ROZREZIST

Project title: Genetics and genomics of rose resistance to black spot disease

Acronym: RozResist

Project duration: 36 months – Start date: 01/10/2017 End date: 30/09/2020

Key-words: *Rosa*, *Diplocarpon rosae*, resistance genes, connected populations, association mapping, transcriptome, diversity

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Summary:

Black spot (caused by the fungal pathogen *Diplocarpon rosae*) is the most severe disease of roses in the outdoor landscape. Most cultivars are susceptible to this disease and its control requires many fungicide treatments. Pathogen attacks have a serious impact on aesthetic quality. It is now crucial to reduce such use of pesticides in ornamental cultures for production cost decrease and also for environmental and consumer health reasons. In this way, use of pesticides will be forbidden in public and private gardens in France in 2017 and 2019, respectively (J. Labbé law). Growing genetically resistant rose cultivars should provide an alternative to chemical control of the disease. Genetic studies have revealed both qualitative resistance conditioned by dominant genes and quantitative (partial) resistance conditioned by multiple genes. In different pathosystems, qualitative resistance is known to be race specific and compromised quickly through pathogen mutation or migration while quantitative resistance is assumed to be race non-specific and could be more durable. A few rose resistance QTL to black spot were identified in only one rose genotype. Here we propose to investigate both genetic and genomic bases of disease resistance. First, we will identify QTL, effective in different genetic backgrounds and against a range of pathogen isolates. Multiparental connected populations will be scored for black spot resistance after both artificial inoculations and natural infections. This project aims also to characterize the candidate-genes underlying resistance QTL that are identified, thanks to positional and transcriptomic approaches. Finally, we will try to validate by association mapping the best candidate-genes previously identified. This will allow to evaluate the efficiency of resistance genes in wider genetic background and to identify different favorable alleles for a same locus. In the end, this thesis aims to supply some sources of genetic resistance that will be used for rose breeding.