On the sequence homology of the ribosomal proteins, *Escherichia coli* S11, yeast rp59 and Chinese hamster S14

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A strong sequence homology was found among the ribosomal proteins of the different species, S11 of *Escherichia coli*, rp59 of *Saccharomyces cerevisiae* and S14 of Chinese hamster ovary cell. The significance of this series of highly conserved proteins is discussed.

Ribosomal protein *Sequence homology* *Evolution*

1. INTRODUCTION

Eukaryotic ribosomes contain a greater number of proteins than prokaryotic ribosomes and the proteins are, on average, larger [1]. Although the patterns of two-dimensional gel electrophoresis of ribosomal proteins are similar among mammals, birds and reptiles [2], or between rat and *Artemia salina* [3], they are very different between yeast and rat [4] or between prokaryotes and eukaryotes. Nevertheless, some lines of evidence suggest the conservation of the structure of some ribosomal proteins during the course of evolution. Antibodies raised against *Escherichia coli* (*E. coli*) L7/L12 crossreacted with acidic ribosomal proteins of rat liver [5]. The primary structures of the acidic proteins corresponding to *E. coli* L7/L12 ('A' proteins) from several kinds of organisms were determined. However, there is only weak, if any, sequence homology in the A proteins of eukaryotes and eubacteria [6]. The Fab fragments of the antibodies raised against *E. coli* ribosomal proteins, S10, S12 and S14 inhibited polyphenylalanine synthesis in a rat liver cell-free system [7]. Immunological evidence for structural homology among *Drosophila* S14, rat S12, yeast S25, *Bacillus subtilis* S6 and *E. coli* S6 was also reported [8]. Recently, we deduced the amino acid sequence of rat S11 from the nucleotide sequence of cloned cDNA and showed that it is well conserved from that of *E. coli* S17 [9], although the function of these proteins is not yet known. Here we examined published sequences of ribosomal proteins and found that the proteins corresponding to Chinese hamster ovary cell (CHO) S14 are highly conserved among prokaryotes, unicellular eukaryotes and mammalian cells.

2. MATERIALS AND METHODS

We keep a data bank of all published amino acid sequences of ribosomal proteins on a microcomputer. Similarity of the amino acid sequences was scored with the computer program based on the algorithm of Dayhoff's ALIGN adopting the log odds matrix for 250 accepted point mutation units with a matrix bias parameter of 2 and a gap penalty of 10 [10].

3. RESULTS AND DISCUSSION

When the amino acid sequence of CHO S14 [11] was compared with those of all the ribosomal proteins in our data bank, it showed significant homology with *E. coli* S11 [12] and *Saccharomyces cerevisiae* rp59 [13] with the alignment scores of

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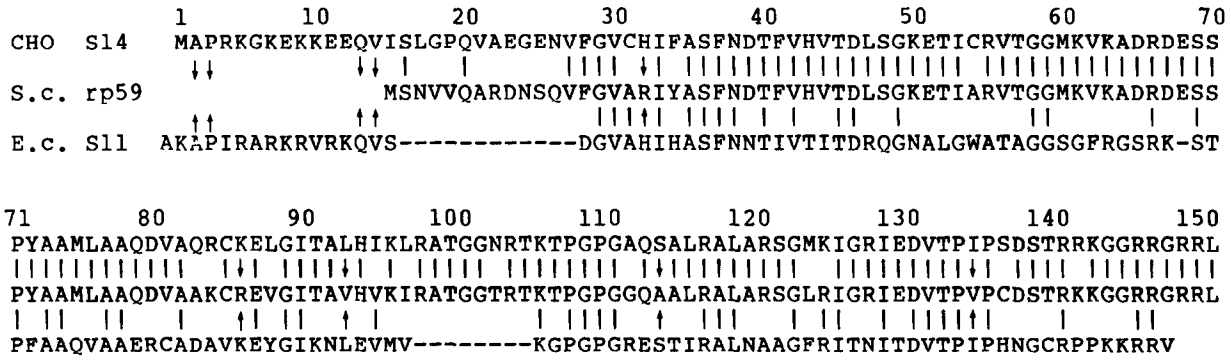

Fig.1. Alignment of the sequences of CHO S14, yeast rp59 and *E. coli* S11. The same amino acids are indicated by '|', the amino acids only common to CHO S14 and *E. coli* S11 being denoted by facing arrows.

11.0 and 37.5 standard deviation units (SD), respectively. The comparisons with the other ribosomal proteins gave values less than 3.0 SD. The amino acid sequence of yeast rp59 was then compared with those of a set of *E. coli* ribosomal small subunit proteins. Again S11 gave the highest value, 12.1 SD, whereas the others were less than 3.0 SD. The sequences of CHO S14 and yeast rp59 are aligned without any gap, but rp59 lacks some 15 amino acids at the N-terminus as shown in fig.1. On the other hand, the sequence of *E. coli* S11 requires three gaps for the proper alignment and also lacks three amino acids at the C-terminus. However, it is one or two (if N-terminal methionine in CHO S14 only acts as the initiator and is removed after the initiation of peptide chain synthesis) amino acids longer than CHO S14 at the N-terminus (fig.1).

The Fab fragment of the antibody raised against *E. coli* S11 was shown to inhibit polyphenylalanine synthesis up to 50% in a rat liver cell-free system [8]. That finding may be explained by the structural homology of *E. coli* S11 and mammalian S14 together with their important role in protein synthesis as discussed below. *E. coli* S11 was reported to play a role in the EF-Tu-dependent aminoacyl-tRNA binding [14]. On the other hand, CHO S14 is responsible for emetine resistance [15]. Emetine inhibits protein synthesis in eukaryotes at the elongation step [16]. Arg at position 149 or Arg-Arg at position 149–150 of S14 are substituted in emetine-resistant mutants of CHO cells, suggesting that a few C-terminal amino acids are important for emetine inhibition [11]. It is very interesting that *E. coli* ribosomes, which resist emetine, lack this part of the protein as shown in fig.1. Thus, both CHO S14 and *E. coli* S11 play an important role in the elongation step. Furthermore, *E. coli* S11 was reported to bind to an AUG analog [17] and to be crosslinked with IF-2 [18] and IF-3 [19] with bifunctional reagents. Rabbit reticulocyte S14 was also reported to be one of the ribosomal proteins crosslinked with eIF-3 [20]. Thus, both *E. coli* S11 and mammalian S14 also have a functional role in the initiation reaction. These results may indicate that this series of proteins play an essential role in common in the wide range of protein synthetic reactions of ribosomes and, therefore, resist the force to evolve proteins.

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