

Journal of Bioengineering and Medical Technology

a SciTe<u>chnol journal</u>

Short Communication

Comparative Insilico Analysis of Ascorbate Peroxidase Protein Sequences from Different Plant Species

Saurabh Pandey , Yogesh Kumar Negi, Soma S. Marla and Sandeep Arora

Abstract

The presence of isoform variety among cancer prevention agent compounds adds to the spatial and transient calibrating of cell reactions. In plants heme restricting ascorbate peroxidase (APX) (EC, 1.11.1.11) presents an essential line of protection against responsive oxygen species. The current investigation plans to give a similar perspective on the practical credits of major isoforms of APX in plants species. A sum of 64 protein groupings of APX were exposed to homology search, different succession arrangement, phylogenetic tree development, and theme investigation. The phylogenetic tree developed uncovered various groups dependent on heme restricting APX in regard of dicot and monocot plants like diverse source of plant species addressed by Oryza sativa, Arabidopsis thaliana, Sorghum bicolor, Zea mays, Ricinus communis, Populus trichocarpa, Vitis vinifera, and Selaginella moellendorffii. The different succession arrangement of these APX protein groupings from various plants showed rationed areas at various stretches with most extreme homology in amino corrosive deposits. The theme investigation uncovered a monitored peroxidase space consistently saw altogether APX independent of variable plant species recommending its conceivable job in underlying and enzymatic capacities. The mark amino acids succession of VFYQMGLSDKDIVALSGGHTLGRCH, NNGL-HIAIRLCQPIKEQFPIITYADFYQLAGVVAVEVTGGPTIPM-HPGRV and LFEDPSFRPYVEKYAKDQDAFFKDYAEAHM-KLSELGF, related with the plant heme restricting peroxidase just as chloroplastic and cytosolic peroxidase mark was oftentimes noticed and appeared to be connected with the construction furthermore, enzymatic capacity on the whole APX protein groupings. The discoveries of the current examination might be helpful for planning degenerate preliminaries or tests explicit for APX and conceivably presents the main line of protection among all the APX isoforms engaged with the phone cancer prevention agent guard pathway, during openness to abiotic stresses

Introduction:

Aerobic life has developed by exploiting the abundance of environmental oxygen (O2) in the atmosphere to oxidize organic

compounds, thus obtaining chemical energy in a highly efficient manner. Paradoxically, the univalent reduction of molecular oxygen in metabolic reactions produces a plethora of partially reduced intermediates, commonly known as reactive oxygen species (ROS). If their levels are not tightly controlled, these chemical species can react with the majority of biological molecules and cause serious cellular damages . ROS are byproducts of aerobic metabolism and are produced in excess within plant cells under abiotic and biotic stresses . However, ROS are also important in many physiological processes and their balance is of the utmost importance. As a result, a complex system, comprising enzymatic and nonenzymatic mechanisms, maintains the delicate balance between oxidant and antioxidant compounds in the cell . Ascorbate peroxidase (APX) is known play the most essential role in scavenging ROS and protecting cells against these toxic effects in higher plants, algae, euglena and other organisms In plants, ascorbate peroxidases (EC, 1.11.1.11) catalyze the conversion of H2 O2 to H2 O2 using ascorbate as the specific electron donor in this enzymatic reaction. APX is the largest class of the nonanimal peroxidase superfamily, and its members are found in all living organisms except Diplomonads, Parabasalids, Apicomplexa, Amoebozoa, and animals Multiple sequence alignment All the sequences of APX were aligned using ClustalW [18] to find out the similarity present among the sequences of the same family. Phylogenetic analysis Phylogenetic analysis of the sequences was done by Molecular Evolutionary Genetic Analysis (MEGA) software (version 4.0.02) [19], using UPGMA method. Each node was tested using the bootstrap approach by taking 1,000 replications and a random seeding of 64,238 to ascertain the reliability of nodes. The number is indicated in percentages against each node. The branch lengths were drawn to scale indicated.

Conclusion:

In silico investigation of ascorbate peroxidase protein arrangements and its examination with other APX has uncovered the grouping based similitude existed among various APX isoforms and bunching in particular gatherings dependent on its source among various plants and nature of the system of enzymatic movement against the cancer prevention agent protection component in plants. In silico area investigation affirms the presence of the various gatherings of ascorbate peroxidase dependent on the presence of special areas, a heme restricting space found on the whole isoforms of APX. The presence or nonappearance of explicit areas was straightforwardly in connection with the underlying and useful association of various isoforms of ascorbate peroxidase.

Keywords: Antioxidant enzyme; Ascorbate peroxidase (APX); Protein sequence



All articles published in Journal of Bioengineering and Medical Technology. are the property of SciTechnol and is protected by copyright laws. Copyright © 2021, SciTechnol, All Rights Reserved