

# Nucleotide sequence of the mustard chloroplast genes *trnH* and *rps19'*

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A 540-ntd mustard chloroplast region containing the genes *trnH* for tRNA<sup>His</sup> and *rps19'* for a 6.8 kDa derived polypeptide with similarity to *E. coli* ribosomal protein S19 (S1) has been sequenced. The two genes are encoded by opposite DNA strands and overlap in part. They are located downstream of the *psbA* gene (2) at the junction between the large single copy region and the right-hand inverted repeat, which resembles the situation e.g. in maize (3), soybean (4), tobacco (5), and spinach (6). Sequence comparison of the polypeptide derived from mustard *rps19'* with those derived from *rps19'* and *rps19* of spinach and tobacco (6, 7) shows 85–87% sequence conservation for the first 39 (N-terminal) residues, whereas no homologies could be found for the remaining 10 amino acids, indicating that codon 39 marks the junction between the single copy region and the right-hand inverted repeat. The mustard tRNA<sup>His</sup> sequence shows 97% and 96% conserved nucleotide positions with those of spinach and tobacco, respectively. In contrast to *rps19'* where the upstream region reveals '–35' and '–10' elements that are identical in several plant species (3–7), the *trnH* 5' flanking region shows little sequence conservation. Although both '–35/–10' and

(internal) 'A/B box' (8) motifs can be assigned, the possibility exists that the *trnH* gene does not have a functional promoter and is cotranscribed with *psbA* *in vivo* (9).

## ACKNOWLEDGEMENTS

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1  GAAAAAACCCGTAACCCCTGGGGTTATCCTGCGCTGGAAAGAACTAGAAAAAGGAAAAATATAGTGAGACTTTGATTCTTCGTC
   -35                                     -10
91  GCGTAGTAAATAGGAGAGAAAAATAGAATTTCTTTCTTCGCTTAAAAAAAATAGGAGTTAATTAAGTGTGACACGTTCACTAAAAAAA
   RBS                                     M T R S L K K
181 ATCCTTTTGTAGCAAAGCATTATTAAGAAAAATAGAGAACTTAATACAAAGCGGAAAAACAATCATAATAACTTGGTCCGGGCCA
   N P F V A K H L L R K I E K L N T K A E K Q I I T W S R A
271 TCACGGGCGAACGACGGGAATTGAACCCGCGATGGTGAATTCACAATCCACTGCCTTAATCCACTTGCTACATCCGCCCTACTATACA
   I T G E R R E L N P R W *
361 TCTTTTTTTTATTGCTAAATAAATAAAAAACGCATCGAATTCAAATAACAATAAACTGGTAGCAAATTACACCTTACTTTTTAT
   trnK ← -10 -35
451 AGAAAAAACGAGCAATATAAGCCTTGAAAAGAGGCTTATATGGCTCGTTTTTTAATAAACTAGGTCTAGACTAACGCTAAAGAATTA

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