Hypothesis

THE ORIGIN OF PLANT CHLOROPLAST 4.5 S RIBOSOMAL RNA

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Received 4 November 1980

1. Introduction

Nazar [1] has recently pointed out the extensive homology (~53%) between trout 5.8 S rRNA (ribosomal ribonucleic acid) and the 5′-terminus of *Escherichia coli* 23 S rRNA, and has suggested that the prokaryotic homologue of eukaryotic 5.8 S exists not as an independent RNA species, but as the 5′-terminus of the 23 S rRNA. This concept is consistent with the observation that the eukaryotic 5.8 S sequence is located proximal to the 5′-end of the 28 S rRNA sequence in a larger precursor RNA species [1]. This approach is used here to consider another small rRNA, the 4.5 S rRNA found in some chloroplast ribosomes [2]. The 4.5 S gene is located 3′ to the 23 S gene and 5′ to the 5 S gene in tobacco chloroplast DNA [3]. This suggests that chloroplast 4.5 S rRNA, with no other known homologue in other types of ribosomes, may be homologous to the 3′-terminus of prokaryotic 23 S rRNA. The complete sequence of *E. coli* 23 S rRNA [4] and the recently reported sequence of tobacco chloroplast 4.5 S rRNA [5] allows this hypothesis to be tested.

2. Sequence homology between chloroplast 4.5 S rRNA and the 3′-terminus of prokaryotic 23 S rRNA

Fig.1 shows the alignment of tobacco chloroplast 4.5 S rRNA with the 3′-terminus of *E. coli* 23 S rRNA. Nucleotides 35–103 of the 4.5 S sequence align easily with no insertions or deletions necessary, and yield homology of 61% for this section. The probability of obtaining this degree of homology between two randomly generated sequences of this length is ≪0.01. Nucleotides 1–34 of the 4.5 S sequence are more difficult to align, with only 24%

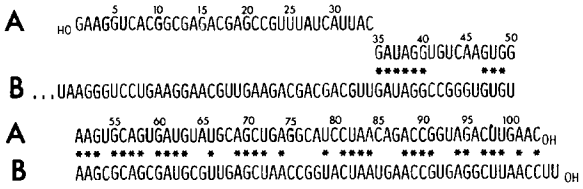

Fig.1. Alignment for maximum homology of (A) tobacco chloroplast 4.5 S rRNA; and (B) the 3′-terminus of *Escherichia coli* 23 S rRNA. Homologous positions are noted by asterisks (*). For reasons outlined in [5], the nucleotides in the 4.5 S rRNA at positions 69 and 70 have been assumed to be A and G, respectively and not G and A.

homology when no insertions or deletions are allowed. Several alternative alignments of this region are possible, if insertions and deletions are used. For example: if, in the 4.5 S sequence, nucleotide 7 and nucleotides 26–34 are considered as insertions, while nucleotides 13 and 14 and nucleotides 21 and 22 each bound single nucleotide deletions, then homology for this region is 53%. The significance of this degree of homology, when several insertions and deletions are postulated within such a short segment, is questionable.

3. Conclusions

The degree of homology observed between nucleotides 35–103 of tobacco chloroplast 4.5 S rRNA and the 3′-terminus of *E. coli* 23 S rRNA supports the hypothesis that these two sequences are derived from a common ancestor, and suggests that they may be functionally equivalent. Restriction mapping of tobacco rDNA [3] indicates the presence of a spacer between the 23 S and 4.5 S genes. This suggests that at some time since the divergence of chloroplasts and prokaryotes there has been either:

(1) An insertion (with or without a transcription terminator for the 23 S gene and a promoter for the 4.5 S gene) in the 23 S gene of the chloroplast; or
(2) A deletion from the 23 S gene of prokaryotes.

Acknowledgements

I thank W. F. Doolittle for encouragement and advice and D. F. Spencer for help in aligning sequences.

References

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