

Cloning of the gene for ribosomal protein S13 from the fission yeast *Schizosaccharomyces pombe*

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Submitted June 30, 1992 EMBL accession no. X67030

Despite much intensive study, the function of the eukaryotic ribosome and many of its individual components remains enigmatic (1). In the course of cloning and analysis of the *S.pombe cdc16*$^{+}$ gene (2), we noticed that the clone which complemented the *cdc16–116* mutation hybridized to two transcripts. Sequencing revealed that one of these transcription units corresponded to the *cdc16* gene (to be reported elsewhere) while the other was the fission yeast equivalent of ribosomal protein S13. Southern blots of *S.pombe* chromosomal DNA digested with a variety of restriction enzymes indicates that the gene is present at single copy in the genome (not shown). The gene comprises four exons, split by introns of 104 bp, 64 bp and 64 bp. The first intron contains two potential stem-loop structures, though whether these play a role in the regulation of the expression of the gene is unknown. The protein is 151 amino acids long and basic in character. It is not known whether the N-terminal methionine is removed as in the case of the rat S13 protein (3). The molecular weight calculated from the DNA sequence is 16953. Ribosomal protein S13 has previously been cloned from rat and the filarial worm, *B.pahangi*, where it was identified as an antigen recognised by the sera of infected people (3, 4). Sequence comparison of the predicted proteins shows that all three are identical at 67% of positions. Pairwise comparisons indicate that the *S.pombe* protein shows 71% and 74% identity with *B.pahangi* and rat, respectively, while the rat and *B.pahangi* proteins are 84% identical (see Figure 1). Examination of the sequence indicates that the imperfect internal repeats identified in the rat protein (3) are also present in the fission yeast rpS13, from residues 32–42 and 83–94. The cloning of a ribosomal protein from a genetically tractable organism such as fission yeast should now permit the application of both classical and reverse genetics to the elucidation of the structure and function of the eukaryotic ribosome. The sequence has been deposited in the EMBL database under the accession number X67030.

ACKNOWLEDGEMENTS

We thank B.Hirt for support. C.Bonnard for assistance with computing and members of the laboratory for constructive criticism and encouragement. This work was supported by the Fonds National, Grant 31-3080.91 and by EC and ISREC fellowships to J.M.

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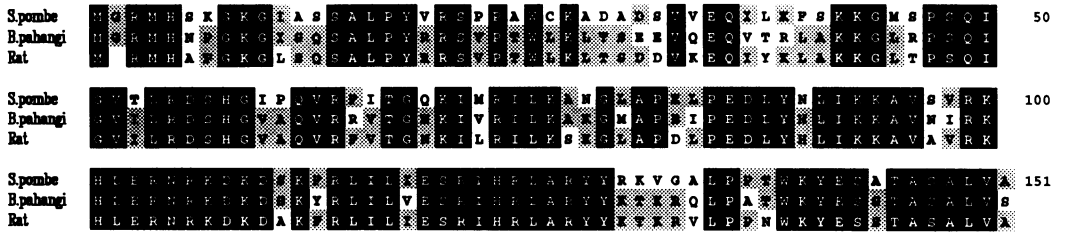

Figure 1. The figure shows an aligment of the predicted protein sequences of the *S.pombe*, *B.pahangi* and rat ribosomal protein S13. Residues conserved in all three proteins are highlighted in black, while those conserved between two are shaded in grey. Numbering is according to the *S.pombe* sequence.

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