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Comparative Computational Analysis of Badh Isozyme of Selected Monocot and Dicot

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Abstract—*Glycine betaine is a key osmoprotectant to protect plants from high salinity. In all betaine producers, it is synthesized by a two-step oxidation of choline. In first step the enzyme choline monooxygenase (CMO) in plants, choline dehydrogenase (CDH) in animals and bacteria and choline oxidase in some bacteria oxidizes choline to an intermediate compound, betaine aldehyde. The second step is catalyzed by betaine aldehyde dehydrogenase (BADH) in the all organisms, to produce the end product, glycine betaine. The betaine aldehyde dehydrogenase (BADH) enzyme is known as the key enzyme for glycine betaine biosynthesis. Comparative genomic analysis is the cornerstone of in-silico based approaches to understand biological systems and processes across plant species in order to identify genes of agronomic interest. Thus, our aim was to use existing computational tools to comparatively analyze BADH isozymes of Hordeum vulgare, Oryza sativa, Sorghum bicolor, Arabidopsis thaliana, Glycine max, Leymus chinensis, Amaranthus hypochondriacus, Chrysanthemum lavandulifolium, Zoysia tenuifolia, Populus euphratica and Atriplex prostrate. In this study, we compiled detailed comparative information about BADH isozymes in selected plants by analyzing their structural features e.g. amino acid content, physico-chemical properties and secondary structural features. Functional characterization was done by predicting motifs, patterns, disulfide bridges and secondary structure. Functional analysis of these proteins includes identification of important 10 to 20 amino acids long motifs arise because specific residues and regions proved to be important for the biological function of a group of proteins, which are conserved in both structure and sequence during evolution. Present investigation will provide an insight for the biologists working with BADH isozymes in order to understand the functionality of BADH.*