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Plant Gene Register

Primary Structure and Characterization of a cDNA Clone of Fructokinase from Potato (*Solanum tuberosum* L. cv Record)[1]

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The major source of carbon for starch synthesis in reserve tissues such as the potato (*Solanum tuberosum* L.) tuber is Suc. In the developing tuber, Suc is hydrolyzed principally by Suc synthase (EC 2.4.1.13) to UDP-Glc and Fru (Preiss, 1982). Fructokinase (EC 2.7.1.4) is believed to catalyze the phosphorylation of the Fru released to yield Fru-6-P. This sugar phosphate can then be used to support starch synthesis following further metabolism in the cytosol and amyloplast. There are some reports (Wolosiuk and Pontis, 1974) that Suc synthase activity can undergo feedback inhibition by free Fru. In this case fructokinase potentially plays an important role in maintaining the flux of carbon toward starch formation.

Fructokinase has been purified from a variety of plants including pea (Turner et al., 1977; Copeland et al., 1984), barley (Baysdorfer et al., 1989), avocado (Copeland and Tanner, 1988), and developing potato tubers (Gardner et al., 1992), but to date the corresponding gene has never been cloned from higher plants. A cDNA clone of the potato fructokinase gene has been isolated as a first step toward investigating more fully the role that fructokinase plays in carbohydrate metabolism in potato (Table I).

Table I. *Characteristics of a cDNA clone encoding potato fructokinase*

Organism:
Potato (*Solanum tuberosum* L. cv Record).

Gene, Function, and Pathway:
Fructokinase (EC 2.7.1.4); phosphorylation of Fru to Fru-6-P in the starch biosynthetic pathway.

Techniques:
cDNA library screen using polyclonal antibody for pea fructokinase; dideoxy sequencing of both strands using successive oligonucleotide primers.

Method of Identification:
Amino acid sequence comparison with *scrK* genes of *Vibrio alginolyticus* (39% identity; 63% similarity using GAP alignment package); cross-reaction with both pea and potato polyclonal antibodies.

Expression Characteristics:
A 1.2-kb transcript detected in swelling stolons, which increased during tuber development. Low levels were detected in leaves and stems taken from tuberizing plants.

Gene Copy Numbers:
Restriction digest analysis of genomic DNA indicated that the fructokinase gene is present in low copy number.

Features of cDNA Structure:
Contains an open reading frame of 957 bp. There is an ATG initiation codon at nucleotide 11 and a TAG termination codon at 968. A polyadenylation signal is present at 1119.

G+C Content:
50.4%.

Structural Features of Protein:
Polypeptide of 323 amino acids with a calculated mol wt of 34,392.

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The GenBank/EMBL accession number for the sequence reported in this article is Z12823.

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