Internship Proposal M2 Research – 2024-2025

Genetic architecture of resistance to Septoria tritici blotch in traditional Tunisian durum wheat landraces.

Context.

Durum wheat (*Triticum turgidum* L. subsp. *durum*) is an important crop worldwide, with the Mediterranean region being the largest production area and the largest consumer of durum wheat (Martínez-Moreno *et al.*, 2020). This traditional crop is mainly used for the production of pasta, couscous, semolina products and bread, which are included in most dishes from the Mediterranean countries. Productivity of durum wheat is highly affected by abiotic and biotic stresses. Septoria tritici blotch (STB) is one of the most devastating disease affecting durum wheat. This fungal disease caused by the ascomycete *Zymoseptoria tritici* is responsible of high yield losses when climatic conditions are favorable. *Z. tritici* has a mixed reproduction system and its populations are highly genetically diversified, conferring to this fungus a great potential to adapt and overcome host resistances. Previous studies identified at least 21 *Stb* major resistance genes and 167 genome regions carrying quantitative trait loci (QTL) or meta-QTL in bread wheat (Brown *et al.*, 2015). Despite the economic importance of durum wheat and the high devastating level of STB on this crop, only few studies have focused on the identification of resistance sources and on the genetic mapping of these resistances. Therefore, pursuing the investigations on the complex genetic architecture of resistance to STB in durum wheat is essential to breed for more resistant varieties and propose efficient deployment strategies of these resistances.

Research project.

Landraces are often considered as interesting sources of resistance genes against diseases as they are highly genetically diversified and locally adapted to their environment (Ouaja *et al.*, 2020). In Tunisia, durum wheat is an important staple crop where traditionally cultivated landraces coexist with the extensive culture of modern varieties. This configuration makes this study area particularly relevant for investigating in a complementary way all the determinants of adaptation of pathogens to their hosts and host resistances. STB exerts a strong disease pressure on durum wheat cultivation in Tunisia. A recent study reported that Tunisian durum wheat landraces were particularly efficient in stopping STB epidemics in farmer's fields (Ben Krima *et al.*, 2020), suggesting that not only the presence of particular resistance genes but also the genetic architecture of resistances within a landrace participate to its success in limiting the disease. Genome-wide association study (GWAS) is a powerful and high-resolution approach to study the genetic architecture of complex traits, such as STB resistance. We will use GWAS to unravel the genetic basis and genetic architecture of resistance to STB within three Tunisian durum wheat landraces. Revealing the number of resistance genes, their effects and their distribution in the bosom of these landraces, successful at stopping STB epidemics, will also allow proposing new scenarios for the efficient deployment of resistance genes in elite varieties and varietal mixtures.

Scientific approach.

The student will conduct a GWAS analysis to reveal the genetic architecture of resistance to STB within three Tunisia durum wheat landraces, i.e. Mahmoudi, Chili and Roussia. The different steps of the analysis comprise:

1. Pathology assays under controlled conditions to determine the level of resistance to STB of lines issued from the three durum wheat landraces;
2. Prepare seed samples to genotype two populations on a SNP array (TaBW35K at GENTYANE, INRAE) and prepare the SNP matrices for genetic analyses;
3. Run GWAS analyses with the GAPIT tool to detect the resistance genes and determine the genetic architecture of resistance to Z. tritici in the three landraces;

Rather as a perspective of the internship:

4. Evaluate the impact of the identified genetic architectures on STB epidemics with the demogenetic model implemented in the R package landsepi (Rimbaud *et al.*, 2018).

Keywords: phytopathology, fungal genomics, quantitative genetics, host adaptation.

Ben Krima S, Slim A, *et al.* (2020). Life story of Tunisian durum wheat landraces revealed by their genetic and phenotypic diversity. *bioRxiv*, 10.1101/2020.08.14.251157.

Brown JKM, Chartrain L, *et al.* (2015). Genetics of resistance to *Zymoseptoria tritici* and applications to wheat breeding. *Fungal Genet Biol* 79: 33-41.

Martínez-Moreno F, Solís I, *et al.* (2020). Durum wheat in the Mediterranean Rim: historical evolution and genetic resources. *Genet Resour Crop Evol* 67(3).

Ouaja M, Aouini L, *et al.* (2020). Identification of valuable sources of resistance to *Zymoseptoria tritici* in the Tunisian durum wheat landraces. *Eur J Plant Pathol* 156: 647–661.

Rimbaud L, Papaïx J, *et al.* (2018). Mosaics, mixtures, rotations or pyramiding: What is the optimal strategy to deploy major gene resistance? *Evol Appl* 11:1791–1810.

Presentation of the Research Unit.

The Research Unit INRAE BIOGER (Biology and Risk Management in Agriculture) is a leading French research center focusing on fungal diseases in major crop plants such as wheat, rapeseed, and grapevines. BIOGER employs multidisciplinary approaches spanning from epidemiology to molecular biology and genomics, and operates across multiple scales, from the gene level to landscape analysis. Our research models encompass pathogenic agents responsible for economically significant fungal diseases, including wheat rusts (*Puccinia striiformis* and *Puccinia triticina*), blackleg of rapeseed (*Leptosphaeria maculans*), septoria leaf blotch of wheat (*Zymoseptoria tritici*), and gray mold (*Botrytis cinerea* - affecting grapevines and various other plants). Our overarching goal is to address societal expectations for sustainable and environmentally friendly strategies in the fight against fungal diseases in major crop plants, and to manage risks associated with the dissemination and adaptive potential of phytopathogenic fungi.

Candidate profile.

The ideal candidate for the internship should have knowledge in one or more of the following areas: genomics, quantitative genetics, plant biology, mycology, or phytopathology. Precision and organization will be crucial for the student to effectively analyse the extensive genomic and genetic datasets at his/her disposal. Willingness to participate in quantitative phenotyping of plant-pathogen interactions is essential. The results obtained during the internship will be presented to the hosting unit.

Stipend: 669,90 €/month

Location: INRAE UR BIOGER, Univ. Paris-Saclay, 22 Place de l'Agronomie, 91120 Palaiseau –FR

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