



Genotype of FLOWERING LOCUS T homologue contributes to flowering time differences in wild and cultivated roses

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Auteur	Otagaki, S. [1], Ogawa, Y. [2], Hibrand-Saint Oyant, Laurence [3], Foucher, Fabrice [4], Kawamura, Koji [5], Horibe, T. [6], Matsumoto, S. [7]
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Mots-clés	CAPS marker [8], flowering [9], FT [10], Rosa [11]
Résumé en anglais	<p>Rose flowers have long delighted humans as ornamental plants. To improve the ornamental value of roses it is necessary to understand the regulatory mechanisms of flowering. We previously found that flowering time is controlled by three minor quantitative trait loci (QTLs) and a major QTL co-localised with RoFT. In this study, we isolated three RoFT alleles encoding completely identical amino acid sequences from the parents of a mapping population. Correlation analysis of the RoFT genotypes and flowering time phenotypes in the mapping population showed that the RoFT_f and RoFT_g alleles contribute to the early-flowering phenotype, while the RoFT_e allele contributes to the late-flowering phenotype. We developed two novel cleaved amplified polymorphic sequence (CAPS) markers based on the genomic sequences of the RoFT alleles and clearly showed that the relationship between RoFT genotype and flowering time was applicable to 12 of 13 cultivated roses grown at the Higashiyama Botanical Gardens, Japan. Allele-specific expression analysis using a reverse transcription CAPS assay suggested that these RoFT alleles are regulated differentially at the transcription level. Furthermore, transgenic <i>Arabidopsis thaliana</i> plants ectopically expressing the RoFT gene showed an early-flowering phenotype. Conversely, in roses, RoFT was continuously expressed after floral bud formation, and RoFT transcript accumulation reached its peak after that of the floral meristem identity gene RoAP1b. These data suggest that RoFT may be essential not only for floral transition but also for normal floral development and flowering in roses.</p>
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Liens

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