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Comparative evolutionary analysis of DNA-binding with one-finger (DOF) transcription-factor family among species from Poaceae, Fabaceae and Malvaceae

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ABSTRACT SUBMISSION

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Text Abstract

The availability of complete genome sequences of numerous plant species has led to the study of various transcription factor families. These insights at the whole genome level can provide evolutionary clues for expansion of gene families and can help to predict their functions. DOF proteins are plant-specific transcription factors which have been implicated in diverse plant processes such as seed germination, seed development, carbohydrate and secondary metabolism, light mediated gene regulation, vascular tissue development, disease response, cell cycle regulation and hormone homeostasis. In this study, a comparative analysis of DOF TF family was carried out in *Oryza sativa*, *Sorghum bicolor*, *Zea mays*, *Arabidopsis thaliana*, *Cajanus cajan*, *Cicer arietinum*, *Glycine max*, *Medicago truncatula*, *Gossypium raimondii* and *Gossypium arboreum*. From the inferred phylogeny, it was observed that DOF family has been expanded with evolutionary process from single-celled green algae *Chlamydomonas reinhardtii* having single *DOF* gene to tetraploid soybean with 78 *DOF* encoding genes. It was also inferred that *DOF* TFs regulating the seed development process in rice, sorghum and maize were evolved in *Poales*-specific lineage. Investigations of gene structure has revealed that the several introns were lost from *CrDof* during evolution, so majority of *DOF* genes in higher plants are either intron-less or have single intron. Some intron re-gain events have also been observed. Segmental as well as tandem duplications seemed to be responsible for expansion of *DOF* family in studied *Poales*. Whereas tandem duplication events seemed to be main route for the expansion of *DOF* family in *Fabales*. Gene duplication studies in *Malvales* suggested that large-scale segmental duplications might have been solely responsible for the *DOF* family expansion in *Gossypium* species. These findings led us to hypothesize that most of the recent expansions of the *DOF* family have involved development-related genes.

App Yes

Approval Confirm

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