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GENOME-WIDE IDENTIFICATION, COMPARISON AND EXPRESSION PROFILING OF ECERIFERUM (CER) GENE FAMILY IN SUNFLOWER AND *ARABIDOPSIS THALIANA*

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Epicuticular wax acts as a first line of defense to protect the plants from biotic and abiotic stresses by sealing the areal parts of land plants. Eceriferum (CER) is class of proteins that play vital role in very long chain fatty acids elongation and epicuticular wax biosynthesis. However, genes coding these proteins have not been yet studied in sunflower because sunflower genome have recently been sequenced and no previous study is available for the genome-wide analysis in this crop. Therefore, present study was designed to exploit the CER gene family in sunflower. A comprehensive genome wide analysis of CER genes/proteins was conducted to identify the genes coding CER proteins in *Helianthus annuus* and *Arabidopsis thaliana* by using computational tools. It was concluded that 44 CER genes were present in sunflower genome and 27 genes in *Arabidopsis Thaliana*. These genes were unevenly distributed in both plant species. Phylogenetic analysis showed that CER genes are clustered in eight clades in these species. From conserved motif analysis, it was observed that there were 19 conserved motifs of CER proteins in both plant species. Cis-regulatory element prediction showed that there were many hormone and stress-related cis-regulatory elements in promoter regions. Expression of CER genes were checked through different drought stress treatments and concluded that activation of these genes and expression analysis showed distinct expression patterns of CER genes under abiotic stress conditions.

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