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Flavie Cussonneau, Carole Constant, Schalk Van Heerden, Marc Bardin,
Benoît Moury, Véronique Lefebvre

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Genetic architecture of powdery mildew resistance in pepper and impact of genetic resistance factors on pathogen diversity

F. Cussonneau (1,3), C. Constant (3), S. Van Heerden (3), M. Bardin (2), B. Moury (2), **V. Lefebvre** (1)

(1) INRAE, GAFL, 84140 Montfavet, France
(2) Pathologie Végétale, INRAE, 84140 Montfavet, France
(3) SAKATA, Sakata Vegetables Europe SAS, Domaine de Sablas, Rue Jean Moulin, 30620 Uchaud

The ascomycete *Leveillula taurica* causes powdery mildew of pepper, resulting in yield losses of up to 40%. This obligate biotrophic fungus has a wide host range including different plant families such as *Solanaceae*, *Asteraceae* and *Cucurbitaceae*. Molecular diversity studies of this pathogen have revealed different clades distributed by host species [1]. On the host side, both monogenic and polygenic resistance to *L. taurica* have been described in pepper (*Capsicum spp.*). However, the identified resistances remain either ineffective under heavy infection or the underlying genetic determinants are insufficiently mapped for breeding. Therefore, we aim to (i) establish a catalogue of resistance loci to *L. taurica*, based on the diversity of *Capsicum annuum*, (ii) characterise the genetic and phenotypic diversity of *L. taurica* worldwide, and (iii) analyse the effect of pepper resistance loci to *L. taurica* on its diversity and that of other pathogens. The catalogue of pepper resistance loci will be based on linkage analysis in progenies and in two core collections by Genome Wide Association Studies. We will collect a large set of *L. taurica* isolates from more than fifteen sites worldwide and assess their aggressiveness on three pepper genotypes contrasted for resistance. In addition, description of *L. taurica* genetic diversity will rely on *de novo* sequencing that will allow building a new reference genome and deriving a SNP matrix in order to genotype the collected isolates. Finally, we will characterize population dynamics not only of *L. taurica*, but also of the oomycete *Phytophthora capsici* and the viruses CMV (*Cucumber mosaic virus*) and PVY (*Potato virus Y*) on a set of lines contrasted for alleles at the QTLs determining resistance to *L. taurica*.

[1] Khodaparast, S. A., Takamatsu, S., Harada, M., Abbasi, M., & Samadi, S. (2012). Additional rDNA ITS sequences and its phylogenetic consequences for the genus *Leveillula* with emphasis on conidium morphology. Mycological Progress, 11(3), 741–752. https://doi.org/10.1007/s11557-011-0785-7

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