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Expression of Sucrose Synthase in Sweet Potato

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Abstract:

PCR amplification of cDNA prepared from the poly (A)⁺ RNA of tuberous roots of sweet potato, using degenerate oligonucleotide primers based on highly conserved regions among sucrose synthase (EC 2. 4. 1. 13) reported previously, yielded a cDNA of 1, 191 bp (IBSUS). The nucleotide sequence of IBSUS exhibited a high degree of homology with the corresponding regions of the potato sucrose synthase cDNA sequences (82 and 86% of identical nucleotides). Less homology (76 ~ 77%) was found in the monocotyledonous sequences (maize, rice and barley). The activity of sucrose synthase in the tuberous roots of sweet potato was higher than that in other parts, namely, leaf blades, petioles, stolons and fibrous roots. The activity of sucrose synthase in roots increased markedly following an increase in sucrose during development of the tuberous roots. Northern blot analysis using IBSUS as a probe revealed that a signal of sucrose synthase mRNA with a size of approximately 2.4 kb was present in petioles, stolons, fibrous roots and tuberous roots, and the levels of sucrose synthase mRNA in different parts and in the roots during development of tuberous roots were highly correlated with enzymatic activities. In petioles, an increase in sucrose concentration led to an increase in the activity of sucrose synthase.

Keywords:

Gene expression, Sucrose, Sucrose synthase (EC 2. 4. 1. 13), Sweet potato

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