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Effector diversity and gene innovations in *Phytophthora*

Francine Govers

Laboratory of Phytopathology, Wageningen University, Wageningen, The Netherlands

francine.govrs@wur.nl

Phytophthora literally means plant destroyer, a name coined by the founding father of mycology, Anton de Bary, when he proved that a microorganism was the causal agent of the devastating potato late blight disease. The genus *Phytophthora* belongs to the oomycetes, a distinct lineage of fungus-like eukaryotes within the supergroup Chromalveolates and related to brown algae and diatoms. The ~ 240 Mb genome of *Phytophthora infestans* is the largest and most complex in the chromalveolate lineage and its sequence reveals features that illuminate its success as a pathogen. Comparison to other *Phytophthora* genomes showed rapid turnover and massive expansion of specific families encoding effector proteins, including the host-translocated effectors sharing an RXLR motif. These fast-evolving effector genes are localized to highly dynamic and expanded regions of the *P. infestans* genome and may attribute to the rapid and successful adaptability of this pathogen to host plants. Other hallmarks reminiscent of a dynamic genome are copy number variations and gene innovations, the latter resulting in proteins with oomycete-specific domain combinations several of which probably have a function in signal transduction.