

## Functional characterization of terpene glycosyltransferases from *Vitis vinifera*

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### Projektbeschreibung

Terpenoids represent one of the major classes of natural products and are used in many applications, from health care and pharmaceutical uses to colour, flavour and fragrance compounds in food and cosmetics. Biosynthesis occurs through either the mevalonic acid or the 1-deoxy-D-xylulose 5-phosphate pathway. In plants, terpenoids are further decorated with sugars which are linked to the active groups OH and/or COOH. In grapes (*Vitis vinifera*) and wines, where the importance of monoterpenes on varietal flavour is widely recognized a major fraction of these compounds is present as non-volatile, aroma-inactive terpene glycosides. Although this water-soluble fraction is a precious source of aroma, little is known about the genes and their encoded enzymes catalyzing the glycosylation of terpenols in grapes. A recent functional analysis of *Arabidopsis thaliana* glycosyltransferase (GT) genes has yielded 27 sequences whose encoded proteins glucosylate a diversity of terpenes. We have extracted 67 homologous, putative GT sequences from the published *Vitis vinifera* genome database which cluster into 8 subgroups. Spatial and temporal expression levels of the potential VvGT genes will be determined in different grapes varieties and will be compared with the levels of terpene glycosides in different tissues to narrow down the number of putative terpene VvGTs. The most promising members of the subgroups will be heterologously expressed and biochemically characterized with a number of potential terpenol substrates. Stereo- and regioselectivity of the recombinant proteins will be determined for a variety of terpenoids. The results can be applied in breeding programs to select for genotypes with low terpene GT activities and, presumably, higher levels of aroma-active, free terpenols and to develop biotechnological processes as alternative to chemical synthesis.

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