

**Sustainable breeding and conservation actions of *Apis mellifera* in Italy**G. Minozzi<sup>1</sup>, G. Gandini<sup>1</sup> and G. Pagnacco<sup>2</sup><sup>1</sup>Università degli Studi di Milano, DIMEVET, Via Celoria 10, 20133, Italy, <sup>2</sup>CNR-IBBA Milano, Via Bassini, 20133, Italy; [giulietta.minozzi@unimi.it](mailto:giulietta.minozzi@unimi.it)

Since the end of the last glaciation, numerous subspecies of *Apis mellifera* appeared in Europe. In Italy the *Ligustica* variety of *A. mellifera* adapted to the mild climate and to the rich floristic biodiversity of the territory. Thanks to its favourable characteristics, this variety has spread since 1800 worldwide. With the arrival of the *Varroa destructor* in the 80s and with the increasingly dramatic use of pesticides in agriculture, the Italian bee is increasingly dependent on human interventions for its survival, both for the control of parasites and for the threat posed by pesticides. More recently, the effects of globalization have favoured in the Italian territory other subspecies of *A. mellifera* more performing in terms of productivity and resistance to pathogens. In this context, there is an urgent need to define strategies for the conservation of local ecotypes and for their valorisation on a productive scale. The control of matings becomes therefore a major point, and in this regard the BEENOMIX project has contributed to implement a specific selection breeding scheme applicable by any breeder able to carry out a selective activity. The BEENOMIX project developed and implemented a selection model based on productivity in terms of kg of honey and hygienic behaviour with a relative emphasis of 1 and 0.4, respectively. Two partially isolated populations are considered. The selection takes place between 108 families per year, from which the 6 best families will be identified and from which the new 108 families of the next cycle will be produced. In addition, from the best family every year a group of sister drone-producing queens (DPQ) is raised. The drones produced by the DPQ will fertilize the 108 virgin queens (VQ) in an isolated mating site. The mating site is chosen on different criteria, in particular to be isolated from the presence of other drones. The research was funded by the BEENOMIX project funded by the Lombardy Region.

**Analysis of the consequences of genetic rescue and its dependence on purging**N. Pérez-Pereira<sup>1</sup>, A. Caballero<sup>1</sup> and A. García-Dorado<sup>2</sup><sup>1</sup>Universidad de Vigo, Departamento de Bioquímica, Genética e Inmunología, Facultad de Biología, 36310 Vigo, Pontevedra, Spain, <sup>2</sup>Universidad Complutense, Departamento de Genética, Facultad de Biología, 28040 Madrid, Spain; [noeperez@uvigo.es](mailto:noeperez@uvigo.es)

Inbreeding depression, the reduction of fitness observed in populations with high inbreeding, has been a main concern in conservation programs. However, effective genetic purging of the recessive deleterious alleles expressed under inbreeding has been confirmed both theoretical and experimentally, especially under slow inbreeding. Therefore, this genetic purging needs to be taken into account to elaborate recommendations of management strategies as it becomes a possible determinant of its success. Particularly, the consequences of genetic purging on genetic rescue programs has not been explored to date. The term genetic rescue is used to refer to the introduction of new genetic variation from another population in order to reduce inbreeding depression and increase genetic diversity. However, despite its potential, the practice of this type of management is still controversial due to the associated risks. One of them is caused by the large inbreeding load that large populations tend to harbour, which can be potentially introduced by migrants and promote an increase of inbreeding depression later on. If the threatened population has reached the current situation by slow progressive reductions of size, the efficiency of genetic purging after the rescue may be lower than the one occurred prior to the rescue, leading to a negative effect on fitness in the medium term. We aim to explore by computer simulations the consequences of genetic purging as a determinant of the circumstances in which the rescue should or should not be recommended. The results indicate that when inbreeding has progressed slowly in the past allowing efficient purging and genetic rescue is performed under conditions in which purging is not effective, initial hybrid vigour is followed by an increased decline in fitness in the medium-long term.



# Analysis of the consequences of genetic rescue and its dependence on purging



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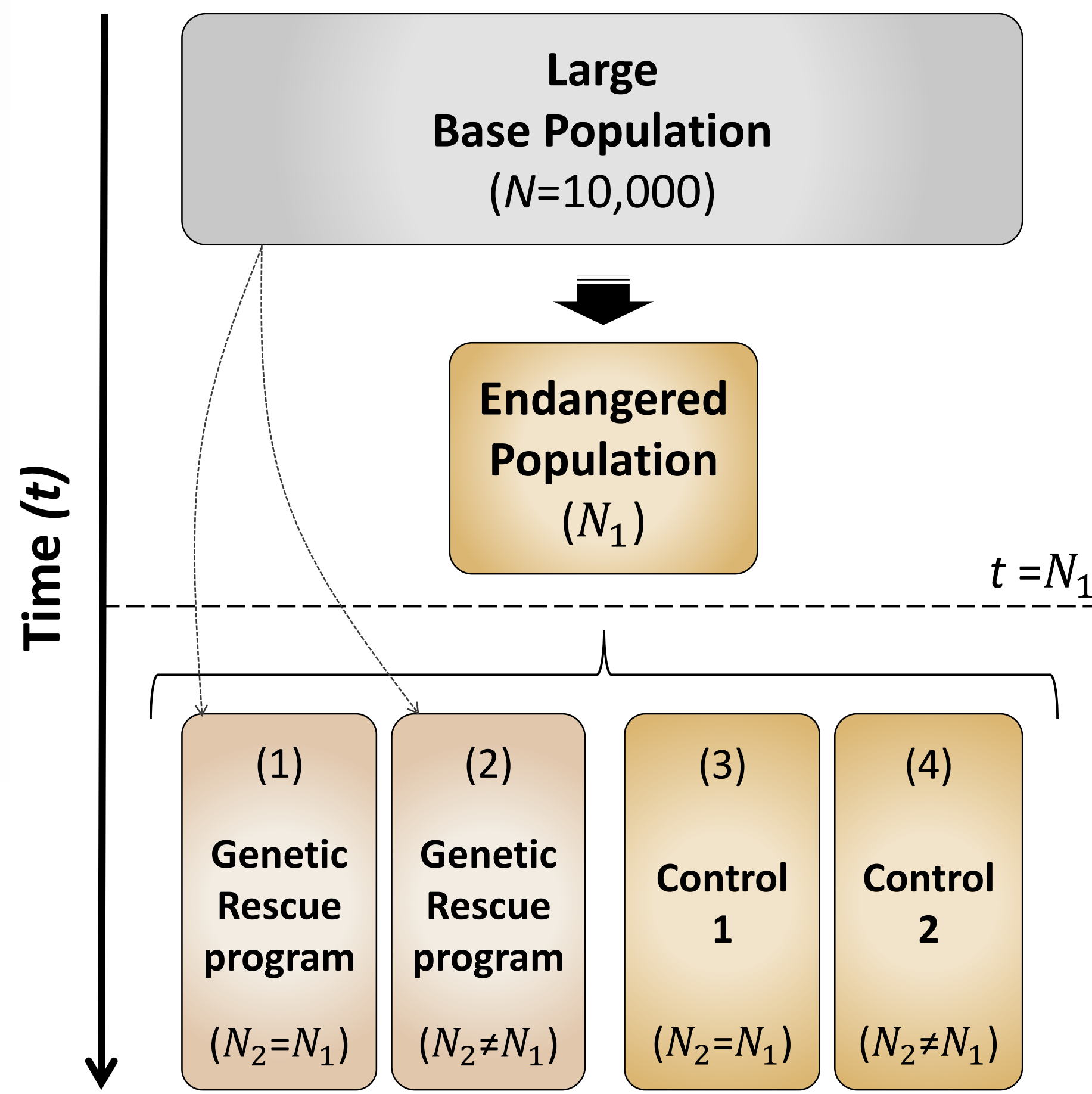


## INTRODUCTION

- Many populations are affected by severe reductions in the effective population size ( $N_e$ ), resulting in increased inbreeding and reduced fitness (**inbreeding depression**; Charlesworth & Charlesworth, 1999).
- When evaluating conservation strategies, the role of natural selection (**genetic purging**) against those deleterious alleles exposed by inbreeding (inbreeding load) is often neglected, despite it has been proven to be efficient with moderate  $N_e$  (García-Dorado, 2012).
- The introduction of individuals from another population (**genetic rescue program**) has resulted in multiple occasions in short term population recovery, but there is very little information about its consequences in the medium to long term (Whiteley *et al.*, 2015).
- One of the **risks** is the introduction of rare detrimental variants (Hedrick & García-Dorado, 2016).

The present work aims to explore the role of genetic purging as a determinant of the circumstances where a genetic rescue program should or should not be recommended.

## COMPUTER SIMULATION



**Figure 1. Simulation scheme.** A small number of individuals ( $N_1$ ) is sampled from the base population to fund a threatened population (TP). After  $t = N_1$  generations, four different scenarios are simulated from the original TP: (1) TP enters a genetic rescue program maintaining the same constant size ( $N_2 = N_1$ ); (2) TP enters a genetic rescue program but the size is simultaneously modified to another value ( $N_2 \neq N_1$ ); (3) and (4) are controls (without a genetic rescue program) of the first and second scenario, respectively. Horizontal dashed line indicates the start of the rescue program.

**Table 1. Mutational parameters (gamma distributed)** (López-Cortegano *et al.*, 2018).

$\lambda$	$\bar{s}$	Shape	$\bar{h}$	$B$
0.2	0.2	0.33	0.283	6.23

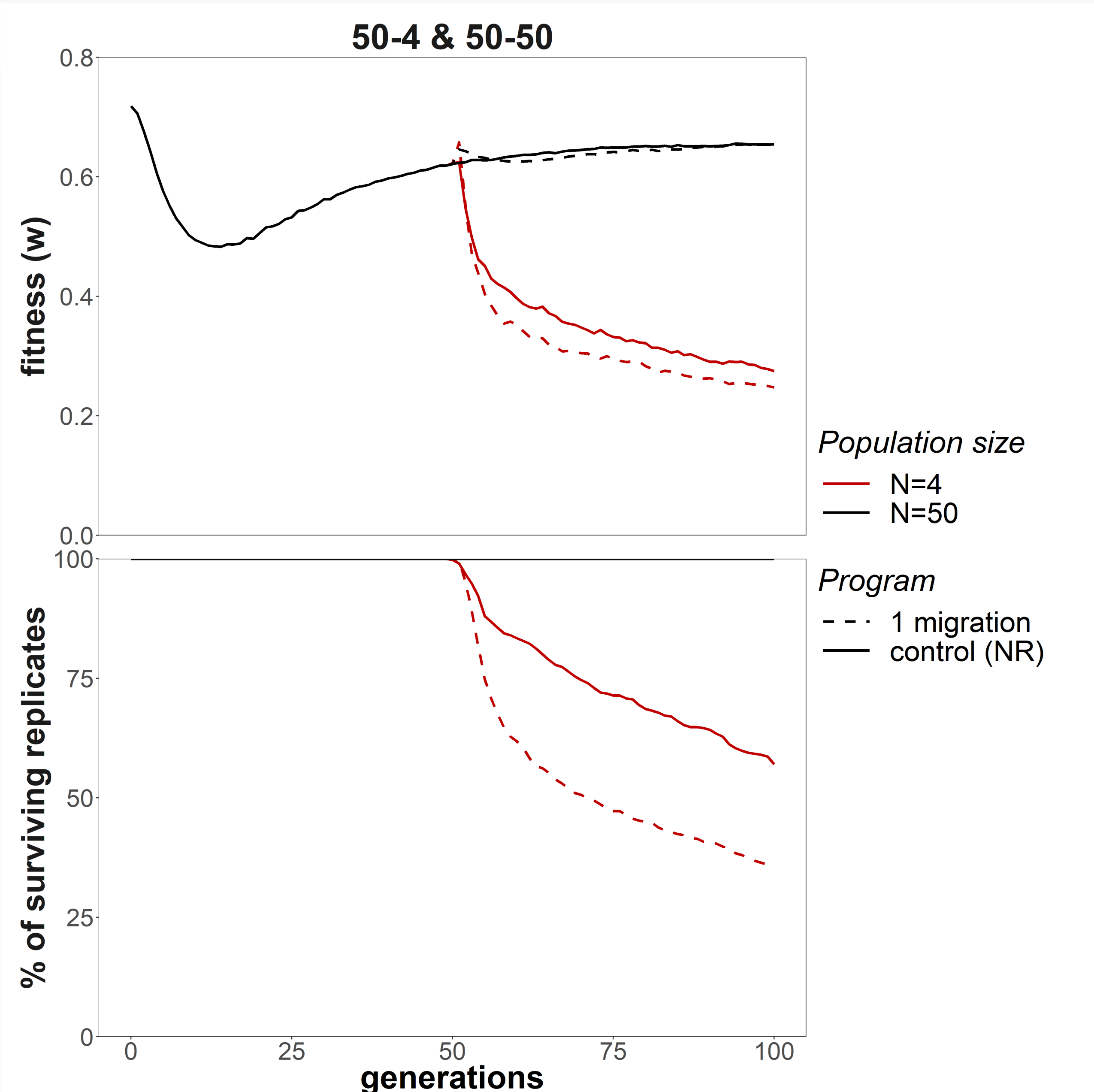
## CONCLUSIONS

- Migration results in a transient hybrid vigor and an increase in genetic diversity, but also of the inbreeding load ( $B$ ).
- With moderately effective population sizes (e.g.  $N_e=50$ ) purging is able to efficiently reduce the inbreeding load, but not with very small sizes (e.g.  $N_e=4$ ).
- If the endangered population had previously suffered a drastic reduction of size, migration will produce an initial hybrid vigor. If the size recovers quickly after migration, the introduced inbreeding load will be efficiently purged, with a **positive fitness effect** (not shown).
- If the endangered population comes from a period of moderate size, migrants can bear higher genetic load than native individuals, with a **negative effect** if the population size becomes smaller.
- Extinction risk** increases due to genetic stochasticity introduced by each migration event.

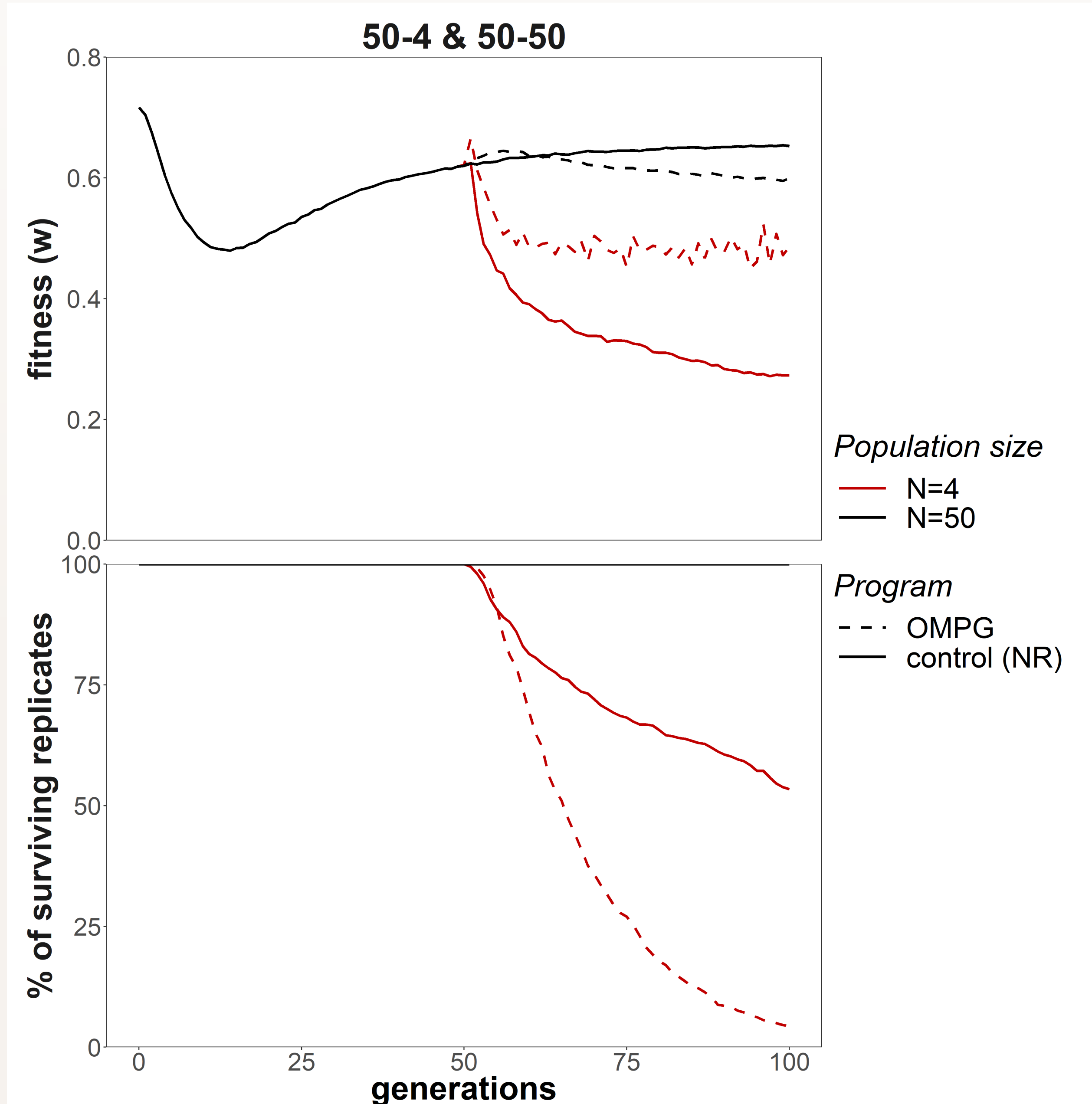
Our results illustrate the need of recovering reasonable population size during rescue programs and of restoring connectivity systems that can alleviate the consequences of migration stochasticity.

## RESULTS

### Occasional migration



### One Migrant Per Generation



**Figures 2 and 3.** Evolution of fitness ( $w$ ) and percentage of surviving replicates of endangered populations entering a genetic rescue program (migration of 5 males if  $N_2=50$ , and 1 male if  $N_2=4$ ; dashed lines) and of control populations (solid lines).



## References

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