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A gene candidate approach to study the control of recurrent blooming in rose.

F. Foucher, D. Lalanne, V. Freslon, C. Bayle and L. Hibrand-Saint Oyant

UMR Génétique et Horticulture (GenHort) - INRA/INH/UA - BP 60057 - 49071 Beaucozú CEDEX - France
Email : foucher@angers.inra.fr

In rose, flowering can occur once a year (non-recurrent blooming) or continuously during the favourable season (recurrent blooming). Recurrent blooming has been shown to be under the control of a major recessive gene, *RB*, which was localized on genetic map (Crespel et al, 2002, fig. 2). In order to understand the molecular basis of recurrent blooming, we have undertaken a gene-candidate approach. Genetic and physiological data suggest that gibberellic acid or floral repressor may be involved in this control. Genes implicated in these pathways have been well characterized in Arabidopsis (fig. 1).

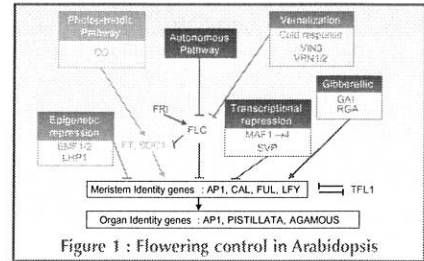


Figure 1 : Flowering control in Arabidopsis

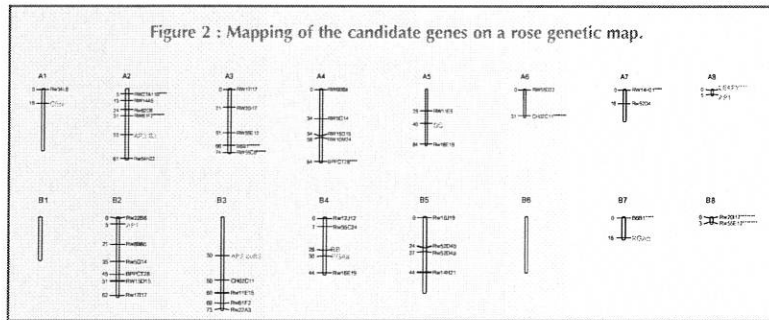


Figure 2 : Mapping of the candidate genes on a rose genetic map.

To look for co-localization with the *RB* gene, we mapped the genes on a genetic map developed in the laboratory with AFLP and SSR markers (fig. 2). A *RGA* homologue, *RGAa*, was mapped in the vicinity of *RB*. To better understand the involvement of these genes in the floral process, we have followed their expression by RT-PCR during the floral process and in different tissues (fig. 3). The genes showed different patterns of expression and almost all the genes are expressed during the floral initiation (between stage Ib and II), suggesting that they may be implicated in this process.

Table 1 : List of the flowering genes isolated in rose.

	Genes	Source	% similarity	Molecular marker	Genetic position
GA perception	<i>RGA</i>	a EST	72	Acryl	A1
		b Primer	84	Acryl	B5
Floral repressors	<i>TFL2/LHP1</i>	Primer	56	no	-
	<i>EMF2</i>	Primer	56	no	-
	<i>CEN/TFL1</i>	Primer	77	Acryl	A1
Floral Control	<i>SOC1</i>	Primer	73	no	-
	<i>LEAFY</i>	Primer	90	no	-
	<i>APETALA1</i>	a Primer	81	Acryl	B2/A8
		b Primer	75	no	-
Flower development	<i>APETALA3</i>	B3 cDNA	67	Acryl	A2
		euB3 cDNA	70	Acryl	B3
	<i>PISTILLATA</i>	cDNA	68	no	-
	<i>AGAMOUS</i>	cDNA	81	no	-

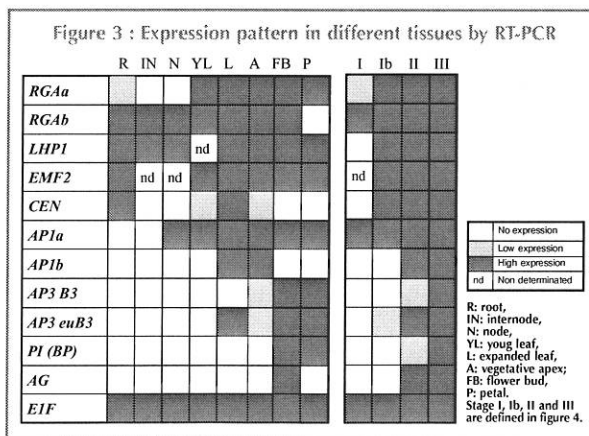


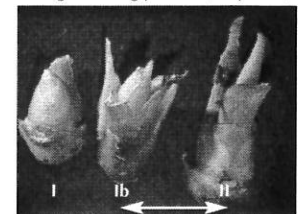
Figure 3 : Expression pattern in different tissues by RT-PCR

Construction of a cDNA libraries and EST production

Two cDNA libraries have been constructed from:

- (1) vegetative apices (*Rosa wichuraiana*)
- (2) apices during the floral transition (*R. hybrida* Black Baccara®, stage I, Ib and II).

Figure 4 : Different stages of the apex during flowering process (*R. hybrida*).



Floral initiation

Histological analysis revealed that the floral initiation takes place between stage Ib and II (data not shown). 5000 EST have been produced from the two libraries and are presently analysed.

Conclusions and perspectives

We were able to isolate in a perennial plant (rose) homologues of genes involved in floral control in an annual one (Arabidopsis). Expression analysis seems indicate that these genes are implicated in the floral process. Production of EST may allow us to develop differential approach to isolate new genes in rose involved in the control of flowering.

Acknowledgements

We thank David Weiss (Hebrew University of Jerusalem) to provide *RGAa* clone, Florence Piola (Université Lyon I, France) for the *RGAb* clone. EST Sequencing was done by Ouest Genopole®.

