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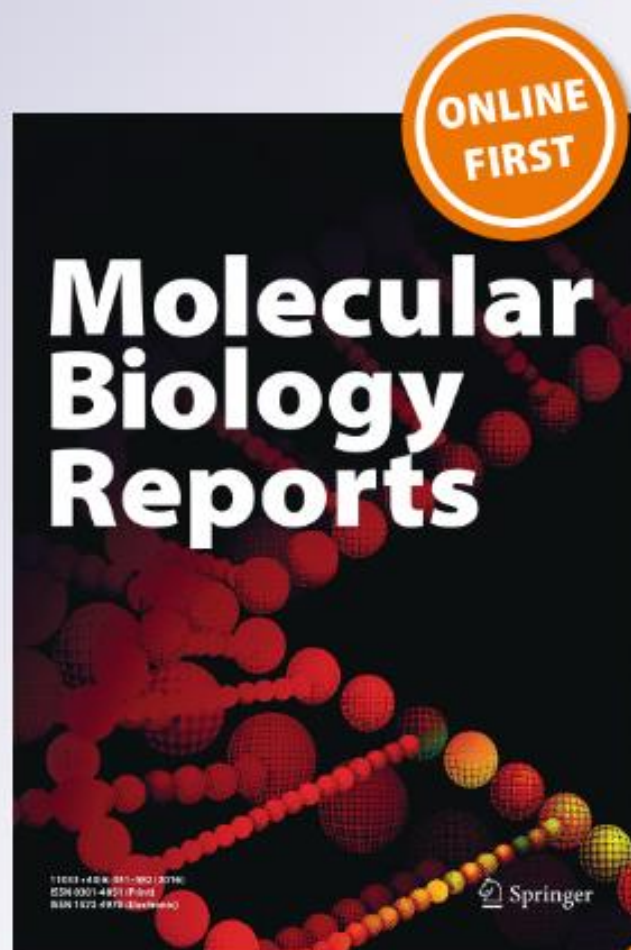
*Molecular cloning and expression profiling
of multiple Dof genes of Sorghum bicolor
(L) Moench*

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SHORT COMMUNICATION

Molecular cloning and expression profiling of multiple *Dof* genes of *Sorghum bicolor* (L) Moench

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Abstract DNA binding with one finger (Dof) proteins represent a family of plant specific transcription factors associated with diverse biological processes, such as seed maturation and germination, phytohormone and light mediated regulation, and plant responses to biotic and abiotic stresses. In present study, a total of 21 *Dof* genes from *Sorghum bicolor* were cloned, sequenced and in silico characterized for homology search, revealing their identity to Dof like proteins. The expression profiling of *SbDof* genes using quantitative RT-PCR in different tissue types and also under drought and salt stresses was attempted. The *SbDof* genes displayed differential expression either in their transcript abundance or in their expression patterns under normal growth condition. Two of the *SbDof* genes namely *SbDof8* and *SbDof12* showed comparatively high level of transcript abundance in all the tissue types tested; whereas some of the *SbDof* genes showed a distinct tissue specific expression pattern. Further a total of 13 *SbDof* genes showed differential expression when subjected to either of the abiotic stress i.e. drought or salinity. Three of the *SbDof* genes namely *SbDof12*, *SbDof19* and *SbDof24* were found to be up-regulated in response to drought and salt stress. Comparative analysis of *SbDof* genes expression revealed existence of a complex transcriptional and functional diversity across plant growth and developmental stages.

Keywords DNA binding with one finger (Dof) · Sorghum · Expression profiling · Abiotic stress · Transcription factor

Introduction

In plants, DNA binding with one finger (Dof) proteins constitute a large family of transcription factors that are associated with various plant specific biological processes [1, 2]. Proteins in this family contain one conserved domain of about 52 amino acid residues, located in the N-terminal region and characterized by presence of a Cys2Cys2 zinc finger [3] that binds specifically to *cis*-regulatory elements containing the common core 5'-T/AAAG-3' [4]. A large number of Dof proteins from different crops revealing functional diversity has been recently reviewed [5]. Dof transcription factors that are involved in response to drought and salt stress have recently been characterized from tomato. *Arabidopsis* plants over-expressing tomato *Dof* genes, *SlCDF1* and *SlCDF3* showed increased drought and salt tolerance by activating the expression of various stress-responsive genes, including *COR15*, *RD29A*, and *RD10* [6].

The Dof family has evolved from a common ancestor in *Chlamydomonas reinhardtii*, where only one *Dof* gene has been reported and expanded into the different taxonomic groups from ferns and mosses to vascular plants [7]. There are 36 Dof family members in *Arabidopsis*, 30 in rice, 41 in poplar, 26 in barley, 31 in wheat, 28 in sorghum, 78 in soybean, 54 in maize, 27 in *Brachypodium*, 34 in tomato and 38 in pigeon pea [5].

Sorghum (*Sorghum bicolor* L. Moench) is an important cereal crops, providing food, fiber, fuel, and feed-stocks across a range of environments and production systems. Worldwide, sorghum is the fifth-most important cereal crop.

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