Structural investigation of Indica rice (Oryza sativa L.) DREB1AP2 domain in response to GCC-BOX DNA: an insight from molecular dynamics

Kundan Singh, Rajpal Singh Jadhao1*, Jitendra Maharana2, Kailash Chandra Samal1, Sukanta Kumar Pradhan2 & Gyana Ranjan Rout1

1Department of Agricultural Biotechnology, College of Agriculture, Orissa University of Agriculture and Technology, Bhubaneswar-751 003, Odisha, India
2Department of Bioinformatics, Centre for Post-Graduate Studies, Orissa University of Agriculture and Technology, Bhubaneswar-751 003, Odisha, India

Received 03 May 2016; revised 27 April 2017

In adverse environmental conditions, genes show specific expression pattern according to their biological and physiological functions. Plant stress tolerance is a genetically complex trait that involves many genes and their expression patterns. Transcription factors (TFs) are vital for sustaining expression of certain genes by interacting with the basal transcription apparatus at target gene promoters to enhance or suppress the target gene functions. DREB proteins are having the conserved domains and functional motifs, which interact with 11 bp of GCC box of promoters and facilitate transcription of stress inducible gene(s). In the present investigation, we predicted the 3D-structure of rice DREB1-AP2 domain from isolated coding sequence of ten indica rice (Oryza sativa L.) cultivars and observed the dynamic interaction of GCC box (DREB1-AP2 domain). The dynamic properties of the DREB1-AP2 domain and its interaction with GCC box DNA were investigated by molecular dynamics simulations. Analysis of protein DNA interface showed that most of the conserved interactions were taking place in the residues of Gly85, Arg87, Arg89, Trp91, Lys93, Arg99, Arg106, Trp108, Ser111, and Tyr122 with GCC box DNA of promoter in Indica rice. In addition, another conserved residue, Arg103 (Lys166 of 1GCC) is interacting with GCC box. Global motion of the protein during MD simulation was analyzed, principal components of backbone atoms of the DREB1-AP2 domain in both apo and holo condition depicted that the higher motion in apo condition, than holo (or, DNA-bound) state. Overall, this study will help to understand the molecular mechanism of a DERB1 protein family in a broader prospective.

Keywords: AP2 domain, DREB, Molecular dynamics simulations, Oryza sativa, Sequence analysis; Transcription factor

Plants are exposed to a wide range of environmental stresses during their life. Abiotic stresses like drought, extreme temperatures, and salinity are the major limiting factors of crop plants leads to water stress, which declines the crop growth and productivity worldwide.12 Plants struggle with these stresses at molecular, physiological and biochemical levels. During these adverse environmental conditions, genes show specific expression patterns in accordance with their biological and physiological functions. However, plants stress tolerance is a genetically complex trait that involves many genes and multiple signalling pathways used to respond to such conditions in plants. Transcription factors (TFs) are vital for sustaining expression of functional protein genes in the genome by interacting with the basal transcription apparatus at target gene promoters to enhance or suppress the target gene function(s). The TFs are interacting with specific cis-acting elements in the promoters regions of various stress-related genes have up-regulated the expression of many downstream genes imparting the tolerance to environmental stress and pathogen attack. Several major transcription factors that are active in response to abiotic stress have been identified in Arabidopsis and rice. In addition, bioinformatics analysis has identified several TFs induced under drought stress and that include TFs like C-repeat binding factor (CBF)/Dehydration responsive element binding (DREB) protein. TFs can be classified in six major families: AP2/ERF (APETAL2/ethylene-response factor) bZIP (Basic leucin-zipper protein), MYB/MYC, Zinc-finger protein, CDT-1 and NAC families and DREB. DREB is one of the largest families of TFs that play vital roles in signalling network which modulates many plant processes, such as abiotic stress tolerance. DREB TFs have been grouped into DREB1.
and DREB2. DREB1 includes 4 additional novel genes that comprise DREB1A (CBF3), DREB1B (CBF1), DREB1C (CBF2), and DREB1D (CBF4), whereas, DREB2 includes 6 genes. In rice, five DREB homologs were identified which includes OsDREB1A, OsDREB1B, OsDREB1C, OsDREB1D, and OsDREB2A. DREB1/CBF and DREB2 TFs function in ABA-independent gene expression, whereas the ABA responsive element (ABRE) binding protein (AREB)/ABRE binding factor (ABF) TF functions in ABA-dependent gene expression. Previous studies demonstrated that DREB1, DREB2, AREB/ABF, and NAC TFs have vital roles in response to abiotic stresses in rice. Members of DREB, MYB, bZIP, and zinc-finger families have been well studied functionally with their roles in the regulation of plant defence and stress responses. Additionally, the DNA-binding specificity of Arabidopsis DREBs is well known. DREB play key roles in plant stress signalling pathways and can bind specifically to DRE/CRT element (G/ACCGAC). It has been shown that both DREB1 and DREB2 specifically bind to six nucleotides (A/GCCGAC) of DRE. An important advancement in the area of understanding plant signal transduction under drought and cold stress was the identification of the DRE. It contains 9 bp (TACGACAT), with a 5 bp core sequence (CCGAC). This consensus sequence is generally referred as GCC-box, thus strongly suggesting that DREB proteins contain GCC-box binding motif and activate the expression of many stress inducible genes. A DREB gene comprises the members of AP2/ERF DNA binding domain of transcription factor family; regulate the biological processes against cold and dehydration stresses. In the plant kingdom, AP2/EREBP (APETALA2/ethylene-responsive element-binding protein) is a large family of TF genes. AP2/EREBP genes contain the highly conserved AP2/ERF DNA binding domain encoded by TFs genes. Homology of an AP2 domain of DREB protein and its binding element has been done in many plants. However, only a few reports exist that reveals the binding properties of this protein with the gene(s) promoter. DREB1 transcription factor seems to be one of the molecular mechanisms of target recognition and to visualize target genes for transcription factors at the genomic level, it is important to examine the relationship between the structure and function of transcription factors.

In the present study, we explored the structure and function of rice DREB1 gene and its binding mechanism with GCC box. Herein, we predicted the 3D model of rice DREB1-AP2 domain and observed the dynamic interaction with GCC-box to understand the dynamic stability and molecular interactions. This is the first report to uncover the novel protein-DNA interface mechanism of AP2/EREBP domain in rice using various computational tools.

### Materials and Methods

#### Genotypes

Based on the reported data (data not shown) of ten promising drought tolerance and susceptible upland as well as lowland cultivars of rice (Oryza sativa L.) viz. ‘Swarupa Sub-1’, ‘Udaygiri’, ‘Lalat’, ‘Bandana’, ‘RGL’, ‘Jagannath’, ‘Daya’, ‘Pary’, ‘Mahalaxmi’, and ‘Khandagiri were collected from the Rice Research Station, Orissa University of Agriculture and Technology, Bhuvaneswar and ICAR-National Rice Research Institute (NRRI), Cuttack, Odisha, India.

#### DNA Extraction and PCR amplification

Fresh leaf tissues (~3g fresh weight) were collected and ground to a fine powder in liquid nitrogen. The genomic DNA of ten rice cultivars was extracted using modified CTAB method and purified DNA of each cultivar was subjected to PCR amplification using designed gene-specific overlapping oligos viz. left 5′CCTCATTGGGTCAGGAAGAA3′ and right 5′GGATCTCAGCCACCCACTTA3′ (Merck Bioscience, India) as described earlier.

#### PCR Product Purification and Sequencing

The single bright amplicon of approximately 0.24 Kbp were eluted and purified from each ten samples using DNA fragments extraction Kit (Gene Aid) with the published protocol. The genomic DNA of ten rice cultivars was extracted using modified CTAB method and purified DNA of each cultivar was subjected to PCR amplification using designed gene-specific overlapping oligos viz. left 5′CCTCATTGGGTCAGGAAGAA3′ and right 5′GGATCTCAGCCACCCACTTA3′ (Merck Bioscience, India) as described earlier.

#### PCR Product Purification and Sequencing

The single bright amplicon of approximately 0.24 Kbp were eluted and purified from each ten samples using DNA fragments extraction Kit (Gene Aid) with the published protocol. The genomic DNA of ten rice cultivars was extracted using modified CTAB method and purified DNA of each cultivar was subjected to PCR amplification using designed gene-specific overlapping oligos viz. left 5′CCTCATTGGGTCAGGAAGAA3′ and right 5′GGATCTCAGCCACCCACTTA3′ (Merck Bioscience, India) as described earlier.

#### Sequence and phylogenetic analysis

After sequencing, the nucleotide sequences of DREB1 were translated into protein sequences using EXPASY translates tool. The resulted sequences from all ten cultivars were aligned in ClustalW program to infer the variation and conserveness in the alignment. The result showed that conserved amino acid sequences for all ten cultivars. These amino acid sequences (from conserved regions) from all ten cultivars were employed as a query sequence for searching the homologous sequences in protein
databases through protein BLAST search (http://blast.ncbi.nlm.nih.gov/Blast.cgi). Phylogenetic analysis was carried out with our query sequences (from conserved regions) against the downloaded database sequences. All the alignment gaps were treated as missing data, and NJ algorithm was used for the calculation of evolutionary distances by applying 1000 bootstraps incorporating Kimura-2 parameter substitution model in MEGA6.

**Domain analysis, homology modeling and model validation**

The translated protein sequence of DREB1 was taken for domain analysis using a combination approach of domain search by using CD-search, SMART, and InterPro tools followed by Pfam database and inter-species multiple sequence alignment in Clustal Omega. The topology of the AP2 domain was drawn in PDB sum (http://www.ebi.ac.uk/pdbsum). The physiochemical properties such as molecular weight, iso-electric point (pI), molecular formula, instability index, aliphatic index, extinction coefficient, and grand average hydropathy of the rice AP2 domain were assessed by using ProtParam tool (http://web.expasy.org/protparam/).

The structural homologue of the AP2 domain was searched through PSI-BLAST for homology modelling. A total of 50 models of the AP2 domain (with/without GCC-box) were generated using MODELLER v9.14 by employing advance modelling protocol. The best model was evaluated based on a discrete optimized protein energy (DOPE) score. Model validation of DREB1-AP2 domain was performed using PROCHECK, ERRAT, and WHATIF programs to conform the accuracy stereo-chemical quality of the built model. The validated model was taken for further structural analyses.

**Molecular dynamics simulation**

Molecular dynamics (MD) simulation was employed to elucidate the structural dynamics of the DREB1-AP2 domain in apo and holo (GCC-bound) condition. MD simulations of both apo and holo systems (AP2 domain and GCC-bound AP2 domain) were carried out in GROMACS using CHARMM22 force field. The simulation systems were solvated using SPC216 water molecules in two different cubic boxes. A minimum distance of 10 Å was kept between protein/complex and box edges. The simulation systems were neutralized by adding a physiological ionic strength (0.15 M) of counter ions. The atomic compositions of both the simulation systems are provided in Table S1. The method and parameters of MD simulations were adopted from a recent work. The trajectory analysis was performed using incorporated tools of GROMACS. To understand the global motion of rice DREB1-AP2 domain in apo and holo condition, Principal component analysis (PCA) was employed using g_covar and g_anaeig programs. The time-dependent secondary structure of the models was analyzed using STRIDE program implemented in visual molecular dynamics (VMD 1.9.1) program. Two-dimensional (2D) graphs were plotted using Grace5.1.23 program (http://plasma-gate.weizmann.ac.il/Grace/).

**Results and Discussion**

**PCR amplification and sequencing**

The sharp and bright bands of 0.24 kbs of a DREB1 gene fragment from template DNA of different rice cultivars were amplified by using designed set of primers (Fig. 1). For the sequencing, large scale amplification was done, and amplified fragments were separated on 2.5% low agarose gel and subsequently used for eluion though Gene aid gel elution kit (www.geneaid.com). The 10 eluted fragments of rice cultivars were sequenced with an ABI 3730 XL genetic analyser with a Big Dye terminator cycle sequencing kit (Xcelris Genomics Ltd., Ahmedabad, India). For the correctness of the sequences, DNAs isolated from independent cultivar was analyzed. The sequences of this amplicon were observed varied from 193 bp to 215 bp long nucleotides. The partial nucleotide sequences were deposited in NCBI GenBank with accession numbers KF545561-KF545569.

![Fig. 1 — Amplification of ten rice cultivars employing DREB1-AP2 gene specific primer. M=Low range DNA markers; Name of cultivars represents on the top of the gel. Numbers on the right side of margin represents molecular weight marker DNA in base pairs (bps).](http://example.com/fig1.png)
Sequence and Phylogenetic Analysis

All nucleotide sequences of rice cultivars were searched for homology in BLASTX program revealed that all ten amplified sequences are bearing the DNA-binding domain with maximum homology with AP2/DREB1 protein. The AP2 domain sequences revealed that the two conserved functional amino acids residues such as valine and glutamic acid at 14th and 19th position (Suppl. Fig.1). Similarly, AP2 domain comprises three strand anti-parallel β-sheets and one α-helix towards N-terminal region and C-terminal end and conserved residues such as valine and glutamic acid at 14th and 19th positions respectively. Further, based on the MSA a phylogenetic tree was drawn for deduced protein along with reported AP2/DREB proteins (Fig. 2). Phylogenetic tree revealed that two distinct clusters I and II, whereas Glycine max as an out group. Oryza sativa cultivar was placed in an Ith cluster along with Oryza sativa subsp. indica and Oryza sativa subsp. japonica with maximum bootstrap value 12. Model plant such as Arabidopsis thaliana and Nicotiana tabacum placed in an IIth cluster with maximum bootstrap value 87. Our analysis implied that DREB subfamily could easily be classified on the basis of AP2 domain. Further computational, biochemical analysis of AP2 domain signifies the molecular weight of 6.64 kDa with theoretical isoelectric point (pI) 10.81. Among 20 essential amino acids, DREB1-AP2 domain encompasses maximum percentage of alanine (A) and arginine (R) with 19% and 15.5% respectively, which indicates DNA binding affinity of the AP2 domain. Through computational observation, about 819 of atoms were encompassed in AP2 domain protein with their atomic composition and formula C298H454N94O79S1 including a total number of negatively charged (Asp + Glu) and positively charged (Arg + Lys) residues 5 and 10 respectively. The computed instability index was 28.65, and grand average of hydropathicity (GRAVY) was −0.622 which indicates the stability of AP2 domain of the DREB1 protein.

Homology modelling and structure analysis

The tertiary structure of DREB1-AP2 domain was modelled in modeling program MODELLER 9.14(http://www.salilab.org/modeller/) by using crystal structure of the GCC-box binding domain of Arabidopsis thaliana (PDB ID: 2GCC). Similarly, the 3D structure of DREB1 and DERB2 from B. napus and T. aestivum was predicted using Python-based protein homology modeling program, Modeller 9.1049,50.Sequence identity and query coverage between target and template were 61% and 96% respectively, indicating the structural and thermodynamic stability of the model.48,51. The developed 3D model structure of the DREB1-AP2 domain of rice was deposited to the PMDB database with model ID: PM007976252. A previous study had indicated that the

![Fig. 2 — Phylogenetic analysis of AP2 domain of translated DREB1 protein. Values on the tree node indicate bootstrap values in per cent.](image-url)
homology modelling and protein’s 3D structure was very much helpful in understanding the protein interactions, functions and localisations, when the experimental 3D-structure of the protein is not available53,54. The model validation was performed in SAVeS server (http://nihserver.mbi.ucla.edu/SAVES). A comparative approach of model validation was considered to know the reliability of the built model. Ramachandran plot analysis by PROCHECK showed ‘94.40 %’ of amino acids in the most favored region and all residues are in accepted range to assure the quality of predicted model43. ProSAz-score report indicated the parameters are within the accepted range. ProQ analysis resulted the model is fairly good. MolProbity server showed no major errors in Cβ-deviation, bad backbone bonds, and angles. Overall the model seems stereo-chemically acceptable for further analysis and details of validation report is depicted in Table 1. The built model consists of one α-helix (with a long coil towards N-terminal) and three β-sheets with connecting coils. Similarly, the β-sheets regions are possibly responsible GCC binding55 (Fig. 3).

Analysis of structural stability
To understand the structural stability of the protein in both apo and holo state, we performed MD simulation for 10 ns time scale in GROMACS 4.5.5 simulation suite. The backbone RMSD of protein in holo condition seems stable than that of apo, which suggests the protein is quite stable in holo condition than that of apo in dynamic state (Fig. 4A). From Cα RMSF, we found a similar type of observation, where, the residual fluctuations were very high in apo than that of holo (Fig. 4B). The evolution of secondary structure from the MD trajectories showed that GCC-bound model retained more conserved secondary structure than that of apo state (Fig. 5).

Molecular interaction
A Living system is a complex network of biomolecules, ions and metabolites and their interactions. Particularly, proteins-DNA interactions serve as a critical role in cellular functions and subsequently modulate the activities of other biomolecules56. Protein-DNA complexes play a critical role in many biological processes like transcriptional regulation and DNA modification57. Therefore it is important to understand the interaction of protein-DNA complexes and to

<table>
<thead>
<tr>
<th>Servers</th>
<th>DREB1 (O. sativa)</th>
<th>ERF1A (A. thaliana)</th>
</tr>
</thead>
<tbody>
<tr>
<td>PROCHECK</td>
<td>94.40</td>
<td>90.60</td>
</tr>
<tr>
<td>Additional allowed regions (%)</td>
<td>3.70</td>
<td>9.40</td>
</tr>
<tr>
<td>Generously allowed regions (%)</td>
<td>1.90</td>
<td>0.00</td>
</tr>
<tr>
<td>Disallowed regions (%)</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>PROSA z-score</td>
<td>-4.09</td>
<td>-3.83</td>
</tr>
<tr>
<td>PROQ LGscore</td>
<td>1.84</td>
<td>1.13</td>
</tr>
<tr>
<td>MaxSub</td>
<td>0.26</td>
<td>0.12</td>
</tr>
<tr>
<td>MolProbity Cβ deviation (%)</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Bad backbone bonds (%)</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>Bad backbone angles (%)</td>
<td>0.00</td>
<td>0.00</td>
</tr>
</tbody>
</table>
study the factors regulating their interaction\textsuperscript{58}. To infer the involvement of critical residues responsible for interaction with DNA, we performed interaction analysis of all complexes (GCC-bound ERF1A (\textit{A. thaliana}); GCC-bound AP2-domain-GCC complex before and after MD by using PyMOL and NukePLOT. The details of the interaction of ERF1A-GCC bound/DREB1-GCC bound (before and after MD) complexes are depicted in Suppl. Fig. 2 & Fig. 6. In ERF1-GCC complex (of \textit{A. thaliana}; 1GCC), the

Fig. 5 — Secondary structure assessment of DREB1-AP2 domain in (A) apo and (B) holo condition during MD simulation. The legends indicate the different secondary structure components.

Fig. 6 — (A) Illustration of DREB1-AP2 domain and GCC-box molecular interaction, (B) Sequence analysis suggests conserved interaction of ERF1-GCC and DREB1-AP2-GCC box. The red arrow indicates the residues interacting in both ERF1 and DREB1, blue and green arrow indicate interaction of GCC with \textit{A. thaliana} DREB1B and rice DREB1-AP2 domain respectively.
established interaction between the residues, Arg147, Gly148, Arg150, Arg152, Trp154, Lys156, Arg162, Arg170, Trp172, Trp75, Trp186, and GCC-box was noticed. The above residues were responsible for H-bond interaction with GCC. The stability of the complex is mainly due to the hydrogen bond (H bond) formation, ionic bonds and Van der waal interaction.

The most of the conserved interactions take place in the residues of Gly85, Arg87, Arg89, Trp91, Lys93, Arg99, Arg106, Trp108, Ser111, and Tyr122 and interacting with GCC in case indica rice. The involvement of conserved Arg84 (Arg147 of 1GCC) in H-bond formation during dynamic condition could not obtained. In addition common residues, another conserved residue, Arg103 (Lys166 of 1GCC) is interacting with GCC box (Fig. 5B). A recent computational study was also advocated that the binding site of AP2 domain is quite different, which contradicts to ERF1-GCC binding interface of *A. thaliana* and our prediction. Overall, the interaction between GCC and rice DREB1-AP2 domain suggested similar type of interaction in ERF1A-GCC bound complex. So, any mutations in these key amino acids may cause change in a protein conformation and may subsequently disturb the AP2-DNA interaction. The details of the interaction of all the complexes were provided in Table 2.

### Principal Component Analysis

The protein-function relay upon their plasticity, elasticity, ligand/substrate recognition, structural stability, etc. Here, to understand the global motion of the protein during MD simulation, we analyzed the principal components of backbone atoms of the DREB1-AP2 domain in both apo and holo condition. We observed that the higher motion in apo condition, than holo (or, DNA-bound) state. In apo condition, the β-sheet region becoming flattened, whereas we found curved structured β-sheets in the holo state. The more helical movement is observed in apo state than holo. A differential motion was noticed in N-terminal coil region; where the coil regions showed inward movement towards the GCC-box in the holo state, whereas in the apo state outward movement was noticed, and from this we assumed, there might have some involvement of additional N-terminal residues other than AP2 domain in GCC-binding (Fig. 7).

<table>
<thead>
<tr>
<th>ERF1A-GCC (PDB ID: 1GCC) (<em>A. thaliana</em>)</th>
<th>DREB1-GCC (O. sativa): Before MD</th>
<th>DREB1-GCC (O. sativa): After MD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Arg147:NH2</td>
<td>DG17:C:OP1</td>
<td>2.89</td>
</tr>
<tr>
<td>Gly148:N</td>
<td>DG18:C:OP2</td>
<td>2.78</td>
</tr>
<tr>
<td>Arg150:NH2</td>
<td>DG20:C:N7</td>
<td>2.85</td>
</tr>
<tr>
<td>Arg150:NH2</td>
<td>DG20:C:O6</td>
<td>2.79</td>
</tr>
<tr>
<td>Arg152:NH1</td>
<td>DG5:B:N7</td>
<td>3.24</td>
</tr>
<tr>
<td>Arg152:NH1</td>
<td>DG21:C:O6</td>
<td>2.91</td>
</tr>
<tr>
<td>Arg152:NH2</td>
<td>DG21:C:O6</td>
<td>2.87</td>
</tr>
<tr>
<td>Trp154:NE1</td>
<td>DA4:B:OP2</td>
<td>2.90</td>
</tr>
<tr>
<td>Lys156:NZ</td>
<td>DA4:B:OP1</td>
<td>2.81</td>
</tr>
<tr>
<td>Arg162:N</td>
<td>DG17:C:OP2</td>
<td>2.99</td>
</tr>
<tr>
<td>Arg162:NA</td>
<td>DG17:C:N7</td>
<td>3.11</td>
</tr>
<tr>
<td>Arg162:NH2</td>
<td>DG17:C:N7</td>
<td>3.17</td>
</tr>
<tr>
<td>Arg162:NH2</td>
<td>DG17:C:O6</td>
<td>2.98</td>
</tr>
<tr>
<td>Arg170:NH2</td>
<td>DC7:B:OP2</td>
<td>2.86</td>
</tr>
<tr>
<td>Arg170:NE</td>
<td>DC7:B:OP2</td>
<td>3.15</td>
</tr>
<tr>
<td>Arg170:NH1</td>
<td>DG8:B:N7</td>
<td>2.93</td>
</tr>
<tr>
<td>Trp172:NE1</td>
<td>DG5:B:OP2</td>
<td>2.77</td>
</tr>
<tr>
<td>Thr175:OG1</td>
<td>DG5:B:OP2</td>
<td>2.76</td>
</tr>
<tr>
<td>Tyr186:OH</td>
<td>DG17:C:OP1</td>
<td>2.63</td>
</tr>
</tbody>
</table>

N.B. Figures (normal font) represents non conserved interactions; Figures (bold font) represents conserved interaction.
Conclusion

Transcription regulation of abiotic stress-related genes is a potential area of interest for improving stress tolerance in plants. In the present study, we have isolated and computationally characterized DREB1-AP2 gene from ten indica rice cultivars to explore the molecular interactions of protein-DNA in a dynamic condition. It is observed that, DREB proteins had the conserved domains and motifs which interact with GCC box of promoters and facilitates the transcription of stress inducible gene(s). The combined approach of molecular modeling, docking, and molecular dynamics simulations are employed to elucidate the molecular interaction between the DREB1-AP2 domain and GCC. It is observed that the interactions of rice DREB1-GCC complex are similar with Arabidopsis ERF1-GCC complex. It was concluded that amino acid residues that interact with DNA bases are highly conserved and any mutations in key residues may lead to the change in protein structure and eventually its function. It is also depicted that the differential structural movement in N-terminal regions of rice DREB1-GCC complex might have some involvement of extra N-terminal residues (other than AP2 domain) in GCC-binding. This study will show a new height and help in better understanding of stress biology in crop plants at the molecular level.

Acknowledgement

The authors wish to acknowledge the Department of Biotechnology, Government of India for providing financial assistance under PG teaching HRD program.

References


