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## #157: Is Phy-P5 a major broad-spectrum resistance QTL conferring resistance to Phytophthora in Solanaceae?

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Blight caused by the pathogen *Phytophthora* spp. (Oomycete) is one of the most damaging diseases of Solanaceae crops. The deployment of resistant varieties is the most effective, economically and environmentally safe control of *Phytophthora*. Contrary to monogenic resistances, polygenic resistances generally confer a durable control of disease severity. Despite the potential importance of quantitative disease resistances, little is known about their molecular bases in plants and the mechanisms of action of the genes controlling them.

A major effect QTL that confers resistance towards *P. capsici* was detected on pepper chromosome P5 from 5 partially resistant parents and with 8 isolates of *P. capsici*. We are not able to determine whether or not the QTL was the same in all populations because of the lack of common markers between published maps. Moreover, comparative mapping indicated colinearities between this pepper QTL and resistance QTLs to *P. infestans* on potato chromosome IV and on tomato chromosome T4.

We aim to anchor the pepper genomic region harbouring the QTL Phy-P5 within the published pepper maps and with the other members of the Solanaceae family in order to determine whether Phy-P5 is a broad-spectrum resistance QTL to *Phytophthora* and to identify candidate genes.

We developed markers in the QTL interval, which allowed the fine anchorage of 4 published pepper genetic maps. Those results showed that Phy-P5 is active against 3 *P. capsici* isolates, in 4 genetic backgrounds. Furthermore, we generated bridge markers linking the tomato, potato and pepper genetic maps. The putative colinear region of Phy-P5 was restricted to 20 cM in tomato and potato, in a region where major *Phytophthora* R genes and QTLs were mapped. Those results provide additional arguments in favour of the conservation of resistance QTLs to *Phytophthora* spp. in these Solanaceae species and made a step forward in the research of functional orthologs underlying the colinear QTLs.