Apple and strawberry MADS-box genes and their function in plant developmental pathways

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MADS-box transcription factors play a crucial role in several plant developmental processes and have been studied in details in the model plant *Arabidopsis thaliana*. However, little is known about their function in crops of important agricultural and commercial value. Our study aims to investigate their role in two representative Rosaceae crops: apple and strawberry. A phylogenetic analysis of apple MADS-box genes indicated the presence of a subclade containing genes involved in important developmental pathways such as flowering induction and dormancy. We investigated the function of these genes in the sequenced apple cultivar 'Golden Delicious'. The open reading frames (ORFs) of these genes were validated experimentally from cDNA libraries of different apple tissues. Expression studies using qPCR seems to indicate that the apple MADS-box genes analyzed are not involved in flower development but are more likely involved in response to winter chill. Real Time gene expression and epigenetic studies of dormant buds collected during the chilling period suggested that the activity of the genes is regulated by long exposure to cold. A potential candidate gene for manipulating the switch to flowering in apple crops was identified.

We also performed a phylogenetic analysis of MADS-box genes in another Rosaceae spp, *Fragaria vesca* (wild strawberry) and selected three MADS-box genes to perform gene expression analyses. These genes were knocked down using RNA interference approach and some regenerants were analyzed at the molecular level. Further information about gene function will be available after the phenotypic analysis of the transgenic lines.