

Nucleotide sequence of the intergenic spacer and the 18S ribosomal RNA gene from the mustard (*Sinapis alba*)

Jörg Rathgeber and Ingrid Capesius

Botanical Institute, University of Heidelberg, Im Neuenheimer Feld, D-6900 Heidelberg, FRG

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From a rRNA repeating unit (9.1 kbp) of mustard we have sequenced the first internal transcribed spacer, the 5.8S rRNA gene, and the second internal transcribed spacer [1]. Here, we present the nucleotide sequence of a 5500 bp fragment containing the 3' end terminus of the 25S gene (486 bp), the intergenic spacer (3204 bp), the 18S gene (1804 bp), and the first 6 nucleotides of the first internal transcribed spacer. The coding regions have been determined in homology to the equivalent genes of rice [2].

The DNA was sequenced according to the method of Maxam and Gilbert.

REFERENCES

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2. Takaiwa, F., Oono, K. and Sugiura, M. (1985) *Plant Mol. Biol.* **4**, 335–364.
3. Maxam, A.M. and Gilbert, W. (1980) *Methods in Enzymology* **65**, 499–560.

1 GAATTCACCA AGTGTGGAT TGTTCCCA CCAATAGGGA ACGTGAGCTG GGTTFAGACC GTCGTGAGAC AGGTTAGTIT TACCCACTG ATGCCCGCGT CGCAGTAGTA
 111 ATTCACACCTA GTACGAGAGG AACCGTTGAT TCGCACAAAT GGTTCATCGCG CTGGTTGAA AAGCCAGTGG CGCGAAGCTA CCGTGCCTG GATTATGACT GAACGCCTCT
 221 AAGTCAGAAT CCGGGCTAGA AGCGACGCAT GTGCCCGCGG CCCGATTGCC GACCCTCAGT AGGAGCTTCG GCTCCCAAAG GCACGTGTG TTGGCTAAGT CCGTTTGGTG
 331 GAAGCGCCGT TCGGACCGCC TTGAATTATA ATTACCACCG AGCGCGGGGT AGAATCCTTT GCAGACGACT TAAATACGCG ACGGGGTATT GTAAGTGGCA GAGTGGCCTT
 441 GCTGCCACGA TCCACTGAGA TTCAGCCCTT TGTGCTAAG ATTCGACCCT CCCCTTAACC TATCAAATGT ACCTCCAAA AACTCGATAA ACAAAAATCC CGAAAATTTT
 551 AAGTATATAA GAAAACGTTG CGCGAGGTTT CAGATTATA CTGGGGTAAA ATCACTCTCG CACCAGATT CCAGAAAAGA ACGACGAAAC GCATCCCGTC ATTACATAGA
 661 TCTGTATCAG ATCATAAAAA ACCAAGGGAA AATGTTTACA CTGGGATGAT CATGCATCCC ATCAGTACTT TCTGGACGGA CCAGGACTGT CCGGACTGGT CCATCAGTCC
 771 ATGAAAATCC GACCCATACG TACTGATGGG CTGTTCTGAT CGAGCTTATC CGTCTGAAAT GGAAGGATT AGCTCAACGG ACCATGGACT GTCCGGACTG GTCCCATCAG
 881 TACGTGAAAA ATGCCCGGTA CGTACTGATA TGCTGATCCG ATCAGCCATC AGTACTGTCT GGACGGACCA GGACTGTCCG GACTGGTCCG TCAGTCCATG AAAATCCGAC
 991 CCATACGCTA TGATGGGCTG TTCTGATCGA GCTTATCCGT CCTGAAATGGA AGGATTTAGC TCAACCGGAC ATGGACTGTC CGGACTGGTC CCATCAGTAC GTGAAAAATG
 1101 CCGCGTACGT ACTGATATGC TGATCCGATC AGCCATCAGT ACTGTCTGGA CGGACCAGGA CTGTCCGGAC TGGTCCATCA GTCCATGAAA ATCCGACCCA TACGCTACTG
 1211 TGGGCTGATG TGATCGAGAC GGACCATGGA CTGTCCGAGC TGGTCCCATC AGTACGTGAA AAAATGCCCG TACGTAATCA TATGCTGATC CGATCAGCCA TCAGTACTGT
 1321 CTGGACGGAC CAGGACTGTC CGGACTGGTC CATCAGTCCA TGA AAAATCCG ACCCATACGT ACTGATGGG TGATCTGATC GAGACGGACC ATGGACTGTC CGGACTGGTC
 1431 CCATCAGTAC GTGAAAATG CCCCCTACGT ACTGATATGC TGATCCGATC AGCCATCAGT ACTGTCTGGA CGGACCAGGA CTGTCCGGAC TGGTCCATCA GTCCATCAAA
 1541 ATCCGACCCA TACGTAATGA TGGGCTGATC TGATCGAGCC GGACCATGGA CTGTCCGGAC TGGTCCCATC AGTACGTGAA AAAATGCCCG TACGTAATCA TATGCTGATC
 1651 CGATCAGCCA TCAGTACTGT CTGGACGGAC CAGGACTGTC CGGACTGGTC CATCAGTCCA TGA AAAATCCG ACCCATACGT ACTGATGGG TGATCTGATC GAGACGGACC
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 2641 TCGAAAAGGA AACATCAAA ATATGTCAAT AAAGAGTTTA AATGTCTCAAG TGTGATCAA AAGTTTCAAT AGACATCCGT TAAGACCCG ACAGCCCGAG CCTTGTAGCA
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 2861 TTTTTTTTAC ATCAAAAATA CTCCCGGAAC AGAATCAATG TCTACTGGTG AGAGACTGAA AAAAAGTATG TTGTATATAT AAGGGGATAG CACTCTCTGT GCCTACCCCG
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 4731 GGGATCAGCG GATGTTGCTT TTAGGACTCC GCTGGCACCT TATGAGAAAT CAAAGTTTTT GGGTCCCGG GGGAGTATGG TCGCAAGGCT CCAACTTAAA GGAATGAGCG
 4841 GAAAGGCACC ACCAGGATGC GAGCCCTCGG CTTAATTTGA CTCACACCG GAAACTTAC CAAGTCCAGA CATAGTAAGG ATTGACAGAC TGAGAGCTCT TCTTTGATTC
 4951 TATGGGTGGT GGTGAGTGC CTTCTTAGT TGTGGAGCG AATTTGCTGG TTAATTCCTG TAACGAACGA GACCTCAGCC TGCTAACTAG CTACGTGGAG GCATCCCTCT
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