Hypothesis

Evolutionary relationship between eukaryotic 29–32 S nucleolar rRNA precursors and the prokaryotic 23 S rRNA

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1. INTRODUCTION

When compared with prokaryotes, the cytoplasmic ribosomes of eukaryotes contain one additional RNA component, the 5.8 S rRNA. This molecule, which is hydrogen bonded to the high-M_r RNA component of the large subunit [1–3] is cotranscribed with the high-M_r rRNAs as part of a much larger precursor molecule [4–6], the 37 S nucleolar RNA in yeast [7]. Although its role in ribosome structure or function has not been established, the molecule is universal to all eukaryotic ribosomes and the sequence is highly conserved [8]; as much as 75% of the sequence is homologous between yeast and man [8].

Because the 5.8 S RNA sequence is so highly conserved, we postulated that it must be very important in ribosome function and, therefore, is probably present in prokaryotes, but simply not as a separate RNA molecule. In eukaryotes, the 5.8 S rRNA is cleaved from the 29–32 S nucleolar RNA precursor which is also a direct precursor of 25–28 S rRNA [4–7]. Since a number of studies [9–11] have indicated that, in rDNA, the 5.8 S RNA sequence is located in the 5′-end of the 29–32 S rRNA precursor sequence we suggested that a 5.8 S-like sequence may be found at, or near, the 5′-end of the prokaryotic 23 S rRNA. Indeed, when eukaryotic 5.8 S rRNA sequences were compared with the 5′-end sequence of the *Escherichia coli* 23 S rRNA a limited sequence homology was observed [12].

If this sequence relationship is correct a second prediction can be made: that sequence homology between the prokaryotic 23 S RNA molecule and the eukaryotic 25–28 S rRNA equivalent should not be observed when the 5′-ends are compared directly but should be present when the 2 molecules are compared with the 5′-end of the 25–28 S rRNA, 150–200 nucleotides in from the 5′-end of the 23 S rRNA.

2. SEQUENCE COMPARISON BETWEEN PROKARYOTIC 23 S rRNA AND EUKARYOTIC 25 S rRNA

A report on the complete nucleotide sequence of the 25 S rRNA from *Saccharomyces cerevisiae* ribosomes [13] permits the comparison with the 23 S rRNA from *Escherichia coli* [14,15]. When the 5′-ends of these molecules are aligned for maximum sequence homology they are not end-to-end, and there is an extra sequence of ~ 150 nucleotides at the 5′-end of the 23 S RNA molecule (fig.1). These are the same nucleotides shown to bear a limited sequence homology with the eukaryotic 5.8 S rRNA in [12].

A more detailed analysis of this sequence homology raises two important points which further support our model. The overall homology is relatively high (~ 75%) in the clearly comparable regions (residues 20–74 in the 25 S rRNA). This is significantly higher than the ~ 50–55% homology observed between 5 S RNAs from prokaryotes and eukaryotes and in the 5.8 S *vs* 23 S rRNA comparison [12]. However, the sequence homology is very low (~ 33%) or not significant in the region of

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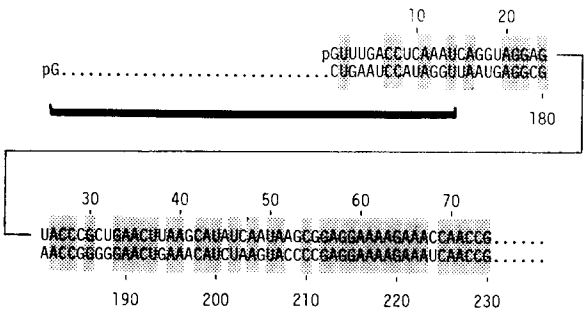

Fig.1. A comparison of 5′-end regions of *S. cerevisiae* 25 S rRNA (upper line) with that of *E. coli* 23 S rRNA (lower line). The shaded areas indicate identical nucleotides; the solid line indicates the nucleotide sequence in *E. coli* 23 S rRNA, shown to bear a limited sequence homology with the eukaryotic 5.8 S rRNA [12]. The residues are identified by the numbers above and below the sequence.

overlap (residues 157–171 in the 23 S rRNA) suggested to be homologous with the 5.8 S rRNA sequence [12].

3. CONCLUSION

Sequence comparisons between eukaryotic 5.8 S rRNAs, the *E. coli* 23 S rRNA and the yeast 25 S rRNA suggest that the mature prokaryotic 23 S rRNA is comparable to the nucleolar 29–32 S rRNA precursor of eukaryotic organisms. Apparently, in the course of evolution, additional processing, acquired by eukaryotes or lost by prokaryotes, cleaves the prokaryotic 23 S RNA sequences into its eukaryotic equivalents. The degree of homology between the eukaryotic 5.8 S RNA sequence and its prokaryotic equivalent is somewhat lower than between the high-M_r RNA components. It is attractive to speculate that these changes may be required for 5.8 S RNA function or structure as an independent molecule. Again, the function of the eukaryotic 5.8 S rRNA will have to be determined before this can be tested experimentally.

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