

GENOME WIDE CHARACTERIZATION OF LIPID TRANSFER PROTEINS (LTPS) MULTIGENIC FAMILY IN A RELEVANT OILSEED CROP: THE SUNFLOWER (*HELIANTHUS ANNUUS* L.) CASE.

VANGELISTI A.*, SIMONI S.*, GIORDANI T.*, USAI G.*, MASCAGNI F.*, VENTIMIGLIA M.*, NATALI L.*, CAVALLINI A.*

*) University of Pisa

sunflower, oilseed, Lipid Transfer Proteins, multigenic family

The sunflower (*Helianthus annuus* L.) is amongst the most widely cultivated crops in the world due to its oilseed production. For this reason lipid metabolism and accumulation in sunflower has been widely studied. In this context, Lipid Transfer Proteins (LTP) show a vast range of functions, including fast mobilization of lipid in the seed. LTPs are low molecular mass proteins forming a broad multigenic family in higher plants, nevertheless these proteins have not been studied in sunflower at genomics level. For this reason, the aim of our work is to exploit the reliable genome sequence of sunflower, constructed using third generation sequencing technology, in order to identify and characterize LTP multigenic family in *H. annuus*. Overall, 101 putative sunflower LTP genes were identified by using homology search from known LTP sequence and by exploiting hidden Markov model algorithm, in order to retrieve possible divergent LTPs in the genome. The selected sequences were characterized by phylogenetic analysis, exon-intron organization and protein structural motifs; results from these analyses allowed the subdivision of sunflower LTPs in four clades which reflected genetical and structural organization. The four clades were further investigated by analyzing possible duplication origins, which showed a prevalence of possible tandem and whole genome duplication events for sunflower LTPs, a result that is in line with polyploidization events occurred during sunflower genome evolution. Furthermore, LTPs expression was evaluated by RPKM values on cDNA libraries constructed on six sunflower tissues (leaf, root, ligul, seed, stamen and pistil) and from leaves and roots treated with stimuli mimicking biotic and abiotic stresses. In particular, three out of four clades responded specifically to external stimuli, especially to abscisic acid, auxin and saline environment. Interestingly, one clade was expressed exclusively in sunflower seed. These results pose the bases for further analyses aimed to identify key genes involved into lipid accumulation in seed, which might be targeted for genome editing experiments.