

# Selected apple and strawberry transcription factors and their relevance to fruit development

Giulia V. Miolli<sup>1</sup>, Henryk Flachowsky<sup>2</sup>, Madga-Viola Hanke<sup>2</sup>, Azeddine Si-Ammour<sup>1</sup>

<sup>1</sup>Julius Kühn-Institut, Institute for Breeding Research on Horticultural and Fruit Crops

<sup>2</sup>Fondazione Edmund Mach/CRI, San Michele all'Adige, Italy

giulia.molli@jki.bund.de

MADS-box transcription factors and their role in flower and fruit development have been widely studied in the model plant *Arabidopsis thaliana*. However, they are poorly studied in major crop plants and fruit trees. Our study aims to extend the knowledge on MADS-box genes of the *Rosaceae* family that includes crops of important agricultural and commercial value. We selected individual genes of this gene family involved in developmental processes and studied their function at the molecular level in two *Rosaceae* representative species. A phylogenetic analysis of apple MADS-box genes suggests the presence of a subclade containing genes that are close to the *Arabidopsis AGL24* gene. Fifteen of these *AGL24*-like genes were investigated with regard to their function in the apple cultivar 'Golden Delicious'. The ORFs of these genes were validated experimentally from cDNA libraries of different apple tissues. Expression studies using qPCR indi-

cate that the apple MADS-box genes belonging to this subclade do not play any role in flower development, but they are more likely involved in response to vernalization (dormancy-associated MADS-box, DAM). Furthermore, we studied also the putative *F. vesca* homologues, but they did not show any expression in the respective tissues of strawberry. Therefore, we focused our study on MADS-box genes with homologues of known function in *Arabidopsis* to perform gene expression and functional analysis. After phylogenetic analysis, three genes that are most likely the strawberry homologues of *Arabidopsis PISTILLATA* and *AGAMOUS* were chosen as candidate genes for post-transcriptional gene silencing using a RNA interference approach. The molecular and phenotypic analysis of the transformants will help to explain how the ABCE model genes act in *Rosaceae*.