

INTERNSHIP PROPOSAL M2 RESEARCH 2025-2026

TITLE: Genetic basis of *Zymoseptoria tritici* virulence on the durum wheat cultivar “Ceedur”

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INTRODUCTION, SCIENTIFIC CONTEXT:

Septoria tritici blotch, caused by the ascomycete *Zymoseptoria tritici*, is one of the most damaging wheat diseases, leading to yield losses about 10–15% annually in France and worldwide, despite the use of resistant cultivars and fungicides (Fones and Gurr, 2015). To mitigate the impact of this disease while reducing fungicide applications, genetic control represents the most sustainable strategy. This approach relies on the development and judicious deployment of wheat varieties resistant to *Z. tritici*. Breeding for resistance requires a comprehensive understanding of the genetic determinism underlying host resistance, as well as the identification of resistance genes or Quantitative Trait Loci (QTL). However, the durability of resistance strongly depends on its management, since the high adaptability and genetic diversity of pathogen populations often lead to a rapid breakdown of newly introduced resistances (Kildea et al., 2020). A deeper understanding of the mechanisms driving *Z. tritici* adaptation is therefore crucial for the efficient use of wheat genetic resources and the development of resistance that is both effective and sustainable. Research on the interaction between bread wheat (*Triticum aestivum*) and *Z. tritici* has already led to the identification of 23 resistance genes (*Stb* genes), numerous QTLs, as well as several avirulence factors (*AvrStb*) and effectors in the pathogen (Brown et al., 2015; Meile et al., 2024). Gene-for-gene interactions are common in this pathosystem, between *Stb* resistance genes in wheat and *AvrStb* genes in *Z. tritici*, which can lead to a qualitative or a quantitative effect on the interaction (Langlands-Perry et al., 2023). Conversely, little is known about the genetic determinants involved in the interaction between durum wheat (*Triticum turgidum*) and *Z. tritici*, despite the nutritional and economic importance of durum wheat, which is exclusively used for the production of semolina and pasta.

RESEARCH PROPOSAL:

This internship is part of a PhD project exploring host specificity in *Z. tritici*, through the study of both the genetic determinism of pathogen virulence and

host resistance in bread and durum wheat. The internship project is focused on the durum wheat cultivar “Ceedur”, which displays remarkable resistance to *Septoria tritici* blotch. Indeed, among 160 isolates of *Z. tritici* collected from durum wheat across several Mediterranean wheat-growing regions, only five were found to be virulent on Ceedur. A QTL mapping approach previously identified two QTLs associated with Ceedur resistance, which colocalize with resistance genes already known in bread wheat; their role is currently under validation. The aim of the internship is to apply a similar QTL mapping approach on the pathogen side, in order to characterize the genetic factors involved in virulence on Ceedur. For this purpose, a progeny from a cross between a Ceedur-virulent strain and an avirulent strain is available (INRA20-TM0285 x INRA20-TM0264, n=200). This progeny, segregating for virulence on Ceedur, will enable the identification of QTLs associated with avirulence that may be interacting in a gene-for-gene manner with the two resistance QTLs previously detected in Ceedur. The identified loci will be characterized using public databases and bioinformatic resources available at BIOGER. The results will be analyzed in relation to Ceedur's resistance factors to provide a comprehensive understanding of this specific host–pathogen interaction.

METHODOLOGIES:

The QTL mapping approach requires both genotypic and phenotypic data, which will be generated during the internship. The workflow can be structured into four main steps:

1. Production of genotypic data: DNA will be extracted from the progeny (*molecular biology*), followed by genome sequencing by short-read Illumina. A marker matrix will then be constructed with the help of the bioinformatic platform of the unit; short sequences will be mapped on a reference *Z. tritici* genome and polymorphisms (SNPs, InDels) will be identified (*bioinformatics*).

2. Production of phenotypic data: The progeny will be phenotyped for virulence on seedlings of the cultivar Ceedur under controlled conditions. The intern will follow a pathoassay protocol involving inoculum preparation (*microbiology*), plant inoculation, and quantitative assessment of disease symptoms (*phytopathology*). Multiple replicates will be conducted, and the data will be analyzed statistically.

3. QTL mapping: Genotypic and phenotypic datasets will be combined to perform QTL mapping using the R/qtl package (*quantitative genetics*).

4. Candidate gene identification: The intern will use the reference genome of *Z. tritici* (IPO323) as well as two PacBio-assembled genomes available in the team to characterize the identified QTL regions, their gene content, and select potential candidate genes. Gene functions will be investigated using online databases and bioinformatic tools, while allelic diversity will be explored through isolate panels available in the team.

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.

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