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## **AvrLm10A/AvrLm10B a part of a multigene family of cooperating effectors largely conserved in Dothideomycetes and Sordariomycetes.**

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With only a few exceptions, fungal effectors (corresponding to small secreted proteins) have long been considered as species- or even isolate-specific. With the increasing availability of high-quality fungal genomes and annotations, including improved strategies to predict fungal effector repertoires and decipher their 3-D structure, trans-species or trans-genera families of effectors are unveiled.

Two avirulence effectors of *Leptosphaeria maculans*, the fungus responsible for stem canker of oilseed rape, *AvrLm10A* and *AvrLm10B*, are members of such a large family of effectors. *AvrLm10A* and *AvrLm10B* are two neighbor genes organized in opposite transcriptional orientation. Both are necessary to trigger recognition by the *Rlm10* resistance gene, and the two corresponding proteins physically interact *in vitro* and *in planta* [1]. Sequence searches within the *L. maculans* genome indicated that *AvrLm10A/AvrLm10B* belong to a multigene family comprising five pairs of genes with a similar tail-to-tail organization, a very unusual feature for this species in which RIP is very active to prevent duplications of genes. A search for homologues in fungal protein databases found that *AvrLm10A* was conserved in more than 30 Dothideomycetes and Sordariomycetes plant pathogenic fungi, with other cases of variable copy numbers within a genome. One of the *AvrLm10A* homologues, SIX5, is an avirulence effector from *Fusarium oxysporum* f.sp. *lycopersici* functioning as a cooperating pair with *Avr2* [2]. Compared to *AvrLm10A*, less *AvrLm10B* homologues were identified and we found that *AvrLm10A* homologues could, in fact, be associated with at least five distinct effector families, suggesting an ability of *AvrLm10A* / SIX5 to cooperate with several effectors. A detailed characterization of the *AvrLm10* family was performed in *L. maculans*, including transcriptomic and functional analyses. The two genes in a pair always had the same expression pattern and, depending on the pair of genes, two expression profiles were distinguished, associated with the biotrophic colonization of cotyledons or petioles and stems. One of the five pairs had no detectable expression and could correspond to pseudogenes. Of the three pairs functionally investigated, two had the ability to physically interact. Since SIX5 and *Avr2* also physically interact, these data point to a general role of the *AvrLm10A* protein as a transporter able to interact with a limited number of effector families whose encoding gene is co-regulated with the neighboring *AvrLm10A* homologue.

[1] Petit-Houdenot, Y., Degrave, A., Meyer, M., Blaise, F., Ollivier, B., Marais, C. L. *et al.* 2019. A two genes-for-one gene interaction between *Leptosphaeria maculans* and *Brassica napus*. *New Phytologist*, 223, 397-411.

[2] Ma L, Houterman PM, Gawehns F, Cao L, Sillo F, Richter H, Clavijo-Ortiz MJ, Schmidt SM, Boeren S, Vervoort J *et al.* 2015. The AVR2-SIX5 gene pair is required to activate I-2-mediated immunity in tomato. *New Phytologist* 208: 507-518.

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