ROGER

Project title: Genetic and genomic of the Rose resistance against Black Spot Disease

Acronym: RoGeR (Rose Genomic Resistance)

Project duration: 24 months - Start date: 01/09/2018   End date: 31/08/2020

Key-words: Rosa, Diplocarpon rosae, resistance genes, connected populations, association genetics, transcriptomic and comparative genomics

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Summary:

Context
In the ornamental sector, the rose is the favourite flower of the consumers (local authorities and private individuals). In 2016, the French market of garden-roses contributed €57 million for a total of 4 millions of units sold essentially as grafted rose in pot or bare-root stock. To dump up the garden rose market, rose professionals created a "red label" that promotes roses with more vigour, floribundity and disease resistance. As the same time, use of pesticides has been forbidden in public gardens in France since the beginning of 2017 and will be âlso forbidden in 2019 for private gardens (J. Labbé and energy transition laws). Therefore, there has been a strong trend in demand by consumers to have resistant garden roses, and as a result, the development by breeders for roses that have a high level of resistance.
Black spot is the most important disease affecting rose aesthetics and was caused by Diplocarpon rosae (Marssonina rosae anamorph), an hemibiotrophic ascomycete fungus. Debener and Byrne (2014) estimated that there was only 7% of Rose with sustainable resistance into the US market.
Rose breeding is a long process (10 years on average) and requires the knowledge of sources of resistance. Several· major genes and QTLs were located on genetic maps by research teams in Germany (University of Hannover) and in France (IRHS-GDO, Angers) (Malek & Debener, 1998; Marolleau et al, 2016; Shupert, 2005; Soufflet-Freslon et al, 2017; Whitaker et al, 2010; Whitaker & Hokanson, 2009).

Goals
The aim of this project is to develop complementary approaches (genetics, genomics, transcriptomics and comparative genomics) to characterise the genes involved in the rose resistance to black spot disease. The long-term objective is to develop new diagnostic markers to hasten the breeding process.

Methodology
For these objectives, we will take advantage of the different resources developed by the GDO team (interconnected progenies, reference genome sequence, and characterized collection of old garden roses, artificial inoculation protocol). Thanks to these resources, we will develop genetic (interconnected progeny to study QTL effects in different genetic backgrounds, candidate-gene association mapping), transcriptomic (comparison of transcripts during the interaction in susceptible and non-susceptible conditions) and comparative genomics (comparison of two pathosystems in the Rosaceae family). We will look for co-localization between genes detected in genetic approach (QTL), annotated genes and differentially-expressed genes.