
The nucleotide sequence of a cDNA clone encoding acyl carrier protein (ACP) from *Brassica campestris* seeds

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Acyl carrier protein (ACP) plays an important role in fatty acid synthesis and metabolism in plants. An ACP cDNA clone was isolated from a cDNA bank prepared from *Brassica campestris* seed tissue using an oligonucleotide derived from a *Brassica napus* ACP protein sequence (1). The sequence surrounding the methionine codon at base 33 differs by two bases from the proposed consensus translation start site for plants (2). Based on an almost perfect match between the protein sequence reported for the mature protein of *B.napus* ACP and that predicted by the open reading frame of the cDNA clone for *B.campestris* seed ACP, we suggest that the mature *B. campestris* seed ACP is coded by bases 186 through 434. Assuming that the translational start is at the methionine at base 33 then this cDNA codes for a precursor protein with a 51 amino acid transit peptide. This transit peptide would share features with those of other nuclear-encoded chloroplast proteins (3) with the notable exception of beginning with MetSer while all others to date start with a MetAla. The amino acid sequence from the leucine codon at base 288 to the phenylalanine codon at base 342 is highly conserved with *E.coli* (4), barley seed (5), and spinach leaf (6) ACP protein sequences. This region is known to be involved in the binding of the phosphopantetheine prosthetic group (6). The cDNA clone ends with seven deoxyadenosines which may be the beginning of a poly (A) tail, however, no obvious polyadenylation signal (7) is found following the stop codon. Both strands were sequenced by dideoxy sequencing (8) using synthetic oligonucleotide primers or by the method of Maxam and Gilbert (9).

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1 TCTCGAGCAGATCTCTCTCGGGAAATATCGACAATGTCGACCACCTTCTGCTCTCCGTCTCCATGCAAGCCACTTCTCTGGCA 83
MetSerThrThrPheCysSerSerValSerMetGlnAlaThrSerLeuAla

84 GCAACAACGAGGATTAGTTTCCAGAAGCCAGCTTTGGTTTCAACGACTAATCTCTCCTTCAACCTCCGCCGTTCAATCCCCAC 166
AlaThrThrArgIleSerPheGlnLysProAlaLeuValSerThrThrAsnLeuSerPheAsnLeuArgArgSerIleProTh

167 TCGTTTCTCAATCTCCTGCGCGGCCAACCCAGAGACGGTTGAGAAAGTGCTAAGATAGTTAAGAAGCAGCTATCACTCAAAG 249
rArgPheSerIleSerCysAlaAlaLysProGluThrValGluLysValSerLysIleValLysLysGlnLeuSerLeuLysA

250 ACGACCAAAGGTCGTTGCGGAGACCAAGTTTGCTGATCTTGAGCAGATTCTCTCGACACTGTTGAGATAGTGATGGGTTTA 332
spAspGlnLysValValAlaGluThrLysPheAlaAspLeuGlyAlaAspSerLeuAspThrValGluIleValMetGlyLeu

333 GAGGAAGAGTTTATCGAAATGGCTGAAGAGAAAGCTCAGAAGATTGCTACTGTGGAGGAAGCTGCTGAACCTATTGAAGA 415
GluGluGluPheAspIleGluMetAlaGluGluLysAlaGlnLysIleAlaThrValGluGluAlaAlaGluLeuIleGluGl

416 GCTCGTTCAACTTAAGAAGTAATTTTAGTATTAAGAGCAGCCAAAGGCTTTGTTGGGTTTGTGTTTTTCATAATCTCTCTGTCA 498
uLeuValGlnLeuLysLys

484 TTTTCTTTTCTTTAATGTGTCAAGCGACTCTGTTGGTTTAAAGTAGTATCTGTTGCCAAAAAAA 564

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