

Phylogenetic analysis of few dehydration-responsive element-binding homologs in Poaceae

T. Sonasree, D. Leena Lavanya

Department of Botany, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore, Tamil Nadu, India

ABSTRACT

Nucleotide sequence of dehydration-responsive element-binding (DREB) gene from *Oryza sativa* was retrieved and taken for the study. BLAST was performed on the retrieved sequence and 10 nucleotide sequences were selected from the hits, which belonged to the family Poaceae. MEGA X software was used to do multiple alignments and to perform phylogenetic analysis. Concerning DREB gene phylogenetic study is carried out among the 10 plants (*O. sativa*, *Oryza glaberrima*, *Oryza brachyantha*, *Oryza coarctata*, *Brachypodium distachyon*, *Avena sativa*, *Poa pratensis*, *Hordeum vulgare*, *Hordeum brevisbulatum*, and *Schedonorus arundinaceus*).

Keywords: BLAST, Dehydration-responsive element-binding gene, MEGA X, Multiple sequence alignment

INTRODUCTION

Grasses (Poaceae) are the fifth largest family of flowering plants in the world, with approximately 11,500 species and about 768 genera (Soreng *et al.*, 2017). The grass family is economically, ecologically, and evolutionarily one of the most successful species-rich groups, due to which it represents as a model family for the study of speciose taxa (Trevor, 2018). A wide range of environmental stress such as drought, high salt, and temperature affects plants all over the world. Due to these environmental changes and stress exerted on the crops, the growth and yield are very much affected. Worldwide, there is about 50% reduction of average yield, and 10% is due to the environmental stresses, particularly drought and salinity (Bray *et al.*, 2000). Response to abiotic stresses is a very complex phenomenon as various stages of plant development can be affected by a particular stress and often several stresses simultaneously affect the plant (Chinnusamy *et al.*, 2004). Dehydration-responsive element-binding protein (DREB) is a type of plant-specific transcription factor which specifically binds to DRE/CRT elements in the response to abiotic stresses such as drought and low temperature and their function was identified in *Arabidopsis* (Gilmour *et al.*, 1998; Liu *et al.*, 1998) at first. DREB1 and DREB2 genes have specific roles in *Arabidopsis* like it can improve the tolerance to drought, and it can increase the survival rate under cold stress, respectively.

METHODOLOGY

BLAST was done with *Oryza sativa* (Acc. no: AY064403.1) nucleotide sequence for DREB gene. The hits list was studied

and nine plants (E-value = 0) belonging to the family Poaceae were selected. Their nucleotide sequences were retrieved from NCBI in FASTA format, and further analysis was performed using MEGA X software for the 10 nucleotide sequences (*O. sativa*, *Oryza glaberrima*, *Oryza brachyantha*, *Oryza coarctata*, *Brachypodium distachyon*, *Avena sativa*, *Poa pratensis*, *Hordeum vulgare*, *Hordeum brevisbulatum*, and *Schedonorus arundinaceus*). To study the positions placed according to taxonomic details among the selected plants, NCBI taxonomic browser was used. Alignment and phylogenetic study was conducted using software Mega X (Tramura *et al.*, 2013). Alignment is done using Clustal W method. Phylogenetic tree was obtained using maximum likelihood method.

RESULTS AND DISCUSSION

The present study deals with the evolutionary aspects of few selected plants with respect to DREB gene through simple phylogenetic analysis. Nucleotide sequence for DREB gene in *O. sativa* was selected and BLAST was run. Sequence selection from the BLAST hits for further analysis is done based on e value (0) and from plants belonging to Poaceae. The details

DOI: 10.30954/2319-5169.2.2020.2

Submission: 06-09-2020

Acceptance: 29-10-2020

Received: 12-09-2020

Published: 17-12-2020

*Corresponding author: D. Leena Lavanya, Department of Botany, Avinashilingam Institute for Home Science and Higher Education for Women, Coimbatore, Tamil Nadu, India.
E-mail: leena.draviam.christy@gmail.com

of pairwise alignment with the query sequence are given in Table 1. FASTA format of selected nucleotide sequences was downloaded for further analysis using MEGA X.

Multiple sequence alignment using Clustal W was done using Molecular Evolution Genetic Analyzer (MEGA X) software. Pairwise distance analysis was conducted using the maximum composite likelihood model (Tamura *et al.*, 2004) [Figure 1] which shows that *Oryza glaberrima* and *O. sativa* are close, while *H. vulgare* and *O. sativa* are found to be far distantly placed.

The evolutionary history was inferred using the minimum evolution method (Rzhetsky and Nei, 1992). The optimal tree with the sum of branch length = 0.92997563 is shown in Figure 2. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were

computed using the maximum composite likelihood method (Tamura *et al.*, 2004) and are in the units of the number of base substitutions per site. The ME tree was searched using the close-neighbor-interchange algorithm (Nei and Kumar, 2000) at a search level of 1. The neighbor-joining algorithm (Saitou and Nei, 1987) was used to generate the initial tree. Evolutionary analyses were conducted in MEGA X (Kumar *et al.*, 2018) and the result shows the same tree division of two main branches of plants belonging to Pooideae and Oryzoideae subfamily. Taxonomic browser results also indicated that all 10 plants belonged to BOP clade under two subfamilies Pooideae (*B. distachyon*, *A. sativa*, *P. pratensis*, *H. vulgare*, *H. brevisbulatum*, and *S. arundinaceus*) and Oryzoideae (*O. sativa*, *O. glaberrima*, *O. brachyantha*, and *O. coarctata*).

Timeline or time tree is performed for the 10 selected plants [Figure 3] using MEGA X software. It shows that genus

Table 1: Results of pairwise alignment with *Oryza sativa*

S. No.	Sequence		Pairing range	E value	Identities	Gaps
	Plant name	Length				
1.	<i>Oryza glaberrima</i>	1449	514–1449	0.0	926/936 (99%)	0/936 (0%)
2.	<i>Oryza brachyantha</i>	3467	355–1347	0.0	904/997 (91%)	7/997 (0%)
3.	<i>Oryza coarctata</i>	849	1–849	0.0	795/849 (94%)	3/849 (0%)
4.	<i>Brachypodium distachyon</i>	8470	493–1517	0.0	830/1031 (81%)	45/1031 (4%)
5.	<i>Avena sativa</i>	1057	32–1052	0.0	820/1028 (80%)	39/1028 (3%)
6.	<i>Poa pratensis</i>	1050	11–990	0.0	786/987 (80%)	34/987 (3%)
7.	<i>Hordeum brevisbulatum</i>	1059	6–1049	0.0	830/1051 (79%)	44/1051 (4%)
8.	<i>Hordeum vulgare</i>	1328	304–1325	0.0	813/1029 (79%)	40/1029 (3%)
9.	<i>Schedonorus arundinaceus</i>	1409	365–1404	0.0	826/1051 (79%)	48/1051 (4%)

```

24 [ 1] #Oryza_sativa
25 [ 2] #Oryza_brachyantha
26 [ 3] #Oryza_glaberrima
27 [ 4] #Oryza_coarctata
28 [ 5] #Brachypodium_distachyon
29 [ 6] #Avena_sativa
30 [ 7] #Poa_pratensis
31 [ 8] #Hordeum_brevisbulatum
32 [ 9] #Hordeum_vulgare
33 [10] #Schedonorus_arundinaceus
34 -
35 [ 1 2 3 4 5 6 7 8 9 10 ]
36 [ 1]
37 [ 2] 0.19109
38 [ 3] 0.00752 0.32638
39 [ 4] 0.06291 0.15321 0.06162
40 [ 5] 0.32470 1.00968 0.57612 0.26539
41 [ 6] 0.24986 0.25306 0.25698 0.26339 0.11667
42 [ 7] 0.24147 0.26369 0.23718 0.24061 0.12688 0.07016
43 [ 8] 0.24443 0.25798 0.25473 0.23876 0.15374 0.12039 0.11427
44 [ 9] 0.35795 0.37349 0.50458 0.29155 0.24974 0.12884 0.12402 0.01869
45 [10] 0.32682 0.49424 0.52374 0.28772 0.32215 0.08336 0.05156 0.12271 0.29275
    
```

Figure 1: Pairwise distance data of evolutionary divergence

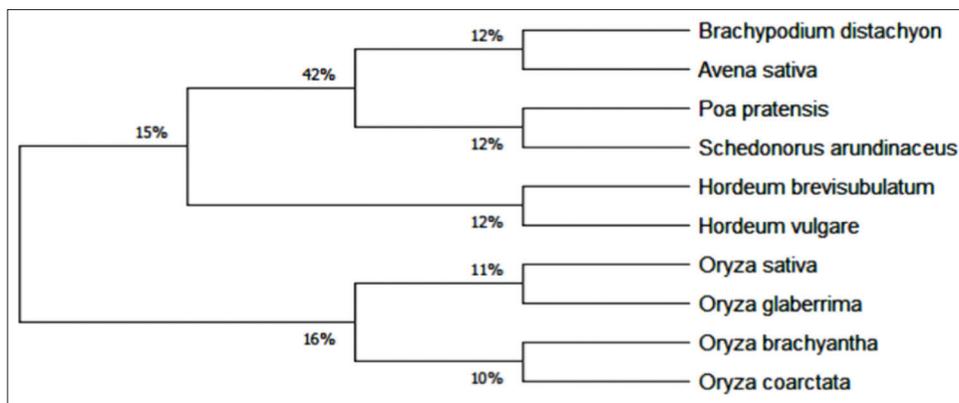


Figure 2: Evolutionary relationships of taxa taken for the study

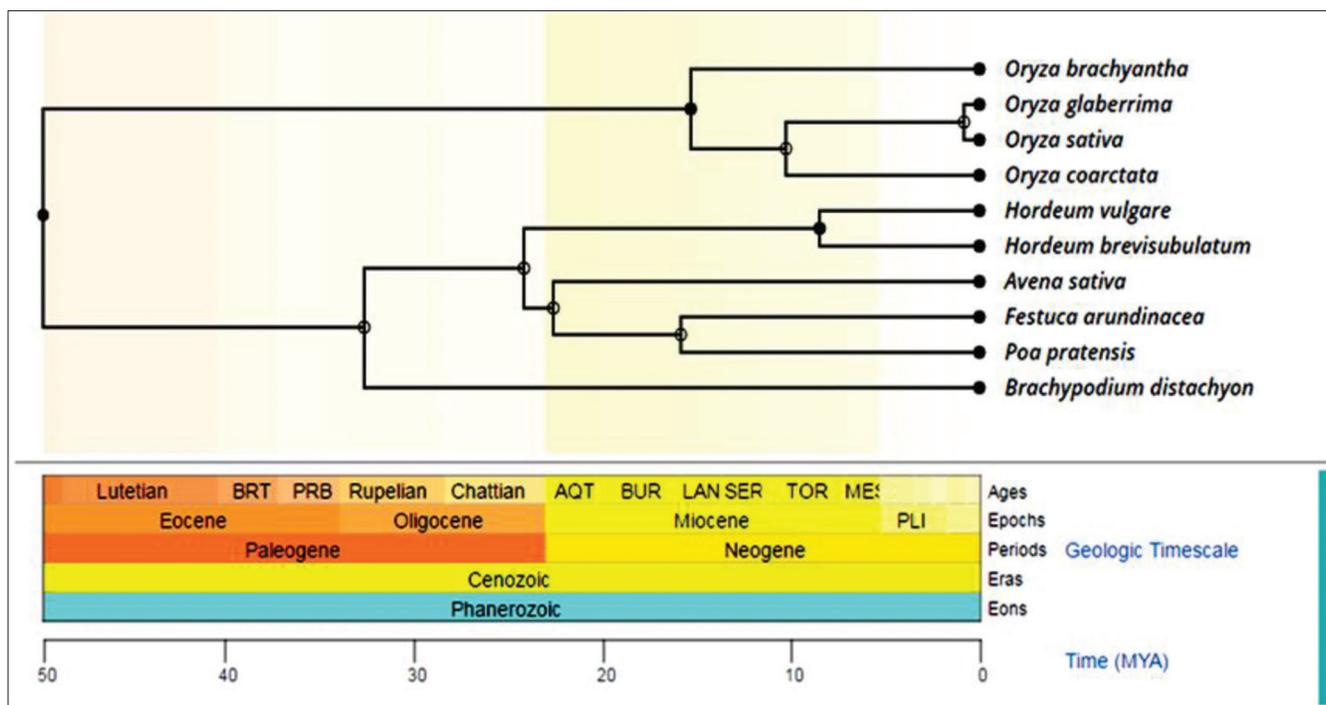


Figure 3: Time line tree for the 10 plants selected for the study

Oryza has evolved during Lutein ages, while the species of *Oryza* evolved during Miocene epochs. *O. glaberrima* and *O. sativa* were found to get evolved PLI epochs. *O. sativa* and *O. glaberrima* are Asian and African rice, respectively, and according to Ndjiondjop *et al.* (2018), both have a narrow genetic diversity.

CONCLUSION

The plants selected for this study belong to BOP clade and subfamilies Pooideae and Oryzoideae. Taxonomic browser tree and the tree generated through MEGA X software using DREB gene showed that the two subfamilies were grouped together. These results show that DREB gene is a homologous gene among the selected plants taken for this study.

Financial Support and Sponsorship

Nil.

Conflicts of Interest

The authors declare that there is no conflict of interest in this work.

REFERENCES

- Bray, E.A., Bailey-Serres, J. and Weretilnyk, E. 2000. Responses to abiotic stresses. In: Buchanan, B.B., Gruissem, W. and Jones, R.L., editors. Biochemistry and Molecular Biology of Plants. American Society of Plant Biologists, Rockville, MD. pp. 1158-1203.

- Chinnusamy, V., Schumaker, K. and Zhu, J. 2004. Molecular genetic perspectives on cross-talk and specificity in abiotic stress signalling in plants. *J. Exp. Bot.*, 55, 225-236.
- Gilmour, S.J., Zarka, D.G., Stockinger, E.J., Salazar, M.P., Houghton, J.M. and Thomashow, M.F. 1998. Low temperature regulation of the Arabidopsis CBF family of AP2 transcriptional activators as an early step in cold induced COR gene expression. *Plant J.*, 16, 433-442.
- Kumar, S., Stecher, G., Li, M., Knyaz, C. and Tamura, K. 2018. MEGA X: Molecular evolutionary genetics analysis across computing platforms. *Mol. Biol. Evol.*, 35(6), 1547-1549.
- Liu, Q., Kasuga, M., Sakuma, Y., Abe, H., Miura, S., Yamaguchi-Shinozaki, K. and Shinozaki, K. 1998. Two transcription factors, DREB1 and DREB2, with an EREBP/AP2 DNA binding domain separate two cellular signal transduction pathways in drought- and low-temperature-responsive gene expression, respectively, in Arabidopsis. *Plant Cell*, 10(8), 1391-1406.
- Ndjiondjop, M.N., Wambugu, P., Sangare, J.R., dro, T., Kpeki, B. and Gnikoua, K. 2018. *Oryza glaberimma* steud. In: Mondal, T. and Henry, R., editors. The Wild *Oryza* genomes. Compendium of Plant Genomes. Springer, Cham.
- Nei, M. and Kumar, S. 2000. Molecular Evolution and Phylogenetics. Oxford University Press, New York.
- Rzhetsky, A. and Nei, M. 1992. Statistical properties of the ordinary least-squares, generalized least-squares, and minimum evolution methods of phylogenetic inference. *J. Mol. Evol.*, 35, 367-375.
- Saitou, N. and Nei, M. 1987. The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.*, 4(4), 406-425.
- Soreng, R.J., Peterson, P.M., Romaschenko, K., Davidse, G., Teisher, J.K., Clark, L.G., Barbera, P., Gillespie, L.J. and Zuloaga, F.O. 2017. A worldwide phylogenetic classification of the *Poaceae* (Gramineae) II. An update and comparison of two 2015 classifications. *J. Syst. Evol.*, 55, 259-290.
- Tamura, K., Nei, M. and Kumar, S. 2004. Prospectus for inferring very large phylogenies by using the neighbor-joining method. *Proc. Natl. Acad. Sci. U. S. A.*, 101, 11030-11035.
- Tamura, K., Stecher, G., Peterson, D., Filipski, A. and Kumar, S. 2013. MEGA6: Molecular evolutionary genetics analysis version 6.0. *Mol. Biol. Evol.*, 30, 2725-2729.
- Trevor, R.H. 2018. Evolution and taxonomy of the grasses (*Poaceae*): A model family for the study of species-rich groups. *Annu. Plant Rev.*, 1, 1-39.

How to cite this article: Sonasree T, Lavanya DL. Phylogenetic analysis of few dehydration-responsive element-binding homologs in Poaceae. *Int. J. Bioinform. Biol. Sci.* 8(2), 7-10.