



HAL
open science

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

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

► To cite this version:

Flavie Cussonneau, Carole Constant, Schalk Van Heerden, Marc Bardin, Benoît Moury, et al.. Genetic architecture of powdery mildew resistance in pepper and impact of genetic resistance factors on pathogen diversity. 13. Rencontres de Phytopathologie - Mycologie, Sep 2022, Aussois (France), France. hal-04133318

HAL Id: hal-04133318

<https://hal.inrae.fr/hal-04133318>

Submitted on 19 Jun 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Public Domain

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>

Keywords: *Leveillula taurica*, Powdery mildew, pepper, *Capsicum annuum*, resistance loci, aggressiveness, genetic diversity, epidemiology