EXPLOITATION OF THE KNOWLEDGE ON OOMYCETE EFFECTORS TO DRIVE THE DISCOVERY OF DURABLE DISEASE RESISTANCE TO DOWNY MILDEW IN SUNFLOWER

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ABSTRACT

Plasmopara halstedii is an obligate biotroph oomycete causing downy mildew disease on sunflower, *Helianthus annuus*, an economically important cultivated crop. Disease symptoms observed in fields, plant dwarfism, leaf bleaching, sporulation and production of infertile flowers, impair strongly seed yield. *P. halstedii* pathotypes are defined by their divergent virulence profiles in a set of sunflower differential hosts carrying different *Pl*resistance genes, not yet cloned. Number of pathotypes increased from 1 to 16 during the last 25 years in France, concomitantly with the breakdown of *Pl* resistance loci used in fields. Finding broad-spectrum *a priori* durable resistance against pathogens would open the doors to efficient, environmentally friendly and cost-effective disease control. In oomycetes, two classes of effectors are translocated into the host plant, RXLRs and CRNs, but oomycete avirulence genes described so far are RXLRs. Through high throughput genomic sequencing of 17 *P.halstedii*pathotype isolates, we selected by stringent *in silico* methods, 74 putative RXLR effectors. 33 show polymorphism with at least one pathotype whereas 41 are conserved in sequence among the 17 pathotypes. Analysing the pathotype effector polymorphism in regard to the content in *Pl* resistant genes of sunflower lines should help us to identify candidates for pathogen avirulence genes. Triggering of defense reactions (Hypersensitive Response) through their transient expression in sunflower lines carrying known resistance genes will be used to validate them. Subcellular localization experiments of selected candidate effectors fused to GFP should give hints to their function in the plant cell. In addition, polymorphic effectors will be used to design molecular markers for rapid pathotype identification. Thirty conserved effectors corresponding to highly expressed genes upon sunflower infection are suspected to be essential genes for the pathogen. They have been cloned and are tested by agroinfiltration on various resistance sources of *H. Annuus* and some of them induce plant cell death. Co-segregation of resistance with cell death activity caused by the effector will have to be tested on segregating populations. If true, these effectors should accelerate the identification, the functional characterization and the mapping of broad-spectrum sunflower resistances potentially sustainable.

Key Words : downy mildew, disease resistance, oomycete effectors