The sequence of the plastid encoded rpl22 protein in marine macroalgae, *Gracilaria tenuistipitata*

Jyh-shyang Kao and Madeline Wu*
Department of Biological Sciences, University of Maryland Baltimore County, Baltimore, MD 21228, USA

Submitted April 2, 1990
EMBL accession no. M32638

A partial library of the plastid DNA EcoRI fragments was constructed in Bluescript vector. Using a heterologous probe from *Chlamydomonas reinhardtii*, several genes coding for ribosomal proteins were located (1). By DNA sequence comparison, an ORF was identified as rpl22, the coding region and its flanking sequences are shown below. At nucleotide level, this gene shares 56.23%, 54.20%, 52.46% and 50.35% with the rpl22 gene of *Marchantia polymorpha* (2), *Nicotiana tabacum* (3), *Spinacia oleracea* and *Zea mays* (4) respectively. At amino acid (aa) level, the homology is 66.96%, 60.87%, 58.26% and 57.73% respectively. The algal rpl22 protein contains 116 aa and the rpl22 protein of liverwort contains 120 aa. Both are considerably smaller than the rpl22 protein of dicot plants, tobacco (156 aa) and spinach (200 aa). The algal rpl22 protein shows high homology to the region of aa 2 to 116 and aa 25–139 in the tobacco and spinach rpl22 protein respectively. The rpl22 gene of maize, a monocot plant, contains 127 aa (4). In the plastid genome of this marine macroalgae, the gene order of 5' rpl22-rps3-rpl16 is identical to that detected in the chloroplast DNA of liverwort (2), tobacco (3) and maize (4).

ACKNOWLEDGEMENT
This work has been supported by NSF grant DCB-8911485.

REFERENCES

1 ACCAGAAATT TCAGAAGCCA TGAAAAAGT GATCAGAAAA ACGAAAAGAT AAATAT

57 ATG ACT AAT AAA ACT ACA AAG ATT CAG GCA ACA GGA AAA TAT GTA

MTNKTGTKIKQATGKYV

102 CGC TTG TCC ACA GCA AAG ACA AGA AGA GTG TTA AATCAAATCAGAAAT

RLSTAKTKRRVNLONIK

147 GGT AAA AAA TAT CAA GAA GCA ATA TTA ATA CTA GAA TTT ATG ACA

GKKYQEAILILEFMTR

192 TAT AAA CCT TGT AAA ATT ATA AAA AAG ATT CTA GAG TCA GCA GGA

YKPKCKIKIKKILESAG

237 AAC AAT GCA TTA AAT CTA AAA TAT GAA AAA CAA AAT TTG ATC ATT

NNALNLKYEKQLII

282 AAA CAA GCT TTT GCT AAC GAT GGC CCA AAA CTA AAA AGA TTG CAA

KQAFANDGPKLKRFQ

327 CCT AGG GCA CAA GGT AGA GCA TTT CGT ATA CAG AAA CCA ACA TGT

PRAQGRAFRIQKPTC

372 CAT ATT ACA ATA AAC TTA AGT ATC AAT TAA TTATATATTA CAAGTATA

HITINLSIN*

462 AATAGAGAACA

* To whom correspondence should be addressed