Adaptive peak shifts with stress-induced mutation

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# Introduction

In 1931, Sewall Wright presented a problem which is still an open problem in evolutionary biology (Wright 1931). Given that the selective value of many alleles depends on other alleles, Wright suggested that "Two superior combinations that differ by two or more gene replacements may both be superior to the intermediate ones" (Wright 1988). The solution Wright suggested was called the "shifting-balance theory" [REF] and is still taught today in many "Introduction to Evolution" courses. This solutions appears to be valid (Crow et al., 1990; Wade and Goodnight, 1991; Coyne et al., 1997) but it seems that the range of parameters for which it works is limited (Moore and Tonsor, 1994; Gavrilets, 1996; Phillips, 1996).

Mutation is a major factor in this process: It creates the new alleles which later fix. If creating new favorable alleles was the only effect of mutation on evolution, a high mutation rate would have been very favored, but of course most mutations are deleterious and the mutation rate is reduced by natural selection to very low levels (Kimura 1967; Lynch 2011).

However, stress-induced mutation, in which stressed individuals increase their mutation rates, is an exception to this rule. In a previous work we have shown that stress-induced mutation is likely to evolve due to natural selection in asexual populations and that it increases the mean fitness of populations due to the increased generation of beneficial mutations in unfit individuals. Additionally, stress-induced mutation has been demonstrated in various species, both prokaryote and eukaryote (Galhardo, Hastings, and Rosenberg 2007; Sharp and Agrawal 2012; MacLean, Torres-Barceló, and Moxon 2013).

Here, we analyze a simple population genetic model of an asexual population with two bi-allelic loci. We derive analytical expressions that suggest that stress-induced mutation greatly increases the population adaptation rate. We use stochastic simulations to validate our analytic approximations.

# Model

Consider the two bi-allelic loci *A/a* and *B/b* and a population that reached a mutation-selection balance (MSB) in an environment in which *ab* is the optimal genotype with a fitness value of 1, single mutants (*Ab* and *aB*) suffer from a selective disadvantage *s* and have a fitness value of *1-s*, and double mutants (*AB)* have a fitness value of *(1-s)2*. This corresponds to a fitness function in which the effect of deleterious mutations are independent of each other and therefore the fitness of an individual is *(1-s)m* where *m* is the number of deleterious mutations the individual has accumulated.

Mutation from *a* to *A* and from *b* to *B* occurs with a probability *µ* at reproduction and we disregard back-mutation. In addition, new deleterious mutations occur across the genome at reproduction, and the number of such mutations follows a Poisson distribution with a mean *U*. Although there is a direct relation between *U* and *µ* (for example, *µ=U/5000*), having two separate parameters helps to distinguish between the two effects of mutation on adaptive evolution – the generation of beneficial mutations (*µ*) and the generation of deleterious mutations (*U*).

We define stress-induced mutation as the case in which an individual with a fitness below 1 hypermutates, increasing both his mutation rates *τ*-fold.

At the MSB, the frequency of wildtype (*ab*) individuals is *1-µ/s+O(µ2)*, the frequency of single mutants (*Ab* and *aB* combined) is *2µ/s+O(µ2)* and the frequency of double mutants (*AB*) is (*µ/s)2+O(µ3)* [REF].

To incorporate random sampling into the model, we denote the population size by *N*.

We are interested in the ability of the population to adapt to a new environment in which the genotype *AB* inhabits a new adaptive peak with a fitness value of *1+sH*, where *H* scales the height of the new peak in comparison with the existing peak at *ab*.

## Constrains on the parameter space

There are several considerations on the relations between the main parameters:

1. The above MSB approximations are only valid when *µ/s<1* or *µ<s*.
2. If *N*(*µ/s)2>1* there are already double mutants and therefore adaptation to the environmental change will be rapid and will not require new mutations.
3. If *Nµ/s<1* then there are no single mutants and double mutatns must be generated by a double mutation in a wild-type individual. Therefore, increasing the mutation rate of individuals with fitness below 1 will have a much smaller effect than if single mutants were abundant.
4. If we assume that individuals loaded with deleterious mutations are "evolutionary dead-ends" and cannot be the origin of adaptation, then the fraction of loaded individuals must be small - *U/s<1*. This replaces the above condition (1) because we expect that *µ* is much smaller than *U*.

Summarizing the above requirements for stress-induced mutation to have an effect on adaptation in this model we get:

|  |  |
| --- | --- |
|  | (1) |
|  | (2) |

For the bacteria species *Escherischia coli* estimations of the selection coefficient and mutation rates are *s=0.01* (Kibota and Lynch 1996), *U=0.0004* (Wielgoss et al. 2011) and *µ =8⋅10-8* (Gordo, Perfeito, and Sousa 2011) which yield a fairly reasonable constraint on the population size - *1.25⋅105 ≤ N ≤ 1.5⋅1010*.

## Appearance of a double mutant

Assuming (3), there are no double mutants (*AB*) at the time of the environmental change. New double mutants can appear either via a double mutation in a wildtype individual (*ab*) or via a single mutation in a single mutant (*Ab* or *aB*). At the MSB the number of deleterious mutations follows a Poisson distribution (Haigh 1978). Therefore, the frequencies of mutation-free wildtype and single mutants are roughly and . The fitness of wildtype and single mutants is 1 and *1-s*, respectively. We assume that individuals with mutations other than in the *A/a* and *B/b* loci are "evolutionary dead ends". Assuming that mutation is a Poisson process, only a fraction of the individuals are of interest. All together, the probability that a newborn is a double mutant can be summarized by:

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

However, if mutation is stress-induced, then the mutation rate of single mutants is increased *τ*-fold and the above probability is:

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

Note that stress-induction only increases the transition from single mutants to other types, but does not change the MSB frequency of single mutants, because that is determined by the mutation rate of the wildtype.

If the mutation rate of wildtype is increased as well, as in the case of constitutive hypermutation, the probability changes to

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

because increased mutation rate in the wildtype affects the MSB frequencies.

The probability that a double mutant would appear a population is . The condition (2) guarantees that *Nq* is very small, and therefore this probability can be approximated by using the Binomial series expansion.

The waiting time for the appearance of a double mutant follows a geometric distribution and therefore the expected time for the appearance of a double mutant in a population without double mutants is:

|  |  |
| --- | --- |
|  | (6) |

## Fixation of a double mutant

Assuming that the advantage of the double mutant is considerable (for example, *H>1)* it has two possible fates after its appearance: fixation and extinction. Following Eshel (1981) the fixation probability of the double mutant is

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| --- | --- |
|  | (7) |

where *α* is the relative fitness of the double mutant normalized by the population mean fitness:

|  |  |
| --- | --- |
|  | (8) |

and assuming that fitness is measured by the number of progeny which is Poisson distributed.

Because the frequency of double mutants is very low at the stage where they are subject to possible extinction by drift, the population mean fitness can be calculated without considering them, so the value we use is the mean fitness of the population at the MSB. Without stress-induced mutation, this evaluates to (Kimura and Maruyama 1966). Therefore, and [REF].

However, as we have shown before (Ram and Hadany 2012), the mean fitness of a population with stress-induced mutation can be different this value if beneficial mutations are allowed. Here, the mean fitness with stress-induced can be calculated by separating the population to the wildtype fraction which has fitness 1 and the non-wildtype fraction . Within the non-wildtype subpopulation, which have at least one mutation, additional mutations are Poisson distributed with expectation because this subpopulation is hypermutating. Therefore the mean fitness of this subpopulation is . Taken together, the mean fitness of a population with stress-induced mutation is

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

Pluging this in (7) and (8) gives a different fixation probability for populations with stress-induced mutation:

|  |  |  |  |
| --- | --- | --- | --- |
|  | (9) |  | (10) |