

**Evolutionary rescue can be impeded by temporary environmental amelioration**

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35 OLP and QGZ analyzed the data. All authors contributed to designing the  
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## **Abstract**

Rapid evolutionary adaptation has the potential to rescue from extinction populations experiencing environmental changes. Little is known, however, about the impact of short-term environmental fluctuations during long-term environmental deterioration, an intrinsic property of realistic environmental changes. Temporary environmental amelioration arising from such fluctuations could either facilitate evolutionary rescue by allowing population recovery (a positive demographic effect) or impede it by relaxing selection for beneficial mutations required for future survival (a negative population genetic effect). We address this uncertainty in an experiment with populations of a bacteriophage virus that evolved under deteriorating conditions (gradually increasing temperature). Periodic environmental amelioration (short periods of reduced temperature) caused demographic recovery during the early phase of the experiment, but ultimately reduced the frequency of evolutionary rescue. These experimental results suggest that environmental fluctuations could reduce the potential of evolutionary rescue.

**Keywords:** adaptation, demographic recovery, environmental change, evolutionary rescue, experimental evolution, microcosm, virus, warming.

## INTRODUCTION

A biological population in decline due to environmental deterioration can recover in abundance if genotypes tolerant of the environmental change increase in frequency and restore population growth sufficiently quickly. This phenomenon is known as evolutionary rescue, and it has the potential to lessen the loss of biodiversity due to environmental changes, including those associated with global climate change (Maynard Smith 1989; Gomulkiewicz & Holt 1995; Bell 2013; Osmond & de Mazancourt 2013; Bourne *et al.* 2014; Carlson *et al.* 2014). Evolutionary rescue depends on the relative rate of demographic decline and evolutionary adaptation. Therefore, more severe stresses and higher rates of environmental changes, which cause higher rates of population decline, can decrease the chance of rescue (Burger & Lynch 1995; Collins *et al.* 2007; Perron *et al.* 2008; Bell & Gonzalez 2009; Collins & de Meaux 2009; Bell & Gonzalez 2011; Lindsey *et al.* 2013). Conversely, larger population sizes and higher genetic variation can promote evolutionary rescue by allowing more time, and more efficient selection, for adaptation (Gomulkiewicz & Holt 1995; Lande & Shannon 1996; Willi *et al.* 2006; Orr & Unckless 2008; Bell & Gonzalez 2009; Samani & Bell 2010; Ramsayer *et al.* 2013). Experimental studies of these questions have all involved monotonic environmental deterioration.

A more realistic scenario of environmental deterioration would show both a directional trend and short-term fluctuations (Karl *et al.* 1995; McLaughlin *et al.* 2002; Bell & Collins 2008). The impact of short-term environmental fluctuations on evolutionary rescue is now poorly understood. When environment fluctuates over

time, periods of extremely harsh environmental conditions can cause dramatic decline in population sizes and likely reduce the chance of evolutionary rescue (Bell 2013; Lindsey *et al.* 2013). The effect of episodes of environmental amelioration is, however, unclear. Temporary environmental amelioration may promote evolutionary rescue by acting as a temporal refuge and allowing populations to recover in abundance, as this can lead to slower demographic decline and thus increase the probability to obtain beneficial mutations before extinction (Wahl *et al.* 2002; Samani & Bell 2010). However, such environmental amelioration may also lead to a relaxation of selection for tolerance of environmental stress and thus reduce the probability of fixation of the beneficial mutations required for adaptation (Uecker & Hermisson 2011; Peischl & Kirkpatrick 2012; Alto *et al.* 2013; Kirkpatrick & Peischl 2013). This may be particularly important when progressive adaptation via fixation of multiple beneficial mutations is needed for populations to survive increasing magnitudes of stress, where later steps of adaptation are contingent on the success of earlier ones (Martin *et al.* 2013). In such cases, the negative effect of environmental amelioration on evolutionary adaptation may amplify through time (Fig. S1). With these antagonistic effects, the net impact of temporary environmental amelioration on evolutionary rescue is not easy to predict, and merits careful examination.

Here we report an experimental evolution study that addresses this question. We use populations of a lytic bacteriophage infecting the bacterium *Pseudomonas fluorescens*. In a previous study, we showed that evolutionary adaptation could

prevent this phage from extinction when temperature was monotonically elevated to a stressful level (Zhang & Buckling 2011). In the present study, populations of the phage were experimentally evolved in gradually warming environments, with or without periodic phases of environmental amelioration (lowered temperature). We also examined the effect of population size, both to confirm that this system behaves as expected (greater chance of evolutionary rescue for larger populations) and to test for an interaction with environmental amelioration in determining the chance of evolutionary rescue. We hypothesize that an interaction may arise, as the positive effects of environmental amelioration are likely to be more important for smaller populations, for which the risk of extinction from demographic stochasticity is higher and evolutionary adaptation is limited by the supply of beneficial mutations to a greater extent (Willi *et al.* 2006; Samani & Bell 2010; Ramsayer *et al.* 2013).

## **METHODS**

### **Strains and culture techniques**

The bacteriophage virus SBW25Φ2 (Buckling & Rainey 2002) and its host bacterium *Pseudomonas fluorescens* SBW25 (Rainey & Bailey 1996) were used in this study. The bacterium grows well at temperatures below 33 °C. The phage fails to reproduce above 30 °C, but may gain tolerance to higher temperature through evolutionary adaptation (Zhang & Buckling 2011). Bacteria and phages were grown in microcosms of 1.5 mL of 0.1KB medium (M9 buffer solution supplemented with 1

g L<sup>-1</sup> glycerol and 2 g L<sup>-1</sup> proteose peptone no. 3) in 24-well microplates, unshaken in temperature-controlled incubators.

Phage population densities were measured by plating phage dilutions onto soft agar plates containing the ancestral bacterial cells and counting the number of plaque forming units (PFUs) after 24 h culture at 29 °C. Isolation of phages from cultures were achieved by mixing 900 µL of culture with 100 µL of chloroform, which was then vortexed to lyse the bacterial cells, and centrifuged at 13,000 rpm for 2 min to pellet the bacteria debris, leaving a suspension of phage in the supernatant.

### **Evolutionary rescue experiment**

Phage populations were allowed to evolve through 20 serial transfers. Each microcosm was initially inoculated with ~10<sup>7</sup> isogenic stationary-phase bacterial cells and ~10<sup>5</sup> isogenic phage particles. Every two days, the phage population from each microcosm was isolated, a portion of which was transferred into a fresh microcosm with ~10<sup>7</sup> ancestral bacteria cells. As the biotic environment, host bacteria, was held in its ancestral state, phage population persistence would be mainly determined by its adaptation to the physical environment (and not result from coevolutionary dynamics with its host).

The experiment followed a split-plot design and considered two factors: environment and population size. Phage populations evolved in a deteriorating environment with: (i) no periodic amelioration, temperature increasing in a stepwise fashion from 29 to 31.4 °C, six steps of 0.4 °C change, one step per three transfers;

and (ii) periodic amelioration, which differed from the ‘no periodic amelioration’ treatment in that, within each 3-transfer step, the second transfer experienced 0.4 °C lower temperature (Fig. 1). After the six steps of temperature increase (transfer 19), phage populations were evolved at 31.4 °C for one more transfer. This ensured that phage persistence at the end of the experiment reflected adaptation to the environment (by ruling out the possibility of transient occurrence of maladapted populations due to the time lag between environmental change and extinction). Four replicate incubators were used for each environmental change regime. Twelve phage lines were grown in each incubator, six with large bottleneck population sizes (1% of phage cultures transferred to new microcosms at each transfer), and six with small bottleneck population sizes (0.1% of phage cultures transferred). Phage population density of each line was measured at every transfer.

In addition, two replicate incubators were used for a constant environment, where temperature was kept at 29 °C. All phage lines in the constant temperature environment persisted throughout the experiment, with highly stable population dynamics (Fig. S2). This confirms that extinction events observed in the deteriorating (temperature-elevated) environments were due to a failure to evolutionarily adapt to higher temperature rather than instability arising from the general lab conditions.

## **Data analysis**

Duration of persistence (time to extinction) of phage lines was analyzed using



parametric survival regression model (with the default Weibull distribution). The status of populations (extinct or persistent) at certain points in time was analyzed with generalized linear mixed model (GLMM), with binomial errors for the response variable. In these analyses, evolution environment (no amelioration or amelioration) and bottleneck population size (large or small) were included as fixed effects, and incubator ID as a random factor. We examined whether the periodic environmental amelioration could cause a demographic recovery by calculating the change in population size for each phage line at each transfer, as  $D_t - D_{t-1}$ , where  $D_t = \log_{10} (\text{PFU mL}^{-1} + 1)$ , representing the population density at transfer  $t$ . We used the software R for data analyses (R Core Team 2014).

## RESULTS

### Population persistence and demographic responses to periodic environmental amelioration

Over the selection experiment, 76 out of 96 phage lines went extinct. Environmental amelioration and small bottleneck population size reduced the duration of persistence by 29% (6.9 transfers) and 39% (9.2 transfers), respectively (Fig. 1; survival regression model, amelioration,  $z = -2.99$ ,  $P = 0.003$ ; bottleneck size,  $z = -5.62$ ,  $P < 0.001$ , interaction,  $z = 0.109$ ,  $P = 0.307$ ).

During the early stage of the experiment, periodic amelioration led to increased population size in most of the phage lines under the amelioration treatment. The

average change in population sizes during amelioration at transfer 3, 6, 9 and 12 for large-bottleneck lines, and at transfer 3 and 6 for small-bottleneck lines, was significantly positive (one sample  $t$  test,  $P < 0.05$ ; Figs 1 & 2). During later episodes of environmental amelioration, however, only some phage lines showed recovery in population size, while most continued to decline and the average of population size change was not positive (Figs 1 & 2).

### **The possibility of progressive adaptation**

Evolutionary rescue under continuously increasing temperature may involve progressive (multiple-step) adaptation. To infer this possibility, we grew phage populations that evolved tolerance to a mildly stressful temperature (30.2 °C; from transfer 10) in a more stressful environment (31 °C); these populations did not show positive growth (Supporting Information Methods). This suggests that adaptation to temperature above 31 °C would need accumulation of additional, and therefore at least two, beneficial mutations.

The observed pattern in population persistence is consistent with our hypothesis that the negative effect of periodic amelioration on evolutionary rescue should be stronger when accumulation of multiple beneficial mutations is required for adaptation in progressively deteriorating environments (see Introduction and Fig. S1). The amelioration treatment showed a significantly negative effect on the chance of population persistence at the end of the experiment when the environment was severely stressful (transfer 20, and 31.4 °C; 76 extinction events in total; GLMM,

amelioration,  $z = -2.86$ ,  $P = 0.004$ ; bottleneck size,  $z = -3.53$ ,  $P < 0.001$ , interaction,  $z = -0.003$ ,  $P = 0.997$ ), but did not have an impact at the mid-point of the experiment when the environment was only mildly harsh (transfer 10, and 30.2 °C; 26 extinction events in total; GLMM, amelioration,  $z = -0.007$ ,  $P = 0.994$ ; bottleneck size,  $z = -0.008$ ,  $P = 0.994$ , interaction,  $z = 0.007$ ,  $P = 0.994$ ).

### **The possibility of reversal of selection for beneficial mutations by periodic environmental amelioration**

The negative effect of periodic amelioration on the spread of beneficial mutations would be stronger if the beneficial mutations incurred fitness costs in the benign environment. In this case, the episodes of environmental amelioration would select against the beneficial mutations needed for adaptation to the future stressful environment. We assayed population growth profiles for certain phage lines, and found that the finally rescued phage populations, regardless of their evolution environments, showed no reduction in growth performance at lower temperature compared with control populations evolved in the temperature-constant environment (Supporting Information Methods; Figs S3 & S4). This suggests that phages carrying mutations conferring tolerance to high temperature suffered no appreciable fitness costs in terms of reduced growth performance at lower temperature. While selection for beneficial mutations may have been relaxed during the amelioration periods, it would not have been reversed.

## DISCUSSION

A large body of research suggests that increasing environmental variability associated with global climate change often, although not always, leads to negative demographic consequences for populations in the long run (McLaughlin *et al.* 2002; Drake 2005; Burgmer & Hillebrand 2011). Studies of evolutionary rescue have, however, paid little attention to the impact of environmental fluctuations, although a realistic scenario of environmental deterioration must observe fluctuations on short-term time scales (Karl *et al.* 1995; Bell & Collins 2008). In an environment with a deteriorating trend, fluctuations may lead to both phases of highly stressful conditions and episodes of more benign environmental conditions. Phases of extremely harsh environmental conditions are akin to very severe environmental deterioration, which is likely to reduce the chance of evolutionary rescue (Bell 2013; Lindsey *et al.* 2013). Our study shows that periodic environmental amelioration can also limit evolutionary rescue. Taken together, these results imply that the potential for rapid evolutionary adaptation to mitigate biodiversity loss might be limited in the face of increased climate variability.

In our experiment, temporary environmental amelioration could cause demographic recovery during the early stage of the experiment (Fig. 2), but ultimately reduced the chance of evolutionary rescue in the late stage (Fig. 1). It is likely that evolutionary rescue in this experimental system was mainly limited by the fixation, not the appearance, of beneficial mutations. Relaxed selection, during the episodes of environmental amelioration, could have reduced the chance of fixation of the

beneficial mutations that were later required for population survival in future, more stressful, environment. Thus the ecological (demographic) benefits of periods of environmental amelioration were outweighed by the evolutionary costs, wherein the failure of evolutionary adaptation diminished any positive effect of environmental amelioration on demography in the late stage of the experiment. The fact that the environmental amelioration treatment did not interact with the bottleneck population size treatment in affecting population persistence (see Results) also suggests that the positive effect of amelioration on demography had little influence on ultimate evolutionary rescue. It could be argued that periodic environmental amelioration can function as an ‘evolutionary trap’ (Ferriere & Legendre 2013; Carlson *et al.* 2014), and populations ‘falling into the trap’ fail to adapt to the future environmental change. The extent to which our findings were contingent on a relatively rapid environmental change combined with modest fluctuations (relative to the rate of the directional change) is unclear. Moreover, our experimental design and study organism preclude the possibility to examine the relevance of other important ecological and evolutionary processes such as recombination and dispersal (Bell 2013; Bourne *et al.* 2014; Carlson *et al.* 2014). More research is therefore required to explore the generality of these findings under a wider range of conditions and in other organisms.

Evolutionary adaptation to changing environments has attracted much interest in population genetics in the past several decades, where adaptation has usually been studied in a sense of relative fitness increase (but see Burger & Lynch 1995; Orr & Unckless 2008). It has been often suggested that lower levels of temporal

autocorrelation in environmental conditions could retard adaptation, and the inconsistency in selection over time has been a major explanation (Lande & Shannon 1996; Lenormand *et al.* 2009; Alto *et al.* 2013; Chevin 2013; Kirkpatrick & Peischl 2013; Kingsolver & Buckley 2015). Interestingly, our periodic amelioration treatment led to reduced temporal autocorrelation compared with the ‘no amelioration’ environment. The consistency of our results with the earlier population genetics studies implies that our conclusion should be fairly robust.

There has been a rich literature on how source-sink dynamics affects population adaptation and persistence in spatially heterogeneous environments. Immigration from benign habitats may help maintain the persistence of populations in harsh habitats through a demographic rescue effect, and meanwhile affect the evolutionary adaptation in the sink environment, either positively by increasing the mutation supply, or negatively by interfering with the fixation of beneficial mutations (Holt & Gomulkiewicz 1997; Perron *et al.* 2007; Venail *et al.* 2008; Bell & Gonzalez 2011; Bourne *et al.* 2014). Similar logic may apply to adaptation in temporally heterogeneous environments, where phases of relatively benign environmental conditions function as temporal refuges that promote population survival but meanwhile may retard the fixation of mutations required for adaptation to harsh future environments. Meanwhile, fundamental differences also exist. For instance, in a spatially heterogeneous environment, a realistic level of migration might not be very high and the negative effect of immigration on the fixation of beneficial mutations in a sink environment should be rather weak. In a temporally heterogeneous

environment, however, all individuals experience both benign and stressful conditions and the negative effect of environmental amelioration on the fixation of mutations for adaptation to harsh conditions is inevitable. Now a major gap in our understanding of what conditions favour evolutionary rescue is the combined effects of spatial and temporal variability (Bell & Gonzalez 2011).

Population persistence in increasingly deteriorating environments may require progressive adaptation via accumulation of multiple beneficial mutations and the chance for such multiple-step adaptation might be more limited (Weinreich *et al.* 2006; Toprak *et al.* 2012; Bell 2013). This seems to be the case in our experiment. Assays of phage growth performance suggested that tolerance to the highly stressful environment required multiple beneficial mutations (Supporting Information Methods). If the relaxation of selection during amelioration periods can delay the fixation of beneficial mutations (Peischl & Kirkpatrick 2012), this effect may accumulate through time and impact the later steps of adaptation to a larger extent (Fig. S1). This is consistent with our observations: environmental amelioration treatment did not show a significant effect on population survival at the mid-point of the experiment when the environmental stress was relatively mild, but showed a negative effect at the end of the experiment when the environment became very harsh. Therefore it will be helpful to explicitly consider evolutionary paths in future studies of evolutionary rescue (Lindsey *et al.* 2013).

The effect of evolutionary rescue in mitigating biodiversity loss can be particularly relevant to microbes, of which we may observe adaptive evolution in real

time. Studies of the causes and consequences of microbial extinction might greatly benefit from taking account of evolutionary processes. For instance, while the impacts of agricultural intensification and land use changes on soil microbial diversity have been recognized (Postma-Blaauw *et al.* 2010; Wagg *et al.* 2014), it is unclear whether environmental variability arising from those anthropogenic activities could have reduced the potential for evolutionary adaptation in the microbes. The concept of evolutionary rescue is also highly relevant for pathogen eradication, where reduced chance of evolution of resistance to chemotherapeutic agents is desirable (Lagator *et al.* 2013; Lindsey *et al.* 2013; Ramsayer *et al.* 2013; Alexander *et al.* 2014; Wu *et al.* 2014). Interestingly, our finding here is consistent with an early suggestion for drug use practice, that temporary low-dose treatments may slow the rate of drug resistance evolution (Read *et al.* 2011; Kouyos *et al.* 2014; Wu *et al.* 2014). The findings highlight the importance of considering both the ecological and population genetic consequences of environmental fluctuations for predicting the likelihood of evolutionary rescue.

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## REFERENCES

1.

Alexander, H.K., Martin, G., Martin, O.Y. & Bonhoeffer, S. (2014). Evolutionary rescue: linking theory for conservation and medicine. *Evol. Appl.*, 7, 1161-1179.

2.

Alto, B.W., Wasik, B.R., Morales, N.M. & Turner, P.E. (2013). Stochastic temperatures impede RNA virus adaptation. *Evolution*, 67, 969-979.

3.

Bell, G. (2013). Evolutionary rescue and the limits of adaptation. *Phil. Trans. R. Soc. B*, 368, 20120080.

4.

Bell, G. & Collins, S. (2008). Adaptation, extinction and global change. *Evol. Appl.*, 1, 3-16.

5.

Bell, G. & Gonzalez, A. (2009). Evolutionary rescue can prevent extinction following environmental change. *Ecol. Lett.*, 12, 942-948.

6.

Bell, G. & Gonzalez, A. (2011). Adaptation and evolutionary rescue in metapopulations experiencing environmental deterioration. *Science*, 332, 1327-1330.

7.

368 Bourne, E.C., Bocedi, G., Travis, J.M.J., Pakeman, R.J., Brooker, R.W. & Schiffrers,  
369 K. (2014). Between migration load and evolutionary rescue: dispersal,  
370 adaptation and the response of spatially structured populations to  
371 environmental change. *Proc. R. Soc. B*, 281, 2013279.

372 8.

373 Buckling, A. & Rainey, P.B. (2002). Antagonistic coevolution between a bacterium  
374 and a bacteriophage. *Proc. R. Soc. B*, 269, 931-936.

375 9.

376 Burger, R. & Lynch, M. (1995). Evolution and extinction in a changing environment:  
377 a quantitative-genetic analysis. *Evolution*, 49, 151–163.

378 10.

379 Burgmer, T. & Hillebrand, H. (2011). Temperature mean and variance alter  
380 phytoplankton biomass and biodiversity in a long-term microcosm experiment.  
381 *Oikos*, 120, 922-933.

382 11.

383 Carlson, S.M., Cunningham, C.J. & Westley, P.A.H. (2014). Evolutionary rescue in a  
384 changing world. *Trends Ecol. Evol.*, 29, 521-530.

385 12.

386 Chevin, L.-M. (2013). Genetic constraints on adaptation to a changing environment.  
387 *Evolution*, 67, 708-721.

388 13.

389 Collins, S. & de Meaux, J. (2009). Adaptation to different rates of environmental

390 change in *Chlamydomonas*. *Evolution*, 63, 2952-2965.

391 14.

392 Collins, S., de Meaux, J. & Acquisti, C. (2007). Adaptive walks toward a moving

393 optimum. *Genetics*, 176, 1089-1099.

394 15.

395 Drake, J.M. (2005). Population effects of increased climate variation. *Proc. R. Soc. B*,

396 272, 1823-1827.

397 16.

398 Ferriere, R. & Legendre, S. (2013). Eco-evolutionary feedbacks, adaptive dynamics

399 and evolutionary rescue theory. *Phil. Trans. R. Soc. B*, 368, 20120081.

400 17.

401 Gomulkiewicz, R. & Holt, R.D. (1995). When does evolution by natural selection

402 prevent extinction? *Evolution*, 49, 201-207.

403 18.

404 Holt, R.D. & Gomulkiewicz, R. (1997). How does immigration influence local

405 adaptation? A reexamination of a familiar paradigm. *Am. Nat.*, 149, 563-572.

406 19.

407 Karl, T.R., Knight, R.W. & Plummer, N. (1995). Trends in high-frequency climate

408 variability in the twentieth century. *Nature*, 377, 217-220.

409 20.

410 Kingsolver, J.G. & Buckley, L.B. (2015). Climate variability slows evolutionary

411 responses of *Colias* butterflies to recent climate change. *Proc. R. Soc. B.*, 282,

412           20142470.

413   21.

414   Kirkpatrick, M. & Peischl, S. (2013). Evolutionary rescue by beneficial mutations in  
415           environments that change in space and time. *Phil. Trans. R. Soc. B*, 368,  
416           20120082.

417   22.

418   Kouyos, R.D., Metcalf, C.J.E., Birger, R., Klein, E.Y., Abel zur Wiesch, P., Ankomah,  
419           P. *et al.* (2014). The path of least resistance: aggressive or moderate treatment?  
420           *Proc. R. Soc. B*, 281, 20140566.

421   23.

422   Lagator, M., Vogwill, T., Colegrave, N. & Neve, P. (2013). Herbicide cycling has  
423           diverse effects on evolution of resistance in *Chlamydomonas reinhardtii*. *Evol.*  
424           *Appl.*, 6, 197-206.

425   24.

426   Lande, R. & Shannon, S. (1996). The role of genetic variation in adaptation and  
427           population persistence in a changing environment. *Evolution*, 50, 434-437.

428   25.

429   Lenormand, T., Roze, D. & Rousset, F. (2009). Stochasticity in evolution. *Trends*  
430           *Ecol. Evol.*, 24, 157-165.

431   26.

432   Lindsey, H.A., Gallie, J., Taylor, S. & Kerr, B. (2013). Evolutionary rescue from  
433           extinction is contingent on a lower rate of environmental change. *Nature*, 494,

434 463-467.

435 27.

436 Martin, G., Aguilee, R., Ramsayer, J., Kaltz, O. & Ronce, O. (2013). The probability  
 437 of evolutionary rescue: towards a quantitative comparison between theory and  
 438 evolution experiments. *Phil. Trans. R. Soc. B*, 368, 20120088.

439 28.

440 Maynard Smith, J. (1989). The causes of extinction. *Phil. Trans. R. Soc. B*, 325,  
 441 241-252.

442 29.

443 McLaughlin, J.F., Hellmann, J.J., Boggs, C.L. & Ehrlich, P.R. (2002). Climate change  
 444 hastens population extinctions. *Proc. Natl. Acad. Sci. USA*, 99, 6070-6074.

445 30.

446 Orr, H.A. & Unckless, R.L. (2008). Population extinction and the genetics of  
 447 adaptation. *Am. Nat.*, 172, 160-169.

448 31.

449 Osmond, M.M. & de Mazancourt, C. (2013). How competition affects evolutionary  
 450 rescue. *Phil. Trans. R. Soc. B*, 368, 20120085.

451 32.

452 Peischl, S. & Kirkpatrick, M. (2012). Establishment of new mutations in changing  
 453 environments. *Genetics*, 191, 895-906.

454 33.

455 Perron, G.G., Gonzalez, A. & Buckling, A. (2007). Source-sink dynamics shape the

456 evolution of antibiotic resistance and its pleiotropic fitness cost. *Proc. R. Soc.*  
457 *B*, 274, 2351-2356.

458 34.

459 Perron, G.G., Gonzalez, A. & Buckling, A. (2008). The rate of environmental change  
460 drives adaptation to an antibiotic sink. *J. Evol. Biol.*, 21, 1724-1731.

461 35.

462 Postma-Blaauw, M.B., de Goede, R.G.M., Bloem, J., Faber, J.H. & Brussaard, L.  
463 (2010). Soil biota community structure and abundance under agricultural  
464 intensification and extensification. *Ecology*, 91, 460-473.

465 36.

466 R Core Team ( 2014). R: A language and environment for statistical computing. R  
467 Foundation for Statistical Computing. Vienna, Austria.

468 37.

469 Rainey, P.B. & Bailey, M.J. (1996). Physical and genetic map of the *Pseudomonas*  
470 *fluorescens* SBW25 chromosome. *Mol. Microbiol.*, 19, 521-533.

471 38.

472 Ramsayer, J., Kaltz, O. & Hochberg, M.E. (2013). Evolutionary rescue in populations  
473 of *Pseudomonas fluorescens* across an antibiotic gradient. *Evol. Appl.*, 6,  
474 608-616.

475 39.

476 Read, A.F., Day, T. & Huijben, S. (2011). The evolution of drug resistance and the  
477 curious orthodoxy of aggressive chemotherapy. *Proc. Natl. Acad. Sci. USA*,

478           108, 10871-10877.

479   40.

480   Samani, P. & Bell, G. (2010). Adaptation of experimental yeast populations to

481           stressful conditions in relation to population size. *J. Evol. Biol.*, 23, 791-796.

482   41.

483   Toprak, E., Veres, A., Michel, J.-B., Chait, R., Hartl, D.L. & Kishony, R. (2012).

484           Evolutionary paths to antibiotic resistance under dynamically sustained drug

485           selection. *Nat. Genet.*, 44, 101-105.

486   42.

487   Uecker, H. & Hermisson, J. (2011). On the fixation process of a beneficial mutation in

488           a variable environment. *Genetics*, 188, 915-U281.

489   43.

490   Venail, P.A., MacLean, R.C., Bouvier, T., Brockhurst, M.A., Hochberg, M.E. &

491           Mouquet, N. (2008). Diversity and productivity peak at intermediate dispersal

492           rate in evolving metacommunities. *Nature*, 452, 210-214.

493   44.

494   Wagg, C., Bender, S.F., Widmer, F. & van der Heijden, M.G.A. (2014). Soil

495           biodiversity and soil community composition determine ecosystem

496           multifunctionality. *Proc. Natl. Acad. Sci. USA*, 111, 5266-5270.

497   45.

498   Wahl, L.M., Gerrish, P.J. & Saika-Voivod, I. (2002). Evaluating the impact of

499           population bottlenecks in experimental evolution. *Genetics*, 162, 961-971.



46.

Weinreich, D.M., Delaney, N.F., DePristo, M.A. & Hartl, D.L. (2006). Darwinian evolution can follow only very few mutational paths to fitter proteins. *Science*, 312, 111-114.

47.

Willi, Y., Van Buskirk, J. & Hoffmann, A.A. (2006). Limits to the adaptive potential of small populations. *Ann. Rev. Ecol. Evol. Syst.*, 37, 433-458.

48.

Wu, Y., Saddler, C.A., Valckenborgh, F. & Tanaka, M.M. (2014). Dynamics of evolutionary rescue in changing environments and the emergence of antibiotic resistance. *J. Theor. Biol.*, 340, 222-231.

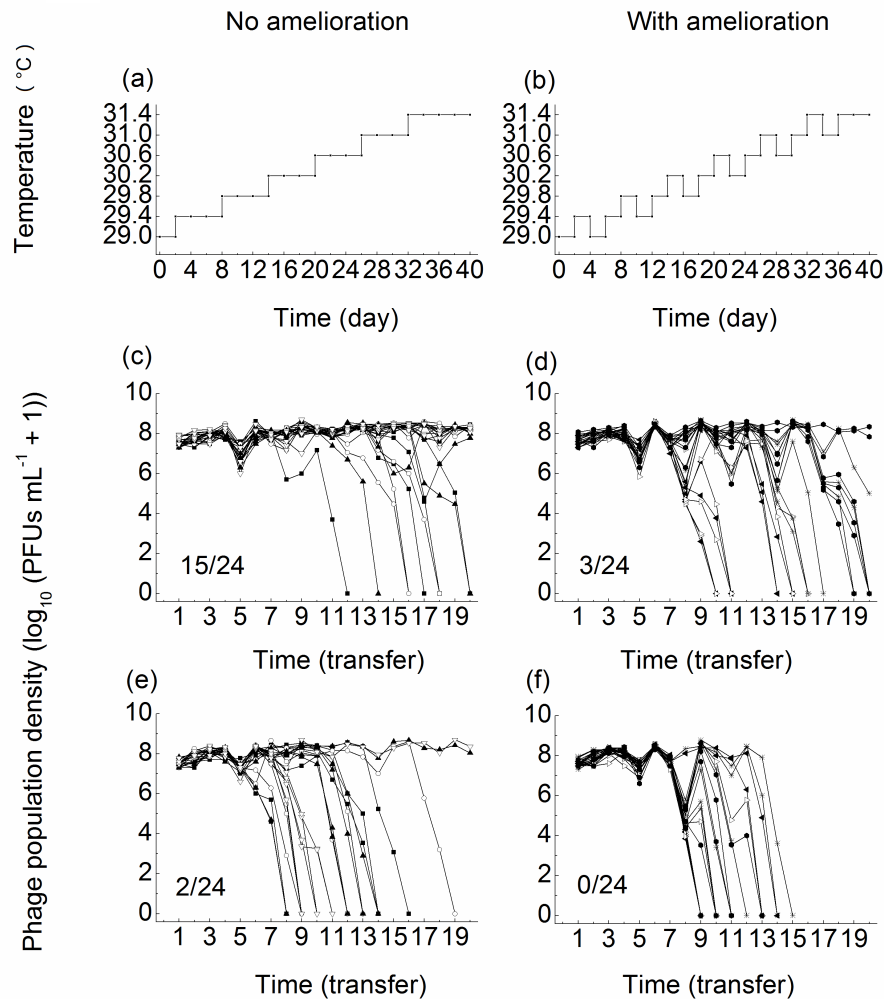
49.

Zhang, Q.-G. & Buckling, A. (2011). Antagonistic coevolution limits population persistence of a virus in a thermally deteriorating environment. *Ecol. Lett.*, 14, 282-288.

## **SUPPORTING INFORMATION**

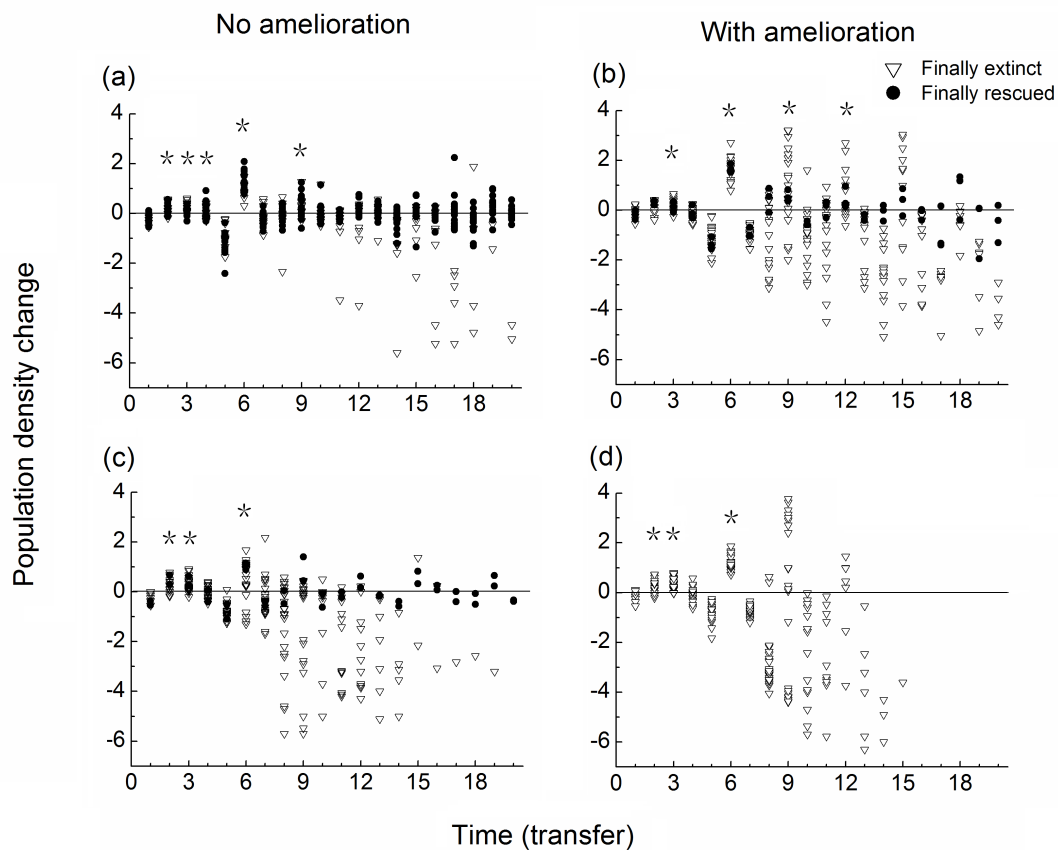
Additional Supporting Information may be downloaded via the online version of this article at Wiley Online Library ([www.ecologyletters.com](http://www.ecologyletters.com)).

# Figure legend



**Figure 1** The trajectory of temperature change during the course of experiment (a-b), and population density of each phage line through time under the large- (c-d) and small-bottleneck size treatments (e-f). ‘Day’ was used as the *x*-axis for (a-b), and ‘transfer’ as the *x*-axis for (c-f). One transfer represents a period of two days; for instance, transfer 1 is the period of day 0-2. Population density at one transfer reflects the population growth performance during a 2-d period. Different symbols in (c-f) indicate phage lines from different individual incubators. And the numbers

in panels indicate the frequency of phage lines that persisted throughout the experiment.



**Figure 2** Change in population density at each transfer ( $D_t - D_{t-1}$ , where  $D_t = \log_{10}$  (PFUs  $\text{mL}^{-1} + 1$ ), population density at transfer  $t$ ) of each phage line through time under the large- (a-b) and small-bottleneck size treatments (c-d). Under the amelioration treatment, episodes of temporary temperature decrease occurred at transfer 3, 6, 9, 12, 15, and 18. Asterisks indicate significantly positive changes in average population densities (one-sample  $t$  test,  $P < 0.05$ ).

## **Evolutionary rescue can be impeded by temporary environmental amelioration**

### **Supporting Information**

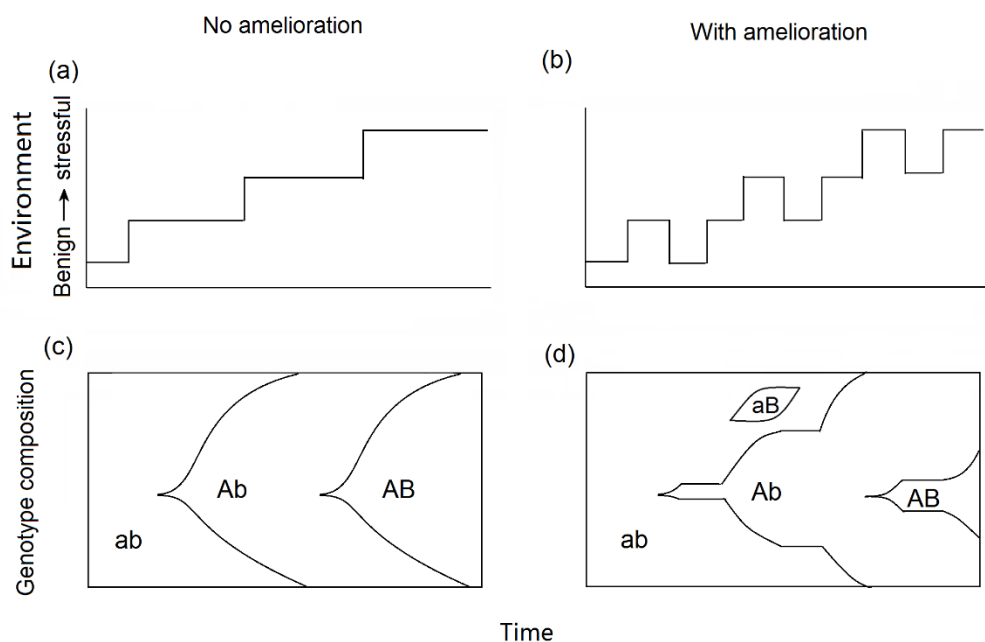
#### **Methods**

We examined whether progressive adaptation via accumulation of multiple beneficial mutations was needed for the persistence of our phage populations in the increasingly deteriorating environments. If phage populations that evolved tolerance to a mildly stressful temperature cannot grow at even higher temperature, it is suggested that multiple beneficial mutations would be required for further adaptation. Our ancestral phage can grow poorly at 29.8 °C, and not above 30 °C (Zhang & Buckling 2011), thus tolerance of temperature > 30 °C would require at least one beneficial mutation. In our experiment, 45 out of 48 large-bottleneck phage populations survived at transfer 10 (30.2 °C). Frozen stocks of these phage populations were reconditioned for 24 h at 30.2 °C (grown with  $\sim 10^7$  ancestral host bacteria cells); 1% of the phage extract was transferred to new microcosms with  $\sim 10^7$  ancestral host bacteria cells, and grown for 48 h at 31 °C. None of these phage lines showed positive growth at 31 °C. This suggests that adaptation to temperature above 31 °C need accumulation of at least two beneficial mutations.

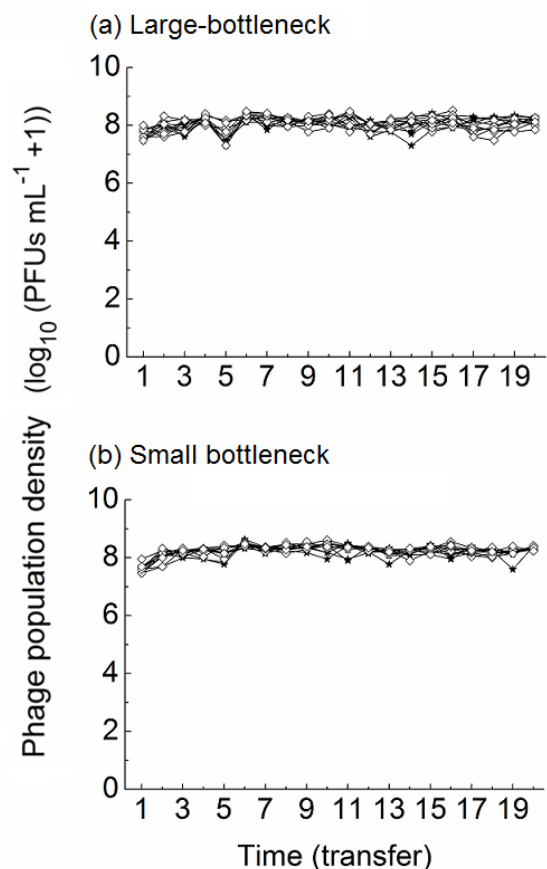
We investigated whether adaptation to high temperature incurred fitness costs in terms of growth performance at lower temperature in our experimental system. Population growth profile at 29 °C was assayed for the ancestral phage and eleven populations from transfer 20 (the end of the experiment), of which two were from the temperature-constant environment, three from the ‘amelioration’ treatment and six from the ‘no amelioration’ treatment. All of the eleven evolved populations were from large-bottleneck lines. Frozen stocks of these populations were first cultured for 24 h at 29 °C; 1% of the phage extract was transferred to new microcosms with  $\sim 10^7$  stationary-phase ancestral bacteria cells, and grown at 29 °C. For each population, 30 replicate microcosms were initiated; three microcosms were randomly chosen at each of the following 10 points in time (0, 0.5, 1, 1.5, 2, 2.5, 3, 4, 8, and

48h), of which phage densities were measured. Mean density of the three replicates were used for assessing the population growth profiles. The log-transformed measurements were used to fit a three-phase linear model for microbial growth (Buchanan *et al.* 1997; Novak *et al.* 2006). The model assumes three distinct growth phases: lag phase with constant population density, log phase with exponentially increasing density, and stationary phase with constant density. Three parameters were obtained from this model: the length of lag phase, the maximum growth rate, and final yield. The goodness of fit of the model was very high: in all cases, the coefficient of determination was  $> 0.99$ . Note that this was an assay of population-level growth performance, but not an assay of ‘one-step’ growth curve. We examined phage populations, rather than individual phage isolates. There may be heterogeneity in growth performance within each population. Stationery-phase, but not exponential-phase, bacteria were used as host cells (consistent with our selection experiment), which may contain both active and less active cells and thus cause further asynchrony in growth within each phage population.

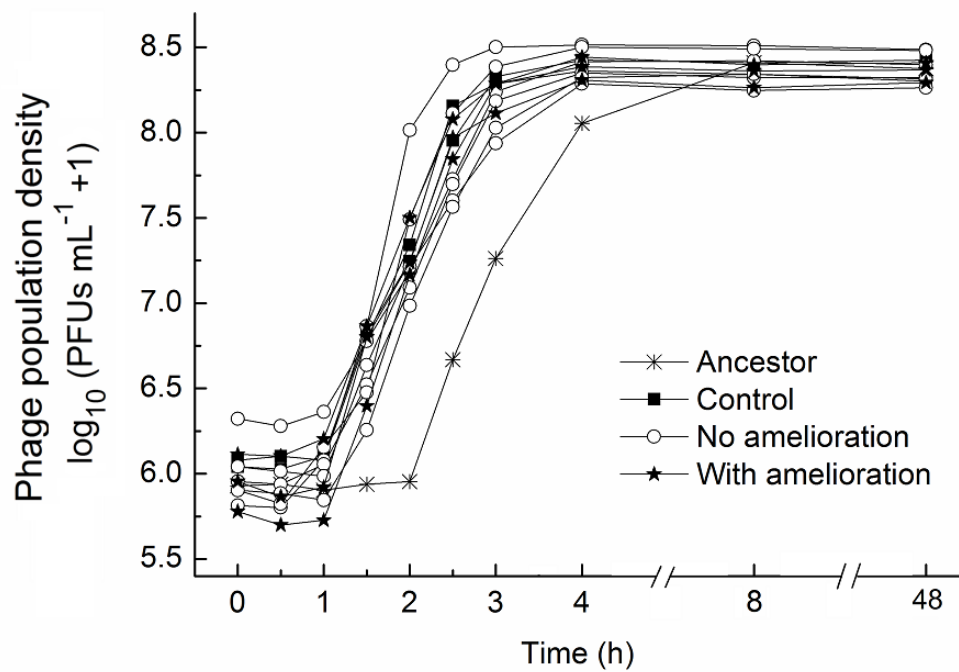
**Figure S1** A graphical illustration of the hypothesis that temporary environmental amelioration during deterioration can slow the fixation of beneficial mutations. In asexual populations, as assumed here, favourable mutations need be established sequentially and thus later steps of adaptation are contingent on the success of earlier ones. Therefore the negative effect of environmental amelioration on the fixation of beneficial mutations may amplify through time. Note that panel (d) assumes a scenario of relaxed, but not reversed, selection for beneficial mutations during the amelioration phases.



**Figure S2** Population density of phage lines that evolved in the temperature-constant environment (29 °C). Two replicate incubators were used for this evolution environment; and within each incubator, twelve populations (six with large bottleneck population size and six with small bottleneck population size) were maintained. Different symbols indicate phage lines from different individual incubators.

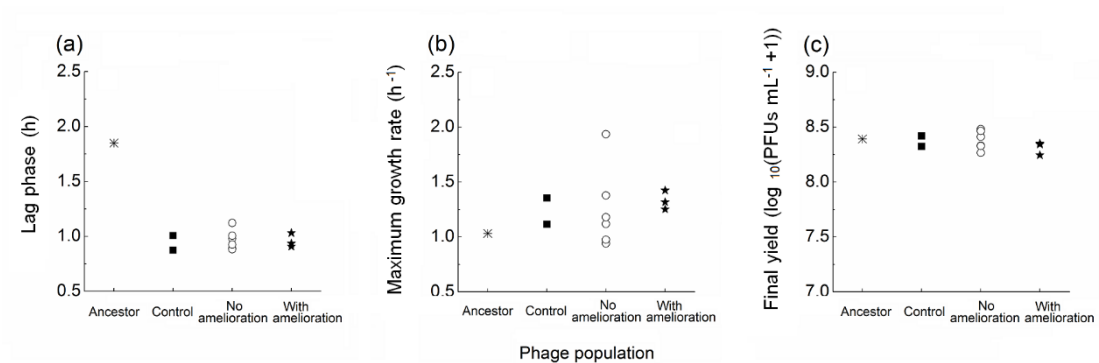


**Figure S3** Growth profile at 29 °C of the ancestral and eleven evolved populations, either from the temperature-constant (control) or deteriorating environments. Each line indicates an individual phage population.





**Figure S4** Phage population growth characteristics, length of lag phase (a), maximum growth rate (b), and final yield (c), of the ancestral phage and eleven evolved phage lines. There is no difference between the rescued lines from the deteriorating environments and those from the temperature-constant (control) environment in the growth characteristics (Mann-Whitney U-test,  $P > 0.1$ ). This suggests tolerance to high temperature does not incur a cost in terms of growth performance at low temperature, and thus in our evolutionary rescue experiment selection for beneficial mutations was relaxed but not reversed during the amelioration periods. Note that the absence of such fitness costs in the finally rescued populations of the ‘amelioration’ environment may result from either (i) that the high temperature-tolerant mutations did not suffer a fitness costs, or (ii) that mutations with fitness costs existed but populations with such mutations went extinct due to the antagonistic selection arising from the environmental fluctuation. But only the first explanation is relevant to the ‘no amelioration’ evolution lines.



## REFERENCES

1.  
Buchanan R.L., Whiting R.C. & Damert W.C. (1997). When is simple good enough: a comparison of the Gompertz, Baranyi, and three-phase linear models for fitting bacterial growth curves. *Food Microbiol.*, 14, 313-326.
2.  
Novak M., Pfeiffer T., Lenski R.E., Sauer U. & Bonhoeffer S. (2006). Experimental tests for an evolutionary trade-off between growth rate and yield in *E. coli*. *Am. Nat.*, 168, 242-251.
3.  
Zhang Q.-G. & Buckling A. (2011). Antagonistic coevolution limits population persistence of a virus in a thermally deteriorating environment. *Ecol. Lett.*, 14, 282-288.