ENGLISH VERSION

Engineering/Master 2's internship - 6 Months in 2026 at INRAE GAFL

Title - Constructing Connected High-Resolution Genetic Maps to Validate Genotype-Phenotype Links in Pepper (*Capsicum annuum* L.)

Host Laboratory – INRAE, GAFL (Génétique et Amélioration des Fruits et Légumes), 67 Allée des Chênes, 84140 Montfavet, France. https://eng-gafl.paca.hub.inrae.fr/

Supervisors – Véronique Lefebvre and Sonia Elbelt

Keywords – SNP calling, genetic map, QTL, candidate genes, disease resistance, agronomic traits, *Capsicum annuum*

Background – Reducing pesticide use in crop systems relies heavily on growing 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. Our current projects aim to leverage these technological advancements to enhance breeding for multi-disease resistance in pepper.

Internship Overview – A genotype–phenotype association identified in genome-wide association studies (GWAS) links specific genetic variants to observable traits in unrelated plant accessions. However, these statistical associations often require validation to confirm their causal relationships. Analysing biparental progenies enables such validation, as the controlled genetic background enhances the detection and strength of the observed effects.

Internship Objectives – The intern's goal will be to develop three connected high-resolution genetic maps based on large biparental pepper progenies, aligned with a common reference genome.

The intern will:
1- perform the SNP (single nucleotide polymorphism) calling from sequencing datasets of three pepper progenies and establish a catalogue of SNPs anchored to a common reference genome,
2- construct three high-resolution genetic maps anchored to each other's,
3- format historical phenotypic datasets according to FAIR (Findable, Accessible, Interoperable, Reusable) data principles,
4- format and store genotypic and phenotypic datasets into the Thaliadb database,
5- perform QTL (quantitative trait locus) and GWA (Genome Wide Association) studies,
6- establish an analytical pipeline that can be reused by the research team,
7- compare the QTL positions among the 3 genetic maps with the GWAS results (McLeod et al. 2023) to refine the SNP-phenotype links.

These results should provide a solid basis for validating genetic effect of SNPs on phenotypes, thereby facilitating more efficient pepper breeding.

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.

Main Activities – Bioinformatics, Mendelian and quantitative genetics, Data management, Application of FAIR principles, Data interpretation, Reporting.

Experience Acquired During the Internship – Proficiency in R and statistical analysis; Experience in Linux and bioinformatics tools; Facilities in FAIR Principles, data management and R script editing; Ability to understand scientific literature; Scientific writing and oral communication skills.

Language Spoken: French for daily interactions, English used as needed for non-French-speaking interns.

Internship Allowance: Approximately 600 € / month (gratification)

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Candidate Profile – A keen interest in plant genetics and management of large datasets; Solid understanding of statistical methods and data analysis; Experience in R programming and Linux; Interest in scientific literature, Problem-solving, Teamwork & communication; Proactive approach; Intellectual curiosity; Commitment to research excellence.

Application: Please send your CV and a cover letter to veronique.lefebvre@inrae.fr **AND** sonia.elbelt@inrae.fr, along with your grades from your M1 and M2 evaluations.

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Some references from the laboratory related to the subject

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⟩

Elbelt S., Lagnel J., Caromel B., David J., Hirsch J., Szadkowski E., Moury B., Caporalino C., Stein N., Giuliano G., Lefebvre V. 2019. A high-density genotyping strategy based on gene capture in pepper: perspectives for genome wide association study and genetic mapping, BG-P/10. ***17th Eucarpia Meeting on Genetics and Breeding of Capsicum and Eggplant***, 11-13 September 2019, Avignon (France). p.192-193. ⟨hal-02737663⟩

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. ***The Plant Journal***, 116(5):1508-1528. DOI 10.1111/tpj.16425. ⟨hal-04185847⟩

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⟩