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Cloning and sequence analysis of the safflower betaine aldehyde dehydrogenase gene

Y.B. Wang[1]*, L.L. Guan[2]*, Y.W. Xu[1], H. Shen[1] and W. Wu[1]

[1]Agronomy College, Chengdu Campus, Sichuan Agricultural University, Wenjiang, China
[2]Tropical Crops Genetic Resources Institute, Chinese Academy of Tropical Agricultural Sciences, Haikou, China

*These authors contributed equally to this study.
Corresponding author: W. Wu
E-mail: ewuwei@sicau.edu.cn / ewuwei@gmail.com

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ABSTRACT. In response to salinity or drought stress, many plants accumulate glycine betaine, which is a regulator of osmosis. In plants, the last step in betaine synthesis is catalyzed by betaine aldehyde dehydrogenase (BADH), a nuclear-encoded chloroplastic enzyme. Based on the conserved oligo amino acid residues of the published *BADH* genes from other higher plant species, a cDNA sequence, designated *CtBADH*, was isolated from safflower (*Carthamus tinctorius* L.) using a polymerase chain reaction approach. The clones were 1.7 kb on average, and contained an open reading frame predicting a polypeptide of 503 amino acids with 84.5% identity to that of *Helianthus annuus*. The deduced amino acid sequence showed a decapeptide, Val-Thr-Leu-Geu-Leu-Gly-Gly-Lys-Ser-Pro and Cys, which is essential for proper functioning of BADH. Phylogenetic analysis indicated that *CtBADH* grouped with other dicotyledonous plant *BADH* genes, and subgrouped in the composite family. Prediction of secondary structure and subcellular localization suggested that the

protein encoded by *CtBADH* contains 33 coils, 15 alpha helixes, and 21 beta strands, and most likely targets the chloroplast or mitochondria.

Key words: Betaine aldehyde dehydrogenase; Phylogenetic analysis; Safflower; Secondary structure; Subcellular localization

