Plant Gene Register

Isolation of a Full-Length cDNA Encoding *Brassica napus* Mitochondrial Chaperonin-60

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Chaperonins are a class of proteins that facilitate the assembly of oligomeric proteins (Hemmingsen et al., 1988). In plants cpn-60 are present in both plastids and the mitochondria, however, the mitochondrial form is different from either subunit of the plastid chaperonin (Martel et al., 1990). Mitochondrial chaperonin has been cloned from a number of plant species including *Arabidopsis*, maize (Prasad and Stewart, 1992), and pumpkin (Tsugeki et al., 1992). The expression of these genes is developmentally regulated during seed germination. They are heat-shock-inducible and are required for mitochondrial biogenesis (Prasad and Stewart, 1992).

We have isolated a full-length *Brassica napus* cDNA clone encoding a mitochondrial cpn-60 (Table I). This clone is 1952 bp in length and contains a 1761-bp open reading frame with 39 bp of a 5′ and 140 bp of a 3′ untranslated sequence. The deduced amino acid sequence has 587 residues and has a predicted molecular mass of 62,355 Da. Alignment of this amino acid sequence with that of the mitochondrial cpn-60, from *Arabidopsis* (Prasad and Stewart, 1992) and pumpkin (Tsugeki et al., 1992) shows that they have a high degree of homology (83%, 91% amino acids). This is considerably higher than the homology with either the α or β subunit of plastid cpn-60 from *Brassica* (40%, 40% amino acids) (Martel et al., 1990). In addition, the transit peptides of *Brassica* and *Arabidopsis* mitochondrial cpn-60 share 50% amino acid identity. Based on the homology to other mitochondrial cpn-60, the NH2-terminal transit peptide of the *Brassica* mitochondrial cpn-60 is predicted to consist of the first 32 amino acids.

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