



A high-quality sequence of *Rosa chinensis* to elucidate genome structure and ornamental traits

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Titre A high-quality sequence of *Rosa chinensis* to elucidate genome structure and ornamental traits

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Résumé en anglais Rose is the world's most important ornamental plant with economic, cultural and symbolic value. Roses are cultivated worldwide and sold as garden roses, cut flowers and potted plants. Rose has a complex genome with high heterozygosity and various ploidy levels. Our objectives were (i) to develop the first high-quality reference genome sequence for the genus *Rosa* by sequencing a doubled haploid, combining long and short read sequencing, and anchoring to a high-density genetic map and (ii) to study the genome structure and the genetic basis of major ornamental traits. We produced a haploid rose line from *R. chinensis* "Old Blush" and generated the first rose genome sequence at the pseudo-molecule scale (512 Mbp with N50 of 3.4 Mb and L75 of 97). The sequence was validated using high-density diploid and tetraploid genetic maps. We delineated hallmark chromosomal features including the pericentromeric regions through annotation of TE families and positioned centromeric repeats using FISH. Genetic diversity was analysed by resequencing eight *Rosa* species. Combining genetic and genomic approaches, we identified potential genetic regulators of key ornamental traits, including prickle density and number of flower petals. A rose APETALA2 homologue is proposed to be the major regulator of petals number in rose. This reference sequence is an important resource for studying polyploidisation, meiosis and developmental processes as we demonstrated for flower and prickle development. This reference sequence will also accelerate breeding through the development of molecular markers linked to traits, the identification of the genes underlying them and the exploitation of synteny across Rosaceae.

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