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Deciphering the genetic determinants of resistance/tolerance to *Phytophthora citrophthora* to develop genomic selection in citrus

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In a context of adaptation to global change, the INRAE-Cirad « Citrus breeding program » aims to improve the ability of citrus crops to adapt to biotic constraints. Among them, the pressure of soil-borne pathogens such as *Phytophthora* spp. affects citrus growth and health, causing significant quality and yield losses (up to 30%) and leading to damping-off, root rot and/or trunk gum diseases. Among these oomycetes, *P. citrophthora* (R. E. Smith et E. H. Smith) Leonian is one of the most destructive and predominant in regions such as the Mediterranean basin. It is known that multiple defence mechanisms are involved in the immune response of citrus against *Phytophthora* spp., and therefore the inheritance of resistance/tolerance is complex. This is the reason why we are developing a pangenomic association genetics project (PAN-GWAS) on a core collection of 250 accessions, which mobilises the genetic and phenotypic diversity of the genus *Citrus* conserved in the biological resource centre (BRC Citrus ISO 9001) of the INRAE centre in Corsica. The aim is to identify allelic variants, candidate genes and genotypes displaying defence mechanisms against *P. citrophthora*. For this purpose, roots of cuttings inoculated with spores are quantitatively phenotyped to assess i) the symptoms of root and aerial infection, ii) the impact of the pathogen on plant physiology and iii) the production of metabolites involved in biotic stress responses (especially antioxidant system). The identified QTLs will serve as the basis for the development of marker-assisted selection (MAS). Resistant/tolerant accessions will be incorporated into the breeding program to introgress multiple genes of interest into the same variety. This project is part of a broader strategy to implement genomic selection (GS) in our breeding program. Thus, both the identified QTLs and the genotyping and phenotyping data will be used in the development of predictive models to speed up breeding for resistance/tolerance to *P. citrophthora*.