



## COMPARISON OF GENE CODING SEQUENCES OF BETAINE ALDEHYDE DEHYDROGENASE AND FERRITIN ENCODING GENES IN SEVERAL CROPS USING BIOINFORMATICS TOOLS

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### Abstract

Improving abiotic stress tolerance traits in crops using transgenic techniques has been highlighted in the recent years. Identification of the potentially hidden regulatory signals within the coding sequences of genes is important in the transfer of such genes via genetic engineering. Identification of short motifs in coding sequences those probably important for gene regulation was the major aim of the study. The bioinformatics analysis was used to study coding sequences of two genes related to drought response which encode Betaine aldehyde dehydrogenase (*BADH*) and Ferritin, in nine different crops including monocots (rice, foxtail millet, sorghum and maize) and dicots (chick pea, pigeon pea, adzuki bean, mung bean and cowpea). Coding Sequences were retrieved from the National Center for Biotechnology Information (NCBI). ClustalW multiple sequence alignment program was performed using MEGA<sub>5</sub> software. Phylogenetic trees following maximum likelihood approach with 100 bootstrap analysis and pairwise distances were obtained using MEGA<sub>5</sub> software. The DnaSP<sub>5</sub> software was used to analyze the conserved regions of two genes. *BADH* and Ferritin genes showed seven and six conserved regions respectively with significant ( $P \leq 0.05$ ) conservation and homozygosity values. Phylogenetic tree of *BADH* showed three distinct clusters whereas only two clusters were observed for Ferritin gene. There was a significant evolutionary divergence among CDS of *BADH* (0.017 - 0.406) and Ferritin (0.009 - 0.509) genes. The observed conserved regions for *BADH* and Ferritin CDS can be considered as the sequences with functional potential. The results indicated that some highly conservative sequences obtained from *BADH* and Ferritin CDS could be used in the phylogeny study to reconstruct the phylogenetic tree of some far related species in the taxonomy. Furthermore, the results of this study suggest that *BADH* and Ferritin encoding genes can be useful sources for genetic engineering of drought tolerance in plant species.

**Keywords:** Coding Sequences (CDS), conserved regions, phylogenetic relationships and evolutionary divergence