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Introduction

e 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.

Materials and Methods

Database search

e sequences of rice genes that are involved in the ascorbate-glutathione pathway such as Ascorbate peroxidise (APX), Monodehydroascorbate reductase (MDHAR), Dehydroascorbate reductase (DHAR), Super oxide dismutase (SOD) and Glutathione reductase (GR) and their upstream regions were retrieved from NCBI databases (http://www.ncbi.nlm.nih.gov).

Identi cation of 5' regulatory region of antioxidant genes involved in ascorbate glutathione pathway in rice genome

All the upstream nucleotide sequences and coding domain sequences concerned in plant stress defences mechanism were con rmed against the *Oryza sativa* genome using Basic local alignment Tool (http://blast.ncbinlm.gov/blast/cgi). Locus link was used to identify genomic sequences of 1 kbp extending 5' from the translation start site of each antioxidant gene family involved in plant stress defence mechanism. ese sequences were used for the computational analysis.

Cis acting regulatory element analysis (CAREs)

1.0 kbp of 5' upstream region of each antioxidant gene family involved in plant stress defence mechanism in were scanned for the presence of putative cis-regulatory element with registered in Plant CARE (http://bioinformatics.psb.ugent-be/webtools/plantcare/html/) and PLACE (http://www.dna.a rc.go.jp/PLACE/signalscan.html) tools. e details of sources of the upstream sequences of antioxidant protein/ enzymes encoding genes in *Oryza Sativa* are given in Table 1.

Evolutionary relationship analysis

For evolutionary relationship, maximum parsimony trees for all ve protein sequences were created using Molecular Evolutionary Genetics Analysis Version 6.0. e relationships between adjacent nodes were based on bootstrap support from 5000 replicates. e number indicated percentages against each node.

In vitro analysis

Plant leaves were collected and treated with sterile solutions of 5.2 mM Methyl Viologen (MV), 5.2 mM H_2O_2, 5.2 mM ethephon (ET) and 5.2 mM salicylic acid (SA), for 12 h. Each treatment was performed in triplicate. Total cellular extracts were prepared at 4°C, and used in activity assays. e activities of APX, GR and SOD were determined through spectrophotometer.

Results

Citation: Pandey S, Subramanaym Reddy C, Yaqoob U, Negi YK, Arora S, et al. (2015) Insilico Analysis of cis acting Regulatory Elements CAREs in Upstream Regions of Ascorbate Glutathione Pathway Genes from Oryza sativa

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