Reversion rates in a leuB auxotroph of Escherichia coli K-12 correlate with ppGpp levels during exponential growth

Barbara E. Wright and Michael F. Minnick

Two isogenic strains of Escherichia coli K-12 differing only in relA, as well as two spoT transductants of the relA- strain, were examined with respect to ppGpp levels and reversion rates of a leuB- allele under nine different conditions. A positive correlation was established between reversion rates and the steady-state concentration of ppGpp during exponential growth. The leu6 genes from two leuB- strains (isogenic except for relA) were cloned and sequenced and found to contain a single mutation, namely, a C-to-T transition at nucleotide 857. This mutation resulted in a serine-to-leucine substitution at amino acid residue 286 of the LeuB protein. PCR products that encompassed the leuB lesion were generated from 53 revertants and then sequenced. Of these revertants, 36 were found to contain nucleotide substitutions that would result in a serine (wild type), valine or methionine at amino acid residue 286 of LeuB, and nearly all of them exhibited generation times similar to wild type. Seventeen of the analysed revertants were found to be suppressors that retained the encoded leucine at residue 286. The majority of the suppressor mutants exhibited generation times that were significantly longer than wild type.

Keywords: stringent response, ppGpp, mutation rates, starvation

INTRODUCTION

The complex of metabolic events triggered by amino acid starvation in Escherichia coli is called the stringent response (reviewed by Cashel & Rudd, 1987). This response is marked by an immediate burst in the accumulation of ppGpp, which acts to reduce the rate of rRNA and tRNA synthesis and to stimulate the rate of synthesis of ‘nutritional stress’ proteins such as amino acid biosynthetic enzymes. The synthesis of ppGpp is primarily controlled by ppGpp synthase I (the relA gene product) and requires mRNA, ribosomes and codon-specified uncharged tRNA bound in the ribosomal A site. The activity of the ppGpp degradative enzyme, (pp)ppGp 3’-pyrophosphohydrolase (the spoT gene product) is also regulated by starvation conditions (Fiil et al., 1972; Gallant et al., 1972). This enzyme, known as ppGpp synthase II, may be bifunctional, i.e. capable of catalysing either synthesis or degradation of ppGpp (Fehr & Richter, 1981; Xiao et al., 1991). Clearly, an increase in ppGpp levels can result from a higher rate of synthesis or from an inhibition of degradation. Evidence indicates that cellular ppGpp levels are regulated by the
effects of the stringent response on reversion rates of point mutations in two isogenic strains of E. coli differing only in relA. Reversion rates of the leuB^- and argH^- alleles in strain CP78 were significantly higher than in the isogenic counterpart, CP79 (relA2). A positive correlation was established between reversion rates and the synthesis of ppGpp during the classical stringent response that occurs within seconds as growth deviates from the exponential phase in amino-acid-limited cultures. The distribution of revertants in mutation rate experiments indicated that most of the mutations occurred during this period of diminishing growth, i.e. the time between the end of exponential growth and the cessation of growth. However, mutations also occurred during exponential growth, especially when the rate of exponential growth was inhibited, for example by serine hydroxamate, which provokes the stringent response as a competitive inhibitor of seryl-tRNA (Cashel & Rudd, 1987; Merzgar et al., 1989; Shand et al., 1989). Under these conditions the mean revertant colony counts on positive plates were abnormally high (data not shown), indicating that the mutation occurred during the exponential growth phase of that culture. According to Cashel & Rudd (1987), effects associated with the classical stringent response also operate during exponential growth to a lesser extent and all relate to the metabolism of ppGpp. Therefore, one goal of the present investigation was to document a possible correlation between mutation rates and the steady-state concentrations of ppGpp during exponential growth, through the use of various strains and culture conditions that produce different levels of cellular ppGpp. To this end, two spoT alleles known to accumulate high ppGpp levels were transduced into CP79 and these strains were grown with and without serine hydroxamate. The CP78 strain was also grown with γ-glutamyl leucine, which apparently served as a poor source of leucine, thereby imposing leucine starvation during exponential growth. The results indicate a positive correlation between reversion rates and ppGpp concentrations during exponential growth.

Another goal of these investigations was to sequence and define the lesion in the leuB^- mutant gene as well as to sequence its revertant, as reversion rates of this mutant allele are being used as a model system to test the hypothesis that enhanced mutation rates result from derepression provoked by amino acid starvation and ppGpp accumulation (Wright, 1997).

### METHODS

#### Strains

The genotypes of the E. coli strains used in this study are summarized in Table 1. To obtain strains with altered ppGpp levels, spoT alleles were transduced using P1 vir into the CP79 relA2 strain, producing strains (Table 1) that grew more slowly than the CP79 relA2 host. Strains with such spoT alleles are known to grow more slowly in relA backgrounds than in ΔrelA hosts, and cells with null alleles in both the relA and spoT genes are multiple auxotrophs (Sarubbi et al., 1988; Xiao et al., 1991). This suggested that relA2 is not a deletion but is a leaky mutation, like relA1. To confirm this, relA2 was replaced in the CP79 ΔspoT207 strain by ΔrelA251 (Table 1). As suspected, a multiple auxotroph was formed, confirming that relA2 is similar to relA1.

#### Growth conditions for mutation rate determinations

Cells were grown at 37°C for 42–48 h in minimal medium consisting of 40 mM glycerol, 50 mM sodium phosphate buffer, pH 6.5, 10 g (NH₄)₂SO₄ l⁻¹, 1 g MgSO₄ l⁻¹, 50 mg thiamin l⁻¹, 0.1 mM hydroxamic acid or substituting 0.5 mM arginine and 0.3 mM histidine. When growth was limited by leucine, the amino acid was present at 0.025 mM; γ-glutamyl leucine was used at 0.06 mM. Cells grown in the presence of 1.5 mM serine hydroxamate and excess leucine (0.04 mM) were washed prior to plating, to prevent growth on the plates due to carry over of leucine. The ‘zero’ method of Luria & Delbrück (1943) was used to determine mutation rates. In a typical experiment, a large culture inoculated with cells from a 7-h-old nutrient agar plate at a cell density of about 5 x 10⁹ ml⁻¹ was prepared and 1.5 ml aliquots were distributed into 40 2-cm-diam. test tubes which were shaken at a 45° angle at 37°C for 24–48 h, depending upon the growth rate of the strain. Each entire culture was then spread onto selective plates. Tenfold dilutions in buffered saline were made of a few identical cultures and the OD₅₆₅ value read to select two typical cultures for appropriate dilutions to determine total viable cell numbers on nutrient agar plates. If the two viable counts differed by more than 25%, the experiment was discarded. The equivalent of viable counts and total cell numbers was assured based on a standard curve comparing the OD₅₆₅ reading to viable counts using exponentially growing cells. Revertant colonies first appear on selective plates about 40 h after plating and final counts were made at 65–78 h. Mutation rates were estimated by the ‘zero’ method (Luria & Delbrück, 1943) according to the expression MR = \( (\ln P_0/N) \), where \( P_0 \) is the proportion of cultures with no revertants, and \( N \) is the total number of cells per culture.

#### Determination of steady-state levels of ppGpp

Cultures were grown at 37°C in the above medium with the exceptions that (1) leucine was present at 0.1 mM, to achieve exponential growth during the ³²P labelling period, and (2) the phosphate buffer was replaced by 40 mM MES buffer, pH 6.5, and the KH₂PO₄ concentration was lowered to 0.3 mM to dilute added ³²P to a minimal extent. To analyse ppGpp concentration during exponential growth, the 16 h cultures were centrifuged and resuspended to an OD₅₆₅ of 0.034 ± 0.005. To analyse ppGpp concentration during exponential growth, the 16 h cultures were centrifuged and resuspended to an OD₅₆₅ of 0.034 ± 0.005 (depending on their growth rate) in fresh medium with or without 1.5 mM serine hydroxamate or substituting 0.06 mM γ-glutamyl leucine for 0.1 mM leucine. Aliquots (1 ml) were removed and their phosphate concentrations determined (Sigma diagnostics, procedure no. 670). Aliquots (1–1.5 ml) were removed to 20 ml glass vials and ³²P (New England Nuclear) added to a final concentration of 100–300 μCi ml⁻¹ (3·7 x 10₆–1.1 x 10⁷ Bq ml⁻¹). Aliquots (15 ml) were transferred to nephelo culture flasks and OD₅₆₅ was monitored every 30–60 min to determine the rate of exponential growth. After 4 h of labelling with ³²P, samples were removed and prepared for polyethyleneimine (PEI) cellulose chromatography. To ensure that the ppGpp pool was saturated with ³²P, a second sample was removed for analysis at 4.5 h. Regardless of the generation time of the culture, the values at 4.5 h and 4.0 h were comparable, indicating saturation of the ppGpp pool. Aliquots of each culture (50 μl) were pipetted into cold microcentrifuge tubes containing 17 μl 23.6 M formic acid (final concn 6 M), mixed and freeze-thawed twice in dry ice/ethanol and a 37°C water bath. After centrifugation, 2 and 3 μl aliquots were spotted onto washed PEI cellulose plates. A 5 μl aliquot of 10 mM GTP prepared in the same manner was spotted as a standard. Ascending chromato-
Table 1. Genotypes of E. coli strains used

<table>
<thead>
<tr>
<th>Strain</th>
<th>Genotype</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>CP78</td>
<td>F- thr-1 leuB6 his65 argH146 thi-1 ara-13 gal-3 malA1 (Δ!) xyl-7 mtl-2 tonA2 supE44</td>
<td>E. coli Genetic Stock Center, Yale, USA</td>
</tr>
<tr>
<td>CP79</td>
<td>As CP78, but relA2</td>
<td>E. coli Genetic Stock Center, Yale, USA</td>
</tr>
<tr>
<td>CP79 ΔspoT207</td>
<td>CF1693 = MG1655 ΔrelA251 : kan ΔspoT207 : cat used as donor to transduce ΔspoT207 into CP79</td>
<td>This study</td>
</tr>
<tr>
<td>CP79 spoT203</td>
<td>CF3042 = CP930 = N99 relA1 zib563 : Tn10 (spoT203) used as donor to transduce spoT203 into CP79</td>
<td>This study</td>
</tr>
<tr>
<td>CP79 ΔspoT207 ΔrelA251</td>
<td>CF1652 = MG1655 ΔrelA251 : kan used as donor to transduce ΔrelA251 into CP79 ΔspoT207</td>
<td>This study</td>
</tr>
<tr>
<td>CP930</td>
<td>relA1zib563 : Tn10 (spoT203)</td>
<td>M. Cashel (Xiao et al., 1991)</td>
</tr>
<tr>
<td>CP1652</td>
<td>ΔrelA251 : kanΔspoT207 : cat</td>
<td>M. Cashel (Xiao et al., 1991)</td>
</tr>
</tbody>
</table>

DNA manipulation. Chromosomal DNA from E. coli was isolated by the methods of Ausubel et al. (1989). Approximately 1 ng purified DNA was PCR amplified using a PCR Core Kit and Taq polymerase according to the manufacturer's instructions (Perkin Elmer Cetus). PCR was done by 30 cycles of 94 °C (1 min), 55 °C (2 min) and 72 °C (1.5 min). Primers for amplifying the entire leuB gene for cloning were based upon the nucleotide sequence of Kirino et al. (1994) (GenBank accession no. D17631) and included 5' GATCC-CTACAGTTTGACGTTCTGC (primer 1) and 5' TTTTCTAGGACACAGGAAAAACGCATGTG (primer 2). For screening revertants, PCR amplification of a 416 bp region encompassing the encoded Ser-286 → Leu lesion of leuB (nt 856-858) was accomplished by using 5' GATCC-ATACAGTTGACCCATGTCGCTGCTG (primer 1) and primer 2. Primers were synthesized with an Applied Biosystems (ABI) model 394 DNA synthesizer at The University of Montana Molecular Biology Facility.

PCR products containing the full-length leuB gene were excised from ethidium-bromide-stained agarose gels and then purified using GeneClean II according to the manufacturer's instructions (Bio101). The DNA was blunt-ended with Klenow fragment and then cloned into the Smal restriction site of pUC19 (Yanisch-Perron et al., 1985) by standard protocol (Sambrook et al., 1989). E. coli DH5α was then transformed with the resulting plasmids by the methods of Chung et al. (1985). Transformants were initially screened for recombinant DNA by blue/white screening on LB medium containing ampicillin (0.1 mg ml⁻¹), IPTG (Gibco BRL) and Bluo-Gal (Gibco BRL). Plasmid DNA from the white colonies was obtained by alkaline minipreps (Sambrook et al., 1989), restriction-endonuclease-digested and then analysed for insert content on ethidium-bromide-stained agarose gels.

Nucleotide sequence analyses were done by the methods of Tracy & Mulcahy (1991) on an ABI automated nucleic acid sequencer (ABI; model 373A). Sequencing-grade templates were prepared by a Midi-Prep Kit (Qiagen) for the 416 bp PCR products from agarose gels. Computer analysis of the sequences was performed using PCGENE 6.8 software (Intelligenetics).

RESULTS

Growth rate determinations

Fig. 1 compares the exponential growth rates of different strains under the various culture conditions used in this investigation. The growth rates ranged from the lowest generation time of 100 min for strains CP78 and CP79 to the highest generation time of 652 min for CP79 in the presence of serine hydroxamate. In the latter case, the low rate of growth was followed for more than 10 h and did not deviate from linearity. The mean values of replicate determinations are summarized in Table 3.

Mutation rate determinations

leuB− reversion rates of the two spoT strains grown with and without serine hydroxamate are shown in Table 2. In the absence of serine hydroxamate, the ΔspoT strain exhibited a reversion rate approximately threefold higher than its parent strain, CP79 (Tables 2 and 3). The reversion rate of CP79ΔspoT207 was only slightly stimulated by serine hydroxamate, in contrast to strain CP79 (Table 3). The reversion rate of the CP79 spoT203 strain was approximately 10-fold higher than that of its parent strain, and was nearly halved by serine hydroxamate (Tables 2 and 3).

To find other conditions that might alter ppGpp levels and reversion rates in the leuB auxotrophs, various leucine derivatives were examined for their ability to
ppGpp levels

The steady-state levels of ppGpp were determined during exponential growth in the strains and under the conditions summarized in Fig. 1 and Table 3. Fig. 2 shows the mutation rates plotted against both the concentration of ppGpp and the generation time. The medium used for measuring ppGpp levels was essentially the same as that used in mutation rate experiments, except that the leucine concentration was necessarily in excess during exponential growth. Leucine was limiting (unless cell growth was inhibited) in mutation rate determinations to achieve a low cell density such that a significant fraction of the cultures would have no revertants. This was necessary to calculate rates by the 'zero' method (Luria & Delbrück, 1943). MES buffer was used in the ppGpp experiments because phosphate levels had to be lowered to minimally dilute the $^{32}$P added. In separate experiments (not shown) it was found that mutation rates using medium with the MES-phosphate buffer were comparable to those in phosphate buffer.

Other investigators measuring ppGpp levels in vivo have labelled at least one (Friesen et al., 1975) or two (Lagosky & Chang, 1980) generations with $^{32}$P prior to sampling. In the experiments reported here, labelling with $^{32}$P occurred for 4 h, which was equivalent to 0.4–2.5 generation times, depending upon the strain and the medium employed (Fig. 1). To ensure that the ppGpp pool was equilibrated with the Pi pool, samples were taken again at 4-5 h. In every case, the 4 and 4.5 h samples were indistinguishable, indicating that the small metabolite pools were turning over rapidly regardless of generation time. As the ppGpp pools were saturated, their concentration could be based on the specific radioactivity of the phosphate in the medium.

Revertant colony sizes

Colony counts on 20 plates from a typical 40-culture mutation rate experiment are shown in Table 4 (see Methods). Because growth was limited by threonine, the $\text{leu}^+$ revertants had no selective advantage. Colony counts at 66 h after plating were used to calculate mutation rates. At least 70% of these proved to be true revertants, regardless of the strain in which they arose.

### Table 2. leuB reversion rates

The values given are the means of at least four independent mutation rate determinations. For experimental conditions and for the method of determining mutation rates, see Methods.

<table>
<thead>
<tr>
<th></th>
<th>CP79 $\Delta\text{spoT207}$</th>
<th>CP79 $\text{spoT203}$</th>
<th>CP78</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Leucine-starved</td>
<td>Seryl-tRNA-starved</td>
<td>Leucine-starved</td>
</tr>
<tr>
<td>$10^8 \times$ Total cell number</td>
<td>$2.8 \pm 0.76$</td>
<td>$0.31 \pm 0.12$</td>
<td>$0.80 \pm 0.14$</td>
</tr>
<tr>
<td>$P_0$ (no. negative plates/total)</td>
<td>$0.79 \pm 0.03$</td>
<td>$0.96 \pm 0.04$</td>
<td>$0.76 \pm 0.04$</td>
</tr>
<tr>
<td>$10^8 \times$ Mutation rate</td>
<td>$0.60 \pm 0.11$</td>
<td>$1.03 \pm 0.09$</td>
<td>$2.5 \pm 0.62$</td>
</tr>
</tbody>
</table>

supply leucine at a low rate, thereby inducing a state of partial starvation and provoking the stringent response. Replacing leucine with the peptide $\gamma$-glutamyl leucine significantly lowered the growth rate of strain CP78 (Fig. 1). When grown in the presence of this peptide, the reversion rate of CP78 was about fourfold higher than in the presence of limiting leucine (Tables 2 and 3).
Table 3. Relationship of mutation rates to levels of ppGpp and generation time

<table>
<thead>
<tr>
<th>Strain and condition*</th>
<th>10^8 × Mutation rate</th>
<th>ppGpp concn [pmol (OD unit)^{-1}]†</th>
<th>Generation time (min)‡</th>
</tr>
</thead>
<tbody>
<tr>
<td>CP78</td>
<td>1.5 ± 0.48§</td>
<td>327 ± 30</td>
<td>100 ± 6</td>
</tr>
<tr>
<td>CP78 + SH</td>
<td>4.9 ± 0.37§</td>
<td>479 ± 40</td>
<td>212 ± 39</td>
</tr>
<tr>
<td>CP78 + γ-Glu-Leu</td>
<td>6.4 ± 1.7</td>
<td>753 ± 81</td>
<td>630 ± 90</td>
</tr>
<tr>
<td>CP79</td>
<td>0.22 ± 0.08§</td>
<td>234 ± 17</td>
<td>102 ± 8</td>
</tr>
<tr>
<td>CP79 + SH</td>
<td>4.4 ± 2.1§</td>
<td>391 ± 29</td>
<td>652 ± 124</td>
</tr>
<tr>
<td>CP79 spoT207</td>
<td>0.60 ± 0.11</td>
<td>267 ± 77</td>
<td>156 ± 22</td>
</tr>
<tr>
<td>CP79 spoT207 + SH</td>
<td>1.0 ± 0.09</td>
<td>395 ± 81</td>
<td>371 ± 45</td>
</tr>
<tr>
<td>CP79 spoT203</td>
<td>2.5 ± 0.62</td>
<td>335 ± 54</td>
<td>207 ± 38</td>
</tr>
<tr>
<td>CP79 spoT203 + SH</td>
<td>1.3 ± 0.32</td>
<td>321 ± 60</td>
<td>494 ± 30</td>
</tr>
</tbody>
</table>

*SH, serine hydroxamate; γ-Glu-Leu, γ-glutamyl leucine.
† Means of four determinations ± SD; see Methods for details.
‡ Means of four to eight determinations ± SD; see Methods for details.
§ Taken from Wright (1996).

Fig. 2. Reversion rate of leuB under different conditions (see Table 2 and Fig. 1) plotted against the generation time (▲) and against the ppGpp concn (●) during exponential growth. Bars indicate SD.

Cloning and sequence analysis

The sequence of the leuB gene, which encodes the enzyme β-isopropyl malate dehydrogenase (EC 1.1.1.83), has been determined (Kirino et al., 1994; GenBank accession no. D17631). Sequence analysis of the cloned leuB genes from the leuB− mutants CP78 and CP79 revealed complete nucleotide sequence identity to the published leuB gene except for C-to-T transitions at nucleotide 857. This point mutation would result in a
serine-to-leucine substitution at amino acid residue 286 of the LeuB protein. The sequence of the leuB\(^{-}\) mutant gene in the region of the mutation is shown in Table 5 and the possible single base substitutions in this codon and the corresponding amino acids are also summarized. Base substitutions encoding serine, valine and methionine were all observed among the revertants; the other possibilities (tryptophan or phenylalanine) were never observed, perhaps because they are too bulky to replace serine. Of the 36 true revertants, two had generation times significantly longer than wild-type cells. Revertants containing the Met-286 substitution were unique to E. coli strain CP79 spoT203. Of the 17 suppressors that were sequenced (i.e. an encoded Leu remained at amino acid residue 286), five had generation times comparable to wild type.

### DISCUSSION

To study the relationship between mutation rates and the stringent response, two isogenic multiple auxotrophs were chosen, namely CP78 and CP79 (Table 1). These strains differ only in relA and have been widely used in investigations of the stringent response over the past 20 years. The leuB allele was chosen for intensive study since (a) the leuB gene has been sequenced (Kirino et al., 1994), (b) revertant colonies appearing after 2 d were all of large uniform size and (c) the reversion rate was conveniently low for using the ‘zero’ method of calculating mutation rates (Luria & Delbrück, 1943). This is preferable to the ‘average’ method (Lea & Coulson, 1949) which does not measure the number of initial mutational events and is subject to various artifacts (Stewart et al., 1990). The validity of the ‘zero’ method depends only upon the survival of each revertant, which has been demonstrated in reconstruction experiments (Wright, 1996). Since the reversion rate depends upon the fraction of plates without colonies, the parental mutant may be grown in medium which may or may not select for the revertants (Ryan, 1955). To obtain a significant fraction of ‘zero’ plates, the final cell concentration is adjusted by the concentration of a required amino acid, or of an inhibitor such as serine hydroxamate.

Using a series of spoT mutant alleles, an inverse linear relationship was found between steady-state rates of growth and ppGpp levels (Sarubbi et al., 1988). The ppGpp concentrations and the reversion rates of leuB\(^{-}\) in the two CP79 spoT strains (Table 2) were higher than in CP79. This would be expected as a result of the blocking of ppGpp degradation by ppGpp synthase II. It is significant that serine hydroxamate did not affect ppGpp levels or mutation rates in these spoT transductants as much as it did in CP79, suggesting that the site of action of this inhibitor is ppGpp degradation. Growth on the \(\gamma\)-glutamyl leucine peptide had the largest effect on ppGpp levels and mutation rates in CP78 (Table 3). Use of this peptide as a substitute for leucine in leu auxotrophs is assumed to be comparable to the use of histidinol or formyl histidine as substitutes for histidine in his auxotrophs (Ames & Garry, 1959; Blasi & Bruni, 1981). Growth on either of these poor sources of histidine imposes partial starvation and provokes the stringent response; genes for the synthetic enzymes are derepressed, which could then result in increased rates of mutation. During exponential growth the most striking effects on ppGpp accumulation and reversion rates in strains CP78 and CP79 were seen when derepression and a low rate of cell division were both maintained due to the presence of 1.5 mM serine hydroxamate or \(\gamma\)-glutamyl leucine (Fig. 1). In S. typhimurium the addition of 2.0 mM serine hydroxamate inhibited growth and provoked an increase in ppGpp levels and his operon expression with a similar time course (Shand et al., 1989).

Two general classes of leu\(^{+}\) revertants were observed: (a) true revertants, with base substitutions encoding serine (wild type), valine or methionine with generation times of about 100 min; and (b) suppressors, which retained the Leu-286 residue of the parental leuB mutant and usually had generation times in excess of 200 min. The distribution of these two classes of revertants suggests that they may arise by different mechanisms. As discussed above, the true revertants appeared with a low variance towards the end of growth when ppGpp levels showed a significant, transient increase from basal levels (Lazzarini et al., 1971; Wright, 1996). Suppressor mutants originated throughout the growth phase of the liquid cultures and appeared with a high variance after 4–7 d incubation on the selective plates. These observations suggest that the mutations resulting in true reversions may have been influenced by the stringent response to a greater extent than the suppressor mutations.

### Table 5. Sequence of the leuB\(^{-}\) mutants and revertants at nt 856–858

<table>
<thead>
<tr>
<th>Single base substitutions observed</th>
<th>Predicted</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sequence</td>
<td>leuB(^{-}) mutant</td>
<td></td>
</tr>
<tr>
<td>ATG</td>
<td>Methionine</td>
<td></td>
</tr>
<tr>
<td>CTG</td>
<td>Valine</td>
<td></td>
</tr>
<tr>
<td>GTG</td>
<td>Phenotypically wild type</td>
<td></td>
</tr>
<tr>
<td>ATG</td>
<td>Methionine</td>
<td></td>
</tr>
</tbody>
</table>

| Predicted amino acid residue 286 in true revertants |
|----------------------------------|-------------|
| Strain               | Amino acid (no. observed) | |
| CP78                   | Ser (7), Val (8) |
| CP79                   | Ser (6), Val (1) |
| CP79 ΔspoT207          | Ser (1), Val (6) |
| CP79 spoT203           | Ser (2), Val (3), Met (2) |
1974; Savić & Kanazir, 1972; Siebenlist et al., 1980; Singer & Kusmierck, 1982; see also Wright, 1997) and repair (Hanawalt & Mellon, 1993; Selby & Sancar, 1994). Cashel & Rudd (1987) believe that all effects of the stringent response can be attributed to the metabolism of ppGpp, and the extensive literature on this subject supports our conclusion that ppGpp stimulates transcription of the leu operon, which in turn affects reversion rates due to an increase in the concentration of single-stranded DNA. Mutation rates have now been correlated with ppGpp levels during exponential growth (Fig. 2) as well as during the transition period between the end of exponential growth and stationary phase (Wright, 1996). Studies in progress will examine the correlation between mutation rates and enzyme and mRNA levels of the leu operon. About 500 pmol ppGpp appears to be optimal to enhance reversion rates of the leuB− allele (Fig. 1). It should be possible to determine whether this level of ppGpp is also optimal for the de novo synthesis of the enzymes encoded by the leu operon in an in vitro transcription–translation system. If so, this would further strengthen the correlation between the stringent response, transcription and mutation rates.

ACKNOWLEDGEMENTS

We thank M. Cashel for spoT mutant strains and for advice, J. B. Sweasy, S. Manning and S. Samuels for helpful criticisms of the manuscript, J. Bernard and J. Reimers for excellent technical assistance, and J. Strange for sequencing and oligonucleotide synthesis. Supported in part by PHS grant GM/OD54279 (to B.E.W.) from the National Institutes of Health and AI34050 (to M.F.M.).

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Received 20 June 1996; revised 30 September 1996; accepted 14 October 1996.