

Sequence of the gene encoding the mitochondrial F<sub>1</sub>-ATPase alpha subunit from *Nicotiana plumbaginifolia*

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A genomic bank of Nicotiana plumbaginifolia mitochondrial DNA was constructed and probed with the gene encoding the alpha subunit of maize mitochondrial F1-APTase (1,2). A 4.7 kb insert was present in the positive clones isolated. After subcloning, a series of progressive deletions were generated. Sequence analysis revealed a region of 1527 nucleotides encoding a polypeptide of 55,162 molecular weight. The amino acid sequence shares respectively 94,3 % et 93,9 % homology with the alpha subunit sequence of maize (1,2) and Oenothera (3).

- 120 GTGCAATTTCTAAGAAGGAATAGAACTGGCCCTTTGATGGAATAAAAAAAGGAGAGACTGGTAGACTGGTAGAGCTCATCTTTGTCAGCGGCAATTCCTCCTCTATCTATCTTGAAT
1 ATGGAACTTTCTCCCGAGCTCGCGGAATCAACAAGTCTATTAGAAAGTCGAATTAGCAACTTTTACACCAATTTTCAAGTGGATGAGATCGGTGCGAGTGGTCTCAGTTGGAGATGGGAT
H E L S F R A A E L T S L L E S R I S N F Y T N F Q V D E I G R V V S V G D G I
121 CGACGTGTTTATGGATTACACGAGATTCAAGCTGGGGAATGGTTGAAATTTGCCAGCGGTGTGAAAGGAATAGCCTTGAATCTTGAGAAATGAGAATGATGGGATCTGTCTTTGCTAGT
A R V Y G L N E I Q A G E H V F A S G V K G I A L N L E N E N V G I V F V G S
241 GATACTGCTATAAAGAGGACACTCTGTCAACCCAGCTGGATCTATTGTGGATGTTCTGCGGGAAAGGCTATCTAGGGCTGTGTGATGGGTTGGCAGTACTGATTCATGCGAAGG
D T A I K E G D L V K R T G S I V D V P A G K A N L G R V V D G L G V P I D G R
361 GGGCTCTAAGCGATCAGGAGCGAAGCGTGTGCAAGTGAAGCCCTGGTATATTGAAGCTAAATCTGTGCAAGCGCTATGCAACACGGGTAAAAGCGGTAGATAGCCTGGTCTCT
G A L S D H E R R R V E V K A P G I E R K S V H E P H Q T G L K A V D S L V P
481 ATAGGTGGCTCAACGAGAATCTATACTCGGACCGACAACTGGAAAACTGCTATGCTATCGATACCATATAAACCAGCAACTGAACTCAAGGGCCACCTCTGAGAGTGG
I G R G Q R E L I I G D R Q T G K T A I A I D T I L N Q K Q L N S R A T S E S E
601 ACATGTATTTGCTCTATGACCGATGACAGAAAGCGTCAACTCTGGCACAATAGTTCAAATCTTTCAGAGCGCAATGCTTGGCAATTTCTATCTTGTAGCAGCCACCGCTCTG
T L Y C V Y V A I G Q K R S T V A Q L V Q I L S E A N A L E Y S I L V A A T A S
721 GATCTGCTCTCTACAATTTTGGCCCATATTTCTGGGTGCCATGGGGGAATATTTCCGGGATAATGGAATGCACCGCATTAATAATCTATGATGATCTTAGTAAACAGCGGTAGCA
D P A P L Q F L A P Y S G C A H G E Y F R D N G M H A L I I Y D D L S K Q A V A
841 TATCGACAAATGTCATTATGTTACCGCGACCCAGGCTGTGAGGCTTTCCAGGGGATGTTTCTATTACATTCGGTCTTGAAGAGCGGCTAACCGATCGGACCCAGCAGCG
Y R Q M S L L R R P P G R E A F P G D V F Y L H S R L L E R A A K R S D Q T G
961 CGAGGTAGCTGACCGCTTACCGCTCAATGAAAACCAAGCTGAGCAGCTATGCTGCTATATTCACCAAGTGTGATGCCATTAAGTCAAGCAAACTCTGTTGGAAGCAGAGCTCTTT
A G S L T A L P V I E T Q A G D V S A Y I P T N V I P I T D G Q I C L E T E L F
1081 TATCGGGAATAGACCTGGGATTAACCTGGCTTATCTGTGAGTGGCGTGGGCTGCGGCTCAGTTGAAAACATGAACAAGCTGCGGTAGTTCAAAATGGAATGGCACAAT
Y R G I R P A I N V G L S V S R V G S A A Q L K T M K Q V C G N S S K L E L A Q Y
1201 CGGGAAGTGGCCCTGCTCAATTTGGCTCAGACCTTGTGCTGCGACTCAGGCATTACTCAATGAGGTGCAAGGCTGACAGCAAGTACCGAAACACCAATATGCCACTGCCA
R E V A A L A Q P F G S D L D A A T Q A L L N R G A R L T E V P K Q P Q Y A P L P
1321 ATTGAAAAACAATTTAGTCTATTATGCAAGTGTCAATGGATTTCTGATGCAATGCCACTAGACAGAATTTCTCAATATGAGAGAGCACTTCCAAATAGTCTCAAACAGAAATTACTA
I E K Q I L V I Y A A V N G F C D R H P L D R I S Q Y E R A I P N S V K P E L L
1441 CAATCGTTTTAGAAAAAGTGGCTTAACACGAAAGAAAGATGGAACACAGATACATCTTAAAAGAAAGTGGTTAGCTTTTATTATAACAATACAGGAAGAAAGAAAGGCTCTCT
Q S F L E K G G L T N E R K M E P D T F L K E S A L A P I \*
1561 AGGGGTACCACAAATAATGGACTACTAGTCTCTTTTCTATCTATGAAGTAGGACGAGTG

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