M2 INTERNSHIP OFFER

TITLE: Toward multi-trait breeding of sweet cherry (*Prunus avium* L.): development and validation of molecular markers

CONTEXT: In perennial fruit species, **climate change** strongly affects many traits and can reduce productivity, further weakening sectors already under pressure from intense international competition. For **sweet cherry** (*P. avium* L.), rising winter temperatures hinder the proper accumulation of chilling requirements for dormant buds, while warmer spring conditions increase the risk of frost damage due to earlier flowering. In addition, heavy summer rainfall promotes fruit cracking. Consequently, climate change threatens the smooth progression of the tree annual cycle.

In this context, **genetic improvement** is a key lever. Various **quantitative genetics** approaches have identified genomic regions associated with variation in important breeding traits, such as **phenology** and **fruit quality**. However, this fundamental research knowledge now needs to be transformed into practical tools for breeders, particularly through marker-assisted selection (**MAS**) strategies.

OBJECTIVES AND EXPECTED RESULTS: The aim of the internship is to **develop and validate molecular markers** for **multi-trait** breeding in **sweet cherry** (*Prunus avium* L.).

The student will first prepare a **literature review** of quantitative genetics studies in sweet cherry that have identified loci associated with various agronomic traits of interest, such as phenology (chilling requirements, flowering date, maturity date, etc.), fruit quality (cracking tolerance, firmness, fruit weight, sugar and acidity content, etc.), and productivity. These studies include work carried out by the host team as well as by international collaborators. The loci reported in the literature may come from genome-wide association studies (GWAS) using genetic resources collections or from quantitative trait locus (QTL) detection in bi- or multi-parental populations.

Following this review, the student will **design molecular primers** for the identified loci. These sequences will be sent to a partner laboratory, BioGEVES, to perform Kompetitive Allele-Specific PCR (KASP, https://www.biosearchtech.com/how-does-kasp-work) on plant material dedicated for validation.

Once these new SNP genotyping data are obtained, the student will analyze them alongside phenotyping data, using **statistical tests** such as ANOVA for quantitative traits or χ^2 tests for binary traits. Phenotyping data will come from the varietal innovation program led by INRAE, under the supervision of José Quero-García, in close collaboration with the private partner CEP Innovation. They will also be complemented with data from the variety evaluation network coordinated by Ctifl.

Validating this marker set will enable the student to **propose marker-assisted selection (MAS) strategies** tailored to the parental lines involved in each cross and to the breeding objectives pursued, involving a variable number of traits.

MAIN TASKS ASSIGNED TO THE INTERN:

- Conduct a literature review to identify loci involved in the variation of multiple traits using quantitative genetics
- Design PCR primers for the development of molecular markers applicable to marker-assisted selection
- Analyze SNP genotyping data and multi-trait phenotyping data

PREREQUISITES:

- Final year of higher education (Master's level, equivalent to BAC + 5)
- Knowledge: Quantitative genetics, breeding methodology
- Practical skills: Molecular biology, data analysis/statistics in R
- Languages: French and English
- Driver's license: Not required
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COMPENSATION: According to the regulations in effect for 2026 (approximately €650/month)

REFERENCES:

- Quero-García, J., Letourmy, P., Campoy, J. A., Branchereau, C., Malchev, S., Barreneche, T., & Dirlewanger, E. (2021). Multi-year analyses on three populations reveal the first stable QTLs for tolerance to rain-induced fruit cracking in sweet cherry (Prunus avium L.). Horticulture Research, 8, 136.
- Branchereau, C., Quero-García, J., Zaracho-Echagüe, N. H., Lambelin, L., Fouché, M., Wenden, B., ... & Dirlewanger, E. (2022). New insights into flowering date in Prunus: fine mapping of a major QTL in sweet cherry. Horticulture research, 9, uhac042.
- Donkpegan, A. S., Bernard, A., Barreneche, T., Quero-García, J., Bonnet, H., Fouché, M., Le Dantec, L., Wenden, B., Dirlewanger, E. (2023). Genome-wide association mapping in a sweet cherry germplasm collection (Prunus avium L.) reveals candidate genes for fruit quality traits. Horticulture Research, 10(10), uhad191.
- Holušová, K., Čmejlová, J., Suran, P., Čmejla, R., Sedlák, J., Zelený, L., & Bartoš, J. (2023). High-resolution genome-wide association study of a large Czech collection of sweet cherry (Prunus avium L.) on fruit maturity and quality traits. Horticulture research, 10(1), uhac233.
- Mccord, P., Crump, W. W., Zhang, Z., & Peace, C. (2024). Improving fruit size in sweet cherry via association mapping and genomic prediction. Tree Genetics & Genomes, 20(5), 26.

KEYWORDS: multi-trait, breeding, MAS, SNP, sweet cherry

SUPERVISOR:

- Anthony BERNARD, Research Scientist
- Address: INRAE Nouvelle-Aquitaine-Bordeaux – UMR 1332 Biologie du Fruit et Pathologie – PrADAm team (*Prunus*: Adaptation, Diversity, Breeding) – 71, avenue Edouard Bourlaux – CS 20032 – 33882 Villenave d'Ornon Cedex – France
- Website of BFP: https://bfp.bordeaux-aquitaine.hub.inrae.fr/
- Email: anthony.bernard@inrae.fr

CO-SUPERVISOR:

- José Quero-García, Sweet Cherry Breeding Program Leader
- Email: jose.quero-garcia@inrae.fr