CHARACTERIZATION OF THE REGULATORY MECHANISMS ASSOCIATED TO THE *SAL*T GENE EXPRESSION IN RICE PLANTS (Oryza sativa L.)

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Plants respond to stress by induction of genes that codify presumable protective proteins. In rice, many proteins are induced by salt stress. Among these, SALT protein was isolated and sequenced. The present work aimed to characterize the regulatory mechanisms associated to the *sal*T gene expression. Western blotting revealed that SALT protein is accumulated in response to several environmental stresses, and such levels are highly variable among cultivars. However, northern blot analysis demonstrated the mRNA accumulation is similar, suggesting the existence of pos-translational regulatory mechanisms. *In silico* analysis of the promoter region showed the presence of two transposons, in some rice cultivars. The results by western blot revealed that the transposable elements don't affect the final protein levels. In addition, a 610bp intron was identified on the 5' untranslated region of *sal*T gene. Thus, the elements responsible for the activation of the *sal*T gene are probably present between the transposable insertion point and the 5' intron, in a 223bp region. Analysis *in silico* of the region of 223bp and the intron showed the presence of sites for regulatory proteins. In the 223bp region were verified 6 transcription factors motifs related with environmental stresses. In the intron several sites for regulatory proteins were identified, suggesting a putative regulatory function of this region.