within the CAZymes (Carbohydrate-Active enZymes) and are grouped into several numbered families (e.g., GH3, GH13, GH16), each number indicating a distinct family based on structural similarity and enzyme specificity.

RESEARCH PROPOSAL:

The objective of this project is to gain a better understanding of the role of wheat cell wall composition in the specialization of *Z. tritici* isolates toward bread wheat and durum wheat. To this end, you will contribute to study the differences in cell wall composition between these two wheat species, as well as the sequence variations in GHs potentially implicated in pathogenicity, depending on the host specialization of the isolates. The results obtained will allow you to determine whether there is a match between the enzymatic cocktails produced by the fungus and the cell wall composition of its hosts.

METHODOLOGIES:

You will be hosted at INRAE BIOGER (in Palaiseau), but the project will be realized in collaboration between the two INRAE units BIOGER and IJPB (in Versailles), respectively specialized in studying plant pathogenic fungi and plant cell walls. You will contribute both to:

- Produce and extract PCW from 10 wheat genotypes (5 bread wheat and 5 durum wheat varieties), under three conditions (non-inoculated, inoculated with bread wheat specialized isolate, inoculated with durum wheat specialized isolate), in three replicates (total 90 points);

- Contribute to the analysis of the PCW composition on the Plant Observatory - Chemistry/Metabolism platform at IJPB, using gas or liquid chromatography coupled with mass spectrometry (Voxeur *et al.*, 2019);

- Make a catalog of all GHs potentially involved in pathogenicity from results available in the literature or from previous genetic analyses realized at BIOGER;

- Study the sequence diversity of GHs in the catalog among 768 *Z. tritici* isolates from which the sequence is already available at BIOGER, by calculating genetic diversity indexes and detecting signals of selection, independently in bread wheat and durum wheat specialized isolates;

You will compare the results concerning the cell wall composition of bread wheat and durum wheat varieties with those obtained for the catalogs of CAZymes and candidate GHs, in order to better understand the role of wheat cell wall composition in the specialization of *Z. tritici* strains toward their host species.

RESEARCH UNIT:

The INRAE BIOGER Research unit (BIOlogy of fungal plant pathogens: from GEnomes to agRo-ecosystems) is a French center of excellence for research into fungal diseases affecting field crops (wheat, rapeseed) and vines. BIOGER develops multidisciplinary approaches (ranging from epidemiology to molecular biology and genomics) and multi-scale approaches (from genes to landscapes). Our main models are pathogens responsible for fungal diseases of major economic importance. Our work is organized into four main research areas: (i) Biological and ecological traits of phytopathogenic fungi, (ii) Fungal infection processes, (iii) Adaptation to the host and control methods, and (iv) Sustainability of fungal disease control strategies. The overall objective of our research is to meet societal expectations in terms of sustainable and environmentally friendly control of fungal diseases in field crops and management of the risks associated with the spread and adaptive potential of phytopathogenic fungi.

REFERENCES (maximum 5):

Munzert KS, Engelsdorf T (2025). Plant cell wall structure and dynamics in plant-pathogen interactions and pathogen defence. *Journal of Experimental Botany* 76(2): 228-242.

Rebaque D, Carrasco-López C, *et al.* (2024). *Zymoseptoria tritici* stealth infection is facilitated by stage-specific down-regulation of a β-glucanase. *bioRxiv*: 2024.12.04.626787.

Voxeur A, Habrylo O, *et al.* (2019). Oligogalacturonide production upon Arabidopsis thaliana–*Botrytis cinerea* interaction. *PNAS* 116(39): 19743–19752.