Differential Gene Expression of Two Apple Cultivars with Contrasting Chilling Requirement

Porto, DD¹; Falavigna, VS¹; Buffon, V¹; Pasquali, G²; Oliveira, PRD¹; Santos, HP¹; Revers, LF^{1*}

¹Laboratório de Biologia Molecular Vegetal, Embrapa Uva e Vinho, Bento Gonçalves, RS, 95700-000. ²Centro de Biotecnologia, Universidade Federal do Rio Grande do Sul, Porto Alegre, RS, 91501-970.

*E-mail: luis@cnpuv.embrapa.br

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Temperate fruit crops are of great economic importance worldwide, and their production depends on developmental processes, mainly the shift from juvenile to reproductive phase, dormancy transitions and flowering. Apple tree development is subjected to regulation by environmental inputs, specially chilling temperatures, which are required to dormancy establishment and release. In this work, we aimed to investigate the differential gene expression between Gala and its derived bud sport Castel Gala that display medium and low chilling requirement, respectively. Bud samples were collected in 2007 at the beginning (May) and end (August) of dormancy period. Total mRNA was isolated by LiCl precipitation, and suppressive subtractive hybridization assays were performed using the PCR-select kit (Clontech Laboratories, Inc.) according to manufacturer instructions. Differentially expressed cDNA tags were sequenced by the Sanger method (ABI3100 Genetic Analyzer, Applied Biosystems). Sequences were manually processed and assembled with CodonCode software. BLAST searches and GO classification assignments and statistics were performed using the Blast2GO suite. Gala buds showed increased number of transcripts related to stress and cold response (metallothioneins, dehydrins, etc.) at both dates. August Gala samples contained several transcripts coding for transcription factors associated to dormancy in the literature, like Kelch repeat-proteins, GRAS family and dormancy-associated MADS box genes. Castel Gala samples were generally enriched in sequences related to cytoskeleton and photosynthesis. Our findings will provide information to help unveil the molecular mechanisms involved in bud dormancy establishment and release in apple.

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