Nucleotide sequence and transcription of the sugar beet mitochondrial F_0F_1-ATPase subunit 9 gene

Yongbiao Xue, Colwyn M.Thomas and D.Roy Davies*

John Innes Institute, AFRC Institute of Plant Science Research, Colney Lane, Norwich NR4 7UH, UK
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The mitochondrial gene for subunit 9 of the F_0F_1-ATPase (*atp9*) from sugar beet was identified by using a heterologous probe containing the coding region of the tobacco *atp9* clone (1). Sequence analysis of a positive clone (pMR300) revealed that it contains the full length *atp9* gene. The deduced amino acid sequence of sugar beet *atp9* displays more than 90% identity with other plant mitochondrial ATP9 sequences (1-4). A short sequence (underlined) shows homology with the consensus of the promoter sequences of sugar beet mitochondrial genes (Xue et al, submitted). A putative ribosome-binding site (boxed), showing 62.5% sequence identity to an octanucleotide sequence capable of binding to the maize 18 S rRNA (5), is located close to the ATG codon. Sequences to form a potential stem-loop structure are found at the 3' flanking region of the *atp9* coding sequence (arrowed). Southern analysis with the coding region of sugar beet mitochondrial *atp9* indicated that multiple bands were detected in restricted mtDNAs from both cytoplasmic male sterile (CMS) and male fertile (MF) mitochondria, suggesting a multiple copy organization of *atp9* in sugar beet mtDNAs. Northern analysis shows that the sugar beet *atp9* gene is transcribed into one major transcript of 0.8 kb in both CMS and MF genotypes, which is different from the complex transcriptional pattern found for the *atp9* gene in tobacco, maize and broad bean (1, 4, 6).

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GAATTCTATCATACCTTCAGCTTCTTCCCCTAGTAGTAGTAGTAGCGCCTCCGGGGATCCTGAAAAGGAGCGCGCTCGTCTAGTAAAAGCATATGACT -312
ATTTCTATAAATCTCTAATCAAGAGGTCCAGGCAGAAGCCCGGCTCCTCTTGAAGAGGAAACTAAGCCTTCGAACTGTTTCGGGGCTTGTCCTTAAGC -214
GGTCACAGAGGCAGTGTTAACTGAGACTTGACCATAGAAGGAGGGGATGCTGGTGAGCTGCTCATAAATCTAAAAAAGGAGCTGGGGCCGGATCACCC -116
TATTATTCAATTTGTTCTAAAAAGGCGAATAAGAGGGAAAATCGACATCGACAAGATGACGAACCATAAATCGTGAATTGAAAAGGCCGTTAGGGCCG  -18
          [atp9] M  L  E  G  A  K  S  I  G  A  G  A  A  T  I  A  S  A  G  A  A  I  G  I  G  N  V
AATTGATCTACTCTGTTATGTTAGAAGGCGCAAAATCAATAGGTGCCGGAGCCGCTACAATTGCTTCAGCGGGAGCTGCTATCGGTATTGGAAACGTT   81
  F  S  S  L  I  H  S  V  A  R  N  P  S  L  A  K  Q  L  F  G  Y  A  I  L  G  F  A  L  S  E  L  I  A
TTTAGTTCCTTGATCCATTCCGTGGCGCGAAATCCGTCATTGGCGAAACAATTATTTGGTTATGCTATTTTGGGCTTGCTCTCTCCGAACTAATCGC  179
  L  F  A  L  M  M  A  F  L  I  L  F  A  F  R  F  F  S  K  K  G  K  L  A  G  A  P  V  *
ATTGTTTGCCCTAATGATGGCCTTTTTGATTTTGTTCGCATTCCGATTTTTTTCAAAGAAAGGGAAGCTGGCGGGGGCCCCAGTTTAAGAGTACACAG  277
ACTGAAAAGGTTGTGAGGTTCCTGCTAGGGCGACTCTCACTCTAGTGGGAAGCGAAGGCAGGTGGGAACGAGCGGAGCGAGAGCAAAGCAAGTTCCAGT  375
GGCGGGCTGTCTTCATGGTCCCATTTCAATCTTTTTCATGGGAAGATATTCTTAGTTCGCTTTTTTCTTCCAAAACCTTTCTTTTTTTTTTCGGTATA  473
CCGTCCGCCAGCAAGGGGCGAACTCAACAAAAAAATGTAGTCTTATGTTCTTCTTTCTTTTTTTTTATAAAATGTTTTCTCTTTCTTTTAAGATGAAG  571
GGCGCCCCGTTCACCGAGAGGGAGGATTTAGGAGACCTGTTTTGCCATGCTGCTTGCTTTGGCGAGATCTAACCCCACCGGCAACGCCAGGGATCATCC  669
TGTCAATAGAACAGAAAGAATTC  692
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*To whom correspondence should be addressed

References

(1) Bland, M.M. et al, (1986) Mol. Gen. Genet. 204, 8-16. (2) Dewey, R.E. et al, (1985) Proc.Natl. Acad. Sci. USA 82, 1015-1019. (3) Young, E.G. et al, (1986) Nucl. Acids Res. 14, 7995-8005. (4) Wahleithner, J.A. and Wolstenholmw, D.R. (1988) Nucl. Acids Res. 16, 6897-6913. (5) Dawson, A.J. et al, (1984) EMBO J. 3, 2107-2113 (6) Mulligan, R.M. et al, (1988) Proc. Natl. Acad. Sci. USA 85, 7998-8002.

