Nucleotide sequence of the *psbA3* gene from the cyanobacterium *Synechocystis* PCC 6803

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The *psbA* gene which encodes the D1 polypeptide of the photosystem two reaction center is present as three different copies in the unicellular cyanobacterium *Synechocystis* sp. PCC 6803 (1). The nucleotide sequences for two of these copies, *psbA1* (2) and *psbA2* (3), have been published. Here we present the nucleotide and deduced amino acid sequences for the remaining copy, *psbA3*, which is located on a 9.4 kb genomic *Hin*dIII fragment (1, 4). The sequence between nucleotides 101 and 1249 was determined from plasmids isolated previously (4). The rest of the sequence was obtained from plasmids containing DNA that had been amplified using the inverted polymerase chain reaction (5).

The *psbA3* gene is highly homologous to the *psbA2* gene (99.4% identity at the nucleotide level) and encodes an identical gene product. Thus *Synechocystis* 6803 contains *psbA* genes that code for two distinct forms of the D1 polypeptide. However, under normal laboratory growth conditions only the *psbA2* and *psbA3* genes appear to be expressed (6).

152 bp downstream of the stop codon for *psbA3* is the putative initiation codon (underlined) for an open reading frame (ORF) that is homologous to the *dnaE* gene of *Bacillus subtilis* (4). Interposon mutagenesis experiments have suggested an essential role for this ORF in cell growth (4).

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  -32   ACATTGACAAATACATAAGGAATTATAACCAAATGACAACGACTCTCCAACAGCGCGAAAGCGCTTCATTGTGGGAACAGTTTTGTCAGT
                                       M  T  T  T  L  Q  Q  R  E  S  A  S  L  W  E  Q  F  C  Q  W
   59   GGGTGACCTCTACCAACAACCGGATTTATGTCGGTTGGTTCGGTACCTTGATGATCCCCACCCTCTTAACTGCCACCACTTGCTTCATCA
         V  T  S  T  N  N  R  I  Y  V  G  W  F  G  T  L  M  I  P  T  L  L  T  A  T  T  C  F  I  I
  149   TTGCCTTCATCGCCGCTCCCCCCGTTGACATCGACGGTATCCGTGAGCCCGTTGCTGGTTCCTTGCTCTACGGTAACAACATCATCTCTG
         A  F  I  A  A  P  P  V  D  I  D  G  I  R  E  P  V  A  G  S  L  L  Y  G  N  N  I  I  S  G
  239   GTGCTGTTGTACCTTCTTCCAACGCTATCGGTTTGCACTTCTACCCCATCTGGGAAGCCGCTTCCTTAGATGAGTGGTTGTACAACGGTG
         A  V  V  P  S  S  N  A  I  G  L  H  F  Y  P  I  W  E  A  A  S  L  D  E  W  L  Y  N  G  G
  329   GTCCTTACCAGTTGGTAGTATTCCACTTCCTCATCGGCATTTTCTGCTACATGGGTCGTCAGTGGGAACTTTCCTACCGCTTAGGTATGC
         P  Y  Q  L  V  V  F  H  F  L  I  G  I  F  C  Y  M  G  R  Q  W  E  L  S  Y  R  L  G  M  R
  419   GTCCTTGGATTTGTGTGGCTTACTCTGCCCCCGTATCCGCTGCCACCGCTGTATTCTTGATCTACCCCATTGGTCAAGGCTCCTTCTCTG
         P  W  I  C  V  A  Y  S  A  P  V  S  A  A  T  A  V  F  L  I  Y  P  I  G  Q  G  S  F  S  D
  509   ATGGTATGCCCTTGGGTATTTCTGGTACCTTCAACTTCATGATCGTGTTCCAAGCTGAGCACAACATCCTGATGCACCCCTTCCACATGT
         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
  599   TAGGTGTGGCTGGTGTATTCGGTGGTAGCTTGTTCTCCGCCATGCACGGTTCCTTGGTAACCTCCTCCTTGGTGCGTGAAACCACCGAAG
         G  V  A  G  V  F  G  G  S  L  F  S  A  M  H  G  S  L  V  T  S  S  L  V  R  E  T  T  E  V
  689   TTGAATCCCAGAACTACGGTTACAAATTCGGTCAAGAAGAAGAAACCTACAACATCGTTGCCGCCCACGGCTACTTTGGTCGGTTGATCT
         E  S  Q  N  Y  G  Y  K  F  G  Q  E  E  E  T  Y  N  I  V  A  A  H  G  Y  F  G  R  L  I  F
  779   TCCAATATGCTTCTTTCAACAACAGCCGTTCCTTGCACTTCTTCTTGGGTGCTTGGCCTGTAATCGGCATCTGGTTCACTGCTATGGGTG
         Q  Y  A  S  F  N  N  S  R  S  L  H  F  F  L  G  A  W  P  V  I  G  I  W  F  T  A  M  G  V
  869   TAAGCACCATGGCGTTCAACCTGAACGGTTTCAACTTCAACCAGTCCATCTTGGATAGCCAAGGCCGTGTAATCGGCACCTGGGCTGATG
         S  T  M  A  F  N  L  N  G  F  N  F  N  Q  S  I  L  D  S  Q  G  R  V  I  G  T  W  A  D  V
  959   TATTGAACCGCGCCAACATCGGTTTTGAAGTAATGCACGAACGCAATGCCCACAACTTCCCCCTCGACTTAGCGTCTGGGGAGCAAGCTC
         L  N  R  A  N  I  G  F  E  V  M  H  E  R  N  A  H  N  F  P  L  D  L  A  S  G  E  Q  A  P
 1049   CTGTGGCTTTGACCGCTCCTGCTGTCAACGGTTAATTCCTTGGTGTAATGCCAACTGAATAATCTGCAAATTGCACTCTCCTTCACCGGG
         V  A  L  T  A  P  A  V  N  G  *
 1139   GGGTGCTTTTTGCTGGTTGACCATGCTTGAGTAGAGCTTAAGTTGACAAGTATCTCTCCCCATCGTCACTCTTAGAAGGAGAGTAGGTTG
 1229   ATTTATCATGGATAACCTCCG   1249
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