

THE DIFFERENTIAL EXPRESSED BRANCHED-CHAIN AMINOTRANSFERASE (HvBCAT-1) FROM BARLEY IS CAPABLE TO COMPLEMENT YEAST DEFICIENCY

M. MALATRASI****, M. CORRADI*, J. T. SVENSSON**, T. J. CLOSE**, M. GULLI*,
N. MARMIROLI*

*) Dipartimento di Scienze Ambientali, Sez. Genetica e Biotecnologie Ambientali, Parco Area delle Scienze, Università di Parma, 43100 Parma, Italy

**) Department of Botany and Plant Sciences, University of California, Riverside, CA 92521-0124, USA

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The BCAs (branched-chain amino acids) are essential amino acids which plants are able to “de novo” synthesize. Very little is known about the last step of the catabolic/anabolic pathway catalyzed by the branched-chain amino acid aminotransferases (BCATs). Analysis of gene expression in barley seedling shoots by Differential Display Reverse Transcriptase Polymerase Chain Reaction (DDRT-PCR) led to the isolation of several drought-, cold- and ABA-induced cDNA short sequences. One of these (DD12) corresponds the HvBCAT-1 gene, which belongs to the BCAT gene family in barley. The structure of HvBCAT-1 has been elucidated: the coding region is interrupted by six introns and contains a predicted mitochondrial transit peptide, the gene has also been mapped on chromosome 4H. A comparative analysis with the homologous genes from rice and *Arabidopsis* has been performed in order to identify conserved structural patterns. Complementation of a yeast (*Saccharomyces cerevisiae*) double knockout strain revealed that HvBCAT-1 can function as the mitochondrial (catabolic) BCATs *in vivo*. The transcriptional levels of HvBCAT-1, analyzed by Northern hybridization, by qualitative and quantitative RT-PCR and by microarray, under several conditions resulted increased in relation to drought condition. Tentatively, (as the first enzyme in BCA catabolic pathway) HvBCAT-1 might have a role in the increased degradation of BCA, previously discussed as a detoxification mechanism that maintains the pool of free branched-chain amino acid at low and not toxic levels in stress condition.