Hypothesis

A 5.8 S rRNA-LIKE SEQUENCE IN PROKARYOTIC 23 S rRNA

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1. Introduction

One of the most striking differences between the cytoplasmic ribosomes of eukaryotes and prokaryotes is the presence (in eukaryotes) of one additional RNA component, the 5.8 S rRNA. This RNA molecule, which is hydrogen bonded to the high molecular weight RNA component of the large subunit [1–3], is about 160 nucleotides long [4] and is cotranscribed with the high molecular weight rRNAs as part of a much larger precursor molecule, the 45 S nucleolar RNA in mammals [5–7]. Although its role in ribosome structure or function has not been established, this molecule has been observed in all eukaryotic cytoplasmic ribosomes that have been examined and its nucleotide sequence appears to be highly conserved in the course of evolution [4]. Indeed, sequence analysis indicate that, in eukaryotes, the 5.8 S rRNA sequence is more highly conserved than that of 5 S rRNA [4]; as much as 75% of the sequence is homologous between yeast and man [4].

Assuming that, because this RNA sequence is so highly conserved, 5.8 S RNA must be important to ribosome function, it is surprising that this component has not been observed in prokaryotes. The possibility exists that the sequence is present in prokaryotic ribosomes but simply not as a separate RNA molecule. In mammals, 5.8 S rRNA is cleaved from the 32 S nucleolar RNA precursor which is also a direct precursor of 28 S rRNA [5–7]. A number of studies [8–10] on the distribution of mature rRNA sequences in rDNA indicate that the 5.8 S rRNA sequence is located in the 5′-end of the 32 S nRNA precursor just proximal to the 28 S rRNA. Accordingly, if a sequence equivalent to 5.8 S rRNA is present in the prokaryotic 23 S rRNA, it is likely to be located at, or near, the 5′-end.

2. Sequence homology between eukaryotic 5.8 S rRNA and prokaryotic 23 S rRNA

Recent reports on the complete nucleotide sequence of 23 S rRNA from *Escherichia coli* ribosomes [11,12] allow a comparison to be made between this prokaryotic RNA and known sequences of 5.8 S RNA. As shown in fig.1, sequence homology is observed between trout 5.8 S RNA [4] and the 5′-terminal sequence of the 23 S RNA molecule. With appropriate insertions and deletions, 94 out of 176 residues (insertions are included as residues) or ~53% of the sequences are homologous. This homology is particularly striking in the first half of the 5.8 S RNA molecule which includes 2 blocks of 8 completely homologous residues. A somewhat lower sequence similarity is observed with the other known 5.8 S rRNA sequences although, because of the high degree of sequence conservation among 5.8 S RNA, most comparisons indicate homologies in the 50% range.

3. Sequence homology between eukaryotic and prokaryotic 5 S rRNA

Although the sequence similarity in fig.1 is unusual, the possibility remains that it is coincidental. Because many 5 S rRNA sequences have been determined for both eukaryotic and prokaryotic species, it is possible to compare the degree of homology among 5 S RNAs with that shown in fig.1. As shown in fig.2, when trout 5 S RNA is compared with that of *E. coli* the overall homology is very similar. With appropriate insertions and deletions, 68 out of 125 residues (insertions are included as residues) or ~54% of the sequences are homologous. The number of insertions, or deletions, is slightly lower (6.4/100 nucleotides vs 8.7/100 nucleotides) but still similar. Other 5 S RNAs

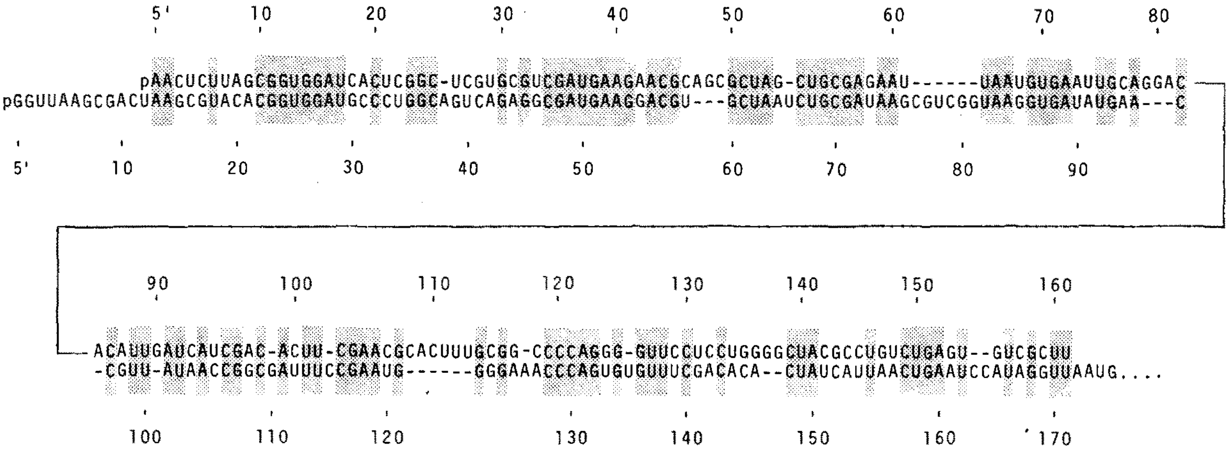

Fig.1. A comparison of the primary nucleotide sequence of trout 5.8 S rRNA (upper line) with the 5′-end region of *E. coli* 23 S rRNA (lower line). The shaded areas indicate identical nucleotides; the residues are identified by the numbers above and below the sequences.

were also examined; the results are summarized in table 1. In each instance the overall degree of homology between eukaryotic and prokaryotic RNAs was similar to that observed in fig.1, suggesting that the comparison between 5.8 S and 23 S rRNA may be significant.

4. Conclusion

Sequence comparisons between eukaryotic 5.8 S rRNAs and *E. coli* 23 S rRNA indicate a 5.8 S RNA-like sequence at the 5′-end of the 23 S RNA molecule. This homology is similar in degree to that observed between eukaryotic and prokaryotic 5 S rRNAs, suggesting that the 5.8 S RNA sequence may exist in prokaryotes but not as an independent molecule. The function of the eukaryotic 5.8 S RNA molecule will have to be determined before this possibility can be tested experimentally.

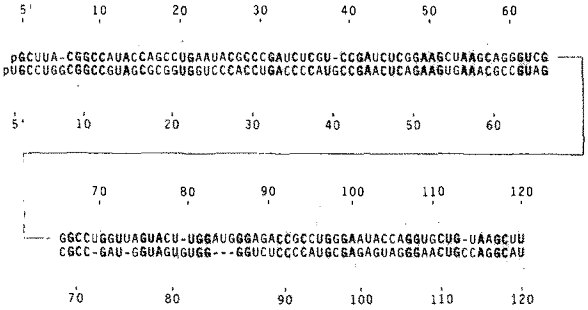

Fig.2. A comparison of the primary nucleotide sequence of trout 5 S rRNA (upper line) with the *E. coli* 5 S RNA molecule (lower line). The shaded areas indicate identical nucleotides; the residues are identified by the numbers above and below the sequences.

Table 1
A comparison of sequence homology between prokaryotic and trout 5 S rRNA

Source of RNA	Ref.	% Sequence homology	Inserts of deletions/ 100 residues
Escherichia coli	[13]	54	6.4
Pseudomonas fluorescens	[14]	52	8.9
Bacillus subtilis	[15]	53	7.3
Thermus aquaticus	[16]	55	6.4
Clostridium pasteurianum	[17]	48	5.0

The % sequence homology was calculated by aligning the sequences for maximum homology as shown in fig.2. The trout 5 S RNA sequence is from [18]

References

[1] Forget, B. G. and Weissman, S. M. (1967) Nature 213, 878–882.

[2] Pene, J. J., Knight, E. jr and Darnell, J. E. jr (1968) J. Mol. Biol. 33, 609–623.

[3] Weinberg, R. A. and Penman, S. (1968) J. Mol. Biol. 38, 289–304.

[4] Nazar, R. N. and Roy, K. L. (1978) J. Biol. Chem. 253, 395–399.

[5] Busch, H. and Smetana, K. (1970) The Nucleolus, pp. 211–284, Academic Press, New York.

[6] Maden, B. E. H. and Robertson, J. S. (1974) J. Mol. Biol. 87, 227–255.

[7] Nazar, R. N., Owens, T. W., Sitz, T. O. and Busch, H. (1975) J. Biol. Chem. 250, 2475–2481.

[8] Speirs, J. and Birnstiel, M. L. (1974) J. Mol. Biol. 87, 237–256.

[9] Dawid, I. B. and Wellauer, P. K. (1976) Cell 8, 443–448.

[10] Bell, G. I., De Gennaro, L. J., Gelfand, D. H., Bishop, R. J., Valenzuela, P. and Rutter, W. J. (1977) J. Biol. Chem. 252, 8118–8125.

[11] Branlant, C., Krol, A., Machatt, M. A. and Ebel, J. P. (1979) FEBS Lett. 107, 177–181.

[12] Brosius, J., Dull, T. J. and Noller, H. F. (1980) Proc. Natl. Acad. Sci. USA 77, 201–204.

[13] Brownlee, G. G. and Sanger, F. (1967) J. Mol. Biol. 23, 337–353.

[14] DuBay, B. and Weissman, S. M. (1971) J. Biol. Chem. 246, 747–761.

[15] Marotta, C. A., Varricchio, F., Smith, I., Weissman, S. M., Sogin, M. L. and Pace, N. R. (1976) J. Biol. Chem. 251, 3122–3127.

[16] Nazar, R. N. and Matheson, A. T. (1977) J. Biol. Chem. 252, 4256–4261.

[17] Pribula, C. D., Fox, G. E. and Woese, C. R. (1976) FEBS Lett. 64, 350–352.

[18] Roy, K. L. (1978) Can. J. Biochem. 56, 60–65.