PHY-ROSE

Project title: Phylogenomics of the genus Rosa - polyploidy and hybridization as diversification forces

Project duration: 36 months – Start date: 1/10/2016 End date: 31/12/2019

Key-words: Phylogeny, Complete Genome, Rosa

Coordinator: FOUCHER Fabrice, IRHS / GDO, fabrice.foucher@angers.inra.fr

Partner: MALECOT Valéry, IRHS / GDO, valery.malecot@agrocampus-ouest.fr

Total cost of the project: 107 770 k€ (Do not include salaries others than those of the people hired for the project)
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Summary:

The rose bush is the most economically important ornamental plant and the model plant for many studies about ornamental traits (flowering, fragrance, disease resistance). The genus *Rosa*, the taxonomic entity to which rose bush is assigned has a complex evolutionary history with interspecific hybridization events and polyploidizations. Little information about these events is presently available, while evolutionary history are mainly based on chloroplastic molecular markers. Recently, as part of an international consortium, co-coordinated by the GDO team, the first version of the genome sequence of rose cultivar (*Rosa chinensis* 'Old Blush') has been obtained. Moreover, as this cultivar is a vegetatively propagated hybrid between *Rosa chinensis* and *Rosa gigantea,* the sequence of 'Old Blush' provides an unrecorded access to gene variation between two poorly related species. **The objective of this project is to understand the evolutionary history of the genus *Rosa***, and especially to focus on the impact of hybridization and polyploidy in the history of the genus, and to benefit from the complete genome to identify the best molecular markers to resolve such phylogeny. From comparison of molecular sequences we will select the best suitable nuclear low copy genes to reconstruct the phylogeny of the genus. Test of these markers will exploit a set of eight sequences acquired through GenoRose project. Then the markers showing the higher sequence variations will by amplified on a sample representing 100 species of *Rosa*, using fluidigmic amplification of amplicons approach. The resulting sequences will be analysed using various phylogenetic tree-based and network-based methods, with a structured methodology regarding the sample (from diploid non hybrid taxa to polyploydes). This project will help to understand the relationships between the different species and to better predict the success of interspecific crosses (introgression of new sources of resistance from wild gene pools still underused), it will also allow looking of evolutionary changes in a set of ornamental characters.