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**Can Evolutionary Rescue Impact Population Recovery in Polluted Environments? Through Migration, Mutation, and Natural Selection**

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**ABSTRACT**

Brown fields are defined as areas that were previously used for industrial purposes but are now neglected or underutilized. These sites are often associated with past industrial activities and pose a major challenge to the survival of biological communities and the conservation of biodiversity in the area due to the potential impact of potentially toxic elements (PTEs). This research proposes a population decline-evolutionary rescue-population recovery process for monitoring biological populations in polluted areas, providing a new perspective on the resistance and recovery of species under pollution stress. This study selected seashells as the target species and established a population model using Rstudio to explore how species in polluted areas achieve population recovery under the combined effects of biological migration, genetic mutation and natural selection, and to explore the effects of different migration rates, mutation rates and environmental stress (decay rate) on the population recovery process. The results show that: 1) Under the premise of ensuring that the selection coefficient is greater than the decay rate, adding a certain number of migratory individuals to the model will cause the population in the polluted area to decay rapidly first and then recover; 2) As the number of migrants increases, the overall population recovery rate increases, but in this process, the increase in foreign migratory individuals will increase the effect of genetic dilution, leading to a plateau period. However, since the wild type dominated the recovery process, the population recovery rate continued to increase; 3) With the increase of mutation rate/environmental stress (decay rate), the population recovery rate increased and decreased respectively. These results provide a basis for future research on ecological restoration and biodiversity conservation in urban industrial areas.

Keywords: Potentially Toxic Element [PTEs]; Environment stress, Evolutionary rescue, Population recovery, Biological migration, Urban sustainability..

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# INTRODUCTION

The term *evolutionary rescue* is used to describe the process by which populations facing environmental stress avoid extinction through genetic adaptation. This entails populations restoring positive growth rates, either by adjusting their size or through adaptive mutations (Freitas and Campos, 2024). This phenomenon is of critical importance for the comprehension of species conservation and the evolution of resistance to stressful factors (Wilson, Pennings and Petrov, 2017). The likelihood of evolutionary rescue depends on factors such as the level of environmental stress, population size, and genetic variation (Anciaux *et al.*, 2018). It is notable that evolutionary rescue is frequently driven by soft selective sweeps, whereby multiple adaptive mutations are disseminated concurrently within the population, thereby enabling a rapid response to stress (Wilson, Pennings and Petrov, 2017). Prior exposure to stressors can also influence the probability of evolutionary rescue. For example, previous adaptation to one stressor may increase resilience to new stressors, although it may initially reduce the likelihood of plastic rescue, which is the immediate survival response of an organism to a new stressor through temporary physiological changes (Samani and Bell, 2016). [The degree of parallel evolution between independent populations under environmental stress is influenced by the initial level of maladaptation and demographic factors](https://edgeservices.bing.com/edgesvc/chat?udsframed=1&form=SHORUN&clientscopes=chat,noheader,udsedgeshop,channelstable,ntpquery,devtoolsapi,udsinwin11,udsdlpconsent,udscstart,cspgrd,&shellsig=cde3649ee30036ed9893316a7f065e2262315ce2&setlang=en-US&lightschemeovr=1&udsps=0&udspp=0" \l "sjevt%7CDiscover.Chat.SydneyClickPageCitation%7Cadpclick%7C0%7C5cd0ec12-11ab-4e07-a254-2a1e687232d1" \t "_blank). These factors affect the likelihood of evolutionary rescue and the level of parallelism in evolutionary responses (Freitas and Campos, 2024). In light of these considerations, a crucial question arises: whether migration and mutation can enable a population to survive and adapt in a polluted environment despite the pressures exerted by pollution.

In the specific context of polluted environments, an understanding of the ways in which populations adapt is of paramount importance for the field of conservation biology. The phenomenon of evolutionary rescue, whereby evolutionary processes serve to prevent extinction in the context of changing environments, can occur through a range of mechanisms. For instance, transgenerational plasticity offers a means of temporary resilience, enabling populations to withstand sudden environmental shifts (Harmon and Pfennig, 2021). It has been demonstrated that certain species, such as the Atlantic killifish, are capable of rapid adaptation to polluted habitats as a result of their large population sizes and significant genetic diversity (Whitehead *et al.*, 2017). Nevertheless, the process of adaptation to pollution frequently results in a reduction in fitness in unpolluted environments. This observation underscores a trade-off between the ability to adapt to stress and overall fitness (Dutilleul *et al.*, 2017). This trade-off is further shaped by mechanisms like frequency-dependent selection, where the fitness of a phenotype depends on its prevalence within the population. Such interactions can significantly influence population persistence, especially when combined with abiotic pressures (Svensson and Connallon, 2019). These studies underscore the complex relationship between evolutionary processes and environmental stressors, highlighting the importance of balancing adaptive potential with associated fitness costs in conservation strategies.

The research on adaptation to polluted environments demonstrates a complex interplay between migration, mutation and selection. In certain cases, adaptive introgression – the transfer of beneficial genes from related species – facilitates rapid evolution, as observed in Gulf killifish, which developed resistance to toxicants (Oziolor *et al.*, 2019). In contrast, studies on Atlantic killifish have revealed an absence of evidence suggestive of mitochondrial DNA selective sweeps in polluted areas, suggesting that population structure is more profoundly influenced by geographic isolation than by pollution levels (Nunez *et al.*, 2018). Theoretical models also indicate that migration can facilitate differentiation in source-sink dynamics, whereby dispersal from a source population to a sink population enhances survival under stress (Mirrahimi and Gandon, 2019). However, as Lenormand (2002) discusses, migration can impose a "migration load," where gene flow counteracts local adaptation by introducing less suited alleles. This dynamic may influence whether locally adapted mutant genotypes in polluted environments persist or are overwhelmed by gene swamping. Moreover, populations of rove beetles in polluted areas demonstrate elevated genetic diversity, which could be attributed to augmented mutation rates resulting from oxidative stress or the migration of individuals from neighbouring populations (Giska *et al.*, 2015). These findings highlight the role of gene flow and genetic diversity in enabling populations to adapt to environmental pollution, though mechanisms may vary across species and pollutants.

All of these cases show the importance of genetic mutation, natural selection, and migration to population recovery in contaminated areas, but they do not provide a good model to describe the relationship between these factors and population recovery. In this study, we will use Rstudio to build a model to describe the decay - evolutionary rescue - recovery process of the population under the influence of the above factors.

# METHODS

## Environment setting

We modeled a riverine environment with two seashell populations of the same species: population A upstream and population B downstream. A stable pollution source between the upstream and downstream areas continuously discharged cyclic hydrocarbon pollutants into the downstream environment. This pollution caused population decay and mutation in the downstream population, while the upstream population remained unaffected. However, as the river flowed, individuals from the upstream population migrated downstream, contributing to the recovery of the downstream population.

## Dynamic changes of population genotypes

We used R Studio to model intergenerational changes in the genotype of population B. The model employed Poisson distributions to calculate the expected absolute number of wild-type individuals. These calculations incorporated the decay rate of wild types, the selection advantage of mutants, and a constant mutation rate to estimate the transition from wild types to mutants. The parameters used in the model are shown in the table below.

It is critical to ensure that the coefficient of natural selection exceeds the decay rate; otherwise, the population will tend toward extinction instead of recovery.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Parameter | Initial Individuals of Wild Type | Initial Individuals of Mutation Type | Decay rate | Coefficient of natural selection | Mutation rate | Migrants per Generation | Maximum Generation |
| Value | 1000 | 0 | 0.1 | 0.3 | 0.001 | 3 | 1000 |

## Tracking population dynamics as migration numbers change

To address our biological questions, we tracked the time required for populations to recover to their maximum carrying capacity under varying migration levels. This analysis aimed to determine how migration influences population recovery and the proportion of different genotypes within the population. Using the previously defined parameters, we executed the model to calculate recovery time for specific migration levels.

To further investigate the effects of migration, we set the number of migrants as a variable and introduced background pollution levels with decay rates of 0.15 and 0.2. This approach highlighted population dynamics under different environmental conditions. Additionally, we analyzed the distribution of genotypes over time to identify which genotype dominated the recovery process at each stage.

## Effects of pollution degree and mutation rate on population

We examined competition within the polluted area and the potential for mutation, focusing on the idea that mutants are typically more resistant to contaminants. These factors are represented in the model as varying decay rates (pollution levels) and mutation rates. Using the parameters defined in Section 2, we modeled population dynamics by treating the decay rate and mutation rate as independent variables, visualizing their effects on population recovery and stability.

# RESULTS

## Intergenerational changes in population size and genotype

As shown in Figure 1, the population size initially declined to a bottleneck before beginning to recover. During the recovery phase, mutants became the dominant genotype, driving the process of evolutionary rescue. Under the combined influence of migrating individuals and gene mutations, the population eventually reached the carrying capacity.

A graph with red and blue lines

Description automatically generatedFigure 1. Intergenerational changes in population size and genotype. The black line represents total population size, the blue line represents the number of wild-type individuals, and the red line represents the number of mutation-type individuals.

## Population dynamics as migration numbers change

The number of migrants is employed as the variable, and the relationship between the time to reach carrying capacity and the mean number of migrants for three decay rates is plotted. The results are presented in the following section.

A graph of different colored lines

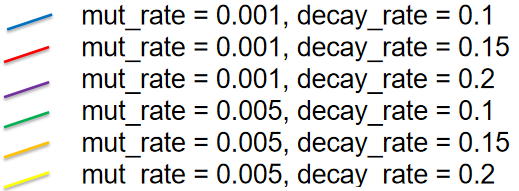
Description automatically generated

Figure 2. Changes in population dynamics with the mean number of migrants at different decay rates and mutation rates. The blue, red, and purple lines represent decay rates of 0.1, 0.15, and 0.2, respectively, under a mutation rate of 0.001. The green, orange, and yellow lines represent decay rates of 0.1, 0.15, and 0.2, respectively, under a mutation rate of 0.005.

At the beginning of Figure 2, the population recovered to the carrying capacity significantly faster due to the input of migrants. However, with the resulting increase in the number of immigrants 4, the time to reach the carrying capacity gradually increased. However, after a turning point5, the rate of population recovery increased with the number of migrants until the number of migrants in each generation could easily supplement the number of deaths in each generation. This indicated that the number of immigrants and deaths became nearly equal, leading to a steady state in population size.

We hypothesized that as the number of migrations increased, the speed of reaching the carrying capacity slowed due to three factors: a constant mutation rate, increased intraspecific competition, and higher genetic dilution. These factors likely caused the wild type to reduce the ecological niche available to the variant, thereby decreasing the efficiency of population recovery and evolutionary rescue. To test this hypothesis, we modified the model by increasing the mutation rate to 0.005 and observed whether the population recovery rate and efficiency of evolutionary rescue improved.

A graph of a number of migrants

Description automatically generatedFigure 3. Changes in population dynamics with the mean number of migrants at different decay rates (blue line: 0.1, red line: 0.15, purple line: 0.2) and a mutation rate of 0.005.

In addition, we analyzed the number of different genotypes for all migration levels. As shown in Figure 3, below a certain threshold, evolutionary rescue is driven by mutants. Beyond this threshold, the recovery process is dominated by wild types.

A graph of a number of migrants

Description automatically generatedA graph of a number of migrants

Description automatically generatedFigure 4. The number of different genotypes in the model (blue line: 0.1, red line: 0.15, purple line: 0.2) with a mutation rate of 0.001.

## Population dynamics change under different pollution degree and mutation rate

We varied the mutation rate and decay rate independently to generate Figure 5 and Figure 6. The upper limit of the decay rate was set at 0.3 to ensure that mutation and natural selection could occur; beyond this threshold, the population would trend toward extinction.

A graph with a line

Description automatically generated

Figure 5. Changes in population dynamics with different mutation rates

A graph of pollution rate

Description automatically generated

Figure 6. Changes in population dynamics with different pollution (decay) rates.

# DISCUSSION

We hypothesized that as the number of migrations increased, the speed of population growth toward carrying capacity slowed. This was due to a constant mutation rate, increased intraspecific competition, and higher genetic dilution, which reduced the ecological niche of the variant, thereby lowering the efficiency of population recovery and evolutionary rescue.

Genetic dilution occurs when increased species diversity in an ecosystem reduces the decay rate of environmental stress. This relationship is negatively correlated, with higher species diversity leading to a lower decay rate (Yao Xiao et al., 2022). In our research, increased migration elevated the proportion of wild types, diluting variant types and raising the attenuation rate. Typically, under natural selection, resistant individuals (mutants) survive outbreaks because they are better at resisting disease, while susceptible individuals (wild types) are more likely to die. However, under conditions of environmental stress and genetic dilution, susceptible individuals may exhibit higher fitness due to growth-defense trade-offs. For example, if resistant individuals face trade-offs in growth or reproduction, susceptible individuals may thrive in environments with abundant resources and low environmental stress by growing faster or reproducing more efficiently (Peng Zhang et al., 2024).

According to Hildegard's research（Hildegard Uecker，et al., 2014）,the dependence of the rescue probability on migration is shaped by four effects: first, migration is advantageous because the old part of the habitat acts as a source for wildtype individuals that might possible mutate. Second, mutants migrate to the old habitat where they have a disadvantage with respect to the wildtype. Migration thus reduces the effective growth rate of mutants. With increasing migration, this effect outweighs the first one such that the rescue probability has a local maximum for intermediate migration. Third, when migration gets very strong, the effect of relaxed competition in the old demes sets in and the rescue probability can become again high. Finally, if mutant fitness in the perturbed demes is density dependent, migration leads to a reduced fitness of mutants in these demes. This result also further explains the trend in our model.

Overall, our study sheds light on how ecological migration contributes to population recovery and how recovery efficiency varies with changing parameters. During the recovery process, we identified the dominant genotype and its role in shaping population dynamics. Furthermore, our findings offer a novel perspective on the mechanisms underlying population recovery.

# CONCLUSIONS

We have described the impact of migrants on population dynamics using models and have compared population dynamics changes under different environmental pressures and variation potential. Through this approach, we aimed to answer our key biological question, "Can migrating individuals promote population recovery when considering the intraspecific competition, environmental pollution and variation potential?".

Our results show that in our simulation, migrating individuals can indeed help the evolutionary rescue of the population, on the other hand, with the increase in the number of migrations, the efficiency of evolutionary rescue decreases due to the action of intraspecific competition and genetic dilution. Furthermore, our results show that when the number of migrations reaches the threshold for wild-type population recovery, the efficiency of population recovery is significantly enhanced, but this process cannot be classified as "evolutionary rescue" because natural selection and variation no longer dominate. Concurrently, by changing the environmental pressure and variation rate respectively, as the environmental pressure increases, the efficiency of population recovery will slow down significantly or even approaches extinction, while as the variation rate increases, the efficiency of population recovery will slowly increase.

In closing, while the results of the study met the initial objectives, there were some limitations. For instance, this project did not consider the interaction of multiple variables, such as the effects of different migration numbers, environmental stress, and mutation rates in a single model. In order to achieve broader and more realistic findings, future studies should include multiple variables and generalize the model to other environments.

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