ILVO LM-UGent GHENT UNIVERSITY FACULTY OF SCIENCES

PhD defense
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Taxonomic revision of *Xanthomonas axonopodis* pv. *dieffenbachiae* strains and pathogenicity on Araceae plants

Wednesday, May 17, 2017 at 16h00
Virginie Lovelinggebouw (VAC Gent) - Koningin Maria Hendrikaplein 70-9000 Gent
Room Jan Hyoens 21.03

Promoters: Em. Prof. Dr. Paul De Vos
Dr. Martine Maes
Prof. Dr. Anne Willems

You are cordially invited to the reception following the defense
Please confirm your presence before May 10
By e-mail (elena.constantin@ilvo.vlaanderen.be) or mobile phone (+32 489697865)

Plants of the Araceae family are important in our region and generally in Europe as ornamentals, best known and of high economic value is Anthurium. In the tropics, several, such as cocoyam, represent important basic food crops. Production of Araceae is threatened by a leaf spot disease caused by *Xanthomonas axonopodis* pv. *dieffenbachiae* (Xad). Due to its virulence and broad plant host range within the Araceae, this pathogen is regulated and figures on the A2 quarantine list of the European and Mediterranean Plant Protection Organization (EPPO). This means that this harmful organism has a limited presence but that further spread has to be prevented. In order to organize efficient control it is essential to know the pathogen and its behavior on the plants, and to reliably detect and identify it. As this was problematic for these *Xanthomonas* bacteria pathogenic to Araceae, this PhD study was initiated.

The study resulted in a taxonomic revision of the *X. axonopodis* species complex. Remarkably, the pathogens on Araceae were proven not to belong to this species *X. axonopodis*, but are a heterogenic group of strains that belong to three other *Xanthomonas* species: *X. citri*, *X. euvesicatoria* en *X. phaseoli*.

It was then important to study and compare the pathogenic potential of these Xad strains belonging to these three different *Xanthomonas* species. A range of Araceae species were infected with strains of the three different *Xanthomonas* species. We could conclude that the strains belonging to *X. citri* and *X. phaseoli* are indeed pathogenic to Araceae, whereas *X. euvesicatoria* strains are only weakly and doubtful pathogenic to these plants. The *X. citri* strains cause leaf spots, but the *X. phaseoli* strains are relatively more virulent, they are able to spread and destroy the whole plant system. Based on all these results, new pathovars were named.

Total genome sequences have been generated from four representative strains in the three different *Xanthomonas* species. Their new taxonomic positions were confirmed. Furthermore, all four strains were shown to have the pathogenicity-related gene content as expected for pathogenic xanthomonads. It suggests that the *X. euvesicatoria* strains are also pathogenic, but probably on different plant hosts, while on Araceae their pathogenicity is not well expressed or suppressed.

The results from this study clearly showed that this important group of pathogenic xanthomonads for Araceae is not to be considered as a single biological unit, and hence should not to be regulated and diagnosed as such. This study provides the basis to redirect phytosanitary control measures, targeting the following 'pathovars' for Araceae, *Xanthomonas phaseoli* pv. *dieffenbachiae* comb. nov., *X. phaseoli* pv. *syngonii* comb. nov., en *X. citri* pv. *aracearum* comb. nov.

Main results of this PhD research were presented in two scientific publications.