Sequence of the F₀-atpase proteolipid (atp9) gene from rice mitochondria

Edward K.Kaleikau, Charles P.André and Virginia Walbot

Department of Biological Sciences, Stanford University, Stanford, CA 94305, USA

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We have cloned and sequenced the F₀-atpase proteolipid (*atp9*) gene from rice mitochondrial DNA. A library of total rice DNA from strain IR36 cloned into the lambda vector EMBL3 was probed with the heterologous mitochondrial gene from maize. We isolated and subcloned a 15kb fragment containing the gene, and this was further subcloned and sequenced. The molecular weight of the rice *atp9* protein is predicted to be 8.945kd. This is larger than in other species because of an additional 13 codons (compared to maize) at the 3' end of the gene. The nucleotide and amino acid sequence homologies to other sequenced plant

atp9 genes (assuming no mRNA editing^{6,7}) are shown in the table below.

REFERENCES

1. Shulte,E. *et al.* (1989) *Nucl. Acids Res.* **17**, 7531.
2. Dewey,R.E. *et al.* (1985) *Proc. Natl. Acad. Sci. USA* **82**, 1015–1019.
3. Rothenberg,M. and Hanson,M.R. (1987) *Mol. Gen. Genet.* **209**, 21–27.
4. Bland,M.M. *et al.* (1986) *Mol. Gen. Genet.* **204**, 8–16.
5. Morikami,A. and Nakamura,K. (1987) *Nucl. Acids Res.* **15**, 4692.
6. Gualberto,J.M. *et al.* (1989) *Nature* **341**, 660–662.
7. Covello,P.S. and Gray,M.W. (1989) *Nature* **341**, 662–666.

Species	Nucleotide sequence homology	Amino Acid sequence homology	Reference
wheat	96.4%	94.6%	1
maize	95.6%	98.7%	2
petunia	91.6%	96.1%	3
tobacco	92.0%	96.1%	4
pea	86.2%	94.7%	5

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-177  ggccgggtgtctaatggtgttatggatctctctttaaatacgagattggtgtggtg
-120  ttcagtctaccgctcatgttcgacgctattatggaccgagaaggaatcaacgaaaaac
-60   ccaggaaagagctgcgaaagaaaagccgtgacgagcaaaagtcaagtctccacgactcgac
+1    atgttagaaggagctaaatcaataggtgccggagctgctacaattgcttttagcgggacgt
      M L E G A K S I G A G A A T I A L A G R
61    gctgtcgggtattgaaacgtcctcagttcttcgattcattccgtggcgcgaaatccttca
      A V G I G N V L S S S I H S V A R N P S
121   ttggctaacaattatgttggttatgccattttgggctttgctctcaccgaagctattgca
      L A K Q L F G Y A I L G F A L T E A I A
181   ttgtttgcccgaatgatggcctttctgatttcattcgttttcgatcacatatttcttggt
      L F A P M M A F L I S F V F D H I F L G
241   gtagatatctctcttttgcaaatagagataccgaggcccccaacctaactagtgtgtggtg
      V D I S L C K *
301   ggggaaagaagagtgggaacgtgggcttctttcacagtgcgtacctctctttctc

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