



Quantitative trait loci for flowering time and inflorescence architecture in rose

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The pattern of development of the inflorescence is an important characteristic in ornamental plants, where the economic value is in the flower. The genetic determinism of inflorescence architecture is poorly understood, especially in woody perennial plants with long life cycles. Our objective was to study the genetic determinism of this characteristic in rose. The genetic architectures of 10 traits associated with the developmental timing and architecture of the inflorescence, and with flower production were investigated in a F₁ diploid garden rose population, based on intensive measurements of phenological and morphological traits in a field. There were substantial genetic variations in inflorescence development traits, with broad-sense heritabilities ranging from 0.82 to 0.93. Genotypic correlations were significant for most (87%) pairs of traits, suggesting either pleiotropy or tight linkage among loci. However, non-significant and low correlations between some pairs of traits revealed two independent developmental pathways controlling inflorescence architecture: (1) the production of inflorescence nodes increased the number of branches and the production of flowers; (2) internode elongation connected with frequent branching increased the number of branches and the production of flowers. QTL mapping identified six common QTL regions (cQTL) for inflorescence developmental traits. A QTL for flowering time and many inflorescence traits were mapped to the same cQTL. Several candidate genes that are known to control inflorescence developmental traits and gibberellin signaling in *Arabidopsis thaliana* were mapped in rose. Rose orthologues of FLOWERING LOCUS T (RoFT), TERMINAL FLOWER 1 (RoKSN), SPINDLY (RoSPINDLY), DELLA (RoDELLA), and SLEEPY (RoSLEEPY) co-localized with cQTL for relevant traits. This is the first report on the genetic basis of complex inflorescence developmental traits in rose.

Résumé en anglais

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