



“Linkage mapping and functional genomics applied to dormancy characterization in apple”

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Keywords: *Malus x domestica*, chilling requirement, flowering time, genetic map, QTL analysis, gene expression.

Apple trees need exposure to cold temperatures (chilling requirement), in order for budbreak to occur promptly and uniformly after winter. In warmer production areas, such as the South region region of Brazil, insufficient winter chilling results in suboptimal budbreak in spring, with negative impacts on apple yield. Therefore, knowledge of the genetic and molecular mechanisms that control bud dormancy is valuable for crop breeding efforts. By integrating a linkage mapping strategy and genomic approaches, we generated a collection of data that is useful to better characterize this complex agronomical trait in apple. A genetic linkage map of apple was constructed based on a population segregating for chilling requirement associated traits from the cross between ‘Fred Hough’ X ‘M13/91’. A total of 1783 SNPs were used for the construction of the genetic linkage maps. For both parents, 17 linkage groups were obtained, corresponding to the apple haploid chromosome number. Major QTLs associated with initial vegetative bud burst and time of flowering, explaining 32,3% to 73,4% of the total variation, respectively, were identified at the end of linkage group 9. Assessing the genomic sequence in this region, two predicted transcripts with similarity to the Flowering Locus C from *Arabidopsis thaliana* were identified. Transcriptomic identification and characterization of genes related to bud dormancy in apple were performed on microarrays representing 57,000 apple genes and by suppression subtraction hybridization. Among the differentially expressed candidates, we identified genes that have potential roles in the circadian clock, hormonal signaling, regulation of growth, flower development and cold response. Differential transcription profiles of candidate genes were reassessed by real time PCR in bud samples from experimental orchards, cold-treated samples under controlled conditions, as well as in different tissues and organs. Our results confirm that a major QTL in the linkage group 9 has important genetic determinants for the control of flowering time and provide additional support to narrow the search for genes related to the control of dormancy progression in apple.