

O-13**Phylogenetic reconstruction of Family 1 UDP-glycosyltransferases: towards a better functional prediction and potential applications**

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Plants have developed the ability to produce an enormous number of secondary metabolites which are of vital importance. It is well known that this huge diversity is produced by multiple decoration of a common skeleton (Gachon *et al.*, 2005). Thus, diversity can only be achieved by concerted evolution and diversification of genes and gene products with altered functionality in regard to modifications. UDP-glycosyltransferases (UGTs) play an important role in the diversification of these metabolites.

For almost a decade, our knowledge on the organisation and functionality of the family 1 UGTs has been limited to the model plant *Arabidopsis thaliana*. The availability of other plant genomes represents an opportunity to obtain a broader view of the family in terms of evolution and organisation but also in functional prediction. A phylogeny reconstruction study was performed to get an insight into the evolution of this multigene family during the adaptation of plants to life on land. More than 1500 putative UGTs were identified in 12 plant genomes based on the highly conserved PSPG motif. Analyses were performed to reconstruct the phylogenetic relationships existing between the sequences. The results of this study clearly show that the UGT family expanded during the transition from algae to vascular plants and that in higher plants the clustering of UGTs into phylogenetic groups appears to be conserved, although gene loss and gene gain events seem to have occurred in certain lineages. Interestingly, two new phylogenetic groups, named O and P, that are not present in *A. thaliana* were discovered (Caputi *et al.*, 2012). The development of such a large 'glycosylation toolbox' appears to be an early acquisition of plants and led to many potential applications in plant breeding and engineering but also in combinatorial synthesis approaches.

References

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