­Stress-Induced Mutagenesis Breaks the Trade-Off Between Adaptability and Adaptedness

Yoav Ram and Lilach Hadany

**Email**: YR - [yoavram@post.tau.ac.il](mailto:yoavram@post.tau.ac.il), LH - [lilach.hadany@gmail.com](mailto:lilach.hadany@gmail.com)

**Address**: Dept. of Molecular Biology and Ecology of Plants, Tel Aviv University

Tel-Aviv 69978, Israel. Tel. +972.3.640.6886

**Running title:** SIM, adaptability, and adaptedness

**Keywords**: adaptation, fitness, models/simulations, mutations, population genetics, trade-offs

**Counts**: X words, X figures, 1 table

**Data archiving**: Dryad

# ­­­­Abstract

Because mutations are mostly deleterious, mutation rates should be reduced by natural selection. However, mutations also provide the raw material for adaptation. Therefore, evolutionary theory suggests that the mutation rate must balance between *adaptability* – the ability to adapt – and *adaptedness* – the ability to remain adapted. We model an asexual population crossing a fitness valley and analyze the adaptation rate with and without stress-induced mutagenesis – the increase of mutation rates in response to stress or maladaptation. We show that stress-induced mutagenesis breaks the evolutionary trade-off between *adaptability* and *adaptedness*, increasing one without reducing the other. Our theoretical results support the hypothesis that stress-induced mutagenesis promotes adaptation and provide quantitative predictions of the adaptation rate with different mutational strategies.

# Introduction

There is experimental, clinical and theoretical evidence that high mutation rates increase the rate of adaptation and that during adaptive evolution, constitutive mutators - alleles that constitutively increase the mutation rate - can rise in frequency because of the beneficial mutations they generate (reviewed in Sniegowski et al. 2000; de Visser 2002; Denamur and Matic 2006). However, during evolution in a stable environment, constitutive mutators become associated with poor genetic backgrounds due to increased accumulation of deleterious mutations – as evidenced both in the lab (Funchain et al. 2000) and in the clinic (Montanari et al. 2007). Classical models suggest the "reduction principle" - natural selection reduces the mutation rate in a stable environment (Kimura 1967; Liberman and Feldman 1986). But many adaptations require new beneficial mutations, especially in asexual populations. This tension between the effects of beneficial and deleterious mutations leads to "the rise and fall of the mutator allele" (Giraud et al. 2001b), where mutator alleles increase in frequency in a maladapted population, only to be eliminated by selection when the population is well-adapted. This dynamic was studied using experimental evolution (Sniegowski et al. 1997; Wielgoss et al. 2012), mathematical analysis, and simulations (Taddei et al. 1997; Kessler and Levine 1998; Tenaillon et al. 1999).

Leigh (1970) suggested that the mutation rate must balance between two evolutionary traits: *adaptability* – the capacity to adapt to new environmental conditions – and *adaptedness* – the capacity to remain adapted to existing conditions.

Stress-induced mutagenesis (SIM), the increase of mutation rates in stressed or maladapted individuals, has been demonstrated in several species, including both prokaryote and eukaryote (Galhardo et al. 2007). SIM was observed in lab strains (Foster 2007; Rosenberg et al. 2012) and natural populations of *Escherichia coli* (Bjedov et al. 2003; but also see Katz and Hershberg 2013), and in other species of bacteria such as Pseudomonads (Kivisaar 2010), *Helicobacter pylori* (Kang et al. 2006), and *Streptococcus pneumonia* (Henderson-Begg et al. 2006). SIM was also observed in yeast (Heidenreich 2007; Rodriguez et al. 2012), algae (Goho and Bell 2000), nematodes (Matsuba et al. 2012), flies (Sharp and Agrawal 2012), and human cancer cells (Bristow and Hill 2008). Several stress responses regulate the mutation rate in bacteria by shifting replication to error-prone DNA polymerases (Ponder et al. 2005) and by inhibiting the mismatch repair system (Debora et al. 2010). In *E. coli* these stress responses include the SOS DNA-damage response, the RpoS-controlled general or starvation stress response, and the RpoE membrane protein stress response (Al Mamun et al. 2012).

It is still not clear how SIM affects evolution and adaptation. Some authors propose that SIM has a significant impact on *adaptability* or *evolvability* (Tenaillon et al. 2004; Cirz and Romesberg 2007; Rosenberg et al. 2012), but there is no theoretical treatment of this impact. On the other hand, the effect of SIM on *adaptedness* was studied with deterministic (Agrawal 2002) and stochastic (Shaw and Baer 2011) models. These works showed that without beneficial mutations SIM doesn't affect the mean fitness of asexual populations in stable environments, in contrast with constitutive mutagenesis, which decreases the population mean fitness. More recently, we showed that with rare beneficial mutations, if maladapted individuals increase their mutation rate then the population mean fitness of asexual populations increases (Ram and Hadany 2012).

Here, we analyze population genetics models of adaptive evolution to explore the rate of adaptation on a rugged fitness landscape, in which adaptations require two separately deleterious mutations (Wright 1931, 1988). We develop analytic approximations and stochastic simulations and compare normal, constitutive, and stress-induced mutagenesis. We show that stress-induced mutagenesis can break the trade-off between *adaptability* and *adaptedness* by increasing the adaptation rate without decreasing the population mean fitness.

# ­Model

We consider a population of *N* haploid asexual individuals with a large number of loci in full linkage. We model the effects of mutation, selection, and genetic drift.

Individuals are characterized by their genotype in two specific bi-allelic loci - *ab*, *Ab*, *aB*, and *AB* – and by the number of deleterious mutations they carry in the rest of the non-specific loci. For example, *aB/3* is the *aB* genotype with additional three deleterious mutations in non-specific loci.

We consider adaptation to a new environment. The fitness of the wildtype *ab/0* is 1, the fitness of the single mutants *Ab*/0 and *aB*/0 is 1-*s*, and the double mutant *AB/0* has the highest fitness 1+*sH*, where *s* is the selection coefficient and *H* is the relative advantage of the double mutant. This is the simplest case of a "rugged fitness landscape": the single mutants *Ab* and *aB* are fitness "valleys" between the local and global fitness peaks *ab*/0 and *AB/0* (Figure 1).

Each deleterious mutation in the non-specific loci independently (multiplicatively) reduces the fitness of the individual by 1-*s*. We assume that mutations occur in the specific loci with probability *µ* and that the number of new mutations per replication in the rest of the genome is Poisson distributed with an average *U*. We neglect back-mutations and compensatory mutations.

We consider three mutational strategies: normal mutagenesis (NM), where there is no increase in the mutation rate; constitutive mutagenesis (CM), where all individuals always increase their mutation rate by *τ*,the mutation rate fold increase; and stress-induced mutagenesis (SIM), where only stressed or maladapted individuals increase their mutation rate by *τ*. Individuals are considered stressed if their fitness is below a specific threshold, so stress can be caused by a deleterious mutation (either in the specific *A/a* and *B/b* loci or in non-specific loci). Our main analysis assumes that with SIM the mutation rate of an individual with fitness *ω* is:

|  |  |
| --- | --- |
| . | (1) |

This models a scenario in which an environmental change – for example, appearance of a new ecological niche or a new carbon source – provides an opportunity for adaptation without affecting the fitness of the current wildtype population. We also study a different scenario in which the environmental change reduces the absolute fitness of the current population, so that the wildtype population is also under stress – see section 3.5.

We are interested in calculating the adaptation rate of a population homogenous for each of the above mutational strategies (NM, CM, or SIM). We separate the adaptation process into two ­­­­distinct stages. In the first stage, a double mutant *AB* appears in the population, usually in a single copy. In the second stage, the double mutant either goes to extinction or avoids extinction, increases in frequency, and goes to fixation.

We analyzed this model with two methods. The first is analytic (Figure 1A), in which we assume that: (i) genotypes with deleterious backgrounds (deleterious alleles in the non-specific loci) do not contribute to the adaptation process; (ii) the number of deleterious alleles per individual before the appearance of a double mutant is at a mutation-selection balance (MSB) and is Poisson distributed with mean *U/s* (Haigh 1978). The former assumption requires that mutation is weaker than selection (); the later assumption only requires that mutation is not much stronger than selection – specifically, that the expected number of mutation-free individuals is at least one ().

The second method is a stochastic Wright-Fisher simulation with selection, mutation and genetic drift (Figure 1B), in which we: (i) allow individuals with a deleterious background to contribute to adaptation; (ii) let a mutation-free population evolve towards a MSB without assuming a Poisson distribution of the number of deleterious alleles. We also use this simulation model to study competitions between the different mutational strategies.

## Wright-Fisher simulations

We divide the individuals to classes according to their genotypes (*ab/x*, *Ab/x*, *aB/x*,and *AB/x*, where *x*≥0 is the number of deleterious alleles in non-specific loci), and track the number of individuals in each class. The simulations start with a single peak smooth fitness landscape and a mutation-free population (all individuals start in the optimal *ab/0* genotype with fitness 1) that accumulates deleterious alleles over the first 5,000 generations of the simulation. With *s*=0.05 and 0.005, 180 and 1,800 generations are enough to get the average number of deleterious alleles per individual to 99.99% of its MSB value, *U/s* (Gordo and Dionisio 2005).

After 5,000 generations the fitness landscape changes to a rugged one, making *AB* the optimal genotype with fitness 1+*sH* (Figure 1B). The simulation then proceeds until an *AB* genotype appears and either fixates in the population or goes extinct (either all or no individuals are in the *AB* classes, respectively). Therefore, each simulation provides one sample of the waiting time for the appearance of a double mutant and one sample of the probability of fixation of a double mutant. At least 1,000 simulations were performed for each parameter set.

Table 1 summarizes the model parameters with estimated values for *E. coli*.

# Results

## Appearance of a double mutant

We are interested in the waiting time for the appearance of a double mutant *AB* either by a double mutation in a wildtype individual *ab*, or via a single mutation in a single mutant *Ab* or *aB* (Figure 1A). Denoting the population size by *N,* we note that (i) if then double mutants are already expected at the MSB and adaptation will not require new mutations; (ii) if then no single mutants are expected at the MSB and double mutants must be generated by a double mutation in a wildtype individual. In this case, increasing the mutation rate of individuals with fitness below 1 will have no effect on the appearance of the double mutant and there is no point in analyzing the effect of SIM.

Combining these two constraints we get this constraint on the population size *N*: . This constraint is reasonable for bacterial populations (see Table 1).

The frequencies of wildtype (*ab*) and single mutants (*aB* and *Ab* combined) that are mutation-free at the MSB are roughly and , respectively. The probability that an offspring of a wildtype or single mutant parent is a double mutant *AB* is and , respectively. The probability that such an offspring is also mutation-free in the rest of its genome (the only mutations that occurred were at the specific loci) is . Therefore, the probability *q* that a random offspring is a double mutant, given there are no double mutants in the current generation, is approximated by:

|  |  |
| --- | --- |
| . | (2) |

The first expression assumes that individuals with a deleterious background don't contribute to adaptation and that the MSB distribution of deleterious alleles is Poisson. The second expression also assumes that mutation is much weaker than selection - *U<<*s.

With SIM the mutation rate of single mutants is increased *τ*-fold and the probability that a random offspring is a double mutant is:

|  |  |
| --- | --- |
| . | (3) |

The first and second expressions make the same assumptions as in eq. 2. The second expression also assumes that .

Appendix 1 includes full derivations of the above formulae. Figure S1 shows a comparison of these approximations with the simulations results.

## Fixation probability of the double mutant

Assuming an advantage to the double mutant (*H*>1)and a large population size (see the former constraint on *N*), a double mutant has two possible fates after its appearance: fixation or extinction. Following Eshel (1981), the fixation probability *ρ* of the double mutant is (see Appendix 2):

|  |  |
| --- | --- |
| . | (4) |

That is, the fixation probability of the double mutant is roughly twice its adaptive advantage. This is a classic result of population genetics theory (Fisher 1930 p. 76).

The fixation probability with SIM equals that of NM and CM because the mutation rate of the wildtype *ab* equals that of the double mutant *AB* (but see an exception in section 3.5).

## Adaptation rate

From the probability *q* that a random offspring is a double mutant, we can derive the probability that one or more double mutants appear in the next generation: . This is a good approximation because *Nq* is very small due to the constraint on *N*. Once a double mutant appears it goes to fixation with probability *ρ*.

The time for adaptation *T* can be approximated by the waiting time for a double mutant that goes to fixation. This is true when fixation is much faster than appearance of *AB*. This waiting time follows a geometric distribution with rate *Nqρ* and therefore the adaptation rate *ν* (the inverse of the waiting time for adaptation) is approximately:

|  |  |
| --- | --- |
| . | (5) |

Plugging eqs. 2-4 in eq. 5, we get these approximations:

|  |  |
| --- | --- |
|  | (6) |
|  | (7) |
|  | (8) |

NM is normal mutagenesis, CM is constitutive mutagenesis, and SIM is stress-induced mutagenesis. The middle expression in each equation is the full approximation, which assumes a Poison distribution and no contribution of deleterious genotypes to adaptation. The right hand side is the first order approximation that assumes mutation is much weaker than selection ( for NM and SIM, for CM) and that 1<τ<1/*U*. See Table 1 for description of model parameters and (Weinreich and Chao 2005) for a result similar to eq. 6.

The main conclusions from eqs. 6-8: First, adaptation with CM is faster than with NM. Second, adaptation with SIM is also faster than with NM, but not as fast as with CM because the mutation-free wildtype (*ab/0*) does not hypermutate.

If mutation is weaker than selection () then the adaptation rate with CM increases with the square of *τ* and the adaptation rate with SIM increases linearly with *τ*. In addition, because the fixation probability is the same for NM, CM and SIM, the difference in adaptation rate is due to differences in the appearance probability *q* (Figure S1), but see section 3.5 for a different scenario in which SIM also increases the fixation probability.

Figure 2A compares the analytic approximations with simulations results for the weak mutation regime (). This regime is relevant for asexual microbes in which the deleterious mutation rate is generally 10-4-10-3 mutations per genome per generation and selection coefficients are estimated to be between 10-1 and 10-2 (see Table 1). When the mutation rate fold increase *τ* is high (>10), the approximations slightly overestimate the adaptation rate because the double mutant *AB* is more likely to appear on a deleterious background - *AB/1* instead of *AB/0*. Because the fitness of *AB/1* is higher than that of the wildtype *ab/0* (guaranteed when *H*>(1-*s*)-1≈1+*s*), the double mutant can go to fixation even when it appears on a deleterious background, sweeping the deleterious alleles with it to fixation in a process called "genetic hitch-hiking" (Smith and Haigh 2009; Hartfield and Otto 2011). However, these sweeps result in a lower fixation probability for the double mutant (Figure S2) and a lower population mean fitness after adaptation.

What happens when mutation is as strong as selection? A shows results for *s*=10*U*. When the average number of deleterious alleles per individual *τU/s* is over one, adaptation with CM is likely to occur on a deleterious background. Because our approximation neglects adaptation on deleterious backgrounds, it underestimates the adaptation rate (Figure 3A). Note that although the adaptation rate continues to increase with *τ*, the population carries more deleterious alleles after adaptation, resulting in a lower population mean fitness (Figure 3B).

With SIM, the average number of deleterious alleles per individual *U/s* does not increase with *τ*, because mutation-free individuals (*ab/0*) do not hypermutate. As in the case of weak mutation, when *τ*>10 the double mutant can appear on a deleterious background, resulting in hitch-hiking and a lower fixation probability, and causing our approximation to overestimate the adaptation rate (Figure 3A).

## The trade-off between *adaptability* and *adaptedness*

Next, we explore how different mutational strategies (NM, CM and SIM) balance between *adaptability* – the ability to adapt to new conditions– and *adaptedness* – the ability to remain adapted to current conditions. For this purpose we define *adaptedness* asthe population mean fitness in a stable environment and *adaptability* as the rate of complex adaptation.

We used the above approximations (eqs. 6-8) to calculate the adaptation rate of populations with NM, CM and SIM. We also extended an existing model (Ram and Hadany 2012) to calculate the population mean fitness at the mutation-selection balance. Our extended model includes beneficial mutations and allows more than one mutation to occur in the same individual and generation. In the *supporting information* we explain how this model is used to calculate the mean fitness of an asexual population with various mutational strategies.

The mutation rate with CM is constant and uniform across the population, and the population mean fitness mainly depends on the fitness and mutation rate of the fittest individuals. Therefore, the population mean fitness decreases when the mutation rate increases - this decrease is due to generation of deleterious mutations in the fittest individuals. The adaptation rate, however, increases with the mutation rate (eq. 7). This trade-off between *adaptability* and *adaptedness* limits the population: after a long period of environmental stability it can lose the potential for adaptation, and after a long period of environmental change the population can be susceptible to reduced fitness and mutational meltdowns (Lynch et al. 1993).

However, this trade-off between *adaptability* and *adaptedness* can be broken if mutation rates are not uniform across the population. Increased mutation rates in unfit individuals increase the population mean fitness, as long as beneficial (compensatory) mutations can occur (Ram and Hadany 2012). Figure S4 shows this advantage of SIM over NM in terms of the difference in population mean fitness (). Moreover, increased mutation rates in unfit individuals also increase the adaptation rate (eq. 8). Therefore, SIM breaks the trade-off between *adaptability* and *adaptedness*.

Figure 4 shows the adaptation rate and population mean fitness of CM and SIM compared to NM for different values of *τ*, the mutation rate fold-increase.

Any realistic rate of adaptation *ν* can be realized using both CM and SIM. The highest mean fitness will always be attained with SIM, which has a small advantage over NM (that cannot be seen in this figure, but see Figure S4) due to the increased generation of beneficial (compensatory) mutations in individuals with low fitness. If for some rate of adaptation the mutation rate fold increase *τ* required by SIM is too high (*i.e.*, *τU*>*s*), the same adaptation rate can be realized by a mixed strategy (dashed line in Figure 4). For example, a 96-fold increase in adaptation rate can be achieved with CM with *τ*=10, with SIM with *τ*=96, or with a mixed strategy with *τCM*=7and *τSIM*=2 in which all individuals increase their mutation rate 7-fold and stressed individuals further increase their mutation rate 2-fold. However, these increases in adaptation rates have a price: the mutational load will decrease the population mean fitness from 0.9996 with NM to 0.996 with CM and 0.9972 with the mixed strategy. This price in not paid by populations with SIM because the mean fitness mainly depends on the mutation rate of fit individuals. In fact, with beneficial mutations the mean fitness with SIM with *τ*=96 is higher than that of NM by ~3⋅10-8.

## Environmental stress

So far, we considered the case where the environmental change creates an opportunity for adaptation without affecting the absolute fitness of the population – for example, a new ecological niche can be favorable without affecting the well-being of the current population. In that scenario, the wildtype *ab* wasn't stressed and did not hypermutate.

Next, we consider a different scenario in which an environmental change affects the well-being of the entire population - for example, exposure to an antibiotic drug or a host's immune response. In this case the environmental change doesn't just create an opportunity for adaptation but also causes stress in the entire population. As before the double mutant *AB* is resistant to the stress (*i.e.* the drug or immune response) and therefore has a higher fitness than either the wildtype or the non-resistant single mutant*s*. However, in this scenario the wildtype *ab* is also stressed and therefore hypermutates with SIM – compare with eq. 1:

|  |  |
| --- | --- |
| . | (9) |

We use a subscript *e* to denote quantities related with this scenario.

This scenario has an important biological relevance, as SIM has been implicated in the evolution of drug resistance in bacteria and yeast (Cirz and Romesberg 2007; Obolski and Hadany 2012; Shor et al. 2013) and could be involved in the evolution of pathogen virulence, as well as drug resistance and progression in cancer cells.

The adaptation rate with SIM in this scenario is (see Appendix 3 for full derivation):

|  |  |
| --- | --- |
| . | (10) |

That is, adaptation with SIMe is faster than with CM. This approximation was verified with simulations (dashed line in Fig. 2A). Adaptation is faster with SIMe because (i) the population quickly evolves towards a MSB and therefore the initial difference in standing variation between CM and SIMe is not significant (with s=0.05 and *U*=0.0004, the average number of deleterious mutations is 0.99∙*U/s* after 90 generations (Gordo and Dionisio 2005)); (ii) the appearance of double mutants is the same as with CM; and (iii) the fixation probability of double mutants is higher with SIMe than with CM, because the mutation rate of double mutants is lower than that of the rest of the population. This difference in mutation rates confers an additional selective advantage to the double mutants (see Appendix 3) which increases their fixation probability:

|  |  |
| --- | --- |
| . | (11) |

This additive advantage increases linearly with *τ* with a slope of , which can be small (*≈*7⋅10-4 for typical values, see Table 1). The increase in fixation probability was verified by simulations (Figure S2).

## Possible relationships between stress and mutation

So far we used a threshold relationship between stress and mutation: if fitness sinks below a threshold (<1 for SIM, ≤1 for SIMe), the mutation rate increases *τ*-fold. But the relationship between stress and mutation can be more complex. For example, Agrawal (2002) used a continuous relationship defined by a curvature parameter *k*. This relationship defines the mutation rate for an individual with fitness *ω*, baseline mutation rate *U*, and a maximal mutation rate fold increase *τ* as:

|  |  |
| --- | --- |
| . | (12) |

When *k* approaches 0 this expression approaches the normal mutagenesis (NM) strategy. When *k* approaches infinity this expression approaches the SIM threshold strategy from eq. 1. See Figure S3 for a visualization of these continuous relationships.

Figure 2B shows the adaptation time for three continuous strategies (*k*=1/10, 1, and 10). Remarkably, the dynamics of a continuous strategy can be approximated by a threshold strategy by matching the mutation rates of single mutants:

|  |  |
| --- | --- |
| . | (13) |

This is equivalent to using a threshold strategy with mutation rate increase *τ*-(*τ*-1)(1-*s*)*k*. The dashed lines in Figure 2B illustrate this approximation. The continuous strategies can be approximated by threshold strategies because the main factor determining the adaptation rate is the mutation rate increase of *ab*, *aB*, and *Ab*. This is because individuals with more than a single mutation do not have a significant contribution to adaptation.

## Competitions between mutational strategies

We also simulated direct competitions between the different mutational strategies (NM, CM, and SIM). In these competitions, when the fitness landscape changes, half of the population alters its mutational strategy to an invading strategy. Each simulation (after the fixation or extinction of the double mutant *AB*) provides a sample of the final frequency of the invading strategy. If the average final frequency is significantly lower or higher than 50% we consider the invading strategy disfavored or favored by selection over the initial strategy. We calculated this statistical significance using a 1-sample 2-tailed t-test.

We simulated direct competitions between the different mutational strategies to determine which is more successful at the individual-level. Figure 5 summarizes these competitions. CM clearly loses to both SIM and NM (first and second panels from the right). SIM is significantly advantageous over NM when the mutation rate increase is large enough (*τ*>2; 2-tail t-test, P<0.0015).

These results show that the evolutionary advantage of SIM at the population-level corresponds to an individual-level advantage and can lead to the evolution of stress-induced mutagenesis by natural selection, even when constitutive mutagenesis is strongly disfavored.

# Discussion

We studied the effect of stress-induced mutagenesis (SIM) on both the *adaptability* – the capacity of populations to adapt to new conditions – and the *adaptedness* – the ability of populations to stay adapted to existing conditions (Leigh 1970). We showed that SIM breaks the trade-off between *adaptability* and *adaptedness*, allowing rapid adaptation to complex environmental changes without compromising the population mean fitness in a constant environment.

In addition to the pure strategies of constitutive mutagenesis (CM) and SIM, our model also considers a mixed mutational strategy. There are two examples of such a mixed strategy. First, if individuals have incomplete information regarding their condition (the case in most realistic biological scenarios) then we expect errors in the stress-induction of mutagenesis - induction of mutagenesis without stress and failure to induce mutagenesis under stress. In this case the population would, on average, use a mixed strategy. Second, a mutator allele can increase the mutation rate constitutively and further increase it under stress – for example, a recent study with *Pseudomonas aeruginosa* found that although the *mutS*, *mutY* and *mutM* mutator alleles always increase the mutation rate in comparison with the wildtype, the level of this increase depends on the level of stress the cell experiences (Torres-Barceló et al. 2013).

Our model does not assume direct fitness costs for any of the mutational strategies. A "cost of DNA replication fidelity" (Dawson 1998) – the energy and time expended in order to maintain a low mutation rate – could make both CM and SIM more successful. The "cost of fidelity" may require further study, but empirical evidence suggests that it doesn't play an important role in the evolution of the mutation rate (Giraud et al. 2001a; Loh et al. 2010; Gentile et al. 2011; Shee et al. 2011). Another fitness cost might be associated with the regulation of the mutation rate: for individuals to determine if their condition calls for the induction of mutagenesis, they must invest resources and energy in costly sensory mechanisms. However, such mechanisms already exist for various unrelated purposes, such as the maintenance of cell cycle and homeostasis. Therefore, we consider these mechanisms as "free" in terms of fitness costs. Moreover, in *E. coli* mutagenesis is induced by several stress responses that serve other cellular functions (Foster 2007; Al Mamun et al. 2012), and this is probably also the case in other organisms.

Our model focuses on asexual populations, ignoring recombination, segregation, and sexual reproduction. These mechanisms are important for adaptation on a rugged fitness landscape both because they help to cope with deleterious mutations and because they allow two different single mutants to produce a double mutant without an increased mutation rate. We expect that recombination will reduce the advantage of SIM over NM in population mean fitness (Agrawal 2002), direct competitions (Tenaillon et al. 2000), and adaptation rate (due to the Fisher-Muller effect).

Mean fitness and adaptation rate are both population-level traits. But just because SIM has the most efficient balance between these traits doesn't mean it will necessarily evolve, because individual-level selection can act in a different direction than population-level selection. In a previous work we demonstrated that 2nd order selection can lead to the evolution of SIM (Ram and Hadany 2012): in an asexual population evolving on a smooth fitness landscape, selection favored SIM over both NM and CM. SIM was favored both in a constant environment and in a constantly changing environment. Here we showed that selection also favors SIM on a rugged fitness landscape (Figure 5).

Complex traits, coded by multiple genes, present an open evolutionary problem, first described by Sewall Wright in 1931 (Wright 1931): if different alleles are separately deleterious but jointly advantageous, how can a population evolve from one co-adapted gene complex to a fitter one, crossing a less fit "valley"? Wright suggested the "shifting-balance theory of evolution" (Wright 1931, 1988). His solution is valid (Crow et al. 1990; Wade and Goodnight 1991; Peck et al. 2000) but possibly limited to specific parameter ranges (Moore and Tonsor 1994; Gavrilets 1996; Coyne et al. 2000; Whitlock and Phillips 2000). As a result, other mechanisms were proposed: increased phenotypic variance after population bottlenecks (Whitlock 1995); environmental fluctuations (Whitlock 1997); environmental heterogeneity (Hadany 2003); fitness-associated recombination (Hadany and Beker 2003); and intermediate recombination rates (Weissman et al. 2010). Our approach is similar to that of Weinreich and Chao (2005), but our model includes various mutational strategies and the effects of stress and deleterious mutations. Our results (Figure 2) suggest that SIM can help resolve the problem of fitness valley crossing by reducing the time required for a population to shift an adaptive peak.

Our results provide theoretical basis to the conjecture that SIM facilitates adaptation. This conjecture can be tested experimentally, for example, with *E. coli*, where it is possible to interfere with the regulation of mutagenesis (Cirz and Romesberg 2007). The adaptation time with and without SIM can be measured in an experimental population adapting to a two-peak fitness landscape (Schrag et al. 1997). These measurements can then be compared to our analytic approximations to determine the relative advantage and disadvantage of the different mutational strategies.

## Conclusions

Stress-induced mutagenesis has been implicated as a driver of adaptive evolution for several decades (Cairns et al. 1988; Tenaillon et al. 2004; Rosenberg et al. 2012). Here we provided theoretical treatment of this concept. We showed that stress-induced mutagenesis increases the rate of complex adaptation, and that in contrast to constitutive mutagenesis it does not jeopardize the fitness of populations under stable conditions. Because mutation is a fundamental force in every biological system, these results have important implications on many fields in the medical and life sciences, including epidemiology, oncology, ecology, and evolutionary biology.

# Acknowledgments

We thank Uri Obolski for advice on statistical analysis. We are very grateful to A.F. Agrawal and two anonymous reviewers for their comments and remarks. This research has been supported in part by the Israeli Science Foundation 1568/13 (LH) and by Marie Curie reintegration grant 2007–224866 (LH).

# Literature cited

Agrawal, A. F. 2002. Genetic loads under fitness-dependent mutation rates. J. Evol. Biol. 15:1004–1010.

Al Mamun, A. A. M., M.-J. Lombardo, C. Shee, A. M. Lisewski, C. Gonzalez, D. Lin, R. B. Nehring, C. Saint-Ruf, J. L. Gibson, R. L. Frisch, O. Lichtarge, P. J. Hastings, and S. M. Rosenberg. 2012. Identity and function of a large gene network underlying mutagenic repair of DNA breaks. Science 338:1344–8.

Berg, O. G. 1996. Selection intensity for codon bias and the effective population size of *Escherichia coli*. Genetics 142:1379–82.

Bjedov, I., O. Tenaillon, B. Gérard, V. Souza, E. Denamur, M. Radman, F. Taddei, and I. Matic. 2003. Stress-induced mutagenesis in bacteria. Science 300:1404–9.

Bristow, R. G., and R. P. Hill. 2008. Hypoxia and metabolism: Hypoxia, DNA repair and genetic instability. Nat. Rev. Cancer 8:180–92.

Cairns, J., J. Overbaugh, and S. Miller. 1988. The origin of mutants. Nature 335:142–5.

Cirz, R. T., and F. E. Romesberg. 2007. Controlling mutation: intervening in evolution as a therapeutic strategy. Crit. Rev. Biochem. Mol. Biol. 42:341–54.

Coyne, J. A., N. H. Barton, and M. Turelli. 2000. Is Wright’s shifting balance process important in evolution? Evolution 54:306–317.

Crow, J. F., W. R. Engels, and C. Denniston. 1990. Phase Three of Wright’s Shifting-Balance Theory. Evolution 44:233.

Dawson, K. J. 1998. Evolutionarily stable mutation rates. J. Theor. Biol. 194:143–57.

De Visser, J. A. G. M. 2002. The fate of microbial mutators. Microbiology 148:1247–52.

Debora, B. N., L. E. Vidales, R. Ramírez, M. Ramírez, E. A. Robleto, R. E. Yasbin, and M. Pedraza-Reyes. 2010. Mismatch Repair Modulation of MutY Activity Drives *Bacillus subtilis* Stationary-Phase Mutagenesis. J. Bacteriol. 193:236–45.

Denamur, E., and I. Matic. 2006. Evolution of mutation rates in bacteria. Mol. Microbiol. 60:820–7.

Drake, J. W., B. Charlesworth, D. Charlesworth, and J. F. Crow. 1998. Rates of spontaneous mutation. Genetics 148:1667–86.

Eshel, I. 1981. On the survival probability of a slightly advantageous mutant gene with a general distribution of progeny size - a branching process model. J. Math. Biol. 12:355–362.

Fisher, R. A. 1930. The Genetical Theory of Natural Selection. Clarendon Press, Oxford.

Foster, P. L. 2007. Stress-induced mutagenesis in bacteria. Crit. Rev. Biochem. Mol. Biol. 42:373–97.

Funchain, P., A. Yeung, J. L. Stewart, R. Lin, M. M. Slupska, and J. H. Miller. 2000. The consequences of growth of a mutator strain of *Escherichia coli* as measured by loss of function among multiple gene targets and loss of fitness. Genetics 154:959–70.

Galhardo, R. S., P. J. Hastings, and S. M. Rosenberg. 2007. Mutation as a stress response and the regulation of evolvability. Crit. Rev. Biochem. Mol. Biol. 42:399–435.

Gavrilets, S. 1996. On phase three of the shifting-balance theory. Evolution 50:1034–1041.

Gentile, C. F., S.-C. Yu, S. A. Serrano, P. J. Gerrish, and P. D. Sniegowski. 2011. Competition between high- and higher-mutating strains of *Escherichia coli*. Biol. Lett. 7:422–4.

Giraud, A., I. Matic, O. Tenaillon, A. Clara, M. Radman, M. Fons, and F. Taddei. 2001a. Costs and benefits of high mutation rates: adaptive evolution of bacteria in the mouse gut. Science 291:2606–8.

Giraud, A., M. Radman, I. Matic, and F. Taddei. 2001b. The rise and fall of mutator bacteria. Curr. Opin. Microbiol. 4:582–585.

Goho, S., and G. Bell. 2000. Mild environmental stress elicits mutations affecting fitness in Chlamydomonas. Proc. R. Soc. B Biol. Sci. 267:123–9.

Gordo, I., and F. Dionisio. 2005. Nonequilibrium model for estimating parameters of deleterious mutations. Phys. Rev. E 71:18–21.

Gordo, I., L. Perfeito, and A. Sousa. 2011. Fitness effects of mutations in bacteria. J. Mol. Microbiol. Biotechnol. 21:20–35.

Hadany, L. 2003. Adaptive peak shifts in a heterogenous environment. Theor. Popul. Biol. 63:41–51.

Hadany, L., and T. Beker. 2003. Fitness-associated recombination on rugged adaptive landscapes. J. Evol. Biol. 16:862–870.

Haigh, J. 1978. The accumulation of deleterious genes in a population - Muller’s Ratchet. Theor. Popul. Biol. 14:251–267.

Hall, L. M. C., and S. K. Henderson-Begg. 2006. Hypermutable bacteria isolated from humans--a critical analysis. Microbiology 152:2505–14.

Hartfield, M., and S. P. Otto. 2011. Recombination and hitchhiking of deleterious alleles. Evolution 65:2421–34.

Heidenreich, E. 2007. Adaptive mutation in *Saccharomyces cerevisiae*. Crit. Rev. Biochem. Mol. Biol. 42:285–311.

Henderson-Begg, S. K., D. M. Livermore, and L. M. C. Hall. 2006. Effect of subinhibitory concentrations of antibiotics on mutation frequency in *Streptococcus pneumoniae*. J. Antimicrob. Chemother. 57:849–54.

Johnson, T., and N. H. Barton. 2002. The effect of deleterious alleles on adaptation in asexual populations. Genetics 162:395–411.

Kang, J. M., N. M. Iovine, and M. J. Blaser. 2006. A paradigm for direct stress-induced mutation in prokaryotes. FASEB J. 20:2476–85.

Katz, S., and R. Hershberg. 2013. Elevated Mutagenesis Does Not Explain the Increased Frequency of Antibiotic Resistant Mutants in Starved Aging Colonies. PLoS Genet. 9:e1003968. Public Library of Science.

Kessler, D. A., and H. Levine. 1998. Mutator Dynamics on a Smooth Evolutionary Landscape. Phys. Rev. Lett. 80:2012–2015.

Kibota, T. T., and M. Lynch. 1996. Estimate of the genomic mutation rate deleterious to overall fitness in *E. coli*. Nature 381:694–6.

Kimura, M. 1967. On the evolutionary adjustment of spontaneous mutation rates. Genet. Res. 9:23–34.

Kivisaar, M. 2010. Mechanisms of stationary-phase mutagenesis in bacteria: mutational processes in pseudomonads. FEMS Microbiol. Lett. 312:1–14.

Leigh, E. G. J. 1970. Natural Selection and Mutability. Am. Nat. 104:301–305.

Liberman, U., and M. W. Feldman. 1986. Modifiers of mutation rate: a general reduction principle. Theor. Popul. Biol. 30:125–42.

Loh, E., J. J. Salk, and L. A. Loeb. 2010. Optimization of DNA polymerase mutation rates during bacterial evolution. Proc. Natl. Acad. Sci. 107:1154–9.

Lynch, M., R. Bürger, D. Butcher, and W. Gabriel. 1993. The mutational meltdown in asexual populations. J. Hered. 84:339–44.

Matsuba, C., D. G. Ostrow, M. P. Salomon, A. Tolani, and C. F. Baer. 2012. Temperature, stress and spontaneous mutation in *Caenorhabditis briggsae* and *Caenorhabditis elegans*. Biol. Lett. 8–12.

Montanari, S., A. Oliver, P. Salerno, A. Mena, G. Bertoni, B. Tümmler, L. Cariani, M. Conese, G. Döring, and A. Bragonzi. 2007. Biological cost of hypermutation in *Pseudomonas aeruginosa* strains from patients with cystic fibrosis. Microbiology 153:1445–54.

Moore, F. B.-G., and S. J. Tonsor. 1994. A Simulation of Wright’s Shifting-Balance Process: Migration and the Three Phases. Evolution 48:69.

Obolski, U., and L. Hadany. 2012. Implications of stress-induced genetic variation for minimizing multidrug resistance in bacteria. BMC Med. 10:1–30.

Peck, S. L., S. P. Ellner, and F. Gould. 2000. Varying migration and deme size and the feasibility of the shifting balance. Evolution 54:324–7.

Ponder, R. G., N. C. Fonville, and S. M. Rosenberg. 2005. A switch from high-fidelity to error-prone DNA double-strand break repair underlies stress-induced mutation. Mol. Cell 19:791–804.

Pupo, G. M., and B. J. Richardson. 1995. Biochemical genetics of a natural population of *Escherichia coli*: seasonal changes in alleles and haplotypes. Microbiology 141:1037–44.

Ram, Y., and L. Hadany. 2012. The evolution of stress-induced hypermutation in asexual populations. Evolution 66:2315–28.

Rodriguez, G. P., N. V Romanova, G. Bao, N. C. Rouf, Y. W. Kow, and G. F. Crouse. 2012. Mismatch repair-dependent mutagenesis in nondividing cells. Proc. Natl. Acad. Sci. 109:6153–8.

Rosenberg, S. M., C. Shee, R. L. Frisch, and P. J. Hastings. 2012. Stress-induced mutation via DNA breaks in *Escherichia coli*: A molecular mechanism with implications for evolution and medicine. BioEssays 1–8.

Schrag, S. J., V. Perrot, and B. R. Levin. 1997. Adaptation to the fitness costs of antibiotic resistance in *Escherichia coli*. Proc. Biol. Sci. 264:1287–91.

Sharp, N. P., and A. F. Agrawal. 2012. Evidence for elevated mutation rates in low-quality genotypes. Proc. Natl. Acad. Sci. 109:6142–6.

Shaw, F. H., and C. F. Baer. 2011. Fitness-dependent mutation rates in finite populations. J. Evol. Biol. 24:1677–84.

Shee, C., J. L. Gibson, M. C. Darrow, C. Gonzalez, and S. M. Rosenberg. 2011. Impact of a stress-inducible switch to mutagenic repair of DNA breaks on mutation in *Escherichia coli*. Proc. Natl. Acad. Sci. 108:13659–13664.

Shor, E., C. a. Fox, and J. R. Broach. 2013. The yeast environmental stress response regulates mutagenesis induced by proteotoxic stress. PLoS Genet. 9:e1003680.

Smith, J. M., and J. Haigh. 2009. The hitch-hiking effect of a favourable gene. Genet. Res. 23:23.

Sniegowski, P. D., P. J. Gerrish, T. Johnson, and A. Shaver. 2000. The evolution of mutation rates: separating causes from consequences. BioEssays 22:1057–66.

Sniegowski, P. D., P. J. Gerrish, and R. E. Lenski. 1997. Evolution of high mutation rates in experimental populations of E. coli. Nature 387:703–5.

Taddei, F., M. Radman, J. Maynard Smith, B. Toupance, P.-H. Gouyon, and B. Godelle. 1997. Role of mutator alleles in adaptive evolution. Nature 387:700–2.

Tenaillon, O., E. Denamur, and I. Matic. 2004. Evolutionary significance of stress-induced mutagenesis in bacteria. Trends Microbiol. 12:264–70.

Tenaillon, O., H. Le Nagard, B. Godelle, and F. Taddei. 2000. Mutators and sex in bacteria: conflict between adaptive strategies. Proc. Natl. Acad. Sci. 97:10465–70.

Tenaillon, O., B. Toupance, H. Le Nagard, F. Taddei, and B. Godelle. 1999. Mutators, population size, adaptive landscape and the adaptation of asexual populations of bacteria. Genetics 152:485–93.

Torres-Barceló, C., G. Cabot, A. Oliver, A. Buckling, and R. C. MacLean. 2013. A trade-off between oxidative stress resistance and DNA repair plays a role in the evolution of elevated mutation rates in bacteria. Proc. Biol. Sci. 280:20130007.

Wade, M. J., and C. J. Goodnight. 1991. Wright’s shifting balance theory: an experimental study. Science 253:1015–8.

Weinreich, D. M., and L. Chao. 2005. Rapid evolutionary escape by large populations from local fitness peaks is likely in nature. Evolution 59:1175–82.

Weissman, D. B., M. W. Feldman, and D. S. Fisher. 2010. The rate of fitness-valley crossing in sexual populations. Genetics 186:1389–410.

Whitlock, M. C. 1997. Founder effects and peak shifts without genetic drift: adaptive peak shifts occur easily when environments fluctuate slightly. Evolution 51:1044.

Whitlock, M. C. 1995. Variance-induced peak shifts. Evolution 49:252.

Whitlock, M. C., and P. C. Phillips. 2000. The exquisite corpse: a shifting view of the shifting balance. Trends Ecol. Evol. 15:347–348.

Wielgoss, S., J. E. Barrick, O. Tenaillon, S. Cruveiller, B. Chane-Woon-Ming, C. Médigue, R. E. Lenski, and D. Schneider. 2011. Mutation rate inferred from synonymous substitutions in a long-term evolution experiment with *Escherichia coli*. G3 1:183–186.

Wielgoss, S., J. E. Barrick, O. Tenaillon, M. J. Wiser, W. J. Dittmar, S. Cruveiller, B. Chane-Woon-Ming, C. Medigue, R. E. Lenski, and D. Schneider. 2012. Mutation rate dynamics in a bacterial population reflect tension between adaptation and genetic load. Proc. Natl. Acad. Sci. 110:222–227.

Wright, S. 1931. Evolution in Mendelian Populations. Genetics 16:97–159.

Wright, S. 1988. Surfaces of selective value revisited. Am. Nat. 131:115–123.

# Appendices

## Appendix 1

In the following analysis we assume that and – see model overview for details. This also means that and . The probability *q* that a random offspring in the next generation is *AB* given there are no *AB* in the current generation can be approximated by:

.

Using the above assumptions, this resolves to:

.

Taking the derivative with respect to *U* and denoting (*g* can be thought of as the number of non-specific loci in the genome):

.

So *q* increases with *U* because the right hand side is guaranteed to be true under the assumption .

For a population with SIM:

.

The last approximation assumes that *.* Rearranging the last result, we find the approximation:

|  |  |
| --- | --- |
| . |  |

Taking the derivative with respect to *τ*:

,

because *q*, *U*, and *τ* are all positive. So the condition guarantees that *qSIM*increases with *τ*, and it is also sufficient for (not shown).

## Appendix 2

Following Eshel (1981), the fixation probability *ρ* of the double mutant *AB* is:

,

where *α* is the fitness of the double mutant relative to the population mean fitness and assuming that fitness is measured by the average number of progeny which is Poisson distributed:

.

Here, we only consider progeny without new deleterious mutations – their fraction is *e-U*. This factor cannot be ignored because there is variation in mutation rates within the population. At this stage, double mutants are still very rare, so we can use the population mean fitness at the MSB.

The mean fitness can be approximated by (see *supporting information*). Therefore:

Assuming *sH* is small () we can approximate this by:

.

## Appendix 3

With SIMe the mutation rate of *ab* is *τU* while that of *AB* is only *U*. We assume the population reached a MSB before the fixation of *AB* because convergence to MSB is much faster than adaptation (Gordo and Dionisio 2005). Following the derivation in Appendix 2 (also see a technical note by Johnson and Barton (2002)), we calculate the relative fitness of SIMe by:

.

Plugging that in the fixation probability:

.

This can be simplified by a 1st order approximation for :

.

Because , the right hand side is greater than 1 and therefore:

.

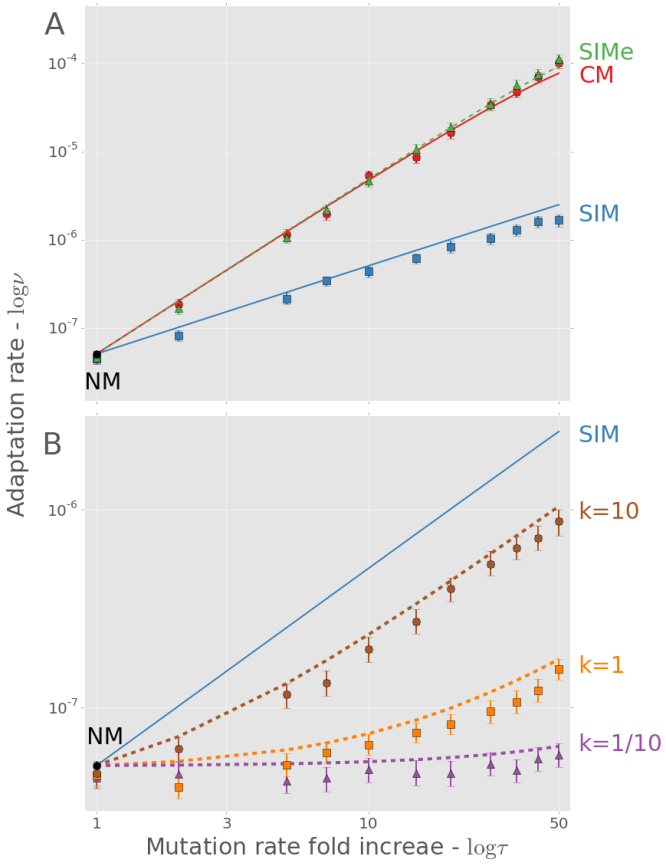
Because the appearance with SIMe is the same as with CM, the adaptation rate with SIMe can be written as:

.

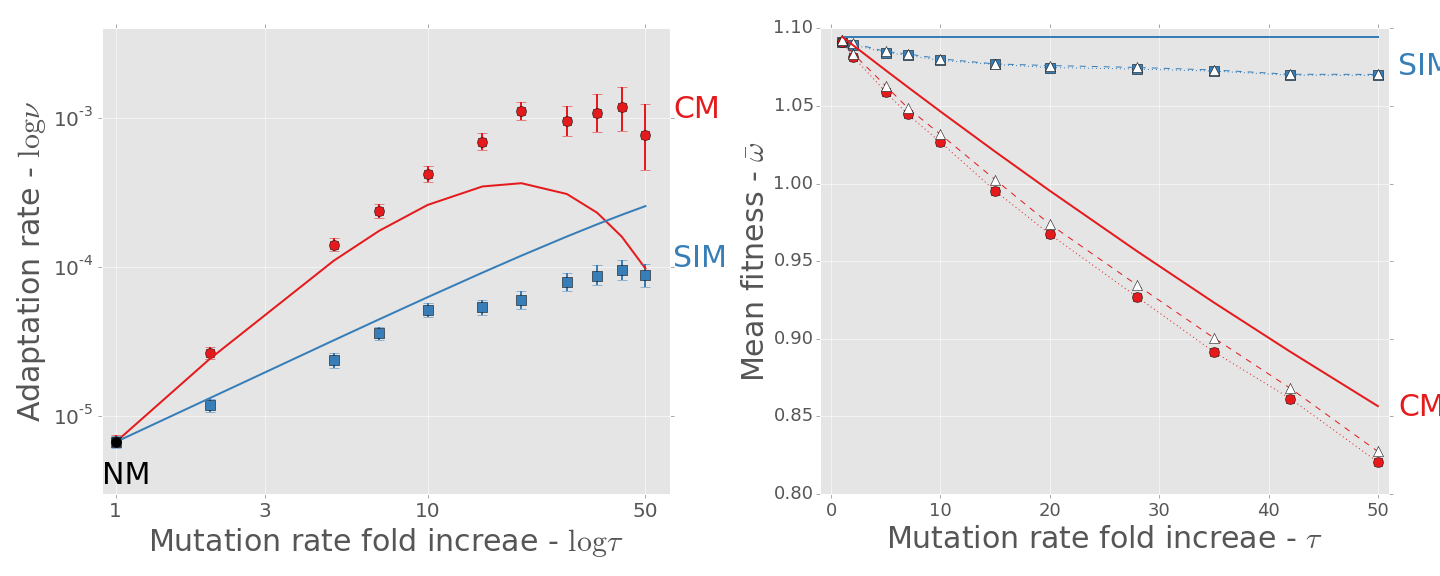
# Figure legends

**D:\workspace\ruggedsim\manuscript\ram_f1.tif**

**Figure 1 – Adaptation on a complex fitness landscape.** Nodes represent genotypes: the alleles *a* or *A* and *b* or *B*. Panel B also includes the number of deleterious alleles across the genome after the forward-slash ('/'). Node brightness represents fitness (see color bar): the fittest genotype, *AB/*0, is white; darker nodes represent genotypes with deleterious alleles, either at the *A/a* and *B/b* loci or at the non-specific loci. Solid arrows represent mutations at the *a/A* and *b/B* loci. Dashed arrows represent deleterious mutations in the rest of the genome. Arrow labels denote the baseline mutation rates without mutagenesis effects. Mutagenesis is induced in stressed genotypes, presented as ellipses (fitness <1). Fit genotypes, presented as squares, (fitness ≥1) do not hypermutate. **(A)** In the analytic model genotypes with deleterious alleles in non-specific loci are considered "evolutionary dead-ends" (marked with RIP) and do not contribute to adaptation. **(B)** In the simulations individuals can accumulate up to 25 deleterious alleles (the figure only shows as much as three). Multiple mutations can occur simultaneously but are not shown for simplicity of the illustration.

****

**Figure 2 – Complex adaptation with different mutational strategies.** The figure shows the adaptation rate *ν* as a function of the mutation rate increase *τ* (both in log scale). **(A)** NM (*τ*=1 and a black circle) is normal mutagenesis; CM (solid lines & circles) is constitutive mutagenesis; SIM (solid lines & squares) is stress-induced mutagenesis; SIMe (dashed lines & triangles) is stress-induced mutagenesis with environmental stress (see section 3.5). Lines are analytic approximations; markers are the means of stochastic simulations results; error bars represent 95% confidence interval of the mean (at least 1,000 replicates per point; computed with bootstrap with 1,000 samples per point). Parameters (see Table 1): *U*=0.0004, *s*=0.05, *β*=0.0002, *H*=2, *N*=106. **(B)** Markers are the results of adaptation with SIM with different continuous relationships between fitness and mutation rate, defined by a curvature parameter *k* and mutation rate fold increase *τ*=10 (see section ‎3.4 and Figure S3)**.** Each dashed line is an analytic approximation of the continuous SIM next to it, using a SIM strategy with a threshold relationship (eq. 13) and with *τ*=4.61, 1.45, and 1.05, top to bottom.

****

**Figure 3 – Adaptation with strong mutation.** When the deleterious mutation rate is high – here *U=s/10* – the adaptation process can lead to hitch-hiking of deleterious alleles with the beneficial double mutant. **(A)** The adaptation rate *ν* as a function of the mutation rate increase *τ* (both in log scale). NM (*τ*=1 and a black circle) is normal mutagenesis; CM (top line and circles) is constitutive mutagenesis; SIM (bottom line and squares) is stress-induced mutagenesis. Lines are analytic approximations; markers are the means of stochastic simulations results; error bars represent 95% confidence interval of the mean (at least 1,000 replicates per point; computed with bootstrap with 1,000 samples per point). Parameters (see Table 1): *U*=0.005, *s*=0.05, *β*=0.0002, *H*=2, *N*=106. **(B)** The population mean fitness after successful fixation of the dobule mutant as a function of the mutation rate increase *τ*. Solid lines are analytic approximations neglecting adaptation from deleterious background *(e-τU*(1+*sH*)); dotted lines with filled squares (SIM) and circles (CM) are the means of stochastic simulation results; dashed lines with white triangles are predictions based on the genotype on which *AB* appeared in the simulations, including MSB but disregarding the effects of drift during the fixation process (which only has a significant effect on CM due to higher mutation rates in the wildtype). Error bars are too small to see. Same paramters as in panel A.



**Figure 4 – The trade-off between *adaptedness* and *adaptability*.** The figure shows the relative *adaptedness* and the relative *adaptability* of different mutational strategies in comparison to normal mutagenesis (NM). *Adaptedness* is defined by the population mean fitness at MSB, (see *supporint information*). *Adaptability* is defined by the adaptation rate, (eqs. 6-8). Constitutive mutagenesis (CM) increases the mutation rate of all individuals *τCM*-fold; Stress-induced mutagenesis (SIM) increases the mutation rate of stressed individuals *τSIM*-fold; Mixed strategies (dashed line; see section 3.4) increase the mutation rate of all individuals *τCM*-fold and of stressed individuals another *τSIM*-fold. SIM breaks off the *adaptability-adaptedness* trade-off of CM, increasing the *adaptability* without compromising the *adaptedness* of the population. Parameters (see Table 1): *N*=106, *U*=­0.0004, *β*=0.0002, *s*=0.05, *H*=2, *τ*<<s/*U*.



Figure 5 – Direct competitions between three mutational strategies. The figure shows the average final frequency of (from right to left): stress-induced mutagenesis (SIM) vs. constitutive mutagenesis (CM); CM vs. normal mutagenesis (NM); SIM vs. NM; and NM vs. NM (control). Initial frequencies are always 0.5. For each strategy several mutation rate fold increases are shown on the x-axis. SIM defeats CM and is significantly advantageous over NM when τ>2 (2-tail t-test, P<0.0015). CM losses to NM and SIM (P≈0). Therefore, SIM is favored by selection over both NM and CM. Changing roles between resident and invader didn't affect the results (not shown). Error bars represent the standard error of the mean (500 replicates per point). Parameters (see Table 1): *U*=0.0004, *s*=0.05, *β*=0.0002, *H*=2, *N*=106.

# Tables

Table 1 – Model parameters and estimated values for *E. coli*

|  |  |  |  |
| --- | --- | --- | --- |
| Symbol | Name | Estimate | References |
| *s* | Selection coefficient | 0.001-0.03 | (Kibota and Lynch 1996; Gordo et al. 2011) |
| *H* | Double mutant advantage | 1-10 | (Gordo et al. 2011) |
| *U* | Genomic deleterious mutation rate | 0.0004-0.003 | (Drake et al. 1998; Wielgoss et al. 2011) |
| *µ* | Site-specific mutation rate | *U*/5000 | (Gordo et al. 2011) |
| *τ* | Fold-increase in mutation rate | 1-100 | (Bjedov et al. 2003; Hall and Henderson-Begg 2006) |
| *N* | Population size | 105-1010 | (Pupo and Richardson 1995; Berg 1996) |

­­­