ANALYSIS OF CANDIDATE GENES INVOLVED IN FLOWERING DATE IN SWEET CHERRY (*Prunus avium*)

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Introduction

In sweet cherry (*Prunus avium*), flowering process is controlled by specific chill and heat requirements. In the context of global climate change, warmer temperatures during winter and spring are responsible for several disruptions already manifested in perennial species and could have important impacts on fruit production. In most temperate-fruit species, the knowledge of the genetic determinism of flowering is necessary to develop new cultivars that will be adapted to increasing temperature.

Material & Methods

Plant material

The two intraspecific F_1 mapping progenies 'Regina' × 'Garnet' (R×G, 117 hybrids) and 'Regina' × 'Lapins' (R×L, 124 hybrids) were planted on their own roots in the orchard. Floral buds of the three parents and 'Cristobalina' were collected between 13th October 2011 and 28th march 2012 (8 data points).

Candidate Genes (CGs) identification and mapping

A list of functional CGs was established based on previous studies from other plant species. Cherry homologues were identified using the sweet cherry Regina transcriptome database, partially resequenced and mapped.

Real-time RT-PCR

Total RNAs were extracted from floral buds and were reverse transcribed with iScript cDNA Synthesis Kit (Biorad). Quantitative real-time PCRs were performed on LightCycler®480 (Roche). The comparative CT (ΔΔCT) method was used to quantify those cDNAs with amplification efficiencies equivalent to the reference actin gene.

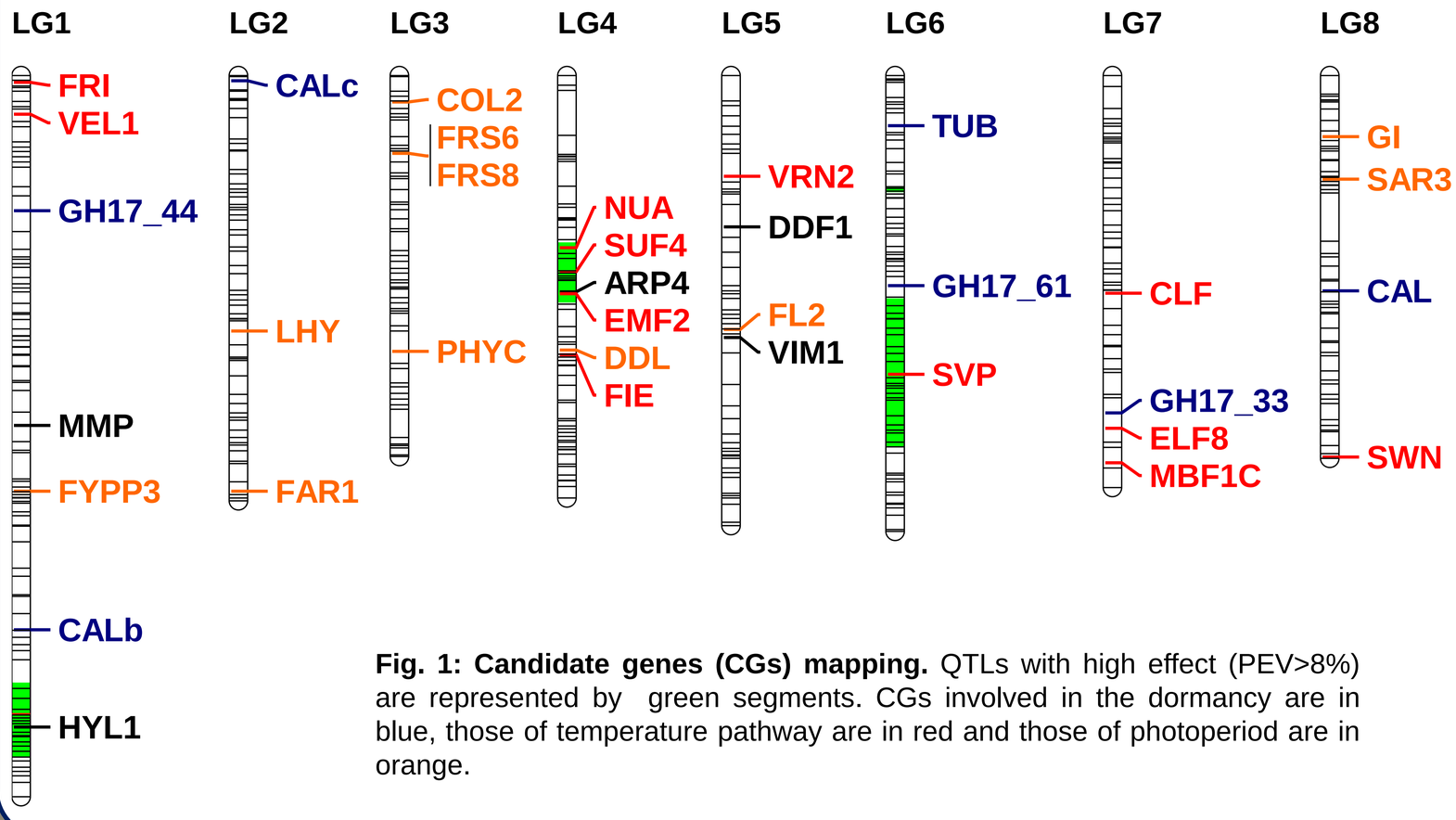
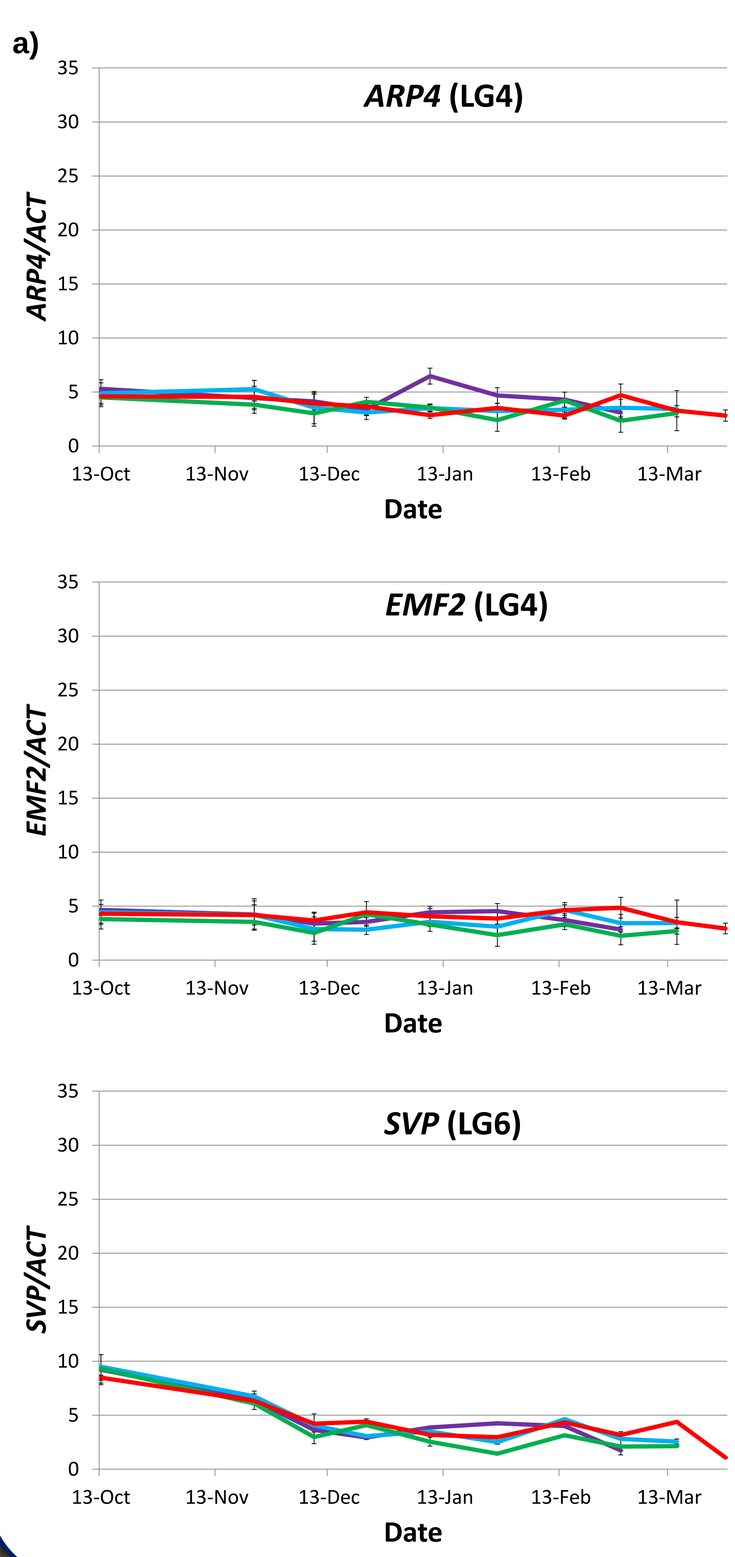


Fig. 1: Candidate genes (CGs) mapping. QTLs with high effect (PEV>8%) are represented by green segments. CGs involved in the dormancy are in blue, those of temperature pathway are in red and those of photoperiod are in orange.



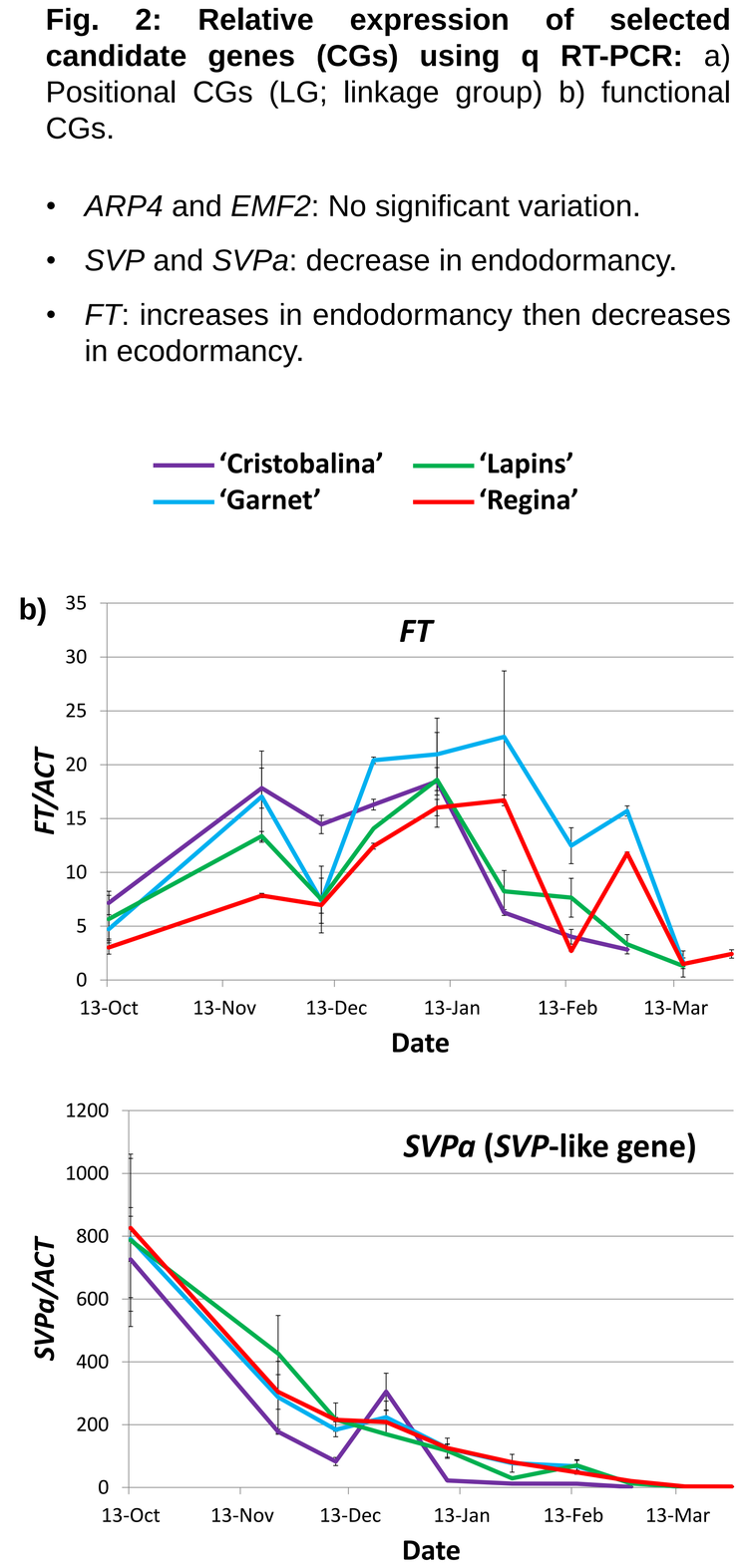


Fig. 2: Relative expression of selected candidate genes (CGs) using q RT-PCR: a) Positional CGs (LG; linkage group) b) functional CGs.

- *ARP4* and *EMF2*: No significant variation.
- *SVP* and *SVPa*: decrease in endodormancy.
- *FT*: increases in endodormancy then decreases in ecodormancy.

Results and conclusions

- 100 CGs involved in flowering have been identified and 34 CGs were mapped on sweet cherry (Fig 1).
- 13 CGs co-localize with QTLs. Among them, 5 CGs are located within the major QTL on linkage group (LG) 4 of 'Regina'.
- The first functional studies using qRT-PCR on five promising CGs show different expression profiles (Fig2).
- No significant differences are observed between each parents.
- Further post-translational modification analyses could complete this study.

Acknowledgements

- This work was supported by the Aquitaine region and INRA (Meta Program ACCAF).
- We thank the Fruit Experimental Unit of INRA – Bordeaux for growing the trees.