

Sequence of the chloroplast-encoded *psbA* gene for the Q_B polypeptide of alfalfaJane Aldrich¹, Barry Cherney² and Ellis Merlin³

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The sequence of the chloroplast-encoded *psbA* gene from *Medicago sativa* cv. Regen S is shown compared to soybean (1) and pea (2). Greater than 99.9% nucleotide sequence homology exists between alfalfa and soybean (55/1069 base pair changes) and alfalfa and pea (26/1059) in the open reading frame (ORF). There are only 5 amino acid changes (4 conservative) between alfalfa and soybean and only 2 amino acid changes (one conservative) between alfalfa and pea in the ORF. The alfalfa 5' flanking region also shares 99.9% nucleotide sequence homology with soybean and pea with none of the base pair substitutions between alfalfa and these two species identical.

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-117   T          T C A T C A C T    TTG          G          G A          -1
       GTGACACCGTATATAAGTCATOTATACCTGAAACAAGCCCTAA-TCTCTACTTATAGAGAATTCTGTGCTGGAGCTCCCTGATAATT-AA----A-TAAACCCA-GATTTTAC
       G          C          G          A          G          A          -1
*1 ATG ACT GCA ATT TTA CG AGA CGG GAT AGC ACC CTA TGG GGT CGC TTC TGT AAC ACC AGC ACT GAA AAC GGT CCT TAC ATT GGA TGG TTT GGT GTT TTG ATG ATT CCC ACC
       M T A I L E R R D S E T L W G R F C K H W I T S T E N R L Y I Q W F G V L M I P T
       psbA          S
       TTA TTG ACC GCA ACT TCT GTA TTT ATT ATC GCT TTC ATC GCA GCC CCT CCA GCA GAT ATT GAT GGT ATC CCT GAT GAO CCT GTT TCT GGA TCT CTA CCT TAC GGA AAC AAT ATT ATT TGC GGT
       L L T A S V F I I A F I A A P P V D I D R P V I A S S L Y I G N H I I C G
       128
       369
       GGC ATT ATT CCT ACT TCT GCG GCT ATC GGT TTG AAC TAC CGG ATA TGG GAA GCA GTC CCT GTT GAT GAA TGG TTA TAC AAC GGT GGT CCT ATT GAA CTA ATT GTT CTA CAC TTC TTA
       A I I I P T S A A I G L H Y P I V A A S V D E V L Y I P T E L I V L
       Pet I          466
       600
       CCT GGT GIA GCT TGT ATG GGT CGT GAG TGG GAA CCT AGT TTT CCT GTO GGT ATG CGC CCT TGG ATT OCT GGT GCA TAT TCA OCT CCT GTT GCA OCT OCT ACT GCA GGT TTG TTO ATC
       L G Y A T C Y M G R E W E L S F R L G M R P V I A V A V A Y S A P V A A A T Y F L I
       728
       TAC CCA ATT GGT GCA CGG AGC ATT TCA GAT GGT ATG CCT CTA CGA ATC CCT GGT ATT ATT GAT GGT ATT GAT GGT GCA GAT CAT ATT ATT CCT ATT CAT CCA CCT TAT CAC ATG TTA
       Y P I G Q G S F D G M P L G I S G T F N F M I V F Q A E H N I L M H P F H M L
       728
       GGT GTA CCT GGT CGT TTC CGC GGT TCC CTA ATT AGT ATG GAC GGT CCT TGG GTA ATT AGT TTC ATC GCA CGG ACC ACA GAA AAA ATT GAA TCT GCT ATT GAA GGT TAC AGA TTC GGT
       G Y A G V F Q G S L F S A M H G S L V T S S L I R E T T E N E S A N E Q Y R F G
       848
       CAA GAG GAA GAA ACC TAT ATT ATT GTA GCA GCT CAT GGT TAT TTT GGC CGA TTO ATC TTC CGA TAT GCT AGT TTC AAC AAC AAC TCT CGT TCT TTA CAT TTC CGT CGT CCT GGT CGT CCT GGT GCA
       Q E E T Y N I V A A H G Y P G R L I F Q Y A A S P F H N S R S L H F F L A K A W P I
       968
       GTA CGT ATC TGG TTT ACC GCA TTA GGT ATC ACC ACT ATG CCT TTC AAC TTA ATT GGT TTC ATT AAC CAA TCA GTA ATT GGT GAT AGT CAA CGT CGT GTA ATT AAC ACC TGG CCT GAT ATT
       V G I W F T A L Q I S T M A F N L G F N F N Q S V Y D S Q G R V I N T W A D I
       1052
       ATT AAC CGT OCT AAC CCT CCT GGT ATG GAA GGT ATT CAT GAA CGT ATT GCT CAT AAC TTC CCT CTA GAC CGA CCT CGG CGT CGG CGG CCT CCA TCT ATA ATT GCA TAA
       I H R A H L G M E V M H E R R H A H N F P L D L A A Y E A P S I N G X
  
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Legend: The alfalfa *psbA* gene spans two adjacent *Pst* I restriction endonuclease fragments of 7.0 kb and 7.1 kb (3). The *Pst* I site at the junction of the 2 fragments is shown at position 464. Nucleotide and amino acid substitutions in soybean are indicated above the alfalfa sequence and pea below with only amino acid substitutions shown in the coding region. Underlined: prokaryotic -16 and -35 promoter sequences and a putative ribosome binding site (4) located an unusual 36 bases upstream of the first ATG in the ORF. Probable transcription initiation by homology to pea (5) is shown as ** at -79 and -80.

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