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Nucleotide sequence of the wheat mitochondrial gene for subunit I of cytochrome oxidase

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The sequence of the wheat mitochondrial gene for cytochrome oxidase subunit I (COI) predicts a hydrophobic protein of 524 amino acids that shows strong similarity to those of maize[1] (99% nucleotide identity), soybean[2] (94%) and Oenothera[3] (93%). Nine of the 30 nucleotide differences seen between the wheat and maize COI genes (arrowheads) lead to amino acid substitutions, many of which occur at the carboxy-terminus. The wheat COI protein is predicted to be four residues shorter than that of maize. No sequence conservation is observed downstream of the coding region. However, upstream of the COI gene, scattered homology is seen between wheat and maize, and at a lower level with soybean (boxed). A 29bp direct repeat precedes that block in wheat (underlined). The wheat COI gene is a single-copy gene and RNA blot analysis shows a single major transcript of approximately 2.2kb.
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-228  AAGCTTCTCAAAAGCATCCAGAAATATCATAGAATGGTGATCGAGATCACCTTCACGGGAATCATCCTTTGCAAATTGGGGGAAGGGAACCAATCAAGT
-129  CACCAAGAAGTTCCCGAAACTTGGTTTAGTATTAAGGTTCTTCTCTTCCAGCGTTTAGTATTCAAGTTCTTCTCTTCCAGCCCCCCGGCCCCTCTTTGA
                                    M  T  N  M  V  R  W  L  F  S  T  N  H  K  D  I  G  T  L  Y  F  I  F
 -30  TAAGGAAAGTTTGCATTTCTCAAATAAAAAATGACAAATATGGTTCGATGGCTCTTCTCTACTAACCACAAGGATATTGGGACTCTCTATTTCATCTTC
       G  A  I  A  G  V  M  G  T  C  F  S  V  L  I  R  M  E  L  A  R  P  G  D  Q  I  L  G  G  N  H  Q  L
  70  GGTGCCATTGCAGGAGTGATGGGCACATGCTTCTCCGTACTGATTCGTATGGAATTAGCCCGACCCGGCGATCAAATTCTTGGTGGGAATCATCAACTT
       Y  N  V  L  I  T  A  H  A  F  L  M  I  F  F  M  V  M  P  A  M  I  G  G  F  G  N  W  F  V  P  I  L
 169  TATAATGTTTTAATAACGGCTCATGCTTTTTTAATGATCTTTTTTATGGTTATGCCGGCGATGATAGGTGGATTTGGTAATTGGTTTGTTCCGATTCTG
       I  G  A  P  D  M  A  F  P  R  L  N  N  I  S  F  W  L  L  P  P  S  L  L  L  L  L  S  S  A  L  V  E
 268  ATAGGTGCACCTGACATGGCATTTCCACGATTAAATAATATATCATTCTGGTTGTTGCCACCAAGTCTCTTGCTCCTATTAAGCTCAGCCTTAGTAGAA
       V  G  S  G  T  G  W  T  V  Y  P  P  L  S  G  I  T  S  H  S  G  G  A  V  D  L  A  I  F  S  L  H  L
 367  GTGGGCAGCGGCACTGGGTGGACAGTCTATCCGCCCTTAAGTGGTATTACCAGCCATTCTGGAGGAGCAGTTGATTTAGCAATTTTTAGTCTTCATCTA
       S  G  I  S  S  I  L  G  S  I  N  F  I  T  T  I  F  N  M  R  G  P  G  M  T  M  H  R  L  P  L  F  V
 466  TCAGGTATTTCATCAATTTTAGGTTCTATCAATTTTATAACAACTATCTTCAACATGCGTGGACCTGGAATGACTATGCATAGATTACCACTTTTTGTG
       W  S  V  L  V  T  A  F  L  L  L  L  S  L  P  V  L  A  G  A  I  T  M  L  L  T  D  R  N  F  N  T  T
 565  TGGTCCGTTCTAGTGACAGCATTCCTACTTTTATTATCACTTCCGGTACTGGCGGGGGCAATTACAATGTTATTAACCGATCGAAACTTTAATACAACC
       F  F  D  P  A  G  G  G  D  P  I  L  Y  Q  H  L  F  W  F  F  G  H  P  E  V  Y  I  L  I  L  P  G  F
 664  TTTTTTGATCCTGCAGGAGGGGGAGACCCAATATTATACCAGCATCTCTTTTGGTTCTTCGGTCATCCAGAGGTGTATATTCTCATTCTGCCTGGATTT
       G  I  I  S  H  I  V  S  T  F  S  R  K  P  V  F  G  Y  L  G  M  V  Y  A  M  I  S  I  G  V  L  G  F
 763  GGTATTATTAGTCATATCGTATCGACCTTTTCAAGAAAACCGGTCTTCGGGTATCTAGGCATGGTTTATGCCATGATAAGTATAGGTGTTCTTGGATTT
       L  V  W  A  H  H  M  F  T  V  G  L  D  V  D  T  R  A  Y  F  T  A  A  T  M  I  I  A  V  P  T  G  I
 862  CTAGTTTGGGCTCATCATATGTTTACTGTGGGCTTAGACGTTGATACGCGTGCCTACTTCACCGCAGCTACCATGATCATAGCTGTGCCCACAGGAATC
       K  I  F  S  W  I  A  T  M  W  G  G  S  I  Q  Y  K  T  P  M  L  F  A  V  G  F  I  F  L  F  T  I  G
 961  AAAATCTTTAGTTGGATCGCTACCATGTGGGGAGGTTCGATACAATACAAAACACCCATGTTATTTGCTGTAGGGTTCATCTTTTTGTTCACCATAGGA
       G  L  T  G  I  V  L  A  N  S  G  L  D  I  A  L  H  D  T  Y  Y  V  V  A  H  F  H  Y  V  L  S  M  G
1060  GGGCTCACTGGAATAGTTCTAGCAAACTCTGGGCTAGACATTGCTCTACATGATACTTATTATGTGGTTGCACATTTCCATTATGTACTTTCTATGGGA
       A  V  F  A  L  F  A  G  F  Y  Y  W  V  G  K  I  F  G  W  T  Y  P  E  T  L  G  Q  I  H  F  W  I  T
1159  GCCGTTTTTGCTTTATTTGCTGGATTTTACTATTGGGTGGGTAAAATCTTTGGTCGGACATATCCTGAAACTTTAGGCCAAATCCATTTTTGGATCACT
       F  F  G  V  N  L  T  F  F  P  M  H  F  L  G  L  S  G  M  P  R  R  I  P  D  Y  P  D  A  Y  A  G  W
1258  TTTTTCGGGGTTAATCTGACCTTCTTTCCCATGCATTTCTTAGGGCTTTCGGGTATGCCACGTCGCATTCCAGATTATCCAGATGCTTACGCCGGATGG
       N  A  L  S  S  F  G  S  Y  I  S  V  V  G  I  R  R  F  F  V  V  V  A  I  T  S  S  S  G  K  N  Q  K
1357  AATGCTCTGAGCAGTTTCGGTTCTTATATATCCGTAGTTGGGATTCGTCGTTTCTTCGTAGTTGTCGCAATCACTTCAAGCAGTGGAAAGAACCAAAAA
       C  A  E  S  P  W  A  V  E  Q  N  P  T  T  L  E  W  L  V  Q  S  P  P  A  F  H  T  F  G  E  L  P  A
1456  TGTGCGGAAAGTCCTTGGGCTGTTGAACAGAATCCAACCACACTAGAATGGTTGGTACAAAGCCCTCCGGCCTTTCATACTTTTGGAGAACTTCCTGCG
       V  K  E  T  K  S  *
1555  GTAAAAGAGACAAAAAGCTAAAAAAAAACCTCTCCTAACTATGAAGGAAGTTTCATAGAGATAGGTGTGGGGAAATAAGTTCTTCATTTGAAGAGTTAG
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