In Silico Analysis of DREB2 Transcription Factor Gene family in *Aeluropus littoralis*

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Abstract: Multiple stresses such as extreme salinity, dehydration and chilling are considered as the major abiotic stresses which affect survival and productivity of many momentous crop species around the world [1]. Plants react to the environmental stimuli conditions through the physiological, cellular and molecular proceedings. The dehydration-responsive element-binding (DREB) proteins (consisting two sub families namely CBF1/DREB1 and DREB2), from the APETALA2 (AP2) transcription factors family, improve the expression of stress-responsive genes by interlocking to the DRE/CRT *cis*-regulatory element existed in their promoter sequences [2]; so play the important role to orchestrate the various stress-related factors. In this study, a total of 9 DREB2 proteins were identified in the *Aeluropus littoralis* genome via RNA-seq data sets, and *in silico* analyses were performed in order to inspect the structure and function of DREB2 family transcription factors. All AlDREB2s revealed the AP2 domain (IPR016177) and atleast one conserved motif was also detected in their sequences. The results showed that AP2 domain sequence was well conserved between some grass species (like *Aegilops tauschii*, *Dichanthelium oligosanthes*, *Setaria italica*, *Panicum hallii*, atc), whereas some amino acids substitutions or insertions were detected in their AP2 domains, which can influence the DNA-binding valency of DREB proteins [2]. The number of amino acids ranged from 236 (DREB2-3) to 448 (DREB2B-3), while the molecular weight varied between 24.92 kDa (DREB2-3) and 48.48 kDa (DREB2B-3). Theoretical pI values showed that most DREBs were of alkalic character; the acidic amino acids (Asp and Glu) ranged from 16 (DREB2-3) to 59 (DREB2B-2), while the alkalic amino acids (Lys and Arg) ranged from 24 (DREB2-3) to 43 (DREB2-2). Post-translational changes are necessary for well-adjusting of developmental and stress responses. The phosphorylation sites were detected on all proteins revealing the crucial role of phosphorylation in *Aeluropus* DREB2s adjustment. All AlDREB2s contained atleast one S-nitrosylation site, except for DREB2B-1, DREB2B-3 and DREB2-3. Multiple ubiquitination sites were also predicted in all proteins except for DREB2A-2. Sumoylation sites were recognized in DREB2B-2, DREB2-1, DREB2A-1 and DREB2C only, illustrating the potential fixing mechanism of them in response to abiotic stress circumstances. The analysis of subcellular localizations indicated that most of the AlDREB2s proteins were predicted to be found in nuclear region supporting that AlDREB2s proteins may contain a specific nuclear localization signal. Our findings can be helpful for understanding the mostly unexplored DREB2s mediated signaling networks which are crucial for the survival of plants under abiotic stress circumstances.

Keywords: *Aeluropus littoralis*; DREB2; *in silico* analysis, Abiotic stress, halophyte

References

[1] M. Akhtar, A. Jaiswal, G. Taj, J. P. Jaiswal, M. I. Qureshi, N. K. Singh, DREB1/CBF transcription factors: their structure, function and role in abiotic stress tolerance in plants, J. Genet., 91(2012) 385-395.

[2] B. Pandey, P. Sharma, M. Saini, D. M. Pandey, I. Sharma, Isolation and characterization of dehydration-responsive element-binding factor 2 (DREB2) from Indian wheat (*Triticum aestivum* L.) cultivars, Aust. J. Crop Sci., 8(2014) 44.