

Nucleotide sequence of the *Oenothera* ATPase subunit 6 gene

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The ATPase subunit 6 is encoded by a single copy gene in *Oenothera* mitochondria. The nucleotide sequence predicts a protein of 316 amino acids. This polypeptide is larger than the maize ATPase subunit 6 (1) due to a reading frame extension at the 3' terminus. The *Oenothera* mitochondrial gene is transcribed in a single mRNA species of 1300 nucleotides as determined by northern blot experiments. S-1 protection analysis of the 5' and 3' mRNA ends locate the termini in classical plant mitochondrial signal regions. The sequence around the 5' terminus shows the consensus sequence for a putative plant mitochondrial promoter. The sequence preceding the 3' mRNA terminus can be folded into stem loop structures (indicated by horizontal arrows in the figure) that have been proposed to function as terminator signals in plant mitochondria (2).

↓ 5' mRNA

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-280 TTGGATCCAATTTCTCTATACATTTGTGAGATTAGAGATCGGCATATATTATCATAGTGGAGAGALCTGATTCAAAATAAAAATAGATGGKALGTAATTCATTCATACGAAGAAC
-160 GTTCCAAAGACAAAAAGAGTTCCTTAGGCCCAAAAAAAGGCCGCCCATGCTTCTGTGTGGTCAACAACACAGCTCTCTAATCAATAGGATCTCTCACTACATCAAGGCTTGAC
-40 GAAGTAAAGCTGTCTGGAGGAATATTATTGCTCAATCA      M K R F Y K T A F F S F I G S F F V S
           ATG AAA AGA TTT TAT AAA ACC GCT TTT TTT TCT GAA ATA GGT AGI GAA GAA GTA AGT
58  H F W A D T M S S H S P L E Q F S I I P L I P M N I G N I Y
CAT TTT TGG GCA GAT ACG ATG TCT TCC CAC AGC CCC CTT GAG CAA TTT TCC ATT CTC CCA TTG ATT CCT ATG AAT ATA GGA AAC TTG TAT
148 F S F T N P S L F M L L T L S L V L L L V N I V I K K G G G
TTC TCA TTC ACA AAT CCA TCT TTG TTT ATG CTG CTA ACT CTC AGT TTG GTC CTA CTT GTG AAT TTT GTT ACT AAA AAG GGA GGA GGA
238 N S V P N A W Q S L V E L I Y D F V P N P V N E Q I G G L S
AAC TCA GTA CCA AAT GCT TGG CAA TCC TTG GTA GAG CTT ATT TAT GAT TTC GTG CCG AAC CCG GTA AAC GAA CAA ATA GGC GGT CTT TCC
328 G N V K Q K F F P R I S V T F T F S L F R N P Q G M I P Y S
GGA AAT GTG AAA CAA AAG TTT TTC CCT CGC ATC TCG GTC ACT TTT ACT TTT TCG TTA TTT CGT AAT CCC CAG GGC ATG ATA CCG TAT AGC
418 F T V T S H F L I T L G L S F S I F I G I T I V G F Q R N G
TTC ACA GTG ACA AGT CAT TTT CTC ATT ACT TTG GGT CTC TCA TTT TCT ATT TTT ATT GGT ATT ACT ATA GTT GGA TTT CAA AGA AAT GGG
508 L H F L S F S L P A G V P L P L A P F L V L L E L E L I P H C F
CCT CAT TTT TTA AGC TTC TCA TTA CCC GCA GGA GTC CCA CTG CCG TTA GCA CCT TTT TTA GTA CCT CTT GAG CTA ATC CCT CAT TGT TTT
598 R A L S S G I R L F A N M M A G H S S V K I L S G G F A W T M
CGC GCA TTA AGC TCA GGA ATA CGT TTA TTT GCT AAT ATG ATG GCC GGT CAT AGT TCA GTA AAG ATT TTA AGT GGG TTC GCG TGG ACT ATG
688 L C M N D L F Y F I G D L G P L F I V L A L T G P E L G V A
CTA TGT ATG AAT GAT CTT TTC TAT TTA ATA GGA GAT CTT GBT CCT TTA TTT ATA GTT CTT GCA TTA ACC GBT CCG GAA TTA GBT GTA GCT
778 I S Q A Y V S T I S I C I Y L N D A T N L M H Q S G W F F F I
ATA TCA CAA GCT TAT GTT TCT ACG ATC TCA ATC TGT ATT TAC TTG AAT GAT GCT ACA AAT CTC CAT CAA ACA AGT GGT TGG TTT TTT ATA
868 I E Q K R K N Q K I K E H R R E R A L N K P R R E L L
ATT GAA CAA AAG CGA AAG AAT CAA AAA ATC AAA GAA CAC AGA AGA GAG GCA CTC CAC AAG CCA AGC AAG AGG TTG TTG TAG ATGATCG
960 GTTCATGCCCCCCCTTAATGTTGTGCGAGGGATTGCCCTTGTGAGTAAATGGGAAGGGAAGCGGGATAGGCCCCCAAGATTCCCGTTAAGAGTTGGGTTCCAAATCTTACTTGGTC
    
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**References**

1. Dewey et al. (1985) Plant Physiol. 79, 914-919
2. Schuster et al. (1986) Nucl. Acids Res. 14, 5943-5954