

Visualizing high error levels during gene expression in living bacterial cells

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Edited* by Susan Gottesman, National Cancer Institute, Bethesda, MD, and approved May 20, 2010 (received for review November 19, 2009)

To monitor inaccuracy in gene expression in living cells, we designed an experimental system in the bacterium *Bacillus subtilis* whereby spontaneous errors can be visualized and quantified at a single-cell level. Our strategy was to introduce mutations into a chromosomally encoded *gfp* allele, such that errors in protein production are reported in real time by the formation of fluorescent GFP molecules. The data reveal that the amount of errors can greatly exceed previous estimates, and that the error rate increases dramatically at lower temperatures and during stationary phase. Furthermore, we demonstrate that when facing an antibiotic threat, an increase in error level is sufficient to allow survival of bacteria carrying a mutated antibiotic-resistance gene. We propose that bacterial gene expression is error prone, frequently yielding protein molecules that differ slightly from the sequence specified by their DNA, thus generating a cellular reservoir of nonidentical protein molecules. This variation may be a key factor in increasing bacterial fitness, expanding the capability of an isogenic population to face environmental challenges.

Bacillus subtilis | translational errors | variations in living cells | translation fidelity

DNA is duplicated with remarkable fidelity to ensure that accurate genetic information is transmitted from one generation to the next. This information is passed from DNA to RNA and from RNA to protein during gene expression; however, the accuracy of these downstream events is relatively less understood. Although RNA and proteins are generally considered short-lived noninherited molecules, several diseases are now known to arise from errors occurring during transcription and translation (1–3), implying that faithful transfer of genetic information from DNA to proteins is crucial for maintaining proper cellular functions.

Interestingly, errors in gene expression can be beneficial, serving as a mechanism to promote noncanonical decoding. This strategy is mostly used by bacteria and viruses to increase diversity of particular proteins and to express alternative translational products (4). In *Escherichia coli* for example, programmed translational frame-shifting in the *dnaX* gene produces DNA polymerase subunits with different enzymatic activities. The canonical product of *dnaX* confers extreme processivity on DNA polymerase, whereas the truncated protein expressed because of translational frame-shifting tempers the polymerase activity (5). In more general terms, errors arising spontaneously during gene expression may increase protein variety and thereby enable genetically identical cells to display heterogeneous phenotypes. This phenomenon is likely to contribute to the robustness of unicellular organisms, allowing them to respond to fluctuating environments without changing their genotype (6–10).

Errors in gene expression emanate from inaccuracies during the processes of transcription or translation. Transcriptional fidelity is determined largely by the capability of the RNA polymerase to sense and discriminate between cognate and noncognate pairing to the DNA template before incorporation of the next nucleotide (11). Faithful translation relies mainly on correct aminoacylation of a given tRNA, selection of the proper tRNA, and maintenance of the correct ORF throughout synthesis (12). In vivo measure-

ments of errors in gene expression in bacteria have been estimated to occur at a rate of 10^{-4} to 10^{-5} per nucleotide during transcription and $\approx 10^{-3}$ to 10^{-4} per codon during translation. These error rates are significantly higher than that attributed to the high-fidelity replication process, where the frequency of errors is as low as 10^{-8} to 10^{-9} per nucleotide (8, 9, 12–20).

For the most part, in vivo error rates in bacterial gene expression have been estimated by measuring the activity of a mutated reporter gene (such as *lacZ*) (14, 17, 18) in a large cell population. However, the resultant measurements represent the average error rates, and thus do not detect the actual error level per cell and the variability, if any, among individuals. Moreover, these assays do not discriminate between errors in gene expression and genetic mutations. Here, we designed an experimental system to visualize and quantify the rate of spontaneous errors in gene expression at a single-cell level in living *Bacillus subtilis* cells. Our strategy was to introduce mutations into the ORF of a chromosomally encoded *gfp* reporter allele, such that errors in protein production would yield functional GFP molecules, visible by fluorescence microscopy. Using this approach, we revealed that gene expression in bacteria is prone to high levels of errors reaching values that are much higher than previously estimated. Moreover, we demonstrate that bacteria have the capability to modify error levels in response to physiological and environmental conditions.

Results

Visualizing Errors in Gene Expression. To visualize errors in gene expression at a single-cell level, we mutated a chromosomally encoded *gfp* reporter allele, such that errors in gene expression would generate functional GFP molecules. We reasoned that the use of highly sensitive fluorescence microscopy would enable us to detect small amounts of GFP molecules. Hence, we inserted frame-shift (*gfp_{fs}*) or nonsense (*gfp_{ns}*) mutations at the beginning of the ORF of an inducible *gfp* gene. Ocher (TAA) was chosen as the nonsense mutation because it is the most abundant stop codon in the *B. subtilis* genome (*SI Appendix*).

To monitor errors in gene expression arising during growth, cells bearing the different alleles were grown to mid-exponential phase and observed by fluorescence microscopy. As expected, a strong fluorescence signal was detected from cells expressing the wild-type *gfp* allele in the presence of the inducer (Fig. 1A). Remarkably however, a clear fluorescent signal was also observed from strains bearing either the *gfp_{fs}* or the *gfp_{ns}* alleles upon induction. In both strains, the signal appeared as a uniformly distributed weak cytoplasmic haze present in all cells. This signal was above background level, as evidenced by the strain lacking the *gfp* gene or a strain

Author contributions: M.M., G.M., and S.B.-Y. designed research, performed research, analyzed data, and wrote the paper.

The authors declare no conflict of interest.

*This Direct Submission article had a prearranged editor.

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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.0912989107/-DCSupplemental.

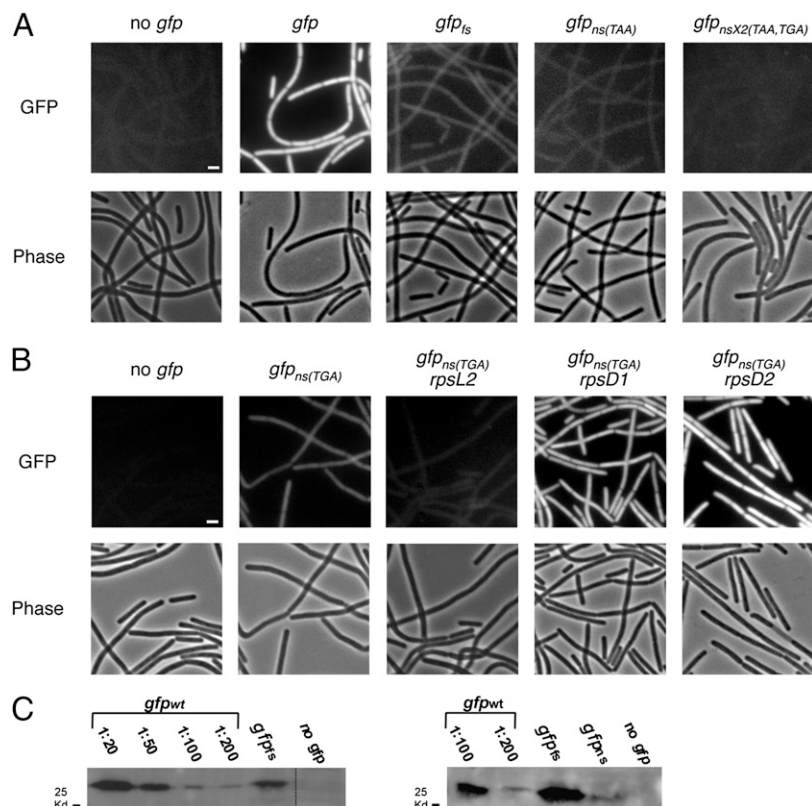


Fig. 1. Observing errors in gene expression at a single cell level. (A) *B. subtilis* strains were grown to mid-exponential phase at 32 °C in hydrolyzed casein (CH) medium supplemented with IPTG and observed by fluorescence microscopy. Fluorescence (Upper) and corresponding phase-contrast (Lower) images of the following strains: PY79 (no *gfp*), SB444 (*gfp_w*), SB448 (*gfp_{fs}*), SB446 (*gfp_{ns(TAA)}*), and SB510 (*gfp_{nsX2(TGA, TAA)}*). Fluorescence images have been normalized to a similar intensity range, apart from the high-intensity image of SB444 strain, which was scaled down for presentation purpose. (Scale bar, 1 μ m.) (B) Fluorescence (Upper) and corresponding phase-contrast (Lower) images of the following strains: PY79 (no *gfp*), SB512 (*gfp_{ns(TGA)}*), SB632 (*rpsL2, gfp_{ns(TGA)}*), SB608 (*rpsD1, gfp_{ns(TGA)}*), and SB616 (*rpsD2, gfp_{ns(TGA)}*). Cells were grown to mid-exponential phase at 32 °C in CH medium. Fluorescence images have been normalized to a similar intensity range. (Scale bar, 1 μ m.) (C) Immunoblot analysis of GFP protein extracts from strains: PY79 (no *gfp*), SB444 (*gfp_w*), SB448 (*gfp_{fs}*), SB446 (*gfp_{ns(TAA)}*) grown at 32 °C to mid-exponential phase. Extracts were incubated with polyclonal anti-GFP antibodies. SB444 extract was diluted as indicated, to serve as a reference for SB446 and SB448 extracts. Right panel was exposed for a longer period than left panel to detect low GFP amounts (SI Appendix, SI Materials and Methods).

containing two nonsense mutations within the *gfp* ORF (Fig. 1A). Moreover, fluorescence recovery after photobleaching experiments showed that 35 min after bleaching, the fluorescent signal displayed by the *gfp* mutant strains was almost restored to its original level, confirming that the signal derived from de novo inaccurate synthesis of protein molecules (SI Appendix, Fig. S1). Importantly, a similar GFP expression pattern was observed for mutations inserted into an endogenous *B. subtilis* gene (*disA*) fused to *gfp* (SI Appendix, Fig. S2) (21), and in strains carrying identical *gfp* alleles controlled by various promoters (SI Appendix, Fig. S3), implying that errors occur constantly regardless of the tested allele or the driving promoter.

We validated the formation of erroneous GFP molecules using Western blot analysis (Fig. 1C). This examination revealed that full-length GFP molecules are produced by the *gfp_{fs}* and the *gfp_{ns}* alleles, indicating that bypass of the mutations is carried out mainly at the beginning of the ORF in the vicinity of the mutations. Evidently, both fluorescent and immunoblot signals appeared to be stronger for the *gfp_{fs}* strain than for *gfp_{ns}* (Fig. 1A and C). This difference most likely emanates from the possibility that nonsense mutation can be read through specifically by erroneous introduction of an amino acid at the stop codon, whereas the frame-shift mutation can be bypassed by any compensatory frame-shift error at various sites in the vicinity of the mutation. Of note, both mutations can be bypassed by transcriptional or translational errors.

Next, we examined the strength and the consistency of our system by replacing the original nonsense mutation (TAA) with a TGA stop codon. TGA was shown to be decoded as tryptophan at low efficiency in *B. subtilis* and thus to increase errors in protein production (22). Accordingly, a strain carrying the *gfp_{ns(TGA)}* allele displayed greater fluorescence than the one containing the *gfp_{ns(TAA)}* allele (SI Appendix, Fig. S4). We then combined the *gfp_{ns(TGA)}* allele with mutations in the genes encoding for the RpsL and RpsD ribosomal proteins. Mutations perturbing RpsL or RpsD activity are known to influence translational fidelity, primarily by affecting the bypass of the TGA codon. Consistent with previous observations (14), a mutation in *rpsL* that represses translational errors decreased the fluorescence emanating from the *gfp_{ns(TGA)}* strain. Conversely, mutations in *rpsD* that elevate translational errors clearly increased the fluorescent signal exhibited by the *gfp_{ns(TGA)}* strain (Fig. 1B).

All together, we established that under standard growth conditions each bacterial cell spontaneously introduces errors during gene expression to a significant level, which can be readily detected using a mutant fluorescent gene.

Quantifying the Rate of Spontaneous Errors in Gene Expression. Next, we estimated the average amount of errors that occur during exponential growth. The GFP signal emanating from the *gfp_{fs}* and *gfp_{ns}* mutant strains was quantified, averaged, and expressed as a percentage of the GFP signal detected in *gfp_w* cells (SI Appendix,

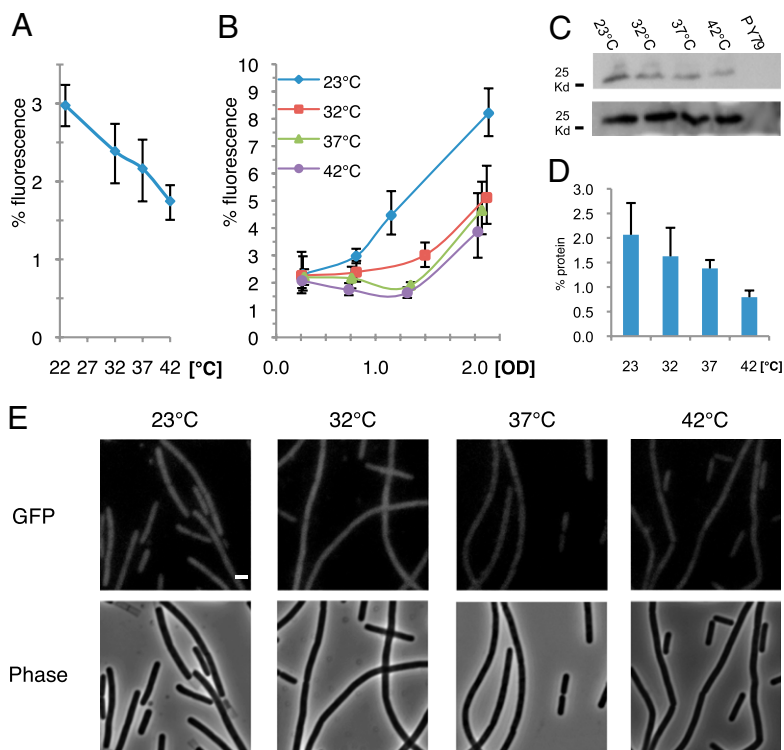


Fig. 2. Error level in gene expression is temperature dependent. (A) Fluorescence levels (%) as a function of temperature in strain SB448 (*gfp_{fs}*) grown to mid-exponential phase. Fluorescence levels (%) are the average fluorescence signal of strain SB448 (*gfp_{fs}*) relative to the average fluorescence signal of strain SB444 (*gfp_{wt}*); both strains were grown to the same OD and at the same temperature (*SI Appendix, SI Materials and Methods*). (B) Fluorescence levels (%) as a function of OD, when strain SB448 (*gfp_{fs}*) was grown at different temperatures. Fluorescence levels (%) were calculated as in A. (C) Immunoblot analysis of GFP protein at different incubation temperatures. Extracts from strains SB448 (*gfp_{fs}*) (Upper), SB444 (*gfp_{wt}*) (Lower) grown at the indicated temperatures and PY79 grown at 23 °C were incubated with polyclonal anti-GFP antibodies. For SB444 only 1/20 of each extract was loaded (*SI Appendix, SI Materials and Methods*). (D) Protein levels (%) as a function of temperature in strain SB448 (*gfp_{fs}*) as calculated from immunoblot analysis. Protein levels (%) are the calculated amount of GFP protein from strain SB448 (*gfp_{fs}*) relative to that of strain SB444 (*gfp_{wt}*); both strains were grown at the same temperature to the same OD₆₀₀ (*SI Appendix, SI Materials and Methods*). (E) Fluorescence (Upper) and corresponding phase-contrast (Lower) images of strain SB448 (*gfp_{fs}*) grown to mid-exponential phase at the indicated temperatures. All fluorescence images were normalized to a similar intensity range. (Scale bar, 1 μ m.)

SI Materials and Methods). Strikingly, the *gfp_{fs}* cells contained $2.4 \pm 0.4\%$ GFP molecules, whereas *gfp_{ns}* contained $0.4 \pm 0.1\%$ fluorescent protein molecules relative to *gfp_{wt}* cells. These values were reproducible, and showed little variation among cells of each strain. Importantly, estimates obtained from different promoters driving the transcription of the mutant *gfp* alleles were similar, and immunoblot signals from *gfp_{fs}* and *gfp_{ns}* resembled that of *gfp_{wt}* diluted 1:50 and 1:200, respectively (Fig. 1C). These measurements could even be underestimates, as mutations situated at the beginning of an ORF are predicted to minimize the error level as they predispose ribosomes to fall off the transcript (17, 23). To further examine if the error rates detected are exceptional or reflect a more standard level, we measured the fluorescence emanated from additional *gfp* mutated alleles. Replacing the nucleotide causing the frame-shift mutation from A to G did not affect the error level (*SI Appendix, Fig. S4*), suggesting that the location rather than the sequence is critical for determining the error level. Moreover, inserting frame-shift and nonsense mutations into additional positions within the *gfp* ORF revealed similar error frequencies (*SI Appendix, Fig. S4*).

A careful comparison of the values obtained using the *gfp_{ns}* alleles (*SI Appendix, Fig. S4*) in *B. subtilis* with those obtained using an other nonsense codon in *E. coli* (15, 17) revealed that our measurements are at least 10-fold higher than previous estimates, raising the possibility that an error occurs approximately once every 200 codons. Errors exceeding 0.1% have been previously reported for specific missense mutations and are generally considered exceptional (e.g. refs. 13 and 15). Our findings suggest that, at least for *B. subtilis*, these values may represent a standard error level, although the mechanisms for generating missense errors or bypassing nonsense codons may differ (24). In addition, we show that frame-shift errors are highly abundant, at least when located at the beginning of the ORF (*SI Appendix, Fig. S4*). Thus, we consider it likely that alternative translational products are produced frequently as a consequence of frame-shift errors. Taken together, the error rates exhibited by the *gfp* mutant alleles support the view that spontaneous errors have been underestimated.

Error Levels in Gene Expression Are Dynamic. In view of our observations that errors are a prominent feature of bacterial gene expression, we reasoned that bacteria in natural habitats modulate error rates. This theory led us to survey the effect of temperature on the level of errors exhibited by *B. subtilis* cells, which naturally reside in the soil. The *gfp_{fs}* strain was used for this analysis because the GFP signal therein is higher than that of the *gfp_{ns}* strain, allowing a greater range of variations to be detected. Samples of *gfp_{fs}* cells at mid-exponential phase grown at temperatures ranging from 23 to 42 °C were collected and their fluorescent intensity was compared with that displayed by *gfp_{wt}* cells incubated at the same temperatures (Fig. 2A and E). We observed an inverse correlation between temperature and error level, such that bacteria grown at the lowest temperature exhibited 70% more errors than bacteria kept at the highest temperature, 3 ± 0.3 and $1.7 \pm 0.2\%$, respectively. Consistently, Western blot analysis showed a similar correlation between the production of erroneous protein molecules and temperature (Fig. 2C and D). Importantly, no significant difference was detected between the levels of wild-type GFP molecules produced at the different temperatures, suggesting that protein stability is not the cause for the observed tendency. Thus, growth temperature has a direct effect on the error level, implying that bacteria can modulate error rates in nature. The reduced error level measured at higher temperatures suggests that raising the temperature imposes the formation of more accurate protein molecules.

Next, we tested whether there is any correlation between growth phase and error level. A time-course experiment was performed whereby the error levels were determined at different growth phases at various temperatures. We found that the error level correlates with optical density, reaching the highest values at stationary phase during when the bacterium is challenged by unfavorable conditions (Fig. 2B). These results were corroborated by Western blot analysis showing a similar trend (*SI Appendix, Fig. S5*). The error rates observed during stationary phase were at least 2.1-fold higher than those observed during exponential phase for all temperatures, with cells grown at the lowest temperature reaching a mean level of more than 8% (Figs. 2B and 3A). To rule

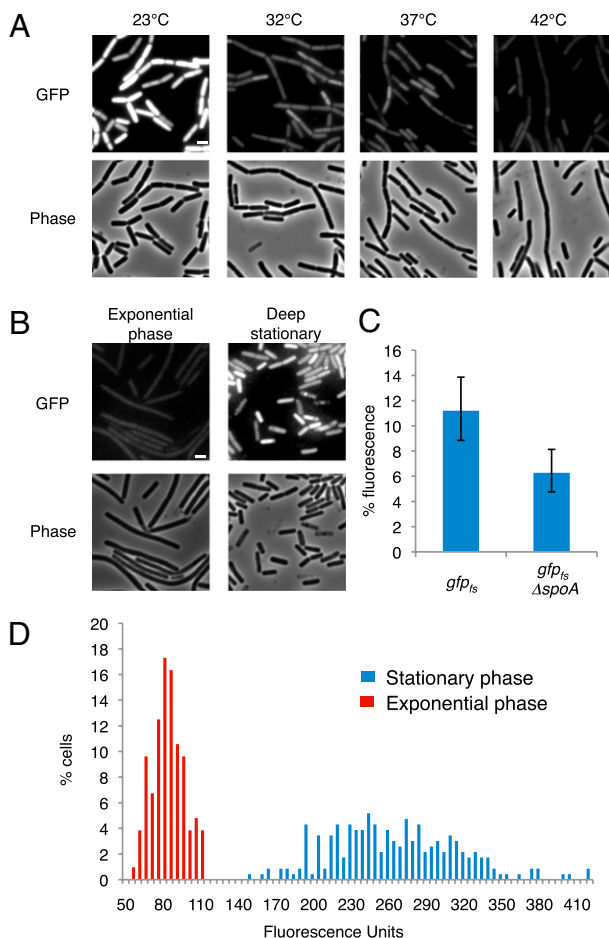


Fig. 3. Error level in gene expression increases during stationary phase. (A) Fluorescence (Upper) and corresponding phase-contrast (Lower) images of strain SB448 (*gfp_{fs}*) during stationary phase at the indicated temperatures. All fluorescence images were normalized to a similar intensity range. (Scale bar, 1 μ m.) (B) Fluorescence (Upper) and corresponding phase-contrast (Lower) images of strain SB448 (*gfp_{fs}*) grown at 32 °C either to mid-exponential phase (Left) or during deep stationary phase (Right) 2 h after the addition of IPTG. Images were normalized to the same intensity range. (Scale bar, 1 μ m.) (C) Fluorescence levels (%) of strains SB448 (*gfp_{fs}*) and SB784 (*gfp_{fs} Δspo0A*) 11 h after entering into stationary phase at 32 °C. Fluorescence levels (%) are the average fluorescence signal of a *gfp* mutant strain relative to the average fluorescence signal of its corresponding wild-type *gfp* strain: SB444 (*gfp_{wt}*) for SB448 and SB782 (*gfp_{wt} Δspo0A*) for SB784 (SI Appendix, SI Materials and Methods). (D) Fluorescence distribution of individual cells of strain SB448 (*gfp_{fs}*) during mid-exponential phase (red bars) and during stationary phase (blue bars) grown at 32 °C. At least 100 cells were scored for each phase.

out the possibility that these high error levels were a consequence of protein accumulation during stationary phase, we induced *gfp_{fs}* expression only during deep stationary phase ($t = 20$ h) for a short window of time. The resultant fluorescence was then compared with that of vegetative *gfp_{fs}* cells induced for the same time period. As shown in Fig. 3B, cells residing in deep stationary phase evidently exhibited higher error levels than exponentially growing cells. Notably, cells unable to properly enter deep stationary phase, because of a mutation in the key transcription factor Spo0A (25), exhibited a lower level of errors than those observed in wild-type cells residing at this stage (Fig. 3C). This result indicates that proper entry into stationary phase is important for the observed increase in error levels. It is therefore possible that either an active induction of errors in gene expression takes place during stationary phase or, alternatively, a fidelity mechanism active during exponential growth shuts off.

A more detailed inspection of fluorescence levels emanating from individual cells revealed greater variation during stationary phase than during exponential phase for all tested temperatures (compare Fig. 2E with Fig. 3A). This increased heterogeneity of stationary cells was readily apparent when the distribution of GFP expression was plotted for cells grown at 32 °C (Fig. 3D). The distribution of fluorescence intensity originated from cells during stationary phase was considerably wider than that observed for exponentially growing cells. Thus, we conclude that individual cells in stationary phase exhibit varying degrees of accuracy in gene expression, expanding the capability of an isogenic population to display heterogeneous phenotypes, a feature that could serve to increase the ability of bacterial cells to face environmental challenges.

High Levels of Errors Can Be Selectively Advantageous. We reasoned that the high amount of errors monitored during bacterial gene expression may be beneficial under certain conditions. To simulate such a situation, we mutated an antibiotic resistance gene and assayed whether errors in gene expression could promote the production of protein molecules valuable for bacterial survival. To this end, mutations were introduced into the ORF of the *cat* gene encoding chloramphenicol resistance protein, and cells were plated on chloramphenicol-containing plates. Remarkably, at 30 °C *cat_{fs}* and *cat_{ns}* mutant strains were able to grow slowly on the selective medium and to display numbers of resistant colonies similar to those of the *cat_{wt}* strain (Fig. 4A and B). Importantly, we confirmed that resistant colonies derived from the mutant strains retained the mutated *cat* allele as well as the mutant phenotypes (Materials and Methods). Moreover, in line with the observed temperature-dependence of error levels, the survival rate on the selective medium increased as growth temperature was reduced. As shown in Fig. 4C, the number of resistant *cat_{fs}* and *cat_{ns}* colonies appearing on the selective medium at 23 °C was similar to the number observed on the nonselective medium,

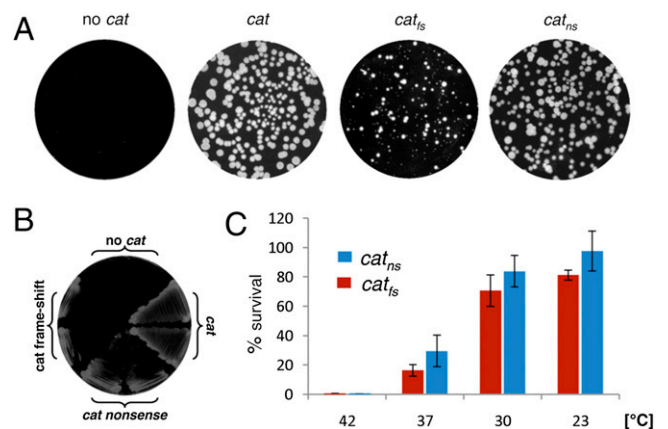


Fig. 4. Errors in gene expression enable survival of strains carrying a mutated antibiotic resistant gene. (A) Strains PY79 (no *cat*), SB463 (*cat*), SB477 (*cat_{fs}*), and SB475 (*cat_{ns}*) were grown on 4- μ g/mL chloramphenicol-containing plates. Plates were imaged after 40 h of incubation at 30 °C. (B) Strains PY79 (no *cat*), SB463 (*cat*), SB477 (*cat_{fs}*), and SB475 (*cat_{ns}*) were streaked on 10- μ g/mL chloramphenicol-containing plates and imaged after 40 h of incubation at 30 °C. (C) The viability (%) of SB477 (*cat_{fs}*) (red bars) and SB475 (*cat_{ns}*) (blue bars) at different temperatures when plated on chloramphenicol-containing plates. Cells were grown in CH medium at the different temperatures in the absence of chloramphenicol, and plated at mid-exponential phase on either LB or LB supplemented with 4- μ g/mL chloramphenicol plates. Percent-viability is the number of colonies growing on chloramphenicol-containing plates relative to the total number of colonies growing on LB plates incubated at the equivalent temperature (Materials and Methods). PY79 (no *cat*) strain did not grow on chloramphenicol-containing plates, whereas SB463 (*cat*) showed \approx 100% viability at any growth temperature. The viability on LB plates of all tested strains was similar, with colony number ranging from 350 to 500.

whereas only a negligible number of colonies was obtained from selective plates incubated at 42 °C. In light of these data, we propose that a high error level could facilitate the expression of pseudogenes containing frame-shift and nonsense mutations, which are a common feature of bacterial genomes (e.g., ref. 26). Thus, pseudogenes may represent a valuable genetic reservoir that can be expressed and become beneficial under certain circumstances. The low amount of full-length proteins produced from pseudogenes may be a strategy used by some bacteria to maintain genetic information with a relatively low cost of protein synthesis.

Discussion

Our data reveal that protein production in the bacterium *B. subtilis* is prone to high levels of errors, a feature that may be widespread among bacteria. Therefore, we propose that in general each genetic locus generates an assortment of closely related protein molecules and that these inaccurate molecules become part of the cellular protein pool. Moreover, the high frequency of spontaneous frame-shifting monitored in our assays suggests that the cellular proteome could also contain large amounts of alternative translational products. Thus, the bacterial genetic code serves as a consensus sequence, on the basis of which protein production generates variations (Fig. 5). Accordingly, in vivo and in vitro experiments from different laboratories indicate that typically, proteins are robust to mutations and can tolerate a significant number of substitutions, even in highly conserved domains, with little change in structure, stability, or function (e.g., refs. 27–33). Furthermore, errors in protein production may be beneficial, as proteins can acquire new properties by only a few amino acid substitutions (e.g., refs. 27, 28, 30, 34). For example, certain mutations in DNA polymerase have been demonstrated to confer higher activity or an ability to incorporate nucleotide analogs (30).

In general, for any organism, the amount of errors represents a compromise between the “error cost,” namely the production of misfolded or dysfunctional proteins, and the “error payoff,” namely the production of beneficial protein variants and increased phenotypic heterogeneity. Several studies have reported large fluctuations in the level of errors among different codons encoding the same protein (14, 15, 17, 18), suggesting a different

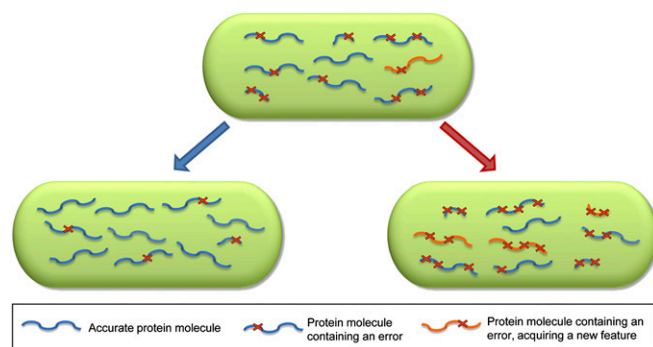


Fig. 5. Heterogeneity of gene products in a bacterium. A schematic illustration of protein molecules produced by a single gene in a bacterium. Proteins are depicted as curly blue or orange lines, and each red X represents an error event in the production of the protein relative to the sequence dictated by the genetic code. Shorter protein molecules represent frame-shift events. (*Upper*) Under normal growth conditions, the bacterial cell contains a mixture of different protein species: accurate molecules (blue), inaccurate molecules (blue and red X), and inaccurate molecules acquiring a new feature (orange and red X). (*Lower Left*) During certain conditions, such as high temperatures, gene expression is more accurate resulting in a less heterogeneous protein pool. (*Lower Right*) During conditions such as low temperatures and stationary phase, an increase in the error level expands the protein pool, resulting in the formation of more protein molecules bearing unique features. These unique features can benefit the bacterium, allowing it to survive during stress conditions and consequently, increase its robustness.

degree of susceptibility to errors along the coding sequence. In this view, evolutionary pressure that shapes codon usage could allow different genes to be prone to unequal error rates according to their cellular function (35).

We observed a significant decrease in the fidelity of protein production during stationary phase in response to other challenging conditions, such as minimal medium, and at lower temperatures. In a similar way, a decrease in translational fidelity was previously observed for *E. coli* cells grown under starvation conditions (36, 37). We hypothesize that in this way, errors in gene expression contribute to bacterial robustness, increasing survival in fluctuating environments or in response to sudden stress (Fig. 5). In addition, challenging conditions could promote expression of pseudogenes, thereby expanding the bacterial protein reservoir. Such plasticity enables cells to adapt to rapid changes that the slow evolutionary process cannot counter (38). Consistent with this idea, it has been proposed that gene-expression errors can contribute to the ability of an organism to develop genetically encoded traits that require multiple mutations. In such evolutionary process, intermediate steps could combine a genetic mutation in one gene with errors in gene expression in another, consequently bypassing the need to undergo two independent mutations simultaneously (10).

The temperature dependence of the error level observed in this study could be simply a result of reduced protein stability at high temperatures. Alternatively, this observation could be explained by temperature-induced expression of chaperones, proteins that were found to mask phenotypic diversity in both prokaryotes and eukaryotes (39–43). The best-studied example is the eukaryotic heat shock protein 90 (Hsp90) that was shown to buffer phenotypic variation in several organisms. Perturbing Hsp90 activity exposes diverse phenotypes and leads to increased population heterogeneity (39–42, 44).

It remains to be resolved whether the high error levels in gene expression observed in bacteria also exist in eukaryotes. It is tempting to speculate that multicellular organisms can modulate the level of errors in different cell types according to their function. In this regard, it has been shown that the proportion of proteins that are defective in certain eukaryotic cell types could exceed 30%; however, these faulty proteins are typically degraded by the proteasome (45, 46). In general, it seems that eukaryotic cells have developed mechanisms to reduce the production of truncated or inaccurate proteins, such as nonsense-mediated RNA decay (47). We suspect that the bacterial need to cope with rapid environmental changes imposes the existence of considerable diversity in their protein reservoir, an attribute that both ensures robustness and contributes to their ability to evolve.

Materials and Methods

Plasmids and Strains. Plasmids, strains, and primers used in this study are described in *SI Appendix, Tables S1–S4*.

General Methods. *B. subtilis* cells were grown in hydrolyzed casein (CH) growth medium at the indicated temperatures (23, 30, 32, 37, or 42 °C). Cultures were inoculated to an OD₆₀₀ of 0.05 using an overnight culture grown in the same medium. Induction of P_{hyper-spank} or P_{spank} promoters was carried out by adding IPTG to a final concentration of 0.5 mM for liquid medium and 1 mM for solid medium.

General Fluorescence Microscopy Methods. Fluorescence microscopy was carried out as described previously (21). For all experiments, cells were visualized and photographed using an Axioplan2 microscope (Zeiss) equipped with a CoolSnap HQ camera (Photometrics; Roper Scientific) or an Axiobserver Z1 microscope (Zeiss) equipped with a CoolSnap HQII camera (Photometrics; Roper Scientific) and X-cite (120PC; EXFO) as a fluorescence illumination light source. All fluorescence-intensity measurements were performed using the latter system because the X-cite provides a more uniform and stable light source in comparison with Mercury lamps. System control and image processing were performed using MetaMorph software (version 7.5; Molecular Devices). Other fluorescence microscopy methods: fluorescence recovery after

photobleaching and fluorescent images processing, are described in *SI Appendix, SI Materials and Methods*.

Monitoring Errors in Gene Expression in Strains Carrying a Mutated Chloramphenicol-Resistant Gene. Strains PY79 (no *cat*), SB463 (*cat*), SB477 (*cat_{ts}*), and SB475 (*cat_{ns}*) were grown in liquid nonselective CH medium at 32 °C to mid-exponential phase and plated on either LB or LB supplemented with 4- μ g/mL chloramphenicol-containing plates. The plates were incubated at different temperatures and the percent-viability was determined by the number of colonies grown on chloramphenicol-containing plates relative to the total number of colonies grown on LB plates incubated at the equivalent temperature. To rule out the possibility that colonies from each mutant strain grown on the selective medium emanated from reversion, suppression, or other genetic modification, at least 100 colonies from each mutant strain were picked and retested for their ability to grow on chloramphenicol. All of the tested colonies

(regardless of the colony size) maintained the mutant phenotypes as they were unable to grow on a high chloramphenicol concentration (20 μ g/mL). In addition, *cat* alleles of at least 20 colonies from each mutant strain were sequenced and none of them contained any genetic alteration. Testing the frequency of colonies gaining the wild-type phenotype (probably by reversions, suppressor mutations, and so forth) was $\approx 10^{-7}$ for the frame-shift or the nonsense alleles, as estimated by plating the mutant cells on high chloramphenicol concentrations.

ACKNOWLEDGMENTS. We thank R. Losick (Harvard University, Boston, MA), D. Kearns (Indiana University), A. Rouvinski (Hebrew University, Jerusalem), Y. Smith (Hebrew University, Jerusalem), and members of the Ben-Yehuda laboratory for valuable comments. We thank K. Ochi (Ibaraki, Japan) for providing *Bacillus subtilis* strains. This work was supported by the European Research Council Starting Grant 209130 and the Israel Science Foundation (696/07) (to S.B.-Y.).

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