OXFORD GENETICS

Environmental and genetic influence on rate and spectrum of spontaneous mutations in *Escherichia coli*

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Abstract

Spontaneous mutations are the ultimate source of novel genetic variation on which evolution operates. While mutation rate is commonly described as a single parameter in evolutionary models, it is increasingly evident that mutation rates vary due to changes in the rate of distinct nucleotide substitutions. Moreover, the rates of these substitutions can be influenced by genomic background and environmental conditions. Here we characterised the spectrum of spontaneous mutations in *Escherichia coli* grown in low and high nutrient environments, conditions known to affect the rate of spontaneous mutation. We compared changes in the mutational spectrum in a wild-type strain and a strain where the response of mutation rate to glucose is greatly diminished (a deletant for *luxS*, a gene involved in both quorum sensing and intracellular methylation regulation). We find an increase in AT>GC transitions in the low glucose environment, suggesting that processes relating to the production or repair of this mutation could drive the response of mutation rate to nutrient concentration. Interestingly, this increase in AT>GC transitions is maintained by the non-responsive Δ*luxS* deletant. Instead, an elevated rate of GC>TA transversions in both nutrient environments 'masks' the effect of AT>GC transitions on overall mutation rate. Our results show how relatively subtle changes, such as the concentration of a carbon substrate or loss of a regulatory gene, can substantially influence the amount and nature of genetic variation available to selection.

Keywords: mutation rate, mutational spectrum, DNA repair, fluctuation assay, thymine starvation, evolution

Introduction

Understanding what governs the occurrence of spontaneous mutations is crucial for predicting evolution. Mutation rate is known to be influenced by genetic variation (e.g. mutators, Matic *et al.* 1997; Oliver *et al.* 2000) and the environment (Foster 2007; Maharjan and Ferenci 2018; Chu *et al.* 2018; Ferenci 2019). Although often described as a single metric, mutation rates actually encompass the cumulative effects of numerous biochemical processes that cause errors in DNA replication to occur and remain uncorrected. Progress in understanding the molecular basis for mutation has been made by characterising the 'mutational spectrum', i.e. the frequency of occurrence of different types of single nucleotide variants (SNVs) and insertion and deletion mutations (indels). For SNVs, this includes a set of six possible mutations, the transitions AT>GC and GC>AT, and the transversions AT>CG, AT>TA, GC>CG, and GC>TA. For indels, the set of possible mutations is much greater (Williams and Wernegreen 2013). Each type of SNV and indel occurs at different rates, which can each respond differently to genetic and environmental factors (e.g. Maharjan and Ferenci 2018; Chu *et al.* 2018; Lee *et al.* 2012; Foster *et al.* 2015; Maharjan and Ferenci 2017; Fajardo-Cavazos *et al.* 2018; Leehan and Nicholson 2021).

Microbial mutation rates are particularly sensitive to environmental effects. We have previously described an inverse relationship between mutation rate and population density, which is now referred to as density-associated mutation rate plasticity (DAMP, Krašovec *et al.* 2014, 2017). DAMP is present in many microbes across all three domains of life (Krašovec *et al.* 2017), and can be demonstrated experimentally by varying the concentration of nutrients accessible to the microbe in its environment (e.g. glucose, Krašovec *et al.* 2014, or rich media, Krašovec *et al.* 2018). The strength of the association between density and mutation rate can vary within organisms from the same species (Krašovec *et al.* 2017; Richards 2019) and can be either enhanced or abolished by certain genetic knockouts (Krašovec *et al.* 2014, 2017; Krašovec *et al.* 2018). Although affected by nutrient concentration, DAMP is a distinct phenomenon from other mutation-generating processes (e.g. stress-induced mutagenesis, Krašovec *et al.* 2018).

Despite the pervasiveness of mutation rate plasticity (Krašovec *et al.* 2017), we currently lack a molecular understanding for the connection between nutrient concentration and mutation rate—in particular, whether the change in mutation rate arises due to changes in all mutational classes, or only some. Previous results indicate that mutation avoidance and repair systems and metabolic effects both seem to play a part. For instance, the association between glucose and mutation rate is diminished

in strains with impaired mutation avoidance and repair (through deletion of *mutS*, *mutH*, *mutL* or *mutT*, Krašovec *et al.* 2017). Yet, not all genes affecting mutagenesis and repair affect mutation rate plasticity; deletion of polymerase IV or polymerase V has no effect (Krašovec *et al.* 2017; Krašovec *et al.* 2018). This shows that the molecular basis for the mutation rate response to glucose may be connected to interactions between metabolism and mutation avoidance and repair.

Intriguingly, the association between glucose concentration and mutation rate was also greatly diminished in a deletion strain, Δ*luxS* (Krašovec *et al.* 2014). In *E. coli*, *luxS* is involved in both AI-2 mediated quorum sensing and the activated methyl cycle (AMC) (Wang *et al.* 2012). This raises the question of whether the response of mutation rate to glucose concentration in the wild-type strain is due to quorum sensing or a role of the AMC in mutation avoidance and repair processes. The AMC generates the methyl-group donor *S*-adenosyl-*L*-methionine (SAM), which is required for DNA methylation and *E. coli*-specific methyl-directed mismatch repair (MMR) (Putnam 2016). Thus, Δ*luxS* could potentially be deficient in methyl-directed MMR. Alternatively, the effect of *luxS* on mutation rate may emerge due to altered gene regulation more generally. Deletion of *luxS* influences gene expression in an environment-dependent manner (Wang *et al.* 2005). In particular, *luxS* affects regulation of metabolism, nutrient acquisition and virulence traits (Mitra *et al.* 2016; Ha *et al.* 2018), which could influence how this strain responds to and metabolises glucose.

Insight into how the mutational spectrum changes has been previously used to characterise the roles of various genes involved in mutation avoidance and repair. For instance, disruption of MMR increases the frequency of the transitions, AT>GC and GC>AT (Schaaper and Dunn 1987). Disruption of GO system genes *mutM* or *mutY*, which typically correct errors induced by oxidative damage, increases the frequency of GC>TA transversions (Foster *et al.* 2015), and disruption of *mutT* increases AT>CG transversions (Lee *et al.* 2012; Yanofsky *et al.* 1966). Differential expression of different DNA polymerase genes can produce striking effects on the mutational spectrum (Curti *et al.* 2009). Similar insights into the molecular underpinnings of mutation rate plasticity may be possible from observing changes in the mutational spectrum associated with the mutation rate response to glucose concentration.

To test how the mutation rate response to glucose potentially relates to metabolism and mutation avoidance and repair systems, we have characterised how the mutational spectrum of *E. coli* changes with growth in high and low glucose environments. We first measured mutation rates using fluctuation tests, and then sequenced resistant isolates to identify spontaneous mutations. Where the wild-type had a higher mutation rate at low glucose, the mutation rate of Δ*luxS* remained relatively unchanged. Changes in the mutational spectrum suggest the molecular mechanism that underpins the response of mutation rate to glucose.

An increase in AT>GC transitions in low glucose conditions suggests that methyl-directed MMR may operate less efficiently under resource-poor conditions, driving the increase in overall mutation rate. This increase is observed for both wild-type and Δ*luxS* deletant, suggesting that the response of mutation rate to density is not driven by quorum sensing. The Δ*luxS* deletant instead showed an increased frequency of another SNV, GC>TA transversions, which occurred independently of glucose concentration. The increase in GC>TA transversions in Δ*luxS* is sufficient to 'mask' the effect of AT>GC transitions on the overall mutation rate. In concert, this suggests that seemingly small-scale genomic and environmental changes can have a significant effect on the quantity and nature of genetic variation available to selection.

Materials and methods

Strains and media

Experiments used *E. coli* str. K-12 substr. MG1655 as the wild-type and a Δ*luxS* deletant (KX1228), which constructed in the same genetic background (Xavier and Bassler 2005)). We used lysogeny broth for routine culturing of strains [LB, 10 g/l tryptone (ThermoFisher Scientific, UK), 5 g/l Bacto yeast extract (BD Biosciences, UK), 10 g/l NaCl (ThermoFisher Scientific, UK)]. Where indicated, LB agar was prepared by adding 12 g/l agar (BD Biosciences, UK).

For fluctuation tests, we used Davis minimal medium [DM, 7 g/l potassium phosphate dibasic trihydrate, 2 g/l potassium phosphate monobasic anhydrous, 1 g/l ammonium sulfate, 0.5 g/l sodium citrate (all obtained from Sigma-Aldrich, UK)]. After autoclaving, we added filter sterilised magnesium sulfate (in each litre of medium, 500 µL of 10% w/v, Fisher Scientific) and thiamine hydrochloride (500 µL of 0.2% w/v, Sigma Aldrich, UK). We supplemented with α-D-glucose (ThermoFisher Scientific, UK) as a carbon source, either to 80 mg/l ('low glucose' treatment), or 250 mg/l ('high glucose' treatment).

For plating of the fluctuation tests, we used tetrazolium agar (TA, 10 g/l tryptone, 1 g/l Bacto yeast extract, 3.75 g/l NaCl, 12 g/l agar) with L(+)-arabinose (3 g/l, Sigma-Aldrich, UK) and 2,3,5-triphenyltetrazolium chloride (50 mg/l, Sigma-Aldrich, UK) added post-autoclaving. Selective media was TA supplemented with 50 mg/l rifampicin (ThermoFisher Scientific, UK), which was dissolved in 99% methanol (ThermoFisher Scientific, UK) before adding to warm (∼55°C) medium.

Fluctuation tests

We estimated mutation rates using a high-throughput variation (Krašovec *et al.* 2019) of the classic fluctuation test (Luria and Delbrück 1943; Rosche and Foster 2000). Briefly, overnight cultures of MG1655 and Δ*luxS* were initiated by inoculating single colonies (streaked on LB agar) into 5 ml LB in 50 ml Falcon conical centrifuge tubes (Corning, USA). Overnight cultures were diluted to 0.3 OD, then subsequently diluted by a factor of 5×10^{-4} to achieve a density of 1×10^3 to 5×10^3 bacterial cells per ml. From these dilutions, 0.5 ml was used to establish 182 independent cultures in 96-well deep well plates (Greiner Bio-One, Austria). Cultures grew at 37°C with 200 RPM shaking for 24 h. Each independent culture was subsequently plated on 5 ml selective media, using 6-well plates (Greiner Bio-One, Austria) as the culture vessel. After 48 h growth, we counted the number of resistant mutants that arose in each parallel culture. We also estimated the population density of a subset of three parallel cultures, by plating dilutions on LB agar in 90 mm Petri dishes.

Isolation of resistant mutants

We used the rifampicin-resistant mutants arising from the fluctuation tests to characterise the spectrum of spontaneous mutations. We isolated resistant colonies from the selective plates and inoculated these into 1 ml cultures of LB for overnight growth, prior to storage in 75% LB and 25% glycerol at −80°C in 96-well

polypropylene plates (ThermoFisher Scientific, UK). To ensure mutations were independent, no more than one colony was isolated from each independent culture where mutants appeared (and nothing was isolated from cultures where no resistant mutants appeared).

Spectrum of spontaneous resistance mutations

Rifampicin resistance typically arises due to mutations in the gene *rpoB*, the β-subunit of RNA polymerase (Jin and Gross 1988; Goldstein 2014). Resistance is generally conferred by SNVs and occasionally by in-frame indels in the 'rifampicin resistance determining region' (RRDR). We therefore amplified a region of the *rpoB* gene containing the RRDR (specifically the region 1328–2235) using forward primer 5′-ATGATATCGACCACCTCGG-3′ and reverse primer 3′-TTCACCCGGATACATCTCG-5 (Integrated DNA Technologies, Belgium). Primers were resuspended and diluted to a stock concentration of 100 µM in nuclease-free water prior to use.

To obtain DNA for Sanger sequencing, resistant mutants were revived from the freezer by inoculating 1 µL of culture on to LB agar using a 96-well pin replicator (Boekel Scientific, USA). Following overnight growth, a pipette tip was used to scrape a small amount of colony material into 10 µL nuclease-free water. Each of 1 µL forward primer stock, 1 µL reverse primer stock, and 12.5 µL master mix (Platinum Green Hot Start PCR Master Mix, ThermoFisher Scientific, UK) was added to each reaction tube, and was mixed gently by pipetting. PCRs were performed as follows: i) initial denaturation (94°C for 5 min), ii) equilibration (30°C for 5 min), iii) denaturation (94°C for 0.5 min), iv) annealing (62°C for 0.5 min), v) extension (72°C for 0.5 min), vi) repeat steps iii–v for 35 cycles, vii) final extension (72°C for 10 min), viii) hold at 4°C. PCR products were purified using the QIAquick PCR Purification Kit (Qiagen, UK). Purified DNA was diluted to approximately 5 ng/µL. Sanger sequencing was performed by Eurofins LightRun service (Eurofins Genomics, Germany) using the reverse primer indicated above as the sequencing primer. Mutations were identified by aligning sequences to *rpoB* from *E. coli* str. K-12 substr. MG1655 using Unipro UGENE version 33 obtained from http://ugene.net (Okonechnikov *et al.* 2012) (data provided in File S1).

Statistical analysis

Data processing and mutation rate estimation Data processing and statistical analyses were performed in R (version 4.0.3) (R Core Team 2020) using functions from the tidyverse (Wickham *et al.* 2019) (analysis code provided in File S2). Figures were produced using ggplot2 (Wickham 2016). We used `mutestim()` (with default settings) from the flan package (version 0.9) (Mazoyer *et al.* 2021) to estimate mutation rates from the mutant counts and population sizes obtained via fluctuation tests (data provided in Files S3 and S4).

Mutation rate comparison We compared ratios of mutation rates measured at different glucose concentrations to see if the wild-type and Δ*luxS* responded differently. We calculated a low-to-high ratio for mutation rates, i.e. a ratio close to 1 indicates a limited response to glucose, a ratio > 1 indicates a higher mutation rate at low glucose, and a ratio < 1 indicates a lower mutation rate at low glucose. We first calculated point estimates of the mean and variance of these ratios (the latter using the 'sigma method' Beyene and Moineddin 2005), and then performed a z-test on the ratio for each strain (for full details, see supplemental material).

Mutational spectrum comparison We assessed the effect of glucose concentration and strain on the overall mutational spectrum by performing multinomial logistic regression using `multinom()` from the nnet package (Venables and Ripley 2002). As their numbers were small, all insertions were grouped into one category, and all deletions into another category. We subsequently looked at individual SNV categories by fitting logistic regression models on each SNV separately using `glm()` with a binomial family. We used Type II ANOVA (with a likelihood-ratio χ^2 as the test statistic) to determine the significance of removing each predictor variable in the presence of other predictor variables using the `Anova()` function from the car package (Fox and Weisberg 2019).

Results and discussion

Figure 1A shows that wild-type and Δ*luxS* deletant have very different mutation rate responses to glucose concentrations in minimal media. To assess the change in mutation rate with environment, we calculated the ratio of mutation rates estimated in the low and high glucose concentration treatments, which we refer to as the 'low-to-high ratio'. We observed a significantly higher mutation rate at low glucose in the wild-type strain [low-to-high ratio: 1.60, 95% CI=$(1.58, 1.62)$], but only a marginal change in Δ*luxS* [low-to-high ratio: 1.06, 95% CI=$(1.00, 1.12)$], which is consistent with our previous research (Krašovec *et al.* 2014, 2017; Richards 2019; Krašovec *et al.* 2018). The wild-type and Δ*luxS* low-to-high ratios were significantly different (z-test: $Z = 2.69$, $p = 0.004$).

To characterise the spectrum of mutations underlying these differences in mutation rate, we sequenced the *rpoB* gene of resistant isolates that arose under low and high glucose conditions (Figure 1B). Mutations were found in the rifampicin resistance determining region for 214 out of 274 sequenced isolates (Table S1 and File S1). The majority of mutations observed were SNVs at loci previously described to give rise to rifampicin resistance (Jin and Gross 1988; Wolff *et al.* 2004; Garibyan *et al.* 2003; Curti *et al.* 2009). We also observed 10 isolates with in-frame insertions or deletions, which were significantly more frequent in the wild-type genetic background, but not significantly affected by glucose concentration (logistic model, glucose concentration: $\chi^2_1 = 0.01$, $p = 0.89$; strain: $\chi^2_1 = 5.47$, $p = 0.019$; interaction: $\chi^2_1 = 0.81$, $p = 0.36$). We observed no indels that would result in frame shifts, which is expected given that *rpoB* is an essential gene (Baba *et al.* 2006).

Across all types of mutations, we found a significant effect of strain, but no significant effect of glucose concentration or their interaction on the mutational spectrum as a whole (multinomial regression model, glucose concentration: $\chi^2_7 = 11.9$, $p = 0.10$; strain: $\chi^2_7 = 15.2$, $p = 0.034$; interaction: $\chi^2_7 = 5.92$, $p = 0.55$). Subsequently, we examined the impact of genotype and environment on the frequency of individual mutational categories. For SNVs, we observed distinct shifts in two classes, AT>GC transitions and GC>TA transversions. AT>GC transitions were significantly higher in the low glucose environment, but were unaffected by strain (logistic model, glucose concentration: $\chi^2_1 = 5.44$, $p = 0.020$; strain: $\chi^2_1 = 0.17$, $p = 0.68$; interaction $\chi^2_1 = 0.67$, $p = 0.41$). In contrast, GC>TA transversions were significantly elevated in the Δ*luxS* deletant, with a slight but non-significant increase in both strains in the high glucose treatment and no significant interaction (logistic model, glucose concentration: $\chi^2_1 = 3.45$, $p = 0.0.063$; strain: $\chi^2_1 = 5.21$, $p = 0.022$; interaction: $\chi^2_1 = 0.50$, $p = 0.48$). For all other SNVs,

there was no significant effect of either glucose concentration or strain (logistic models, all $p > 0.1$).

The increase in AT>GC transitions under low glucose indicates two molecular processes that may be involved in the mutation rate response to glucose. Elevated rates of AT>GC transitions are associated with deficient MMR, which typically repairs both types of transition mutations, AT>GC and GC>AT. Consistent with this finding, we previously observed that deletion of key MMR genes diminishes the response of mutation rate to glucose (Krašovec *et al.* 2017). Although we did not detect a significant increase in GC>AT transitions in low glucose (in fact, the proportion of GC>AT transitions is smaller in low than high glucose: 0.21 vs 0.28), the relative proportion of this class of SNVs is much smaller overall. An elevated rate of AT>GC transitions, without a similar elevation of GC>AT transitions, has also been observed under conditions inducing thymine starvation in *E. coli* and other organisms, suggesting a common mechanism involving cellular pyrimidine availability (Kunz and Glickman 1985).

Intriguingly, the loss of the mutation rate response to glucose in the Δ*luxS* deletant (Figure 1A) likely did not arise from deficient MMR, as we observed similar effects of glucose on AT>GC transitions in both strains (Figure 1B). This is contrary to the idea that the disruption of SAM production in Δ*luxS* deletants (Halliday *et al.* 2010) decreases the efficiency of methyl-directed MMR. Instead, increased frequencies of GC>TA transversions in the Δ*luxS* strain masked the increase in AT>GC transitions under low glucose conditions. Elevated GC>TA transversions are typically associated with oxidative damage, and are usually corrected by the GO system involving MutM and MutY. That similar effects are observed for Δ*luxS* raises the possibility that *luxS* has a role in regulating either the GO system or the oxidative stress response that has yet to be characterised in *E. coli*. Several other lines of evidence also suggest this possibility. In *Streptococcus mutans*, *luxS* is involved in regulating genes involved in recombination and base excision repair, namely *recA*, and the apurinic/apyrimidinic AP endonucleases *smnA* and *nth*), as well as oxidative stress response genes (Wen and Burne 2004; Wen *et al.* 2011). In *E. coli*, similar AP endonucleases are required for filling in nucleotide gaps caused by the GO system (Mendoza-Chamizo *et al.* 2018). Deletion of *E. coli luxS* also affects expression of multiple genes (Haigh *et al.* 2013), including several involved in oxidative damage response (Wang *et al.* 2005), carbon utilisation, and biofilm formation (Niu *et al.* 2013).

Our results indicate that mutation rate plasticity associated with growth to different population densities results from changes in the rate of a specific mutational class, AT>GC transitions, and not an overall increase in mutation rate. The resulting effect on mutation rate can be masked by increases in the relative frequencies of other mutational classes that have a different response to the glucose environment. As the response of AT>GC transitions to glucose concentration occurred in both wild-type and Δ*luxS* strains, the association between population density and mutation rate observed in many microbes (Krašovec *et al.* 2014, 2017; Richards 2019; Krašovec *et al.* 2018) is not likely driven by quorum sensing (Krašovec *et al.* 2014), but instead potentially due to deficiencies in mutation repair under low nutrient conditions. As the mutational spectrum can have downstream consequences for adaptive evolution (Cano *et al.* 2022; Sane *et al.* 2022), understanding how population growth and density affect mutation generation, avoidance, and repair processes will be essential for understanding adaptive potential.

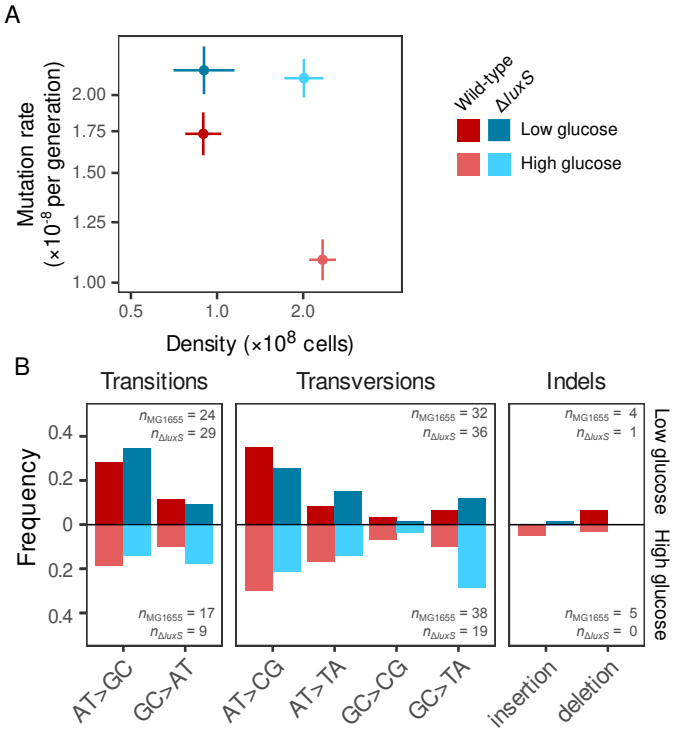

Figure 1 Effect of glucose concentration on rate and spectrum of mutations in *E. coli* str. K-12. wild-type and Δ*luxS* deletant. A) Spontaneous mutation rate measured by fluctuation test (mean±SE from $n = 182$ independent populations for each estimate). B) Spectrum of spontaneous mutations in wild-type MG1655 and Δ*luxS* deletant under high and low glucose treatments, showing increased AT>GC transitions in low glucose for both strains ($\chi^2_1 = 6.07$, $p = 0.014$), elevated GC>TA transversions for the Δ*luxS* deletant ($\chi^2_1 = 5.21$, $p = 0.022$), and a greater frequency of indels in the wild-type MG1655 background ($\chi^2_1 = 5.46$, $p = 0.019$).

Data availability

Strains are available upon request. File S1 contains the mutations found in sequenced rifampicin-resistant strains originating from fluctuation test and used to assess changes in mutational spectrum. File S2 contains the R analysis code used to perform all statistical analyses and generate figures. File S3 contains mutant counts used to estimate mutation rates to rifampicin resistance for MG1655 and Δ*luxS* strains grown at low and high glucose in the fluctuation test. File S4 contains population density data (N_t) for MG1655 and Δ*luxS* strains grown at low and high glucose in the fluctuation test.

Acknowledgments

The authors thank Karina Xavier (Instituto Gulbenkian de Ciência) for the gift of the Δ*luxS* deletant strain KX1228 and its MG1655 parent strain.

Funding

This project was funded by the BBSRC (EM: part of BB/M011208/1), UKRI (DRG: MR/R024936/1, RK: MR/T021225/1), and the Wellcome Trust (AB, DRG, CGK: part of 204796/Z/16/Z).

Conflicts of interest

The authors state no conflicts of interest.

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