Towards the rose genome sequence and its use in research and breeding

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Résumé en anglais	Rose is one of the most economically important ornamental crops worldwide. Rosa sp. can become a model for woody ornamentals. Its genome size is relatively small (560 Mb), its genetic history with ploïdy events is well documented, and rose has a short life for a woody plant. Furthermore, different tools are available, including transcriptomic tools, genetic maps and genetic transformation protocols. Rose represents an original model for studying some ornamental traits that cannot be addressed in other model plant species such as Arabidopsis. Some of these traits, such recurrent blooming, flower morphogenesis or scent production and emission, are of economic interest. Different groups involved in rose genetics and genomics gathered to form the 'Rose Genome Sequence Initiative'. Our objective is to obtain a high quality rose genome sequence of the diploid R. chinensis 'Old Blush'. One important issue is the high level of heterozygosity of roses. To tackle this issue, different strategies are proposed: production of a haploid and development a high density genetic map to anchor the genome. This genetic map will be developed from a cross between 'Old Blush' and R. wichurana. The genotype R. chinensis 'Old Blush' will be sequenced using NGS technologies. The data will be assembled and arranged using the high-density map. In order to increase ESTs and to facilitate genome annotation, we have recently produced ESTs from various tissues of 'Old Blush' under different conditions. Digital expression (RNA Seq) was obtained from the different tissues and data are available on the following web site (https://iant.toulouse.inra.fr/plants/rosa/FATAL/). The rose genome sequence will be a great step to help identifying the molecular basis of ornamental traits and also to study genetic diversity and genome evolution in the genus Rosa and in the Rosaceae family.
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