

GENOME-WIDE COMPARATIVE AND EVOLUTIONARY STUDY OF XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE GENES IN FOUR CULTIVATED PLANT FAMILIES.

GUADAGNO A.*, DUBLINO R.*, ANDOLFO G.*, ERCOLANO M. R.*

*) Department of Agricultural Science, University of Naples Federico II, Portici, NA

genome-wide, xyloglucan endotransglucosylase/hydrolase, hemicellulose, cellulose, cell wall

Xyloglucan endotransglucosylase/hydrolases (XTHs) belong to a multigene family that plays key roles in plant growth and development as well as in biotic and abiotic stress response. They are involved in construction, remodelling and extensibility of plant cell wall through the cleavage and polymerization of xyloglucan molecules. Xyloglucan is the most abundant hemicellulose found in the primary plant cell wall, it is linked to cellulose by a non-covalent bond and it cooperates in the formation of cellulose microfibrils. In this study, an *in silico* analysis was performed on xyloglucan endotransglucosylase/hydrolase gene family in four plant families *Solanaceae*, *Cucurbitaceae*, *Graminaceae* and *Brassicaceae*, including 11 cultivated plant species (*Solanum lycopersicum*, *Nicotiana tabacum*, *Solanum melongena*, *Cucurbita pepo*, *Cucurbita moschata*, *Cucurbita melo*, *Brachipodium distachlyon*, *Oryza sativa*, *Triticum turgidum* ssp. *Durum*, *Raphanus sativus*, *Brassica oleracea*) and a model species (*Arabidopsis thaliana*). About 500 genes were identified in the 12 species analysed and most of them contain two conserved domain proteins (Glyco_hydro_16 and XET_C domain) characteristic for the XTH enzymes. The conserved motives analysis showed that the proteins contain a typical catalyze enzymatic reaction motif (HDEIDFEFLG), in which the first glutamic acid residue (E) is an affinity site and the second is a proton donor. The gene structure organization of the XTHs genes varied in the analysed species. The study of spatial arrangement of the XTHs genes along the chromosomes showed that they are mainly organized in cluster and in singleton. The phylogenetic analysis in the different plant families displayed that the XTH family are

organized in 3 or 4 groups with few duplication. In conclusion, although, the XTH gene family has been identified and characterized for many plants, our comparative and evolutionary study of XTHs genes provide an extensive knowledge on this gene family in 12 plant species, with important implications for further investigations on this gene family as well as for the genetic improvement of cell wall properties.