



Genetic analysis of the flowering date and number of petals in rose

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Rose is the ornamental species with the highest financial impact. Floral traits such as the number of petals and the date of flowering are major characteristics of ornamental plants. Our objective is to study the genetic determinism of floral traits: date of flowering and number of petals, which are a major issue for rose breeders. The study was conducted on two interspecific populations interconnected by the male parent: H190 x hybrid of *Rosa wichurana* (referred to as HW) and "The Fairy" x hybrid of *Rosa wichurana* (referred to as FW). The number of petals and the date of flowering were scored over 2 and 8 years, respectively. A new HW genetic map covering 468 cM and the already available genetic map of the FW population (Kawamura et al. TAG Theor Appl Genet 122:661-675, 2011) were used for the genetic determinism studies. In each population, half of the hybrids exhibited single flowers (less than 10 petals), whereas the other half revealed double flowers. The number of petals is controlled by the NP gene located on LG3. Additionally, we detected two new major quantitative trait loci (QTLs) on LG2 and LG5, close to RoAP1b and RoRAG, respectively, two genes involved in the control of floral identity. For the date of flowering, three QTLs with a major effect and high stability between years were found on linkage groups 3, 4, and 6, indicating a high stability of QTLs to the changing environment. Candidate genes underlying these QTLs were investigated and key genes were identified. These major QTLs were linked to candidate genes, i.e., the identified QTL on LG4 was linked to RoFT, the one on LG3 to genes involved in gibberellin pathways, and the one on LG6 to RoFD. These QTLs, which are very stable over time, are good candidates to develop markers applicable in marker-assisted selection (MAS).

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