Hypothesis

PROPOSED SEQUENCE HOMOLOGY BETWEEN THE 5′-END REGIONS OF PROKARYOTIC 23 S rRNA AND EUKARYOTIC 28 S rRNA

Relevance to the hypothesis that 5.8 S rRNA is homologous to the 5′-end region of 23 S rRNA

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1. Introduction

It was proposed in [1] that the 5′-end region of prokaryotic 23 S rRNA may be homologous with, and the functional equivalent of, 5.8 S rRNA in eukaryotes. The significance of the proposed whole sequence identities between trout (*Salmo gairdneri*) 5.8 S rRNA and the 5′-end region of *Escherichia coli* 23 S rRNA [1] was recently questioned [2], given the large number of assumed deletions and insertions, and a more convincing case was presented based upon a selective high percentage identity between only highly conserved nucleotide positions in 5.8 S and proposed homologous positions in *E. coli* 23 S rRNA. The question arose whether a sequence homologous with 5.8 S and the 5′-end regions of 23 S rRNA exists at or near the 5′-end in eukaryotic 28 S rRNA. This question was left unanswered as no adequate data was then known. Such data on the 5′-end region of *Xenopus laevis* 28 S has now become available [3]. An alignment of homologous positions in the 5′-end region of *E. coli* 23 S and *Xenopus* 28 S rRNA is proposed here and the favorable implications for the hypothesis that 5.8 S rRNA is homologous with the 5′-end region of prokaryotic 23 S rRNA are noted.

2. Proposed alignment of 5′-end regions of *E. coli* 23 S and *Xenopus* 28 S rRNA

Comparison of the *Xenopus* 28 S rRNA partial sequence [3] with the 5′-end region of *E. coli* 23 S rRNA [4] (fig.1) reveals a high percentage (72%) identity between positions 1–118 in the 28 S sequence and positions 158–275 in the 23 S rRNA sequence (as far as the 28 S rRNA was sequenced). Only 2 single nucleotide deletions or insertions are assumed, both in the region nearest the 5′-end of the 28 S rRNA, which shows a lower percentage identity than the more interior region.

3. Apparent partial overlap of regions of homology in 5.8 S, 23 S and 28 S rRNA

The first 15 positions of the proposed 23 S–28 S rRNA alignment overlaps with the last 13 positions on the 3′-end region of 5.8 S rRNA, according to the alignment proposed in fig.1. This alignment differs from the proposed alignment of 5.8 S and *E. coli* 23 S rRNA [1] in that the GUC sequence in positions 155–157 has been shifted one position toward the

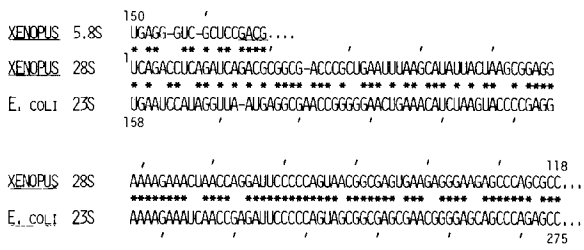

Fig.1. Proposed alignment of the 3′-end region of *Xenopus laevis* somatic 5.8 S rRNA and the 5′-end regions of *X. laevis* 28 S and *Escherichia coli* 23 S rRNA, beginning at positions 150, 1 and 158 from the 5′-end, respectively. The underlined positions in the 5.8 S rRNA partial sequence are spacer positions according to [3]. Asterisks denote positions with identical nucleotides in the sequences on either side.

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5′-end. Furthur sequence data may provide a more confident judgement as to which of these alignments is more likely. The first 4 nucleotides of the spacer between *Xenopus* 5.8 S and 28 S rRNA [3] are identical to possible homologous positions in *Xenopus* 28 S rRNA (fig.1). Thus, 12/19 positions, including these spacer positions, or 8/15 positions without them in the proposed region of 5.8 S–28 S rRNA overlap have identical nucleotides. This compares to a mean of 8.5/15 identities in this region between *Xenopus* and *Vicia faba* bean [5], wheat [6], yeast [7] or *Neurospora* [8] 5.8 S rRNA.

It is unfortunate that the region of proposed 5.8 S–28 S rRNA overlap is part of a region of comparatively high variability within 5.8 S rRNA sequences [2] and between the 23 S–28 S rRNA comparison (fig.1). Comparisons between a variety of eukaryotic 5.8 S and 28 S rRNA and prokaryotic 23 S rRNA may provide a more definitive test of the hypothesis that some positions homologous with the 3′-end region of eukaryotic 5.8 S rRNA are present on the 5′-end of eukaryotic 28 S rRNA.

4. Conclusions

The 5′-end region of *Xenopus* 28 S rRNA is proposed to be homologous with a region of *E. coli* 23 S rRNA beginning 158 nucleotides from the 5′-end of the 23 S rRNA. The apparent absence of a sequence in the 5′-end region of *Xenopus* 28 S rRNA homologous with the 5′-terminal 157 nucleotides of *E. coli* 23 S rRNA (approximating in length that of eukaryotic 5.8 S rRNA) adds furthur credence to the hypothesis [1,2] that eukaryotic 5.8 S rRNA is homologous with and possibly functionally equivalent to the 5′-end region of prokaryotic 23 S rRNA. A small proposed overlap in homology between the 3 representative sequences of 5.8 S, 23 S and 28 S rRNA provides a suggestion that 5.8 S rRNA may once have been part of a 28 S rRNA-like molecule in eukaryotes.

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