Homology of Ribosomal Ribonucleic Acid of Diverse Bacterial Species with Escherichia coli and Bacillus stearothermophilus

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Hybridization competition experiments were used to examine the ribosomal ribonucleic acid (rRNA) homologies of 22 bacteria and 3 higher organisms with *Esch*erichia coli and Bacillus stearothermophilus. Although little or no homology was observed with the higher organisms, the bacteria showed a wide range of homologies. Organisms whose rRNA showed closer homology to E. coli rRNA showed less rRNA homology to B. stearothermophilus rRNA and vice versa.

The observed differences in the thermal stability of ribosomes of Escherichia coli, Bacillus stearothermophilus, and other Bacillus species (4, 6) led Pace and Campbell (12) to examine the thermal stability of ribosomes from a variety of bacteria possessing widely different maximal growth temperatures. A positive correlation was demonstrated between the maximal growth temperature and the thermal stability of the ribosomes of the organisms studied. Although the thermal stability of the ribosomes tended to increase with increasing guanine plus cytosine (GC) content of the ribosomal ribonucleic acid (rRNA), no positive correlation could be demonstrated. Further, the GC content of the deoxyribonucleic acid (DNA) exhibited no apparent correlation to that of the rRNA of the organisms examined (12).

The differences in base composition and thermal stability of the ribosomes and rRNA have prompted us to examine the rRNA primary structural homology within the group of organisms previously studied to determine if the observed functional relationship of ribosome thermal stability was reflected in the genetic relationship of the ribosomal DNA. The refinement of the DNA-RNA hybridization technique by Gillespie and Spiegelman (8) permits RNA homologies from a variety of organisms to be quantitatively examined. Several studies on the rRNA primary structure homology of ^a number of microorganisms with E. coli, various Bacillus species, and Desulfovibrio vulgaris have been reported (2, 3, 10, 11, 13, 17).

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This paper reports the homologies of rRNA (as judged by hybridization competition experiments) from a group of organisms to the homologous DNA of E. coli and B. stearothermophilus. The rRNA homologies did not correlate with the thermal stability of the ribosomes and rRNA of the organisms studied. Nevertheless, the results are interesting from a phylogenetic viewpoint in that the rRNA of E. coli and B. stearothermophilus showed a continuum of homologies with the rRNA of the other organisms examined.

MATERIALS AND METHODS

Organisms and growth media. B. stearothermophilus strains 10 and 1503R and unclassified thermophiles T-107, 194, and B (Tecce), B. megaterium strain Paris, B. subtilis SB-19, Aerobacter aerogenes, Alcaligenes faecalis, Proteus vulgaris, and Serratia marcescens were grown at their optimal temperatures (65 C for the thermophiles; 37 C for A. faecalis, P. vulgaris, B. megaterium, and B . subtilis; and 30 C for A . aerogenes and S. marcescens) in TYC medium containing per liter of distilled water: 20 g of Trypticase (BBL), 3 g of yeast extract, 8.5 g of NaCl, 1.47 g of $CaCl₂ \cdot 2H₂O$, 7 mg of $FeCl_3 \cdot 6H_2O$, 15 mg of $MgSO_4 \cdot 7H_2O$, and 1 mg of $MnCl_2 \cdot 4H_2O$. The pH was adjusted to 7.3. Twenty grams of agar per liter were added for plates and slants. B. coagulans strain 43P was grown at ⁴⁵ C in TYC medium minus yeast extract.

E. coli strain K38 was grown in ^a modified 3XD (5) medium as described by Pace and Campbell (13).

Organisms 2-1 and 7E-3 (unidentified psychrophiles obtained from J. L. Ingraham) were grown at 30 and 18 C, respectively, in Trypticase Soy Broth (16).

Vibrio marinus strains 15381 and 15382, obtained from the American Type Culture Collection, were grown at ¹⁸ and 30 C, respectively, in ^a medium (1) containing per liter of distilled water: 10 g of Proteose

FIG. 1. Hybridization competition of Escherichia \ coli $\mathbf{r} \mathbf{R} \mathbf{N} \mathbf{A}$ by homologous $\mathbf{R} \mathbf{N} \mathbf{A}$. Membrane filters $\mathbf{s} \circ \mathbf{S}$ with 8 μ g of ³H-labeled E. coli DNA were immersed in 0.5 ml of $2 \times SSC$ containing 3 μ g of ³²P-labeled 60 methylated-albumin-kieselguhr (MAK) -purified E. coli $\frac{mR}{4}$ and the indicated guarante of unlabeled MAK rRNA and the indicated amounts of unlabeled MAK-
purified E. coli rRNA or E. coli bulk RNA and held at
65 C for 8 hr. After the annealing period. filters were purified E . coli rRNA or E . coli bulk RNA and held at 65 C for 8 hr. After the annealing period, filters were \tilde{x} washed, treated with ribonuclease, again washed, and \tilde{z} monitored for 3H and ${}^{32}P$ radioactivity as detailed in \tilde{z} Methods and Materials. washed, treated with ribonuclease, again washed, and massive, we have not allocated the monitored for $3H$ and $32P$ radioactivity as detailed in Methods and Materials. Data are expressed as per cent of $32P$ hybridized relative to samples containing no 8^{100} competing RNA. All points are the average of two identical filters. (A) ³²P-labeled E. coli rRNA competed by unlabeled, MAK-purified E. coli rRNA. (B) $32P$ -labeled E. coli rRNA competed by unlabeled E. coli bulk RNA .

Peptone, ³ g of yeast extract, and 25.2 g of artificial sea salt. The pH was adjusted to 7.2.

cans strain 8351, D. africanus strain Benghazi, D. desulfuricans strain VC, D. vulgaris strain 8303, and D. FIG. 2. Hybridization competition of Escherichia
salexigens strain British Guiana were grown as de- coli rRNA by heterologous bulk RNA. Membrane filsalexigens strain British Guiana were grown as de-

nisms from which $32P$ -labeled rRNA was isolated were transferred to their respective low-phosphate media marinus; \blacktriangle , Serratia marcescens. B. \blacktriangleright , Bacillus sub-
containing ³²P (orthophosphate). After the first one-
illis strain SB-19; O, Alcaligenes faecalis; \blacktriangle third to one-half of the exponential phase of growth, a bacter aerogenes.

 \overline{A} 200-fold excess of Na₂HPO₄, pH 7.3, was added and \vert the cells were grown for a further one to two generations. E. coli K38 was grown in a modified SC (14) medium ⁸⁰ containing: ² g of NH4Cl, ⁵ ^g of NaCl, 0.37 ^g of KCI, 1 ml of a 1% solution of $MgCl₂$, 2.6 ml of a 1% solution of Na2SO4, 300 ml of tap water, and 694 ml of distilled water. After autoclaving, the following sterile components were added: 0.175 ml of a 0.0668% solu-40 tion of FeCl₃, 5 ml of 1 M tris(hydroxymethyl)amino-
methane (Tris), pH 7.3, 0.1 ml of 2 M CaCl₂, 4 ml of ²⁰²⁰ \. 5% glucose, and ^I ml of 0.05 ^M Na2HPO4. B. stearo- thermophilus strain ¹⁰ was grown in 1% peptone plus 0.1% fructose.

Tritiated DNA was extracted from E. coli grown in $\begin{array}{|c|c|c|c|c|c|c|c|c|}\n\hline\n\text{the presence of } ^3\text{H-thymidine in } ^3\text{XD medium (5). } B. \\
\hline\n\text{stearothermophilus strain, 10 DNA was labeled with}\n\hline\n\end{array}$ stearothermophilus strain 10 DNA was labeled with

ponential phase of growth were washed twice with TM3 buffer $(0.01 \text{ m Tris}, pH 7.3, 0.001 \text{ m MgCl}_2)$ and ponential phase of growth were washed twice with

TM3 buffer (0.01 M Tris, pH 7.3, 0.001 M MgCl₂) and

suspended in 2 volumes TM3 buffer. Lysozyme (400
 μ g/ml) and deoxyribonuclease (10 μ g/ml) were added

and the μ g/ml) and deoxyribonuclease (10 μ g/ml) were added 40 $\frac{1}{2}$ and the suspension was disrupted by three freeze-thaw cycles. In addition to this procedure, it was necessary
to incubate yeast cells for 5 hr with 1% Glusulase 20 to incubate yeast cells for ⁵ hr with 1% Glusulase (snail gut enzyme). RNA was extracted from these ly-

scribed by Pace and Campbell (13). ters with 8 μ g of 3H-labeled E. coli DNA were im-
Saccharomyces chevalieri Y32 was grown at 37 C in mersed in 0.5 ml of 2 \times SSC containing 3 μ g of ³²P-Saccharomyces chevalieri Y32 was grown at 37 C in mersed in 0.5 ml of $2 \times SSC$ containing 3 μ g of ³²P-
5% glucose plus 0.5% yeast extract.
labeled, methylated-albumin-kieselguhr-purified E. coli labeled, methylated-albumin-kieselguhr-purified E. coli Tetrahymena pyriformis variety 1 strain C16643 was rRNA and the indicated quantities of bulk RNA from
grown at 30 C in 1% Proteose Peptone plus 0.1% yeast the following organisms. Hybridizations were carried the following organisms. Hybridizations were carried extract. out as detailed in Methods and Materials and the **Isotopic labeling of bacterial nucleic acids.** Orga- *legend to Fig. 1. All data are from duplicate filters (A)* $\sum_{n=1}^{\infty}$ and filters (A) $\sum_{n=1}^{\infty}$ and $\sum_{n=1}^{\infty}$ $\sum_{n=1}^{\infty}$ $\sum_{n=1}^{\infty}$ $\sum_{n=1}^{\infty$ tilis strain SB-19; O, Alcaligenes faecalis; A, Aero-

TABLE 1. Homology of heterologous ribonucleic acid (RNA) species to ribosomal RNA (r RNA) of Escherichia colia

$\%$ Homol- ogy of rRNA	\mathcal{G}_0 Homol- ogy of bulk RNA
88	77
83	79
	76
55	52
	53
	36
31	30
31	23
	24
	24
	22
	22
	17
	20
	19
	18
	17
	16
	12
	11
	9
	9
	7
	6
	21 0

^a Filters with 8 μ g of ³H-labeled *Escherichia coli* deoxyribonucleic acid were immersed in 0.5 ml of 2 \times SSC containing $3 \mu g$ ³²P-labeled, methylated-albuminkieselguhr-purified E. coli rRNA and up to 108 μ g of unlabeled RNA. Hybridizations were carried out as detailed in Methods and Materials and the legend to Fig. 1.

 \overline{b} Kindly provided by C. Radcliffe.

sates, which were diluted in TM3 buffer to ¹⁰ to ²⁰ ml per g of cells, by a modification of the procedure of Gierer and Schramm (7), in the presence of 0.5% sodium dodecyl sulfate. Phenol was removed from the final aqueous layer by three extractions with 3 volumes of anhydrous ether, or by ethanol precipitation three times. The RNA pellet was dried and suspended in TE buffer $(0.01 \text{ M} \text{ Tris}, pH 7.3; 0.001 \text{ M} \text{ ethylene dia-}$ minetetraacetic acid).

DNA extraction. DNA was prepared by ^a slight modification of the procedure of Saito and Miura (15) as described by Pace and Campbell (13).

Methylated-albumin-kieselguhr (MAK) chromatography. MAK columns were prepared by the procedure of Mandell and Hershey (9) as detailed by Pace and Campbell (13). The RNA was eluted with ^a 0.7 to 1.1 M NaCl linear gradient. The isolated 165 and 23S peak fractions (free of 5S RNA) were pooled, ethanol precipitated, and suspended in $2 \times SSC$ (0.15 M NaCl plus 0.015 M sodium citrate, $pH 7$).

DNA-RNA hybridizations. The DNA-RNA hybridization technique of Gillespie and Spiegelman (8) was employed exactly as described by Pace and Campbell (13) except that $6 \times SSC$ was occasionally used in place of $2 \times SSC$ in some of the experiments. Hybridizations were carried out by immersing the filters in 0.5 or 1.3 ml of a $2 \times SSC$ solution of RNA of the desired concentration and incubating for 8 to 10 hr at 65 C. After chilling the tubes in an ice bath, the DNA and the blank control filters were washed with 50 ml of 2 \times SSC on each side by suction filtration and immersed in a solution of 2 \times SSC containing 25 μ g of pancreatic ribonuclease per ml (EC 2.7.7.16) and 5 μ g of T₁ ribonuclease per ml. After incubation at ³⁷ C for 60 min the tubes were chilled and the filters were washed, dried, and counted in a Tri-Carb liquid scintillation counter (model 3002; Packard Instrument Co., Inc., Downers Grove, Ill.). DNA remaining on the filter was determined from the tritium counts and the amount of RNA hybridized was calculated from the 32P counts on the DNA filter minus those on the blank filter.

FIG. 3. Hybridization competition of Bacillus stearothermophilis strain 10 rRNA by heterologous bulk RNA. Membrane filters containing 3μ g of $3H$ -labeled B. stearothermophilus DNA were immersed in 0.5 ml of 2 \times SSC containing 1.5 μ g of ³²P-labeled, methylated-albumin-kieselguhr-purified B. stearothermophilus rRNA and the indicated quantities of bulk RNA from the following organisms. Hybridizations were carried out as detailed in Methods and Materials and the legend to Fig. 1. All data are from duplicate filters. (A) 0, Saccharomyces chevalieri; 0, Vibrio marinus strain 15382; \blacktriangle , 7E-3. (B) \blacktriangleright , Serratia marcescens; \bigcirc , Desulfovibrio africanus strain Benghazi; A, Bacillus stearothermophilus strain 10.

TABLE 2. Homology of heterologous ribonucleic acid (RNA) species to ribosomal RNA (rRNA) of Bacillus stearothermophilus strain 10

Organism	% Homol- ogy of bulk RNA
Bacillus stearothermophilus 1503R	95
Bacillus subtilis SB-19	90
Thermophile $T-107$	89
Bacillus coagulans 43P	82
Thermophile 194	81
Bacillus megaterium Paris	78
Psychrophile 7E-3	71
Desulfotomaculum nigrificans 8351	65
Desulfovibrio salexigens British Guiana	51
Spirillum itersonii SI-1	51
Desulfovibrio africanus Benghazi	45
Thermophile B (Tecce)	45
Alcaligenes faecalis	44
Desulfovibrio desulfuricans VC	43
Desulfovibrio vulgaris 8303	43
Psychrophile 2-1	41
Proteus vulgaris	39
Vibrio marinus 15382	37
Vibrio marinus 15381	37
Aerobacter aerogenes	36
Escherichia coli K38	33
Serratia marcescens	25
Saccharomyces chevalieri	15
Tetrahymena pyriformis	0

^a Membrane filters containing $3 \mu g$ of ³H-labeled Bacillus stearothermophilus deoxyribonucleic acid were immersed in 0.5 ml of 2 \times SSC containing 1.5 μ g of $32P$ -labeled, methylated-albumin-kieselguhr-purified B. stearothermophilus rRNA and up to 108 μ g of unlabeled RNA. Hybridizations were carried out as detailed in Methods and Materials and the legend to Fig. 1.

RESULTS AND DISCUSSION

By using the competition hybridization technique, the homologies of homologous and heterologous bulk and rRNA species to E. coli rRNA were determined. Figure ^I illustrates the hybridization competition profiles of E . coli rRNA with its homologous rRNA and bulk RNA. The rRNA competition approximates the theoretical dilution curve, and it is apparent that the bulk RNA approaches the dilution asymptote.

Representative bulk RNA competitions of E. coli rRNA are shown in Fig. 2. D. desulfuricans, V. marinus 15381, S. marcescens, B. subtilis, A. faecalis, and A. aerogenes have homologies of 17, 52, 76, 16, 30, and 77%, respectively. Table ^I lists the rRNA homologies of ²² bacteria and ³ higher organisms to E. coli rRNA.

The rRNA homologies of the same group of organisms for B. stearothermophilus rRNA were also determined. Representative hybridization competition experiments are illustrated in Fig. 3. In Fig. 3A, Saccharomyces, V. marinus 15382, 7E-3, and *B. subtilis* are seen to have homologies of 15, 37, 71, and 90%, respectively. In Fig. 3B the respective homologies of S. marcescens, D a fricanus, B . megaterium, and homologous B . stearothermophilus are 25, 45, 78, and 97%. Table ² lists the rRNA homologies of the organisms examined to B. stearothermophilus rRNA.

Although the data obtained in this study do not reveal a correlation between the genetic relatedness of the rDNA and the thermal stability of the ribosomes and rRNA of the organisms examined (12), ^a wide range of rRNA homologies was observed for E . coli and B . stearothermophilus with diverse bacterial species. E. coli and B. stearothermophilus appears to represent the extremes of homology among the bacterial species examined; the other species are distributed between these two organisms with regard to homology. Of note is the observation that the rRNA species possessing near relationships to E. \textit{coli} are correspondingly less related to $\textit{B.}$ stearothermophilus and vice versa. This approximately reciprocal relationship would seem to justify the use of rRNA homologies as one means of generating a numerical spectrum (in the sense of ordering) of genetic relatedness, based on primary sequence homologies of a particular class of functional molecules.

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