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Update section

Sequence

Nucleotide sequence of an osmotin cDNA from the *Nicotiana tabacum* cv. White Burley generated by the polymerase chain reaction

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Salt stress-induced changes in gene expression have been observed in a number of plant species, in both whole plants and cultured cells. In tobacco and tomato salt adaptation is associated with the accumulation of a 26 kDa protein, which has been termed osmotin in tobacco [1, 2, 3]. Highly homologous cDNA clones encoding osmotin or an osmotin-like protein have been isolated and sequenced from libraries constructed from the roots of salt-adapted tomato (*Lycopersicon esculentum* VFNT) plants, and from salt-adapted suspension cultures of tobacco (*Nicotiana tabacum* Wisconsin-38) [3, 4].

The present communication describes the nucleotide sequence of a PCR-amplified osmotin cDNA from salt-adapted suspension cultures of the tobacco cultivar White Burley, using primers derived from published sequence from the Wisconsin-38 cultivar [4]. The cDNA was cloned in both orientations into the phagemid vector pTZ (Pharmacia) and the sequence determined by the dideoxynucleotide chain termination method [5], each position being determined on average three times. The coding region is 738 bp, 6 bp longer than that of Wisconsin-38, and the predicted molecular mass of the encoded preprotein is 26697 Da. Assuming a signal processing site identical to the Wisconsin-38 osmotin [6], the molecular mass of the mature protein would be 24283 Da.

The main differences between the White Burley sequence, shown in Fig. 1, and the Wisconsin-38 sequence [4] can be summarised as follows: (a) nucleotide substitutions occur at 11 positions, 4 of them resulting in no change in amino acid. The remaining substitutions result in 5 changes in amino acid sequence, 3 of them being conservative changes; (b) there are 7 nucleotide insertions and 1 deletion, resulting in 2 additional amino acids; (c) there is a region of considerable variation from nucleotide positions 446–465 where 2 nucleotide substitutions followed by an insertion and a compensatory deletion result in changes in 7 consecutive amino acids.

Although the physiological function of osmotin is unknown, we are currently investigating its role in salt adaptation by introducing the gene into a different cellular environment.

The nucleotide sequence data reported will appear in the EMBL, GenBank and DDBJ Nucleotide Sequence Databases under the accession number X61679.

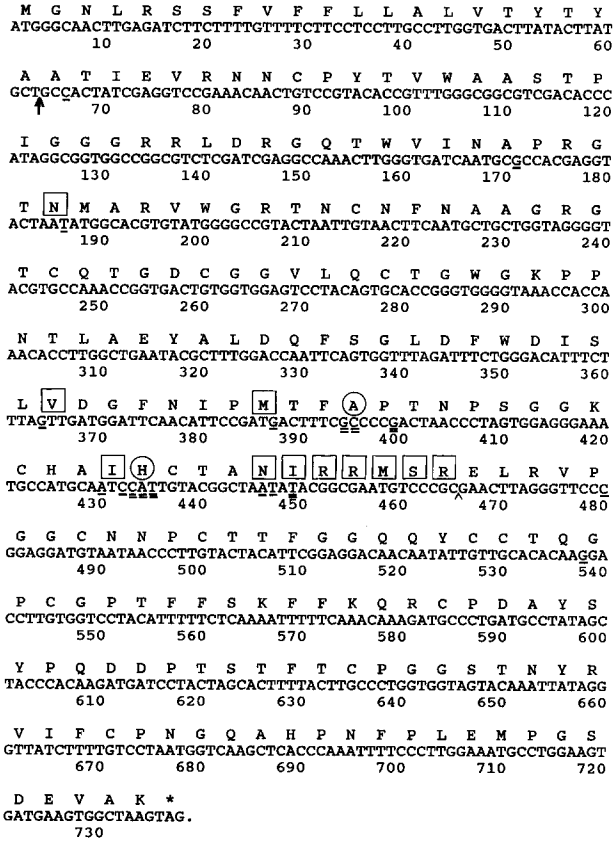

Fig. 1. Nucleotide sequence and derived amino acid sequence of an osmotin cDNA clone from tobacco (*Nicotiana tabacum* cv. White Burley). The arrow indicates the likely cleavage site for the removal of the signal sequence. Variations with the Wisconsin-38 sequence are indicated: nucleotide substitutions are underlined once, insertions are underlined twice and the deletion point is indicated by ^. Amino acid substitutions are boxed and insertions are circled.

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