

CARO

Project title: Deciphering the genetic determinism of ornamental traits in rose by complementary approaches (GWAS and linkage-based mapping) as a case to develop genetic markers for selection.

Acronym: **CARO**

Project duration: 19 months - Start date: 01/09/2020 End date: 31/03/2022

Key-words: GWAS, QTLs, Number of petals

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Total cost of the project : 211 300 €

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Summary:

Rose is one of the most essential ornamental plants worldwide. Since a few years, important efforts of the rose research community have led to the development of new knowledge and tools for rose breeding. Thus, several studies have focused on traits of interest including number of petals, disease resistance, fragrance, date of flowering, flower color, flower development and vernalization response and allowed the characterization of the genetic determinism of these characters, largely using progenies produced by crossing (F1 populations). These populations enable precise mapping, but only for those traits that are in contrast between the two selected parents, and only for those genes in which the parents differ, so this produces very limited information on interaction among genes underlying the trait. The recent completion of the rose genome sequence and a microarray of SNP markers make it possible to envisage new methods of analysis to locate precisely the genes involved in the traits of interest. Notably, genome-wide association studies promise to produce information of several genes involved and their interaction in different genetic backgrounds, which is essential information for DNA-informed breeding strategies. Further improvements in efficiency may come from combining information from various populations and panels.

In this project, we propose to study a specific trait (the number of petals) as a proof of concept of meta-analysis of several mapping methods.

The number of petals is controlled by a major gene which was recently identified and controlled single vs double petals and at least, three QTLs. The aim of this project is to identify markers of these QTLs to predict the number of petals. The concerned methods are (i) Genome-wide association study (GWAS) that will be carried out on a large collection of rose (including modern versus old/botanical roses and garden versus cut flower roses) and (ii) linkage-based mapping for which several data on the genetic determinism are already available. Combining these methods will help to make a fine mapping of the QTLs and define molecular markers to predict the number of petals in rose for marker assisted selection.