

Sequence and secondary structure of *Porphyra umbilicalis* 5S rRNA. Relevance for the evolutionary origin of red algae

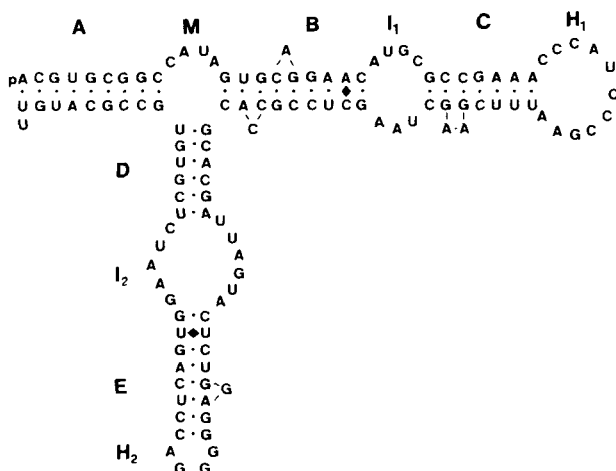
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The sequence of the cytoplasmic 5S rRNA of the red alga *Porphyra umbilicalis* was determined and fits the following secondary structure model:



This model, applicable to all red algal 5S rRNAs (1), has certain features reminiscent of bacterial rather than eukaryotic 5S rRNAs, as documented below:

Feature (see also refs. 2 and 3)	Archae- bacteria	Eubacteria	Eukaryotes	
			red algae	other
Presence of bulge on 5'-strand of helix B	yes	yes	yes	no
N ^o of bases in helix C + loop H ₁	27	27	27	26
Symmetry of loop I ₁	sym.	sym.	asym.	asym.
Presence of bulge(s) on helix E	sometimes	no	yes	yes

This pattern can be explained by assuming that the ancestral eukaryotic 5S rRNA shared the first two features with the archaeobacterial and eubacterial 5S rRNAs, and that these were altered in the eukaryotic branch of evolution only after the divergence of the red algae, the latter conserving these ancestral features until the present time. As such, the study of 5S rRNA secondary structure consolidates phylogenetic studies (4) based on 5S rRNA sequences and pointing to the red algae as the earliest diverging branch of the eukaryotes.

References:

- 1) Lim, B.-L. et al. (1986) Jpn. J. Genet. 61, 169-176.
- 2) Willekens, P. et al. (1986) Syst. Appl. Microbiol. 7, 151-157.
- 3) Van den Eynde, H., De Wachter, R. (1987) FEBS Lett. 217, 191-196.
- 4) Hori, H., Osawa, S. (1987) Mol. Biol. Evol. 4, 445-472.