

Metabolons and the biosynthesis of *Gerbera hybrida* flavonoids

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The formation of protein complexes, metabolons, and the channeling of intermediates of secondary metabolism has been discussed for at least 30 years. Metabolons and channeling enable plants to perform a highly effective synthesis of specific natural products without or with reduced metabolic interference and avoiding accumulation of toxic intermediates. In spite of a long tradition of the concept, precise examples of complete metabolons are very scarce. Our aim is to define flavone and anthocyanidin specific metabolons in the ornamental plant *Gerbera hybrida*. Our earlier data shows that specific genes are expressed early in development (*PAL* and *CHS3*) and others late (*PAL*, *CHS1* and *DFR*), possibly correlating with flavone and anthocyanin biosynthesis. Furthermore, transformation of the pelargonidin type *Gerbera* cultivar Terra Regina with a *MYB*-type regulatory gene induces cyanidin biosynthesis without interfering with the background pelargonidin biosynthesis. Using our large set of EST, the expanding genomic sequence resource of *Gerbera* and new data from Illumina sequences for wild type of Regina and *MYB* transgenic lines, we are establishing correlations in expression and patterns of protein-protein interactions for the whole flavonoid metabolism isoenzyme complex in our model plant.

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