Nucleotide sequence of a cDNA encoding the beta subunit of the mitochondrial ATP synthase from *Zea mays*

B.M.Winning*, B.Bathgate[1], P.E.Purdue[2] and C.J.Leaver[3]

Department of Botany and [1]Department of Microbiology, The King's Buildings, University of Edinburgh, Mayfield Road, Edinburgh EH9 3JH, [2]Biochemical Genetics Research Group, MRC Clinical Research Centre, Watford Road, Harrow, Middlesex HA1 3UJ and [3]Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB, UK

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The beta subunit of the mitochondrial F_1-F_0 ATP synthase is a nuclear encoded protein which is located in the F_1 component of the enzyme. The F_1 domain is made up of five distinct subunits, the alpha and beta subunits of which are thought to be involved in the catalytic activity of F_1 and in the binding of nucleotides. The *N. plumbaginofolia* beta subunit cDNA, corresponding to the *atp*2-1 gene, was used as a probe to screen a λgt10 cDNA library prepared from mRNA isolated from three day old dark grown coleoptiles of *Zea mays* (line MUTIND-FR7205034). Two cDNA clones were isolated, the sequence of one of these is presented here. The deduced amino acid sequence shares 93% homology with that of the *N. plumbaginofolia atp*2-1 sequence and 100% homology with a recently published *Zea mays* sequence (1). There are four differences at the nucleotide sequence (these are underlined in the sequence). The three occurring in the coding region are conservative changes. This sequence includes an additional 48 nucleotides at the 5′ end and the position of the poly A tail is altered. It should be noted that these cDNAs were isolated from libraries derived from different maize lines and this may account for sequence variations.

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REFERENCE

1. Ehrenshaft and Brambl (1990) *Plant Physiol.* **93**, 295–304.

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   1 CAGCCGCCGCAACCCAGCGTCCCCCGAAGTCTAACCCTAGATCCGGACCGGCCATGGCGTCCCGCCGGGTCGTCTCCTCGCTCCTCCGCTCCGCGTCCCGCCTGCGGGCCGCCTCGCCCG   120
                                                                M  A  S  R  R  V  V  S  S  L  L  R  S  A  S  R  L  R  A  A  S  P  A
 121 CTGCTCCACGCCCGCCGCGCGCCACCGCACCGCCCGTCCCCGGCCGGGTACCTCTTCAACCGCGCTGCCGCCTACGCCTCTTCCGCCCGCGGCCCAGGCGGCACCTGCCACCCCGCCGCCGG   240
      A  P  R  P  R  A  P  P  H  R  P  S  P  A  G  Y  L  F  N  R  A  A  A  Y  A  S  S  A  A  A  Q  A  A  P  A  T  P  P  P  A
 241 CCACCGGGAAGACCGGGGGCGGCAAGATCACCGACGAGTTCACCGGCGCTGGCGCCATCGGCCAGGTGTGCCAGGTGATCGGCGCCGTCGTTGACGTGCGCTTCGATGAGGGCCTCCCGC   360
      T  G  K  T  G  G  G  K  I  T  D  E  F  T  G  A  G  A  I  G  Q  V  C  Q  V  I  G  A  V  V  D  V  R  F  D  E  G  L  P  P
 361 CCATCCTCACGGCGCTCGAGGTGCTCGACAACAACATCCGCCTCGTGCTCGAGGTGGCGCAGCACCTTGGCGAGAACATGGTGCGCACCATCGCTATGGACGGCACGGAGGGGCTCGTCC   480
      I  L  T  A  L  E  V  L  D  N  N  I  R  L  V  L  E  V  A  Q  H  L  G  E  N  M  V  R  T  I  A  M  D  G  T  E  G  L  V  R
 481 GCGGCCAGCGCGTCCTCAACACTGGCTCCCCCATCACCGTGCCTGTTGGCAGGGCTACCCTTGGACGCATCATAAATGTTATTGGTGAACCGATTGATGAGAAGGGTGACATAAAGACAA   600
      G  Q  R  V  L  N  T  G  S  P  I  T  V  P  V  G  R  A  T  L  G  R  I  I  N  V  I  G  E  P  I  D  E  K  G  D  I  K  T  N
 601 ACCACTTCCTCCCTATTCATCGTGAAGCCCCTGCCTTTGTTGAGCAGGCCACTGAGCAGCAAATTCTTGTTACTGGAATCAAGGTCGTGGATCTTCTTGCACCCTACCAAAGGGGTGGAA   720
      I  L  V  T  G  I  K  V  V  D  L  L  A  P  Y  Q  R  G  G  K  H  F  L  P  I  H  R  E  A  P  A  F  V  E  Q  A  T  E  Q  Q
 721 AGATTGGTCTCTTCGGTGGTGCAGGAGTGGGTAAAACTGTGCTCATTATGGAGTTGATCAACAATGTTGCTAAGGCCCATGGTGGTTTCTCTGTGTTTGCTGGTGTTGGAGAACGTACCC   840
      I  G  L  F  G  G  A  G  V  G  K  T  V  L  I  M  E  L  I  N  N  V  A  K  A  H  G  G  F  S  V  F  A  G  V  G  E  R  T  R
 841 GTGAAGGTAATGATCTGTACAGGGAAATGATTGAAAGTGGTGTCATTAAGCTAGATGACAAGCAGAGCGAAAGCAAGTGTGCTCTTGTTTACGGGCAGATGAATGAGCCCCCGGGTGCTC   960
      E  G  N  D  L  Y  R  E  M  I  E  S  G  V  I  K  L  D  D  K  Q  S  E  S  K  C  A  L  V  Y  G  Q  M  N  E  P  P  G  A  R
 961 GTGCTCGTGTTGGGTTGACTGGTTTGACTGTTGCTGAACATTTCCGTGATGCTGAAGGACAAGATGTGCTTCTGTTTATTGACAACATTTTCCGTTTTACTCAGGCAAACTCTGAGGTGT  1080
      A  R  V  G  L  T  G  L  T  V  A  E  H  F  R  D  A  E  G  Q  D  V  L  L  F  I  D  N  I  F  R  F  T  Q  A  N  S  E  V  S
1081 CTGCTCTTCTTGGACGTATCCCATCTGCTGTGGGATACCAGCCAACCCTTGCCACTGATCTTGGAGGACTGCAAGAGCGTATTACGACAACAAAGAAGGGTTCTATTACATCTGTGCAGG  1200
      G  G  L  Q  E  R  I  T  T  T  K  K  G  S  I  T  S  V  Q  A  A  L  L  G  R  I  P  S  A  V  G  Y  Q  P  T  L  A  T  D  L
1201 CCATCTACGTGCCTGCCGATGACTTGACGGATCCTGCTCCTGCTACTACCTTTGCCCATCTTGATGCTACAACTGTGTTGTCACGACAGATCTCTGAGCTTGGTATTTATCCTGCTGTTG  1320
      I  Y  V  P  A  D  D  L  T  D  P  A  P  A  T  T  F  A  H  L  D  A  T  T  V  L  S  R  Q  I  S  E  L  G  I  Y  P  A  V  D
1321 ATCCACTGGATTCCACATCAAGAATGCTTTCTCCCCACGTGCTGGGTGAGGATCACTACAACACTGCTCGTGGTGTGCAGAAGGTTCTTCAGAACTACAAAAATCTTCAGGATATTATTG  1440
      P  L  D  S  T  S  R  M  L  S  P  H  V  L  G  E  D  H  Y  N  T  A  R  G  V  Q  K  V  L  Q  N  Y  K  N  L  Q  D  I  I  A
1441 CTATCTTGGGTATGGATGAGCTCAGTGAGGATGACAAGCTGACAGTCGCCCGTGCAAGAAAGATTCAGCGTTTCCTGAGCCAGCCTTTCCATGTCGCTGAAGTTTTCACGGGTGCTCCAG  1560
      I  L  G  M  D  E  L  S  E  D  D  K  L  T  V  A  R  A  R  K  I  Q  R  F  L  S  Q  P  F  H  V  A  E  V  F  T  G  A  P  G
1561 GAAAGTATGTGGAGCTGAAGGAAAGCGTGAAGAGTTTCCAGGGTGTTTTGGATGGGAAGTATGATGACCTCCCTGAGCAGTCATTCTACATGGTTGGTGGCATTGAGGAAGTCATTGCTA  1680
      K  Y  V  E  L  K  E  S  V  K  S  F  Q  G  V  L  D  G  K  Y  D  D  L  P  E  Q  S  F  Y  M  V  G  G  I  E  E  V  I  A  K
1681 AGGCTGAGAAAATTGCCAAGGAGTCTGCTTCATAAGGAGGCTTCTTGCTTGTTCAACCCTGTACAAGTTCCATTTTTGGATTTTAAGCGTTTATTTATGCTTTTCCCAGTTAGGCATGAC  1800
      A  E  K  I  A  K  E  S  A  S  *
1801 GAGCTGGAGAGTCCATCTCCTGCTGAGAGATGTTTGTTTTACCCTTCTTTGCTTCCTCCACCTTACACCCAAATAAGCAACTGCAGTGACGTTGGTTTTGGCTGCACCCAAACTACATGA  1920

1921 CTGAAGAAACTTGTGGCCTGTGTAACGCGAATCCATCAGAACGCCAAAGTTATGGCTTCTGGTTGTGGCAAATTATGGTTCCTCCCTGTTCGGTTGAAAAAAAAAAAAA              2029
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* To whom correspondence should be addressed