

Characterization of genes encoding target enzymes related in amino acid biosynthesis and herbicide resistance

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Herbicide resistance is important to study basic and applied agricultural research in transgenic plants. Acetolactate synthase (ALS) or chorismate synthase (CS) are the targets of several classes of herbicides that are effective to protect broad range of crops. ALS is a thiamine diphosphate-dependent enzyme in the biosynthetic pathway for isoleucine, valine and leucine and CS roles on the branch point for the synthesis of aromatic amino acids such as phenylalanine, tyrosine, and tryptophan in plants. The functional analysis of the genes encoding for ALS or CS from rice (*OsALS* or *OsCS*) is performed, respectively. Sequence analysis of ESTs and rice genome revealed that the full-length open reading frame for *OsALS* or *OsCS* are predicted with the protein of approximate molecular weight of 69.4 kDa or 46.9 kDa. The predicted amino acid sequences of *OsALS* or *OsCS* are highly homologous to those of the corresponding proteins from bacteria and plants. The *OsALS* or *OsCS* expression in *Escherichia coli* showed that the genes were functionally capable of complementing the *ilvH* or *AroC* mutant strains of *E. coli*, respectively. Expression of *OsCS* in *Escherichia coli* with or without bathophenanthroline, an inhibitor of CS, showed that the growth of the *AroC* mutant strain of *E. coli* with the inhibitor was severely retarded compared to wild type. These results indicate that the target genes encoding ALS or CS for amino acid synthesis and modulation by inhibitors including herbicides are able to characterize by molecular genetics and bioinformatics approaches.

Keywords : herbicide resistance, gene, functional complementation, acetolactate synthase, chorismate synthase, rice