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The effect of selection history on extinction risk during severe environmental change

Josianne Lachapelle¹²*, Nick Colegrave² and Graham Bell³

¹ Department of Biology, University of Toronto Mississauga, William G. Davis Building, 3359 Mississauga Road, Mississauga, Ontario, Canada L5L 1C6
² School of Biological Sciences, University of Edinburgh, King’s Buildings, Ashworth Laboratories, Charlotte Auerbach Road, Edinburgh, UK EH9 3FL
³ Department of Biology, McGill University, Stewart Biology Building, Montreal, Quebec, Canada H3A 1B1

*Corresponding author
josianne.lachapelle@utoronto.ca
Tel +1 416 662 2077
Fax +1 905 828 3792

Running head: Selection history and extinction risk
Abstract
Environments rarely remain the same over time, and populations are therefore frequently at risk of going extinct when changes are significant enough to reduce fitness. While many studies have investigated what attributes of the new environments and of the populations experiencing these changes will affect their probability of going extinct, limited work has been directed toward determining the role of population history on the probability of going extinct during severe environmental change. Here we compare the extinction risk of populations with a history of selection in a benign environment, to populations with a history of selection in one or two stressful environments. We exposed spores and lines of the green alga *Chlamydomonas reinhardtii* from these three different histories to a range of severe environmental changes. We found that the extinction risk was higher for populations with a history of selection in stressful environments compared to populations with a history of selection in a benign environment. This effect was not due to differences in initial population sizes. Finally, the rates of extinction were highly repeatable within histories, indicating strong historical contingency of extinction risk. Hence, information on the selection history of a population can be used to predict their probability of going extinct during environmental change.

Keywords: Evolutionary rescue, historical contingency, stressor, repeatability, *Chlamydomonas reinhardtii*
**Introduction**

Determining what factors favour survival is critical for predicting the outcome of severe environmental changes. We know from experiments that the probability of survival is higher in larger populations (Willi & Hoffmann, 2009; Bell & Gonzalez, 2009), with higher amounts of genetic variation (Agashe et al., 2011; Lachapelle & Bell, 2012), immigration (Bell & Gonzalez, 2011; Lagator et al., 2014b), and lower rates of environmental change (Perron et al., 2008; Bell & Gonzalez, 2011; Lindsey et al., 2013). However, lineages also differ in the number and type of environmental changes they have survived in the past. We tested whether a history of selection in stressful environments, compared to selection in a benign environment, affects extinction risks during further environmental change.

In the context of this report, a stressful environment is one that severely reduces fitness to the point of population decline and possibly extinction. A benign environment is one where population survival is not at risk. A stressful environment can become benign once a population successfully adapts to it, and similarly a previously benign environment can become a stressful environment after evolution in another environment. A history of selection in stressful environments, compared to selection in a benign environment, might affect extinction risks if it consistently affects evolvability or costs of adaptation (Colegrave & Collins, 2008). For example, history can affect the ability of a population to respond to natural selection by favouring genes that constitutively increase the genomic mutation rate (Shaver et al., 2002) or modulate the mutation rate (Metzgar & Wills, 2000; Erill et al., 2006), and hence increase the supply of variation; by favouring mechanisms
that promote gene exchange or recombination such as conjugation, viral infection (Poon & Chao, 2004), and sex (Colegrave, 2002; Lachapelle & Bell, 2012; McDonald et al., 2016); or by changing the type of interactions between genes to promote a more modular genome (Weinreich et al., 2006; Colegrave & Collins, 2008). History can also affect evolvability through differences in the proportion of beneficial mutations that arise because of changes in the distribution of fitness effects of mutations. For example, in rugged landscapes, the probability of jumping from one fitness peak to another decreases as the population climbs a peak because the probability of a mutation with effect size large enough to make the jump decreases (Buckling et al., 2003). Hence specialisation in one environment can reduce the ability to diversify and consequently thrive in other environments.

Evolutionary history may also affect extinction risks if it mediates costs of adaptation through pleiotropy or mutation accumulation. For example, alleles favoured in one environment can have negative impacts on fitness in other environments through antagonistic pleiotropy (MacLean et al., 2004) and therefore lower the probability of survival during environmental change. Similarly, mutations with neutral effects in the current environment but deleterious effects in the new environment can accumulate over time (Kawecki, 1994; Fry, 1996) and lower the probability of survival during environmental change. On the other hand, alleles favoured in one environment can have positive impacts on fitness in other environments through positive pleiotropy, such as when the evolution of resistance to the current stressor indirectly increases resistance to a range of other stressors (Walley et al., 1974; Trindade et al., 2009; Ward et al., 2009;
It remains unclear whether a history of environmental stress will increase or decrease the probability of extinction during severe environmental change. We make use of a unique set of experimental populations of *C. reinhardtii* that have survived and adapted to two back-to-back stressful environments in the laboratory to study the effect of selection history on extinction risks, and on variance among populations and individuals within these populations in extinction risk. We sampled from different time points in the history of these populations: before exposure to any stressful environments, after survival and adaptation to the first stressful environment (i.e. the dark), and after survival and adaptation to the second stressful environment (i.e. high salt). We exposed the populations from each time point to each of the three selection environments, as well as to a range of different novel environments. We compared population density and extinction rates across and within time points to determine if selection history affects the overall response to environmental change as well as the variability in responses. In our experiment, previous selection shapes the amount of standing genetic variation and its relevance to survival after any possible change in the environment. Hence, evolutionary rescue (i.e. survival) occurs not as direct result of evolution in the novel environments, but as a correlated response to selection in the previous environment.

**Materials and Methods**
Selection history

The selection history of the lineages used in this experiment is depicted in Figure 1. In 1997, experimental lines of the unicellular green alga *Chlamydomonas reinhardtii* were set-up using spores from a cross among standard laboratory strains (CC-124 x [CC-1952 x (CC-1952 x CC-2343)]). Four types of lines were set-up as described in Bell (2005): sexual mass-transfer (obligately sexual propagated by many zygotes); sexual single-zygote (obligately sexual propagated by single zygote); unselected (sexual lines where unmated cells are not killed at transfer); and asexual (obligately asexual lines propagated en masse). These lines were propagated on Bold’s minimal medium solidified with agar, phototrophically in the light. We refer to them as the light lines or L. They have been evolving in a benign environment in one of our laboratories for about 20 years.

A decade later, three of the sexual mass-transfer L lines were used to initiate 2880 lines which were propagated in the dark in Bold’s minimal medium supplemented with 1.2 gL⁻¹ sodium acetate as described in Bell (2012). Only 241 lines (8.4%) survived. We refer to these lines as the LD lines, for light then dark, and they have survived and adapted to one stressful environment.

In 2011, forty of the LD lines were used to initiate 96 salt lines which were propagated in steadily increasing concentrations of NaCl as described in Lachapelle and Bell (2012) and Lachapelle *et al.* (2015). Ten lines are now surviving in 36 gL⁻¹ NaCl. We refer to these lines as the LDS lines, for light then dark then salt, and they have survived and
adapted to two back-to-back stressful environments, first the dark, then a reversion to light with no acetate and added salt (Figure 1).

**Extinction assay**

We isolated four spores from each of five lines from each of the three histories. Since there are only three ancestral lines for the LD lines, we used the three ancestral lines (i.e. sexual mass-transfer lines) as well as two of the asexual L lines, which have been propagated in parallel. We chose to use the asexual L lines as opposed to the single zygote or unselected lines because the asexuals have been propagated en masse like the sexual mass-transfer lines, and to avoid the ambiguity of the unselected lines, which by being facultative sexuals, have an unclear history in terms of how much of the progeny is recombinant and how much clonal. Each spore was assayed three times, in each of six environments for a total of 1080 cultures. To determine if there has been a direct response to selection, that is if spores from a given selection history have a lower probability of going extinct and a higher yield in their selection environment than spores from other selection histories, we assayed the spores in the three selection environments, i.e. Bold’s minimal liquid media (referred to as ‘Bolds’; (Harris, 2009); Bold’s supplemented with 1.2 gL$^{-1}$ sodium acetate and maintained in the dark (referred to as ‘Dark’); Bold’s supplemented with 20 gL$^{-1}$ NaCl (referred to as ‘NaCl’). The growth of the L and LD lines in NaCl does not itself represent a direct response to selection, as they have not been selected in NaCl. The direct response is usually determined by comparing the fitness of evolved lines to the fitness of their ancestors. Here the L and LD lines therefore serve as the ancestors to which to compare the fitness of the LDS lines. To determine the indirect
response to selection, that is consequence of selection in one environment on the
probability of going extinct and the yield in other environments, we assayed the spores in
three novel environments, i.e. Bold’s media supplemented with 0.4M Atrazine, a
herbicide (referred to as ‘Atrazine’); Bold’s supplemented with 0.1 µM CuSO₄ (referred
to as CuSO₄); and Bold’s buffered to pH4 with a phosphate solution (0.43 gL⁻¹ Na₂HPO₄
+ 3.36 gL⁻¹ KH₂PO₄; referred to as pH4). All cultures were grown phototrophically in the
light, except in the Dark environment where all growth had to be heterotrophic.

The concentrations used for the three novel environments Atrazine, CuSO₄, and pH4
were determined by running preliminary growth assays with six wild-type strains (CC-
1690, CC-1952, CC-2342, CC-2344, CC-2931, CC-2937). The use of wild-type strains in
these preliminary assays ensured that the choice of concentration was independent of the
biological material used in the extinction assay. The wild-type strains were grown in a
range of different concentrations of Atrazine, CuSO₄ and pH, and the concentration that
reduced cell densities to just above the detection limit of the spectrophotometer after two
growth cycles was chosen. This ensured that the concentration was severe enough to
reduce growth, but would not lead to immediate extinctions (which would limit our
ability to detect variance in extinction risk).

To start the extinction assay each spore was grown from a single colony into a population
in its home environment (i.e. L lines in Bold’s, LD lines in Dark, LDS lines in NaCl). We
chose to grow the spores into different environments because we could find no single
common environment that would not severely disfavour the growth of one history over
that of the others. The populations were therefore isogenic at the start of the assays except for any mutation that would have arisen during the growth of the single colony into a population (about four generations). After one cycle of growth, the spores were transferred to all six assay environments. Cultures were then serially transferred once every 7 days by diluting 10 µL of culture into 190 µL fresh media in 96-well plates. To maintain a constant size a population therefore needs to undergo about 4.3 divisions over a week. The cultures were incubated at 26 degrees Celsius, 60% air humidity, and 7150 Lux constant light intensity.

At the end of each growth cycle, every culture was inspected using an inverted microscope to record the presence or absence of living cells. A culture was deemed extinct if the absence of living cells was recorded for two cycles in a row. The cell density was also estimated at the end of each growth cycle by measuring the optical density at 750 nm with a spectrophotometer. The assay was terminated after 11 cycles (about 55 generations) or later in the case of some environments, whenever the number of extinctions had stabilised for two cycles and none of the cultures were on the brink of extinction.

Statistical analyses
All analyses were done in R version 3.2.1. We examined the effect of selection history on extinction in two different ways. First, the extinction dynamics, i.e. the proportion of lines alive over time, were analysed by performing survival analyses using Cox proportional hazards with mixed effects, which assume Gaussian random effects, with the
‘coxme’ R package (Therneau, 2015). In all models we included a ‘Censor’ variable for spores that had not gone extinct by the end of the assay. Second, the extinction risk, i.e. the proportion of lines extinct by the end of the experiment, was analysed by computing two-tailed Fisher’s exact tests for independence of number of extinction events and selection history in a contingency table. We report both survival analyses and Fisher’s exact test results except in assay environments where the survival analysis could not be fitted, i.e. in cases where extinctions did not occur in all selection histories. This is because proper model fitting requires at least one event to have occurred in each level of the fixed factor. In those cases, we report only the extinction risk.

Yield of surviving spores at the end of the assay was analysed by fitting mixed effect models using the lmer function in the R package ‘lme4’ (Bates et al., 2015). Our estimate of yield is the optical density at the end of the extinction assay (cycle 11) when populations had stabilised. While the assay lasted more than 11 cycles in some environments, we decided to use the yield at the end of cycle 11 to be consistent across all environments. P values were obtained using the R package ‘lmerTest’ (Kuznetsova et al., 2014) with type III sum of squares in an analysis of variance and Satterthwaite approximation for degrees of freedom by using the normal approximation.

More precisely, we divided our analyses into two sections: the direct response to selection and the indirect response to selection. First, to determine if in a given environment, there are fewer extinctions in the selection history most recently selected in that environment than in the other selection histories, we compared the extinction risk
and extinction dynamics of the three selection histories in each selection environment (i.e. Bold’s, Dark, NaCl). That is we fitted a coxme survival model with selection history as a fixed factor, and line and spore within line as random factors. The model was applied to each environment individually. To determine if in a given environment, yield is higher for the selection history most recently selected in that environment than for the other selection histories, we fitted a mixed effects model with selection history as a fixed factor, and line and spore within line as random factors.

Second, to determine if past selection in a stressful environment affects the extinction risk and the dynamics of extinction in novel environments compared to selection in a benign environment, we computed Fisher’s tests and fitted a coxme survival model with selection history as a fixed factor, and assay environment, line, and spore within line as random factors. Only the three novel environments (Atrazine, CuSO₄, pH4) are included in this model. All the novel environments we used had constant lighting and no acetate. Therefore, unlike the L lines and LDS lines, the extinction risk of the LD lines will not only include the general extinction risk due to selection in a stressful environment, but also a special risk associated with the presence of light and lack of acetate. To estimate the general extinction risk of the LD lines we assumed that the effects of novel stressful compounds is additive to the effects of constant light and no acetate (i.e. measured risk = general risk + special risk), which has been shown to be a reasonable assumption in the case of NaCl (Lachapelle et al., 2015). More precisely, we calculated \[1 - (\text{proportion of LD lines alive in Bold’s at time } t - \text{proportion of LD lines alive in novel environment } x \text{ at time } t)\]. From this corrected proportion of lines alive, back calculated the corrected time
of extinction. That is, we multiplied the corrected proportion of lines alive by 20 (total number of cultures) to get \( n \), the corrected absolute number of lines alive at each time point. We created a new data set with \( n \) rows for lines alive followed by \((20 - n)\) rows for lines extinct. We assigned a number from 1 to 20 to each row. For each line number, we counted the number of time points where the line was alive, and used that number as the corrected time of extinction. Finally, given that the order in which lines go extinct after correction is the same as before correction since the correction is simply a subtraction, we matched the initial and corrected datasets after ordering them by time of extinction to obtain the actual line and replicate number. We report the corrected extinction risk as the general extinction risk in the analyses of the extinction risk in the novel environments.

To determine if yield of surviving spores in novel environments differs between selection histories, we fitted a mixed effects model for each novel environment with selection history as a fixed factor, and line and spore within line as random factors.

Finally, to estimate variance in the dynamics of extinction in novel environments, we fitted a coxme survival model for each selection history with line, spore within line, environment (including only the novel environments Atrazine, CuSO\(_4\), and pH4), the combination of line and environment, the combination of spore and environment, as random factors. Note that the coxme function does not accept interaction terms for the random factors, and therefore we created two new variables by pasting line and environment or spore and environment together. Similarly, variance in yield of surviving lines in novel environments was compared among selection histories using a lmer model.
with assay environment (including only the novel environments Atrazine, CuSO₄, pH4), line, spore within line, the interaction between line and assay environment, and the interaction between spore and environment as random factors. The significance of the differences in variance between selection histories was determined using F ratios. The degrees of freedom were calculated based on an analysis of variance model.

Results

Selection reduces extinction risk in most recent environment

To measure the direct response to selection we did a reciprocal transplant, growing the three selection histories in all three selection environments (Figure 2; Figure 4; Table 1). A direct response is detected if spores from a given selection history have a lower extinction risk and higher yield in their selection environment than spores from other selection histories.

In the Dark environment, none of the LD lines go extinct, while on average 67% and 70% of L lines and LDS lines, respectively, go extinct. As such, selection in the Dark has significantly lowered extinction risk (LD line to L line comparison using Fisher’s exact test: $P = 7.3 \times 10^{-17}$; LD line to LDS line comparison using Fisher’s exact test: $P = 4.4 \times 10^{-18}$). The extinction risk of the LDS line is no different from that of the L lines ($P = 0.84$). Also, the LD lines reach higher yield than the surviving L lines ($t_{12} = -2.9, P = 0.012$) and the surviving LDS lines ($t_{12} = -3.2, P = 0.0079$) by cycle 11. Hence, long-term
selection in the Dark increased the capacity for heterotrophic growth that arises spontaneously in unselected populations.

In the NaCl environment, all L lines and all LD lines go extinct, while only 20% of LDS lines on average go extinct. As such, selection in NaCl has significantly lowered the extinction risk (LDS line to LD line and LDS line to L line comparison using Fisher’s exact test: $P = 3.2 \times 10^{-22}$). The extinction risk of the LD lines is no different from that of the L lines ($P = 1.00$), although the LD lines go extinct more rapidly than the L lines (coxme survival model: $z = -2.71$, $P = 0.0067$). None of the LD lines or L lines survive to cycle 11, such that we cannot compare their yield to that of the LDS lines.

Finally, in the Bold’s environment, which is the benign environment, none of the L lines and none of the LDS lines go extinct, while 25% of the LD lines on average go extinct. The extinction risk of the L lines and LDS lines is significantly lower than that of the LD lines (Fisher’s exact test: $P = 5.6 \times 10^{-8}$). The yield of surviving LD lines is no different from that of L lines ($t_{12} = 1.2$, $P = 0.24$) and no different from that of LDS lines ($t_{12} = 0.14$, $P = 0.89$).

Overall extinction risk in novel environments is lowest in the L lines. To determine if the risk of extinction in novel environments is lower for populations with a history of selection in stressful environments than for populations with a history of selection in a benign environment, we compared the general extinction risk (see Methods) of the LD lines and the LDS lines to that of the L lines.
We find that adaptation to a stressful environment increases the extinction risk in a novel environment in comparison to adaptation to a benign environment. That is, over all novel environments, the LD lines and LDS lines, with 39% and 29% of spores extinct on average respectively, have a higher general extinction risk than the L lines with 24% of spores extinct on average over all novel environments (Fisher’s exact test: LD – L comparison: P = 0.0031; LDS - L comparison: P = 0.28). Although the LDS lines do not have a significantly higher probability of extinction than the L lines, they do go extinct at a significantly faster rate (coxme survival model: L – LDS comparison z = 1.98, P = 0.048; L – LD comparison z = 1.85, P = 0.064). While the LDS lines have a lower extinction risk than the LD lines, this difference is not statistically significant (Fisher’s exact test: P = 0.075) nor are the extinction dynamics significantly different (coxme survival model z = 0.14; P = 0.89). The difference in extinction dynamics between the selection histories cannot be explained by differences in population size at the start of the assays (coxme survival analysis using yield at the end of cycle 1 in the home environments as a proxy for population size at the start of the assay, and assay environment, line, and spore as explanatory variables: z = -1.16, P = 0.25).

Examination of the general extinction risk in each novel environment reveals the same overall pattern of higher extinction risk in lines with prior selection in stressful environments: in Atrazine the LD lines have a significantly greater extinction risk than the light and LDS lines (Fisher’s exact test: P = 1.5 x 10^-8 for both LD - L and LD – LDS comparisons; L – LDS comparison: P = 1.0); and in pH4, the LDS and LD lines have a
significantly greater extinction risk than the L lines (Fisher’s exact test: LD - L P = 0.12; L - LDS P = 0.038; LD - LDS P = 0.79) and significantly different extinction dynamics (coxme survival model: LD - L comparison: z = -3.12, P = 0.0018; L - LDS comparison: z = 1.70, P = 0.0073; LD -LDS comparison: z = -0.45, P = 0.66). This is with the exception of the CuSO₄ environment where all lines have an equivalent extinction risk (Fisher’s exact test: P = 0.11 for both LD - L and LD - LDS comparisons).

Yield of surviving lines in novel environment is similar no matter selection history

The surviving lines all reach similar yields in the novel environments (Figure 4; Atrazine: L - LDS comparison t₁₁ = -1.4, P = 0.19; CuSO₄: LD - L comparison t₁₂ = -1.5, P = 0.16, LDS - L comparison t₁₂ = -0.73, P = 0.48; pH4: LDS - L comparison: t₁₁ = 0.41, P = 0.69), except in Atrazine, where the L lines reach greater yield by cycle 11 than the surviving LD lines (t₁₁ = -2.9, P = 0.014).

Repeatability of extinction

The amount of variance in the extinction dynamics provides an estimate of the repeatability of extinction. That is, if all populations from a given history go extinct at the same rate or all survive, variance in extinction will be low and repeatability high. High repeatability is an indication that history plays an important role in extinction. If populations from a given history respond in different ways to environmental change, variance in extinction will be high, and repeatability of extinction low. Low repeatability is an indication that chance plays an important role in extinction.
By estimating variance among lines within selection histories, among spores within lines, and among novel environments, we found that the repeatability of extinction is highest in the LD lines, and lowest in the salt and L lines (Table 2, Figure 3). Both the LDS and L lines are very sensitive to different environments, having either very high or very low extinction rates depending on the environment, and thus a high amount of variance across environments. The LD lines on the other hand tend to have more similar and intermediate rates of extinction across all environments, and hence much lower environmental variance. On the other hand, genetic variance is higher in the LD lines, as seen by the significantly higher variance among lines, and in the spore by environment interaction. This result is driven mainly by one of the five LD lines consistently having higher extinction rates than the other four lines. Hence, the repeatability of extinction is higher in the LD lines because of a more consistent albeit poor ability to survive in a range of novel environments.

Variance in yield of surviving populations
The amount of variance in proportion to mean yield, i.e. the variance-to-mean ratio, can provide an estimate of the ability of populations to respond to natural selection, with larger ratios predicted to increase rates of adaptation, and lower ratios predicted to slow or even prevent adaptation. Hence the variance-to-mean ratio is an indication of the evolvability of populations (Houle, 2002). We estimated the variance-to-mean ratio among lines, among spores (i.e. within lines), among environments, and among line by environment and spore by environment interactions. The total ratio is the sum of all these ratios. The total amount of variation in yield is highest in the surviving LD lines, with
close to two times more variation than in the surviving L lines, and more than three times
more variation than in the surviving LDS lines (Table 3, Figure 5). We obtain the same
qualitative results when using variance instead of the variance-to-mean ratio.

Contrary to variance in extinction which is driven mainly by variance among
environments, we find that variation in yield is driven mainly by genetic and gene by
environment variation. The L lines have high line-by-environment and spore-by-
environment variation, indicating that the surviving spores and lines from the light history
respond differently to different environments. The LD lines have the highest amount of
line-by-environment variation, and almost no other sources of variation, indicating
limited variation within lines, but high variability among lines in their response to
different environments. Finally, the LDS lines have the highest amount of variation
among lines, indicating significant differences among lines that are independent of the
environment of assay.

Discussion

We made use of lineages that have undergone two back-to-back events of selection in
stressful environments to test for a role of selection history on extinction risk in novel
environments. Survival in this case occurs as a correlated response to selection in the
previous environment. We exposed four spores from each of five lines from before any
selection in stressful environments (L lines), after selection in one stressful environment
(LD lines), and after selection in two stressful environments (LDS lines) to a range of
novel and severe environmental changes. The general extinction risk in a novel environment tended to be higher for lines with a history of selection in stressful environments than for lines with a history of selection in a benign environment.

Our main finding of greater extinction risk after selection in stressful environments is in agreement with what Samani and Bell (2016) found in yeast populations, where populations that had been exposed to long-term starvation had a higher probability of going extinct after exposure to a novel stressor than populations selected in conditions of plenitude. It is also in part in agreement with findings by Gonzalez and Bell (2013) who selected replicate populations of two species of yeast, *Saccharomyces cerevisiae* and *S. paradoxus* in different concentrations of salt before exposing all surviving populations to an initially lethal concentration of 150 gL$^{-1}$ NaCl. In accordance with our results, in *S. cerevisiae*, selection in stressful salt concentrations increased the extinction risk. However, the opposite was found in *S. paradoxus*, where selection in stressful salt concentrations reduced the extinction risk. Hence, while there is evidence that selection in stressful environments increases extinction risks during environmental change, other factors, such as species identity, can mediate the effect of selection history.

**Extinction risk depends on latest stress encountered**

Given that our experimental lines have survived two back-to-back stressful environments, it gives us the opportunity to ask whether the number of past stressful environments itself, i.e. one or two, affects the extinction risk. If stressful environments select for greater evolvability or positive genetic correlations for fitness among environments, selection in
two back-to-back stressful environments should lead to even lower extinction risks than
after selection in one stressful environment. We found that there was no general trend of
increasing or decreasing extinction risk with number of stressful environments survived
in the past. How much of this result is down to the history of stress per se, and how much
down to the specific stresses that these populations have encountered is impossible to say
from this data. Replication of this study using different selection histories would be
needed to determine the generality of the results with regards to the effect of the number
of events of evolutionary rescue on extinction risk. The lack of general trend in extinction
risk with number of stressful environment survived in the past could be because it is only
the latest stressful environment that determines evolvability and/or costs of adaptation
(i.e. there is no accumulation of effects from multiple stressful environments), or
although additive, the effects of different stressful environments can be opposite in
direction and/or magnitude and thus can lead to a reduction in extinction risk over
sequential selection in stressful environments.

The fact that the LDS lines have the same extinction risk in the Dark environment as the
L lines, and that LDS lines have significantly different patterns of variance in extinction
risk and yield in novel environments than the LD lines, suggests that selection in salt
erased the prior signature of selection in the dark. Hence, our results suggest that the
latest stressful environment to have survived is more important than the accumulation of
evolutionary rescue events. This is in agreement with findings by Lagator et al. (2014a)
who selected replicate populations of the green alga *Chlamydomonas reinhardtii* in one
of three herbicides before exposing all surviving populations to the two other herbicides
sequentially. Survivability during exposure to the second and third herbicides was either
increased, decreased, or not affected, depending on what herbicide in particular was used
for the initial selection phase.

The importance of the particular stressor experienced is also indicated by the different
results in different novel environment. The CuSO$_4$ environment was not stressful enough
and barely any populations went extinct in it. It was therefore not very informative for
distinguishing extinction risks between selection histories. As for the other two novel
environments, in Atrazine, it is the LD lines that have the highest extinction risk and rate
of extinction, whereas in pH4 it is the LDS lines that have the highest extinction risk and
both LD and LDS have the highest rate of extinction. Hence, selection history in stressful
environments leads to higher extinction risks and rates overall, but this effect does vary
between novel environments depending on the identity of the previous stressor.

Factors other than the stress per se can also affect extinction risks and evolutionary
responses. For example, differences in the severity of the stress can affect population
sizes and the fraction of beneficial mutations available (Gonzalez & Bell, 2013; Samani & Bell, 2016); differences in the genetic basis of adaptation to different stresses, such as
the presence and amplitude of antagonistic epistasis, can lead to differences in how much
of a reduction there is in the fitness costs of resistance mutations (Lagator et al., 2014a);
and finally, the tempo of environmental change, such as a gradual increase in the stressor
or a sudden exposure to high levels of the stressor, can lead to differences in the
magnitude of costs of adaptation (Collins & De Meaux, 2009; Lindsey et al., 2013). We
therefore cannot exclude the possibility that the greater extinction risk of the LD lines is
due, for example, to the fact that survival in the LD lines occurred after a sudden change,
which has been shown to involve greater costs than adaptation to gradually changing
environments such as in the LDS lines (Collins & De Meaux, 2009; Lindsey et al., 2013).

The role of plasticity in extinction in novel environments

The spores that survived in the novel environments follow a diverse range of dynamics in
yield over time, from constant, to steady increase, steady increase followed by a plateau,
and U-shaped dynamics (Figure 4). All populations were initiated from a single spore.
The only genetic variation present at the time of environmental change was therefore
limited to novel mutations generated during the four generations of growth prior to the
assay. Population decline upon environmental change would have also reduced the
supply of mutations and reduced the probability of fixation. Changes in yield over time
are therefore unlikely to be due to genetic changes given the absence of standing genetic
variation, and the short evolutionary timescale of the experiment. They are more likely to
be due to physiological acclimation or positive growth rates in initially bottlenecked
populations. Given that most of the spores that go extinct do so within the first five cycles
(about 25 generations) in the new environment, survival during severe environmental
change will depend almost entirely on the presence of spores in the population that can
either plastically respond or constitutively withstand the novel stressor enough to prevent
population extinction. Significant differences in the magnitude of the plastic response to
novel stressors have been found in yeast populations with different selection histories
(Samani & Bell, 2016). Hence prior selection regimes can affect the probability of
survival in novel environments by favouring or hindering the evolution of plastic responses (Lande, 2009) or by altering the health of the population and therefore its ability to physiologically respond to stressors.

Within and among line variance in extinction risk

By characterizing the rates of extinction of different spores within lines, of different independent lines within selection histories, and of different selection histories, in multiple novel environments, we are able to quantify precisely the repeatability of extinction across a whole range of environments. History played an important role in driving the repeatability of extinction, as lines and spores from each given history tended to go extinct at a similar rate in a given novel environment. Almost all variation in extinction rates arose from differences among novel environments, as histories tended to go extinct at different rates in different novel environments. This is with the exception of the LD lines, which showed even greater levels of repeatability than the L and LDS lines, by having similar rates of extinction in all novel environments.

Repeatability in yield differed significantly from repeatability of extinction in terms of what is the source of variation. The environment appears to be the most important determinant of the probability of extinction given it is the largest source of variation in extinction, whereas genetic and gene by environment interactions appear to be the most important determinants of yield. This suggests that chance plays an important role in yield and contributes to low repeatability of yield. The difference between extinction and yield in the main source of variation could be due to extinction being a binary trait (rather
than a continuous trait like yield), meaning that subtler genetic differences are not detected; it could be due to the fact that variation in yield was calculated for surviving populations, thus eliminating all the values of zero and leading to a much reduced environmental variance; or it could be due to differences in the genetic underpinning of extinction risk and yield. It is interesting to note that although the extinction risk was overall highest for the LD lines, the LD lines had the highest overall variance in yield amongst surviving populations. Hence, surviving LD lines have the highest potential evolvability in spite of sustaining the highest rate of extinction.

To conclude, selection in stressful environments tends to increase the risk of extinction in novel environments compared to selection in benign conditions. We also found that back-to-back episodes of selection in stressful environments did not increase or decrease that risk further, suggesting that effects of selection in stressful environments do not accumulate over time. Rather, our results suggest that it is the latest environment of selection that determines the evolvability of the population and the magnitude of costs of adaptation. By examining not only averages but also the amount variation in extinction risk and yield, we found that rates of extinction were highly repeatable within selection histories, despite there being significant amounts of genetic and gene by environment variation in yield within histories. Hence, lineages from the same selection history will have a similar probability of going extinction during environmental change, and this probability will be higher if the last selection environment was stressful.
Acknowledgements

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References


Bates, D., Maechler, M., Bolker, B. & Walker, S. 2015. Package “lme4.”


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**Tables**

Table 1. Proportion of spores extinct per line per selection history, in each of the assay environments. The proportions for the LD lines in novel assay environments (i.e. Atrazine, CuSO₄, and pH4) are corrected proportions (see Methods). The proportions represent the number of spores over three assays that were extinct by the end of the assay (4 spores x 3 replicate assays = 12 total spores), such that a number of 1 means
that all 12 spores went extinct. Each row represents one of five lines.

<table>
<thead>
<tr>
<th>Assay environment</th>
<th>Selection history</th>
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<tbody>
<tr>
<td>Bold’s</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>0.75</td>
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<td></td>
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<td></td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>0.42</td>
</tr>
<tr>
<td>Dark</td>
<td>0.75</td>
</tr>
<tr>
<td></td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>0.33</td>
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<td>0.83</td>
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<td></td>
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<td></td>
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</tr>
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<td>CuSO₄</td>
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<td>0.67</td>
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</tr>
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</tr>
</tbody>
</table>

Table 2. Significance of differences in variance in extinction dynamics in novel environments between selection histories. Only data from the three novel environments (i.e. Atrazine, CuSO₄, pH4) are included in the model.

<table>
<thead>
<tr>
<th>Source</th>
<th>Selection histories</th>
<th>Df (numerator, denominator)</th>
<th>F ratio</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Line</td>
<td>LD - LDS</td>
<td>1, 1</td>
<td>7.86 x 10³</td>
<td>7.18 x 10⁻³</td>
</tr>
<tr>
<td></td>
<td>LD - L</td>
<td>1, 1</td>
<td>7.90 x 10³</td>
<td>7.16 x 10⁻³</td>
</tr>
<tr>
<td></td>
<td>LDS - L</td>
<td>1, 1</td>
<td>1.00</td>
<td>0.499</td>
</tr>
<tr>
<td>Line : Environment</td>
<td>LD - L</td>
<td>1, 1</td>
<td>1.87</td>
<td>0.402</td>
</tr>
<tr>
<td></td>
<td>LD - LDS</td>
<td>1, 1</td>
<td>1.91</td>
<td>0.399</td>
</tr>
<tr>
<td></td>
<td>L - LDS</td>
<td>1, 1</td>
<td>1.02</td>
<td>0.497</td>
</tr>
</tbody>
</table>
Table 3. Significance of differences in variance-to-mean ratios in optical density between selection histories when cultured in all three novel environments (i.e. Atrazine, CuSO$_4$, pH4).

<table>
<thead>
<tr>
<th>Source</th>
<th>Selection histories</th>
<th>Df (numerator, denominator)</th>
<th>F ratio</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Line</strong></td>
<td>L - LD</td>
<td>4, 4</td>
<td>Inf</td>
<td>0.00</td>
</tr>
<tr>
<td></td>
<td>LDS - L</td>
<td>4, 4</td>
<td>4.20</td>
<td>0.0969</td>
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<tr>
<td></td>
<td>LDS - LD</td>
<td>4, 4</td>
<td>Inf</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Line : Environment</strong></td>
<td>L - LDS</td>
<td>6, 4</td>
<td>Inf</td>
<td>0.00</td>
</tr>
<tr>
<td></td>
<td>LD - L</td>
<td>3, 6</td>
<td>3.97</td>
<td>0.0710</td>
</tr>
<tr>
<td></td>
<td>LD - LDS</td>
<td>3, 4</td>
<td>Inf</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Spore</strong></td>
<td>L - LD</td>
<td>15, 12</td>
<td>4.90</td>
<td>4.23 x 10$^{-3}$</td>
</tr>
<tr>
<td></td>
<td>L - LDS</td>
<td>15, 15</td>
<td>4.05</td>
<td>5.13 x 10$^{-3}$</td>
</tr>
<tr>
<td></td>
<td>LDS - LD</td>
<td>15, 12</td>
<td>1.21</td>
<td>0.374</td>
</tr>
<tr>
<td><strong>Spore : Environment</strong></td>
<td>L - LDS</td>
<td>22, 9</td>
<td>27.7</td>
<td>8.48 x 10$^{-6}$</td>
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<tr>
<td></td>
<td>LD - LDS</td>
<td>9, 17</td>
<td>Inf</td>
<td>0.00</td>
</tr>
<tr>
<td><strong>Environment</strong></td>
<td>LD - L</td>
<td>1, 2</td>
<td>Inf</td>
<td>0.00</td>
</tr>
<tr>
<td></td>
<td>LDS - L</td>
<td>2, 2</td>
<td>Inf</td>
<td>0.00</td>
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<tr>
<td></td>
<td>LDS - LD</td>
<td>2, 1</td>
<td>8.72 x 10$^{13}$</td>
<td>7.57 x 10$^{-6}$</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>L - LDS</td>
<td>49, 42</td>
<td>2.88</td>
<td>3.28 x 10$^{-4}$</td>
</tr>
<tr>
<td></td>
<td>LD - L</td>
<td>29, 49</td>
<td>1.92</td>
<td>0.0218</td>
</tr>
<tr>
<td></td>
<td>LD - LDS</td>
<td>29, 42</td>
<td>5.52</td>
<td>3.56 x 10$^{-7}$</td>
</tr>
</tbody>
</table>
Figure 1. Schematic of the selection history of the L, LD, and LDS lines.

Figure 2. Extinction dynamics of the different selection histories in each assay environment. Survivorship in the selection environments (i.e. Bold, Dark, NaCl) corresponds to the proportion of lines and spores alive, whereas survivorship in the novel environments corresponds to the proportion of lines and spores alive corrected by the special risk of constant light and no acetate in the case of the LD lines. The survivorship sometimes increases in the novel environments due to correction. That is, when at a given time point survivorship decreased in Bold but not in the novel environment, this leads to an increase in survivorship in the novel environment. There are three lines per selection history, one for each of the three replicate assays. In the Bold, Atrazine, and CuSO₄ environments, the extinction dynamics of the L and LDS lines are exactly the same and fall exactly on top of each other at 1. Time corresponds to the growth cycle number.

Figure 3. Variance in extinction in novel environments depending on selection history.

Figure 4. Yield over time of the L, LD, and LDS spores and lines that survived to the end of the assay in each of the three historical environments and the three novel environments. Each point represents one replicate (total of 3 replicates per spore per line). Curves are smoothed trend lines fitted using loess, with 95% confidence interval shading. Time corresponds to the growth cycle number.

Figure 5. Variance-to-mean ratio in yield in novel environments at the end of the assay depending on selection history.
<table>
<thead>
<tr>
<th>Year</th>
<th>Event</th>
</tr>
</thead>
<tbody>
<tr>
<td>1997</td>
<td>Cross between lab strains using progeny from a light line are assembled</td>
</tr>
<tr>
<td>2008</td>
<td>Light lines are assembled</td>
</tr>
<tr>
<td>2011</td>
<td>The light lines assembled using three of 96 salt lines are</td>
</tr>
<tr>
<td>2015</td>
<td>The surviving dark lines assembled using 40 of 241 lines surviving</td>
</tr>
<tr>
<td>2017</td>
<td>Extinct</td>
</tr>
</tbody>
</table>

### Timeline

- **1997**: Cross between lab strains using progeny from a light line are assembled.
- **2008**: Light lines are assembled.
- **2011**: The light lines assembled using three of 96 salt lines are.
- **2015**: The surviving dark lines assembled using 40 of 241 lines surviving.
- **2017**: Extinct.
Selection history
- L lines
- LD lines
- LDS lines

Variance in extinction dynamics

Source
- Line
- Line:Environment
- Spore
- Spore:Environment
- Environment
- Total