

Insilico Analysis of cis acting Regulatory Elements CAREs in Upstream Regions of Ascorbate Glutathione Pathway Genes from *Oryza sativa*

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CAREs play an important role in plant stress tolerance by interacting with transcription factors and controlling the expression of many stress related potential genes. Recognition of promoters and their regulatory elements is one of the crucial challenges in biotechnology. In this study, we examine cis acting regulatory element in 5' upstream regions (~1 kb) of Asc-Glu pathway genes such as SOD, APX, MDHAR, DHAR, and GR. The evolutionary relationships amongst these sequences were deciphered using MEGA v. 6.0. The promoter region these genes contain various cis acting regulatory elements such as MBS, DRE/C repeat, W box, HSE, TCA element, LTR, ABRE box, ARE box, Wun and DRE that have significant role in stress tolerance Asc-Glu promoter sequences analysis revealed their specific responsiveness or overlapping in various environment stress and significantly contribute toward plant growth and development.

Plants have evolved complex molecular mechanisms by which they adapt and tolerate these adverse conditions. When they perceive stress conditions, plant cells reprogram their cellular processes by triggering a network of signalling events leading to changes in gene expression and eventually altered cellular response. Exposure of plants to unfavourable environmental conditions such as extreme temperature, heavy metals, drought, water availability, air pollutants, nutrient deficiency or salt stress can increase the production of ROS. To protect themselves against these toxic oxygen intermediates, plant cells and cell organelles like chloroplast, mitochondria and peroxisomes employ antioxidant defence systems. A great contract of research has established that the induction of the cellular antioxidant machinery is important for protection against plant stresses. The components of antioxidant defence system are enzymatic and non-enzymatic. Enzymatic include SOD, CAT, APX, MDHAR, DHAR and GR and non-enzymatic are GSH, ascorbic acid, carotenoids and tocopherols. The above said antioxidants found in almost all cellular compartments, demonstrating the importance of ROS detoxification for cellular survival.

The finding of the ascorbate-glutathione pathway genes in almost all cellular compartments as well as the high affinity of APX for H₂O₂ plays a crucial role in controlling the level of reactive oxygen species in these compartments. Plants acclimate to stresses by triggering a cascade or network of

events that starts with stress perception and ends with the expression of a series of target genes. The key components of the stress response association are illustrated. These are stress stimulus, signals, transducers, transcription regulators, target genes, and stress responses, including morphological, biochemical, and physiological changes. Cis-acting regulatory elements (CARE) are key switches for the transcriptional regulation of a dynamic network of gene expression controlling different biological processes, including abiotic stress responses, hormone responses and developmental processes. Especially, understanding regulatory gene networks in stress response cascades depends on victorious functional analyses of cis acting elements. The ever-improving accuracy of transcriptome expression profiling has led to the identification of various stresses responsive. CARE in the promoter regions of stress-inducible genes involved in stress and hormone responses. Different transcription factors interact with CARE in promoter regions and make a transcriptional initiation complex on the TATA box core promoter upstream of the transcriptional initiation sites. In this process, different interactions between CARE and transcription factors function as molecular switches for transcription to determine transcription initiation events. The roles of CAREs play in transcription are well defined in higher plants, and these include core promoter elements, enhancers, silencers and insulator sequences. The core promoter motifs are located ~35 bp, either upstream region of the transcription start site and include TATA box or initiator. Plant stress signals activate transcription factors by induction of genes, proteins activation by phosphorylation, and proteins degradation via proteasome. We consider that it is potential to determine CAREs in the stress responsive promoters to understand the molecular switches of stress inducible genes which are binding sites for transcription factor located in the promoter regions of genes are the functional elements that determine the timing and location of transcriptional activity. Long year, wide promoter analyses have identified a large number of which are major molecular switches involved in the transcriptional regulation of a dynamic network of gene activities controlling many biological activity and plant stress response. CARE also involved in the dehydration, salinity, heat, cold and ABA responsive transcription of APX, SOD, MDHAR, DHAR, and GR genes. As well acknowledged, regulation of gene expression includes a broad range of

mechanisms that are used by cells to enhance or reduce the construction of specific gene products is informally termed gene regulation.

The present study was aimed to examine to in silico analysis of promoters of (APX), superoxide dismutase (SOD), monodehydroascorbate reductase (MDHAR), dehydroascorbate

reductase (DHAR), and glutathione peroxidase (GR) sequences present up to 1000 bp upstream region and evolutionary relationship of major ascorbate glutathione pathway genes of *Oryza sativa* in involve plant defence responses against plant stress tolerance.