DIHYDROCHALCONE BIOSYNTHESIS: INNOVATIVE TARGET FOR BREEDING IN ROSACEAE AND BIOTECHNOLOGICAL APPROACHES

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The apple tree is an agriculturally and economically important tree commonly used in food and beverages. Apple has also drawn attention in recent years due to its potential pharmaceutical and nutraceutical applications which are correlated with secondary metabolites. The major phenolic compounds found in apple belong to the class of dihydrochalcones (DHCs), represented by various phloretin derivatives (e.g. phloridzin, sieboldin, trilobatin). Beside their contribution to the bitter taste of cider and the colour of apple juices due to oxidation products and they were also associated with health effects of apple fruits, and their processed products. Metabolite fingerprints of *Malus* species revealed significant variation in the DHC pattern. Several unknown metabolites could be tentatively identified. However, the specific reactions that leads to the synthesis different DHC patterns has not yet been determined. The availability of apple genomic and transcriptomic resources make apple an ideal plant to elucidate these activities that leads to the production of many valuable DHCs in apple but also in other plants. To identify genes involved in the synthesis of dihydrophenolic compounds the existing genome database of the Rosaceae was screened for apple genes with significant sequence similarity to e.g. Arabidopsis alkenal double-bond reductase. The functionally expressed apple double bond reductase exhibits p-coumaroyl-CoA reductase activity generating dihydrocoumaroyl-CoA. This finding contributes significantly to our understanding of dihydrophenol formation in plants. Further focus is on the different glycosylation and hydroxylation pattern of DHCs.