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Nucleotide sequence of the *frx*B gene in wheat chloroplast DNA

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DNA sequence analysis of part of the small single copy region of wheat (Triticum aestivum cv. Mardler) chloroplast DNA has revealed an open reading frame of 528 bp. This open reading frame is located in the 11.0 kbp PstI fragment (P5), approximately 6.5 kbp from the 3' end of the nearer copy of the gene for the 23S rRNA (1). The gene is transcribed in the same direction as the nearer rRNA operon. The deduced amino acid sequence indicates a polypeptide of 176 amino acid residues which contains 70% residues identical to the product of a gene termed frxB in liverwort chloroplast DNA (2) and 78% residues identical to the product of ORF167 in the tobacco chloroplast genome (3). Wheat frxB encodes a polypeptide of molecular weight 20393 which is predicted to carry two 4Fe-4S centres (4).

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                                                                M  N  M  F  P  M  V  T  G  F  M  S  Y  G  Q  Q  T  I  R
TATTTCAACACAAAGCTCTCTCAAACAAGAGAAAGAAACATATCTTTTTCATAGATATTTAGAATGAATATGTTCCCTATGGTAACTGGGTTCATGAGTTATGGTCAACAAACAATACG
      10        20        30        40        50        60        70        80        90        100       110       120

  A  T  R  Y  I  G  Q  S  F  I  T  T  L  S  H  T  N  R  L  P  I  T  I  H  Y  P  Y  E  K  S  I  T  P  E  R  F  R  G  R  I
TGCTACAAGGTACATAGGTCAAAGTTTCATAACTACCTTATCCCACACAAATCGTTTACCTATAACGATTCACTACCCTTATGAAAAATCAATTACACCAGAGCGTTTCCGAGGGCGAAT
      130       140       150       160       170       180       190       200       210       220       230       240

  H  F  E  F  D  K  C  I  A  C  E  V  C  V  G  V  C  P  I  D  L  P  V  V  D  W  R  F  E  K  D  I  K  K  K  Q  L  L  N  Y
CCACTTTGAATTTGATAAATGTATTGCTTGTGAAGTATGTGTTGGCGTATGTCCGATAGATCTACCCGTTGTGGATTGGAGATTTGAAAAGGATATTAAAAAGAAACAATTGCTTAATTA
      250       260       270       280       290       300       310       320       330       340       350       360

  S  I  D  F  G  V  C  I  F  C  G  N  C  V  E  Y  C  P  T  S  C  L  S  M  T  E  E  Y  E  L  S  T  Y  D  R  H  E  L  N  Y
TAGTATTGATTTCGGAGTTTGTATATTTTGTGGCAATTGTGTTGAGTACTGTCCAACAAGCTGTTTATCAATGACTGAAGAATATGAACTTTCTACCTATGATCGTCATGAATTGAATTA
      370       380       390       400       410       420       430       440       450       460       470       480

  N  Q  I  A  L  S  R  L  P  I  S  I  M  G  D  Y  T  I  Q  T  I  R  N  S  S  E  S  K  I  N  K  E  K  S  S  N  S  *
CAATCAAATTGCTTTAAGTCGGTTACCAATCTCCATAATGGGAGATTACACAATTCAAACAATTAGGAATTCGTCTGAAAGTAAAATAAACAAAGAAAAATCTTCGAATTCCTAATTGTT
      490       500       510       520       530       540       550       560       570       580       590       600

TGAATTGTGTAATCTCCCATTATGGAGATTGGTAACCGACTTAAAGCAATTTGATTGT
      610       620       630       640       650
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