

Search for genetic resistance to three viral species infecting melon

Location: Plant Pathology Unit (PV) and Genetics and Improvement of Fruit and Vegetables Unit (GAFL) at INRAE Avignon

Duration: 6 months

Dates: Start between February and March 2024

Supervisors: Cécile Desbiez (PV) and Lucie Tamisier (GAFL)

Project Leader: Nathalie Boissot (GAFL)

Context

Melon (*Cucumis melo* L., *Cucurbitaceae* family) is a crop of worldwide economic importance. Its production is constantly threatened by various pathogens, including viruses from different families such as *Watermelon mosaic virus* (WMV, *Potyvirus* genus, *Potyviridae* family), *Zucchini yellow mosaic virus* (ZYMV, *Potyvirus* genus, *Potyviridae* family), and *Tomato leaf curl New Delhi virus* (ToLCNDV, *Begomovirus* genus, *Geminiviridae* family). WMV and ZYMV are widespread in production areas (Desbiez et al., 2020), while ToLCNDV is a quarantine-emergent virus identified in France in 2020. Currently, these viruses are primarily controlled by the use of insecticides targeting vector insects. To reduce the use of chemical inputs, the use of genetically resistant plant varieties is considered an effective and environmentally friendly alternative.

However, few genetic resistances to these viruses are currently known. Two major-effect Quantitative Trait Loci (QTLs) controlling resistance to WMV and ToLCNDV, respectively, have been identified on chromosome 11 (Pérez-de-Castro et al., 2019; Sáez et al., 2017). Among the candidate genes, the VPS4 protein belonging to the Endosomal Sorting Complexes Required for Transport (ESCRT) complex has recently been described as a new sensitivity factor to WMV in melon (Agaoua et al., 2022). The Fn gene is also known to trigger necrosis formation in response to certain ZYMV strains (Desbiez et al., 2002).

Objectives

The objective of the internship is to identify new genomic regions controlling resistance to these viruses and/or confirm previously identified QTLs. The study of three viral species will determine if QTLs have a broad or specific spectrum of action, as previously demonstrated in cucumber (Monnot et al., 2022). The student will phenotype 200 melon accessions to assess their resistance levels to WMV and ToLCNDV, while trials for ZYMV will be conducted by a private partner. The evolution of symptoms over time will be monitored. Since the 200 melon accessions have been previously genotyped, Genome-Wide Association Studies (GWAS) will be conducted to identify resistance QTLs.

Among the already identified resistance QTLs, some are located in gene-rich regions of NLR (nucleotide-binding domain leucine-rich repeat), known to confer resistance to pathogens and pests. Our team is currently sequencing genomic regions containing NLR in melon. If QTLs located in these regions are identified during the internship, NLR sequencing will be used to refine the list of candidate genes underlying the QTLs.

Finally, other phenotypes of interest for resistance, such as the viral load, will be studied in the team. The viral load of 180 melon genotypes inoculated with different WMV strains is planned to be measured. As part of the internship, the student will assist in developing a precise, high-throughput, and unbiased method for measuring viral load. Several methods will be compared, including RT-qPCR, high-throughput sequencing, and dot-blot hybridization.

Tasks

- Setting up phenotyping trials for 200 melon accessions in greenhouses (WMV) and S3 confinement greenhouses (ToLCNDV).
- Phenotyping melon accessions for their resistance levels to WMV and ToLCNDV by monitoring symptoms over time.
- Statistical analysis (GWAS for the three viruses).
- Contribution to the development of a high-throughput phenotyping method to quantify viral load in melon.

Profile

- M2 level in plant biology.
- Interest in plant health and molecular biology.
- Knowledge of Genome-Wide Association Studies.
- Management of experiments with large plant populations.
- Experimental rigor and organizational skills.
- Ability to work as part of a team.

Application

Send a resume and a cover letter to cecile.desbiez@inrae.fr and lucie.tamisier@inrae.fr

References

- Agaoua, A., Rittener, V., Troadec, C., Desbiez, C., Bendahmane, A., Moquet, F., and Dogimont, C.** (2022). A single substitution in Vacuolar protein sorting 4 is responsible for resistance to Watermelon mosaic virus in melon. *J. Exp. Bot.* **73**: 4008–4021.
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- Desbiez, C., Wipf-Scheibel, C., Millot, P., Berthier, K., Girardot, G., Gognalons, P., Hirsch, J., Moury, B., Nozeran, K., and Piry, S.** (2020). Distribution and evolution of the major viruses infecting cucurbitaceous and solanaceous crops in the French Mediterranean area. *Virus Res.* **286**: 198042.

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- Pérez-de-Castro, A., Esteras, C., Alfaro-Fernández, A., Daròs, J.-A., Monforte, A.J., Picó, B., and Gómez-Guillamón, M.L.** (2019). Fine mapping of wmv 1551, a resistance gene to Watermelon mosaic virus in melon. *Mol. Breed.* **39**: 1–15.
- Sáez, C., Esteras, C., Martínez, C., Ferriol, M., Dhillon, N.P., López, C., and Picó, B.** (2017). Resistance to tomato leaf curl New Delhi virus in melon is controlled by a major QTL located in chromosome 11. *Plant Cell Rep.* **36**: 1571–1584.