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► **To cite this version:**

Jérémy Just, Mohammed Bendahmane. Rosa spp.. Trends in Genetics, 2020, 36 (2), pp.146-147.  
10.1016/j.tig.2019.11.002 . hal-03153174

**HAL Id: hal-03153174**

**<https://hal.inrae.fr/hal-03153174>**

Submitted on 21 Jul 2022

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## ***Rosa sp***

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Roses hold high cultural and economic values and have been cultivated by humans since antiquity as ornamental plants and for therapeutic and cosmetic use. *Rosa* genus comprises about 200 species<sup>1</sup>, among them 8 to 20 have contributed to the creation of nearly 35 000 hybrid rose cultivars<sup>2</sup>, exhibiting huge diversity in floral phenotype and perfume. *Rosa* species have a highly heterozygous genome, of varying level of ploidy, making it challenging to sequence and assemble. To reduce its complexity, a homozygous plant material was created from a diploid species that participated to domestication. This material allowed the generation of a high-quality rose genome assembly, considered among the three most continuous plant genomes sequenced to date<sup>3</sup>. The genome, which includes annotation of coding and non-coding genes, and transposable elements, as well as the genome-wide polymorphism of 14 other rose genotypes, provide a solid base knowledge for future work to understand genomic variation associated with floral and scent diversity.

### **GENOME FACTS:**

The genome of *Rosa sp.* is composed of seven chromosomes.

The assembly covers 504 Mb with transposable elements (TEs) spanning 67.9 % of the assembly (including 50.6 % long-terminal-repeat retrotransposons).

The rose genome comprises 36,377 inferred protein-coding genes (70 % of them being available as allele pairs) and is predicted to contain 3,971 long noncoding RNAs and 207 miRNA precursors<sup>4</sup>.

### **SPECIES FACTS:**

Rose belongs to the Rosaceae family that comprises over 90 genera and 2,500 species, many among which are economically important crops<sup>5</sup>.

Fruit-producing Rosaceae crops include pear, apple, raspberries, strawberries and stone fruits such as peach/nectarine, apricot, plum, cherry and almond.

The rose represents an ideal model plant to study many biological aspects for many of these Rosacea crops, because:

- (i) Rose shares many agronomic traits with Rosaceae tree crops
- (ii) Rose is easily propagated by cuttings
- (iii) Cuttings are able to flower the same year, an advantage over other Rosaceae crops requiring many years of growth before flowering
- (iv) The availability of omics resources, including transcriptomics database<sup>6-8</sup> and a very high-quality assembled and annotated Rose genome<sup>4</sup>

- (v) The availability of efficient Rose transformation protocol<sup>9</sup>

**TAXONOMY AND CLASSIFICATION:** [SEP]

|             |                     |
|-------------|---------------------|
| KINGDOM:    | Plantae [SEP]       |
| DIVISION:   | Magnoliophyta       |
| CLASS:      | Magnoliopsida [SEP] |
| ORDER:      | [SEP] Rosales       |
| FAMILY:     | Rosaceae [SEP]      |
| SUB-FAMILY: | Rosoideae           |
| TRIBE:      | Roseae              |
| GENUS:      | <i>Rosa</i> [SEP]   |

**FUN FACT ABOUT THE GENOME:**

Roses exhibit one of the richest diversity of flower fragrance and color. Rose scent compounds belong to 3 major classes: terpenoids, benzenoids/phenylpropanoids and fatty acid derivatives. Modern roses have inherited scent from both European and Chinese lineages through many manmade crosses. The diverse fragrances are linked to the expression of the different enzymatic pathways inherited from wild species. Extensive literature has dealt with the chemistry of rose scent. The production of high quality rose genome assembly complemented these previous studies by providing information on the enzymes responsible for synthesizing these major scent compounds and their transcription regulatory pathways<sup>4</sup>. It permitted the identification of biosynthetic steps that have not been characterized in the rose and/or in other species<sup>4</sup>. The analyses also identified an interconnected regulation and coordinated biosynthesis of certain scent compounds and flower color<sup>4</sup>. Such co-regulation may explain the difficulties breeders have in combining some pigments with specific scents in rose hybrids. Functional characterization of such gene regulatory pathways has thus become one of the major goals in rose research.

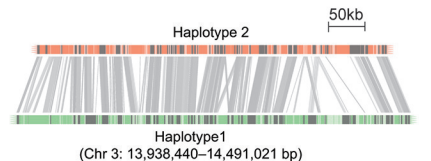
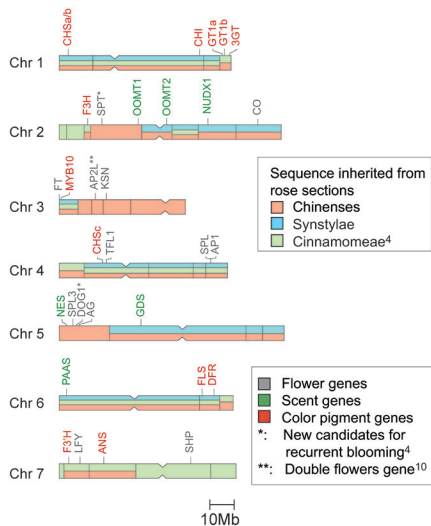
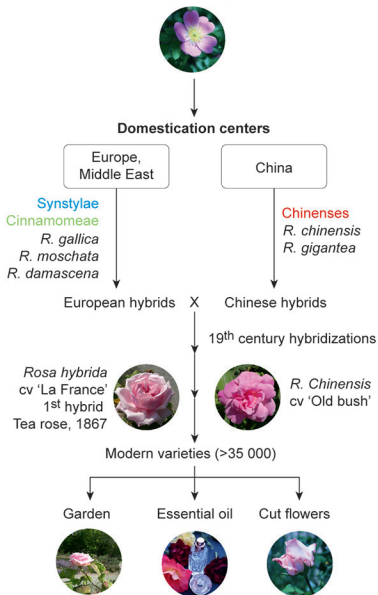
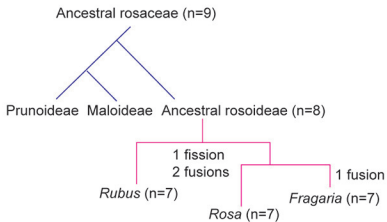
**References:**

1. Fougere-Danezan, M. *et al.* *Ann Bot* **115**, 275-91 (2015).
2. De Vries, D.P. *et al.* *Acta Horticulturae* **424**, 241-248 (1996).
3. Belser, C. *et al.* *Nat Plants* **4**, 879-887 (2018).
4. Raymond, O. *et al.* *Nat Genet* **50**, 772-777 (2018).
5. Hummer, K.E. *et al.* in *Genetics and Genomics of Rosaceae*, Vol. 6 (eds. Gardiner, S.E. & Folta, K.M.) 1-17 (Springer, New York, 2009).
6. Dubois, A. *et al.* *BMC Genomics* **13**, 638 (2012).
7. Yan, H. *et al.* *Gene* **540**, 96-103 (2014).
8. Yan, H. *et al.* *Front Plant Sci* **7**, 996 (2016).
9. Vergne, P. *et al.* *Plant Cell Tissue and Organ Culture* **100**, 73-81 (2010).
10. Francois, L. *et al.* *Sci Rep* **8**, 12912 (2018).









Example showing the high sequence divergence between haplotypes. Black bars: genes; red or green; transposable elements.