Elucidation of phloridzin biosynthesis in apple - tissue-specific expression pattern of a candidate gene presumed to play a key role in phloridzin formation

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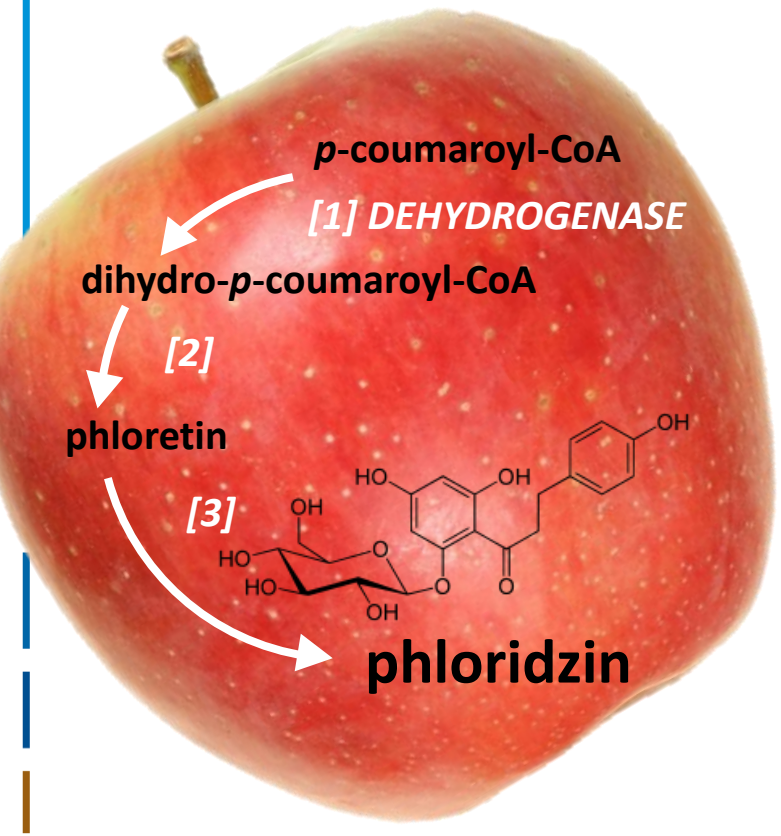

Figure 1: Biosynthetic formation of phloridzin. [1] Formation of dihydro-*p*-coumaroyl-CoA from *p*-coumaroyl-CoA by an NADPH-dependent dehydrogenase, [2] formation of phloretin by a chalcone synthase (CHS), [3] glucosylation of phloretin at position 2' leading to phloridzin.

INTRODUCTION

- Dihydrochalcone phloridzin represents more than 90% of the soluble phenolic components in apple leaves
- Health-promoting properties of phloridzin for the human diet
- Large amounts of phloridzin is unique to *Malus* species
- Physiological role of phloridzin in apple and its first step of biosynthesis **(Fig. 1)** are still unknown

AIM of the PROJECT

- Investigation of a candidate gene encoding for a dehydrogenase potentially catalyzing the first step in phloridzin biosynthesis

PRELIMINARY RESULTS

- Candidate gene is expressed in leaf and flower tissue with varying expression levels, dependent on tissue type, tissue age, and cultivar **(Fig. 2)**
- Generation of RNAi apple lines with reduced candidate gene expression (to 10 – 30%)
- Establishment of transgenic *Arabidopis thaliana* lines for heterologous expression of the candidate gene **(Fig. 3)**

OUTLOOK

- Metabolite analysis (e.g. phloridzin, phloretin)
- Functional studies (resistance to stresses) using transgenic apple and *Arabidopsis* lines

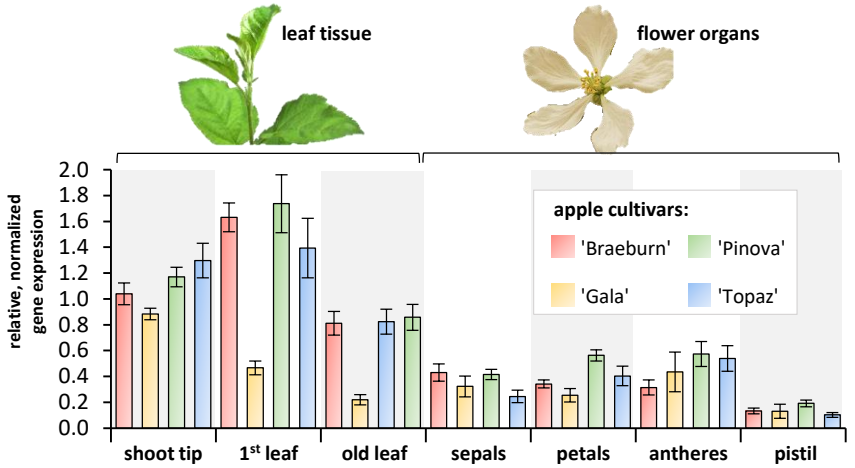

Figure 2: Dehydrogenase candidate gene expression. qPCR were performed with material from leaves and flowers of different apple cultivars.

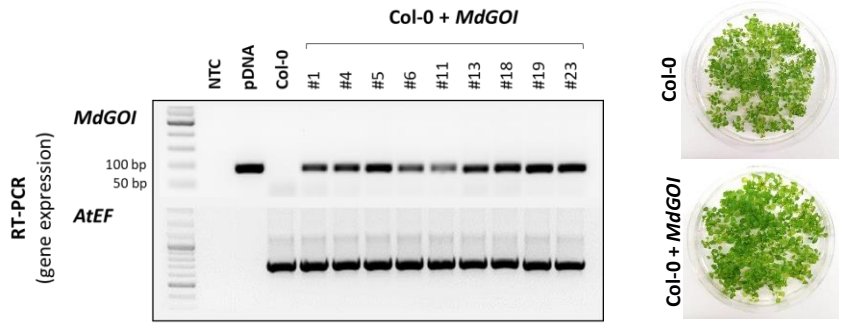

Figure 3: Heterologous expression of the candidate gene from apple in *A. thaliana*. Transgenic lines were generated using *Agrobacterium*-mediated transformation of the wild type Col-0. The expression of the candidate gene (*MdGOI*) was detected by RT-PCR.

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