

ISOLATION AND CHARACTERIZATION OF THE PROMOTER REGION OF A BETA-AMYLASE GENE EXPRESSED DURING BANANA RIPENING

Astorino Filho, R.¹, Lajolo, F.M.¹, Nascimento, J.R.O.¹

¹Departamento de Alimentos e Nutrição Experimental, Faculdade de Ciências Farmacêuticas, Universidade de São Paulo, São Paulo, Brasil.

Transcription of banana beta-amylase gene is highly induced during the climacteric rise and it is concomitant to starch degradation during ripening. Previous data from molecular, enzymatic and immunological analysis suggest that beta-amylase could contribute to the starch breakdown and the transcription of its gene would play an important role in the regulation of this process. A better understanding on how ethylene, auxin and others factors modulate the expression of this gene would be provided by the isolation and characterization of the promoter region. In order to identify possible regulatory motifs present in this region, a 2,527 bp fragment corresponding to the 5' upstream region of a beta-amylase gene was cloned and compared to motif databases. The transcription initiation site was precisely determined by primer extension and the functionality of the promoter was accessed by transient expression assays using the GUS report gene. *In silico* analysis allowed the identification of putative ethylene and auxin responsive motifs and the transient expressions revealed a functional TATA-box located at -29 bp from the transcription-starting site. A fragment of 142 bp carrying the TATA-box was able to efficiently promote the transcription of the GUS gene, indicating that the genomic fragment correspond to a functional promoter from banana. We thank CNPq for the graduate fellowship and FAPESP for the financial support.