ENGLISH VERSION

Master 2‘s internship - 6 Months in 2025 at INRAE GAFL

Title - Construction of a High-Density Genetic Map, QTL Identification, and Candidate Genes for Multiple Disease Resistance in *Capsicum annuum* L.

Laboratory – INRAE, GAFL, 67 Allée des Chênes, 84140 Montfavet, France. https://eng-gafl.paca.hub.inrae.fr/

Supervisors – Sonia Elbelt and Véronique Lefebvre

Keywords – genetic map, selective genotyping, QTL, candidate genes, disease resistance, multi-resistance, *Capsicum annuum* L., oomycete, ascomycete, virus

Project Overview – Reducing pesticide use in crop systems relies heavily on cultivating disease-resistant plants, but traditional breeding to transfer resistance traits into new cultivars is a time-consuming process, especially when considering several pathogens. Moreover, many major resistance genes often become ineffective against evolved pathogen variants. By contrast, quantitative resistance—governed by multiple loci or QTLs (Quantitative Trait Loci)— has proved to offer generally more durable plant health.

Pepper (*Capsicum annuum* L.), cultivated worldwide, faces threats from a wide array of pests and pathogens. While several genetic maps and QTLs related to disease resistance in peppers have been published, recent advances in genotyping now enable the development of high-density genetic maps from larger progenies, facilitating the identification of a short list of candidate genes for quantitative resistance. This project aims to leverage these technological advancements to enhance breeding for multi-disease resistance in pepper.

Internship Objectives – The intern will work on developing a comprehensive genetic analysis pipeline, with the following core objectives:

1. Genomic Data Processing: Analyze ALLEGRO read data targeting 6,000 genomic regions, ensuring high-quality SNP matrix, with chosen filters, using a GAFL pipeline.
2. High-Density Genetic Map Construction: Generate a novel, higher-resolution map using SNP data from a 350-lines progeny, and perfom selective genotyping for phenotyping, with analyses conducted in R.
3. Disease Resistance Phenotyping: Evaluation of progeny selected for resistance to a specific pathogen.
4. Descriptive analysis of phenotypic data collected on the progeny towards three pathogens, and possibly additional agronomic traits, with R.
5. Statistical and QTL Analysis: Conduct detailed statistical analysis of phenotypic data, followed by QTL mapping to identify candidate resistance genes, in R.
6. Genomic Comparison: Synthesize findings on QTL distributions over the whole genome, compare results with previous maps and GWAS studies from the lab and the literature, identify clusters or loci associated with multi-disease resistance.

Throughout, the intern will align with INRAE’s open science policy, ensuring that data and code adhere to the FAIR principles (Findable, Accessible, Interoperable, and Reusable) and are stored in appropriate repositories.

Candidate Profile – A keen interest in plant genetics and data analysis, experience with statistics and R software, interest in scientific literature, a proactive approach, intellectual curiosity, a commitment to research excellence.

Experience acquired during the internship

- Proficiency in R and statistical analysis, with experience in Linux and bioinformatics tools
- Facilities in data management and FAIR practices
- Ability to understand scientific literature in English
- Scientific writing skills

Language spoken – French for daily interactions, English used as needed for non-French-speaking interns.

Internship allowance – approximately 600 euros per month

Application – Please send your CV and a cover letter to sonia.elbelt@inrae.fr AND veronique.lefebvre@inrae.fr

Literature

Barchi L., Lefebvre V., Sage-Palloix A.M., Lanteri S., Palloix A. **2009**. QTL analysis of plant development and fruit traits in pepper and performance of selective phenotyping. ***TAG Theoretical and Applied Genetics***, 118(6):1157-1171. DOI 10.1007/s00122-009-0970-0. ⟨hal-02661978⟩

Caranta, C., Palloix, A., Lefebvre, V., Daubèze, A.M. **1997**. QTLs for a component of partial resistance to cucumber mosaic virus in pepper: restriction of virus installation in host-cells. ***TAG Theoretical and Applied Genetics***, 94, 431-438. DOI 10.1007/s001220050433. ⟨hal-02684785⟩

Caranta, C., Pflieger, S., Lefebvre, V., Daubèze, A.M., Thabuis, A., Palloix, A. **2002**. QTLs involved in restriction of cucumber mosaic virus (CMV) long-distance movement in pepper. ***TAG Theoretical and Applied Genetics***, 104 (4), 586-591. DOI 10.1007/s001220100753. ⟨hal-02677230⟩

Lefebvre, V., Daubèze, A.M., Rouppe van der Voort, J., Peleman, J., Bardin, M., Palloix, A. **2003**. QTLs for resistance to powdery mildew in pepper under natural and artificial infections. ***TAG Theoretical and Applied Genetics***, 107, 661-666. DOI 10.1007/s00122-003-1307-z. ⟨hal-02681019⟩

Lefebvre, V., Pflieger, S., Thabuis, A., Caranta, C., Blattes, A., Chauvet, JC., Daubèze, A.M., Palloix, A. **2002**. Towards the saturation of the pepper linkage map by alignment of three intraspecific maps including known-function genes. ***Genome***, 45, 839-854. DOI 10.1139/G02-053. ⟨hal-02680049⟩

McLeod L, Barchi L, Tumino G, Tripodi P, Salinier J, Gros C, Boyaci HF, Ozalp R, Borovsky Y, Schafleitner R, Barchenger D, Finkers R, Brouwer M, Stein N, Rabanus-Wallace MT, Giuliano G, Voorrips R, Paran I, Lefebvre V. **2023**. Multi-environment association study highlights candidate genes for robust agronomic quantitative trait loci in a novel worldwide *Capsicum* core collection. ***Plant Journal***, 116(5):1508-1528. https://doi.org/10.1111/tpj.16425 ⟨hal-04185847⟩

Pflieger S, Lefebvre V, Causse M. **2001**. The candidate gene approach in plant genetics: a review. ***Molecular Breeding***, 7 (4), 275-291.

Thabuis, A., Palloix, A., Pflieger, S., Daubèze, A.M., Caranta, C., Lefebvre, V. **2003**. Comparative mapping of *Phytophthora* resistance loci in pepper germplasm: evidence for conserved resistance loci across *Solanaceae* and for a large genetic diversity. ***TAG Theoretical and Applied Genetics***, 106 (8), 1473-1485. DOI 10.1007/s00122-003-1206-3. ⟨hal-02681630⟩