

IDENTIFICATION AND *IN PLANTA* FUNCTIONAL ANALYSES OF RxLR EFFECTORS OF THE OOMYCETE *PHYTOPHTHORA PARASITICA*

INTRODUCTION

The oomycete genus *Phytophthora* represents plant destroyers that cause devastating diseases on agricultural crops and plants in diverse ecosystems (Erwin & Ribeiro, 1996). To establish infection, adapted *Phytophthora* species employ diverse pathogenicity mechanisms including delivery of the RxLR class of cytoplasmic effectors (Jones & Dangl, 2006). The cytoplasm and or its subcellular compartments are exploited for a permissive environment by the RxLR effectors to induce modulations to various essential physiological processes including suppression of plant immunity for pathogen success (Jones & Dangl, 2006, Whisson et al., 2007).

Plants have in turn evolved resistant (R) genes to antagonise effector-mediated modulation of cell function and prevent disease establishment. Currently the most efficient, cost and environmentally friendly management of *Phytophthora* diseases is the use of resistant germplasm that host cognate R-genes (Dangl et al., 2013, Zhang & Coaker, 2017). However, R-gene resistance is undermined by their relationship with the RxLR effectors, perceived as an ongoing co-evolutionary arms race (Jones & Dangl, 2006, Boller & He, 2009). The RxLR effectors seem to have an upper hand in this race, mirrored by the remarkable records of devastation *Phytophthora* disease as they continue to pose a threat to food security and ecological balance in diverse plant communities (Erwin & Ribeiro, 1996, Kamoun et al., 2015). To advance a sound understanding of RxLR effector biology and their role in *Phytophthora* pathogenesis, this study employs a bioinformatics analytical pipeline developed around the modular structure of RxLR effectors to identify putative RxLR effector proteins from *Phytophthora parasitica*. Further, the identified RxLR effectors will be functionally characterised *in planta*.

Phytophthora parasitica has been highlighted as a model *Phytophthora* organism for study of *Phytophthora*-plant interactions (Meng et al., 2014). Further, the pathogen has a broad agro-economic and ecological significance (Kamoun et al., 2015, Panabieres et al., 2016) making it a suitable model for enquiry of *Phytophthora* pathogenesis.

REFERENCES

1. Boller T, He SY, 2009. Innate immunity in plants: an arms race between pattern recognition receptors in plants and effectors in microbial pathogens. *Science* **324**, 742-4.
2. Dangl JL, Horvath DM, Staskawicz BJ, 2013. Pivoting the plant immune system from dissection to deployment. *Science* **341**, 746-51.
3. Erwin DC, Ribeiro OK, 1996. *Phytophthora diseases worldwide*. American Phytopathological Society (APS Press).
4. Jones JD, Dangl JL, 2006. The plant immune system. *nature* **444**, 323.
5. Kamoun S, Furzer O, Jones JD, *et al.*, 2015. The Top 10 oomycete pathogens in molecular plant pathology. *Molecular plant pathology* **16**, 413-34.
6. Meng Y, Zhang Q, Ding W, Shan W, 2014. *Phytophthora parasitica*: a model oomycete plant pathogen. *Mycology* **5**, 43-51.
7. Panabieres F, Ali GS, Allagui MB, *et al.*, 2016. *Phytophthora nicotianae* diseases worldwide: new knowledge of a long-recognised pathogen. *Phytopathologia Mediterranea* **55**, 20-40.
8. Whisson SC, Boevink PC, Moleleki L, *et al.*, 2007. A translocation signal for delivery of oomycete effector proteins into host plant cells. *nature* **450**, 115.
9. Zhang M, Coaker G, 2017. Harnessing effector-triggered immunity for durable disease resistance. *Phytopathology* **107**, 912-9.