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W181

### DEVELOPMENT OF A GENETIC LINKAGE MAP AND STUDY OF CANDIDATE GENES FOR FLOWERING CONTROL IN ROSE

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A research program has been started at INRA of Angers to study the rose genome as a model for woody and ornamental plants. Rose was selected as a model species because it has a small genome (about 4 times the size of *Arabidopsis thaliana* genome), a short generation time, and a high level of variability of phenotypic traits. Genetic maps have been developed previously in rose using different markers, such as AFLP, RAPD or SSR. SSR markers developed from rose, peach and apple were positioned on two genetic linkage maps previously constructed from a segregating population of 91 hybrids obtained by cross between a dihaploid rose (H190) and diploid (*Rosa wichuraiana*) species (Crespel et al., 2002 Theoretical and Applied Genetics 1207-1214). Placement of these SSR markers increased the map length and provided anchoring points between female (H190) and male (*R. wichuraiana*) linkage groups. Two important ornamental characters, resistance to black spot fungus and shoot colour, were also placed on the maps. We are also focusing on understanding the flowering characters in rose. Based on floral studies in model plants (*Arabidopsis* and rice), homologues of candidate genes (*LEAFY*, *CENTRORADIALIS*, *LHP1*, *EMF2*, *RGA/GAI*) for flowering control have been isolated from rose using degenerate primers. *CEN* and *RGA/GAI* genes were mapped on female and male maps, respectively. Expression studies in different tissues by RT-PCR reveal that some genes (*LEAFY*, *CEN* and *RGA/GAI*) are differentially regulated whereas others, such as *LHP1*, are constitutively expressed. These results contribute to our knowledge on flowering behaviour of rose as well as other Rosaceae genomes.

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