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EXPLORING A MODEL FOR THE FORMATION OF NOVEL GENES FROM TRANSPOSONS IN PLANTS

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

*) Department of Agriculture, Food and Environment, University of Pisa, Via del Borghetto 80, 56124 Pisa (Italy)
**) Department of Biotechnology, University of Verona, Cà Vignal 1, Strada Le Grazie 15, 37134 Verona (Italy)
***) Center for Desert Agriculture, Biological and Environmental Sciences & Engineering Division (BESE), King Abdullah University of Science and Technology (KAUST), Thuwal 23955-6900 (Saudi Arabia)

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The sunflower (*Helianthus annuus* L.) has an estimated genome size of 3.6 Gbp composed mainly of repetitive DNA, which amounts to about 80% of the genome and is mostly represented by transposable elements (TEs). Being able to move across the genome, TEs are responsible for rapid genome remodelling by creating structural rearrangements and new regulatory gene networks. A less investigated aspect concerns the molecular domestication of TEs, which leads to the formation of novel genes through exaptation. Through this mechanism, a TE with positive phenotypic effects to the host loses its ability to move and assumes the characteristics of a conventional gene evolving under selective phenotypic pressure. After setting up a protocol for systematically discovering exapted transposable elements (ETEs) in large genome species, we identified and validated 3,530 sunflower ETEs standing out from their ancestral TEs by repetitiveness, expression, siRNA coverage and similarity with already known TEs. We performed a comparative genomic investigation to infer the evolutionary history of sunflower ETEs with lettuce and artichoke as representatives of Asterids II, coffee for Asterids I, and grape and Arabidopsis outgroup species. From this analysis, the bulk of ETEs resulted specific to the sunflower, suggesting that the genomes undertook different evolutionary dynamics after speciation. ETE

orthologous sequences, identified based on similarity and synteny, were mostly retrieved in lettuce and artichoke. At the same time, few ETEs presented orthologues in the genome of all the analyzed species making the hypothesis of a conserved function. We investigated the expression pattern across several tissues/organs to gain insight into the potential functionality of sunflower ETEs to highlight tissue-specific expressions. Overall, ETEs resulted more activated in pistil and root, whereas leaf and seed showed the lower expression values. Differential expression of these genes was observed in roots, comparing control cDNA libraries with different libraries of treatments mimicking biotic and abiotic stimuli: auxin, ethylene, gibberellic acid, salicylic acid, kinetin, abscisic acid, strigolactones, brassinosteroids, polyethylene glycol, jasmonic acid and salt. A core of 1,499 ETEs was detected as differentially regulated, indicating that auxin, abscisic acid and jasmonic acid treatments triggered over and under expression of ETEs while other stimuli showed no effect. Furthermore, the distribution of functional domains of differentially regulated ETEs, identified by Pfam, revealed that a relevant fraction is related to pentatricopeptide repeat (PPR) and PPR repeat domains, which are RNA-binding proteins involved in many aspects of RNA editing. The identification of sunflower ETEs can be considered further proof of the fundamental contribution that TEs had in the rising of genetic novelties, probably influencing different biological processes during the evolution of the sunflower.