SEQUENCE ANALYSIS OF UDP-GLUCOSE: PROTEIN TRANSGLUCOSYLASE cDNAs IN POTATO AND mRNA EXPRESSION STUDIES

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UDP-Glucose:protein transglucosylase (UPTG) (EC 2.4.1.112) is a self-glucosylating protein (38 kDa) that can initiate protein-bound α–glucan synthesis *in vitro*. Its participation in the initiation of starch synthesis has been proposed (Bocca *et al.*, 1997).
The present paper reports the sequence analysis and the expression analysis at the mRNA level of two cDNAs coding for potato UPTG.
Two cDNAs, called E2 and E11, coding for potato UPTG were sequenced. These two cDNAs were isolated by screening a cDNA expression library, prepared from potato swelling stolon tips, with antibodies raised against the purified potato tuber UPTG (Bocca *et al.*, in press).
The two potato cDNAs sequenced are different in length, are highly similar in a central 1045-bp region and less conserved at their 3' ends. They code for a 365-amino acid and a 366-amino acid polypeptide respectively.
Database searches with the nucleotide and the amino acid sequences of E11 and E2 revealed several homologous sequences of plant origin. Some of these sequences present complete ORFs and code for proteins putatively involved in the biosynthesis of cell wall polysaccharides. Some of these proteins present biochemical properties similar to those of potato UPTG, like K_m for UDP-Glucose, activation by Mn^{2+}, kinetics of the reaction and sugar donor specificity (Delgado *et al.*, 1998; Dhugga *et al.*, 1997).
Northern Blot analysis of mRNA isolated from different potato tissues, by using the complete E11 cDNA as probe, shows that UPTG mRNA is present in all tested organs. Northern blot analyses using probes designed on the 3' end regions (partly untranslated) of E11 and E2 show different expression patterns at the mRNA level for these two cDNAs.

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