

The structure of the yeast ribosomal RNA genes. I. The complete nucleotide sequence of the

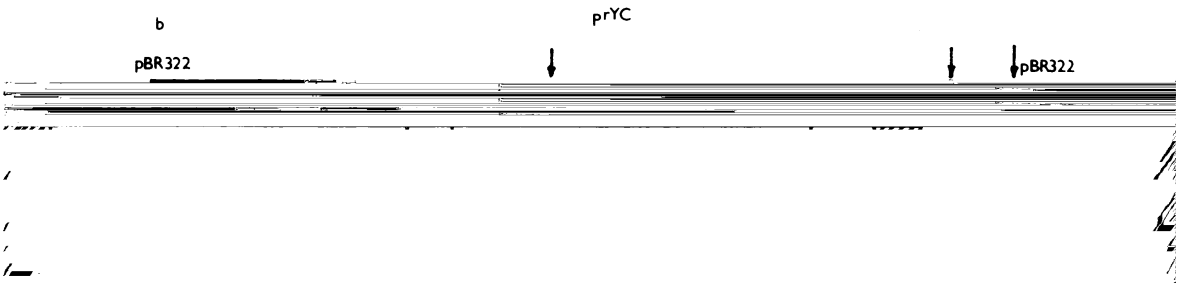
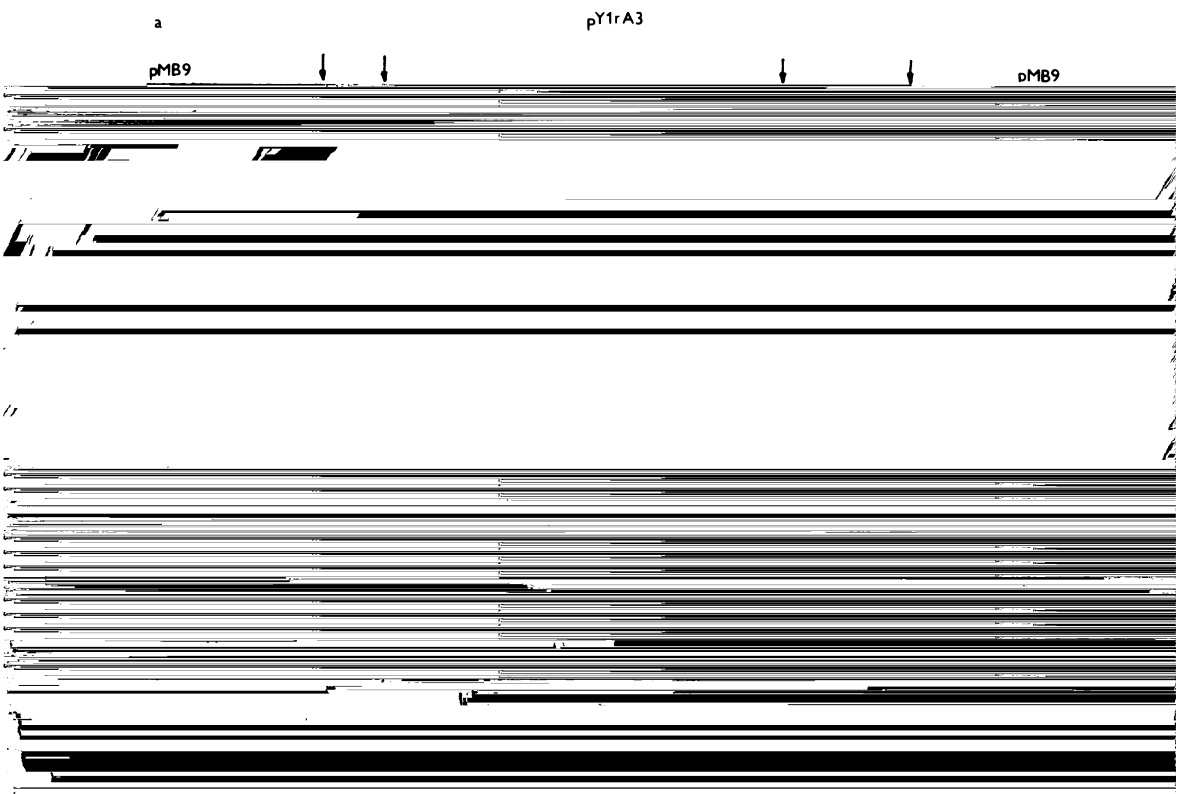
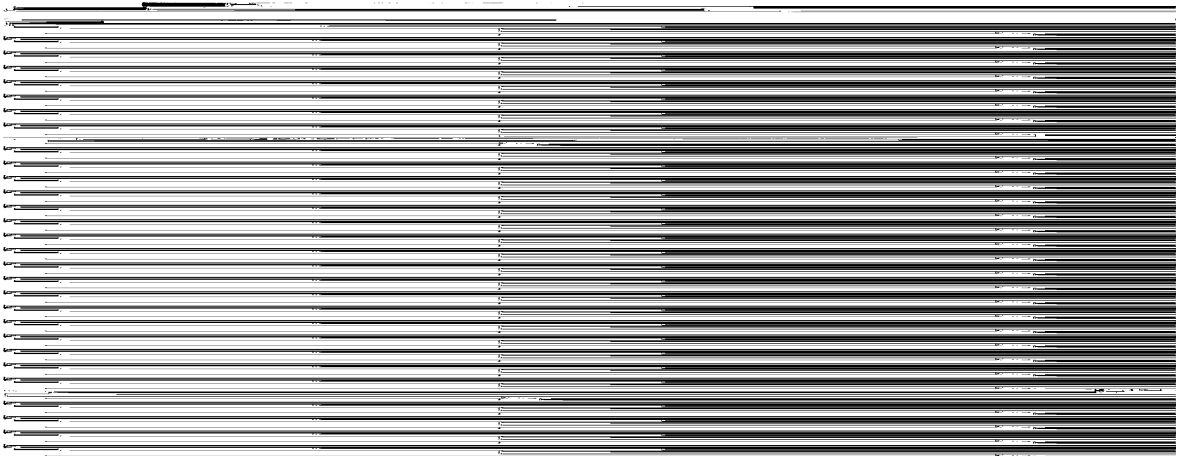
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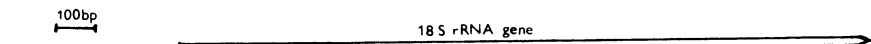
and the identification of evolutionary divergence of different

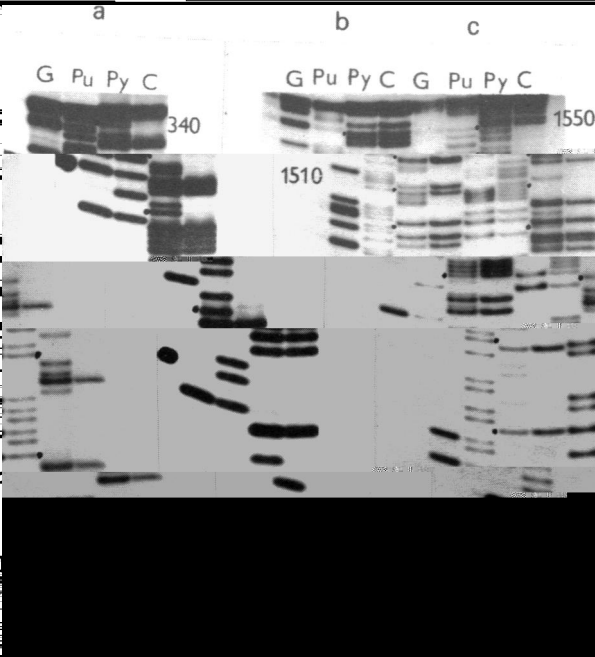


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mixture, to which "stop-solution" has already been added.

method of Glynn and Chappel (17). The 18 S rRNA from the





(fig. 4). T

the



Figure 4. Autoradiograph of 10% non-denaturing acrylamide

strand.

a. appr. 0.05 μ g the 5'end labelled DNA fragment
was denaturated in 5XSSC and 50% formamide in

3'-end of eucaryotic 18 S RNAs is a strikingly conserved region.

The 3'-end of the 16 S rRNA molecule: as pointed out by Shine-Dalgarno model, is involved in a complex with an mRNA that is indispensable for effective translation. the

interaction do occurring via the sequence CCUCC (27). All

cular sequence (28). So does the *S.cerevisiae* rRNA, though it shows striking homology with adjacent region of 16 S

90 100
GAACUGC GAUAGCCUA

190 200
UUCUGACC CUUUGGAGAG

290 300
UUGCGAUG GUUCAUUCAG

390 400
UGGAGAGGG AGCCUGAGAG

490 500
UACAGGGCC CAUUCGGGUC

590 600
UCCAGCUCC AAUAGCGUAU

690 700
CCACAGGGG CCUUUCUUC

790 800
UGCUCGAU AUUUAAGCAU

890 900
UUGGUAUUC AAUUGUGAG

990 1000
GAGGGAUCU GAUACCGUCG

0 5 0 5 0 0 0 4 0 0 0 5 0 0 0

UGG UCA UCU GAU GAG UGC UCC ue

Identical sequences are underlined

approximately 250 nucleotides left to the end of the 18 S

RNA gene of *X. leavis* (31), *D. melanogaster* (32);

(d) The T1 oligonucleotide possessing the unique 18 S RNA hypermodified nucleotide $m^1\text{cap}^3\psi$ was found both in

oligonucleotide was proposed to be A-A-C- $m^1\text{cap}^3\psi$ -C-A-C-A-

C-Gp.

We could not find such oligonucleotide within *S. cerevisiae* 18 S RNA sequence. The only appropriate T1 oligonucleotide which could be deduced was A-C-U-C-A-A-C-A-C-Gp.

not contradict the results of the RNase A and U_2 digestions

of the oligonucleotide which was obtained by Maden et al.

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17. Glynn, I.M. and Chappel, J.B. (1964) Biochem. J. 90.

18. Ferguson, J. and Davis, R.W. (1978) J. Mol. Biol. 123, 417-430.

19. deJonge, P., Klootwijk, J. and Planta, R.J. (1977) Europ. J.Biochem. 72, 361-369.

20. Donis-Keller, H., Maxam, A.M. and Gilbert, W. (1977) Nucleic Acids Res., 4, 2527-2538.

21. Dudov, K.P., Dabeva, M.D. and Hadjiolov, A.A. (1976)

Anal. Biochem. 76, 250-258.

22. Carbon, P., Ehresmann, C., Ehresmann, B. and Ebel, J.-P. (1978) FEBS Lett. 94, 152-156.

23. Brosius, J., Palmer, M.L., Kennely, P.J. and Noller, H.F.

24. Eperon I. personal communication.

25. Schwarz, Zs. and Kössel, H. (1980) Nature. 283. 739-742.

26. Samols, D.R., Hagenbuchle, O. and Gage L.P. (1979)