Correction to: Reviewing the consequences of genetic purging on the success of rescue programs

Noelia Pérez-Pereira¹ · Armando Caballero¹ · Aurora García-Dorado²

Published online: 6 November 2021
© The Author(s) 2021

Correction to: Conservation Genetics
<https://doi.org/10.1007/s10592-021-01405-7>

In the original publication of the article, Figs. 5 and 6 were published incorrectly. The correct Figs. 5 and 6 are given in this correction.

The original article has been corrected.

The original article can be found online at <https://doi.org/10.1007/s10592-021-01405-7>.

✉ Aurora García-Dorado
augardo@ucm.es

¹ Centro de Investigación Mariña, Universidade de Vigo, Facultade de Bioloxía, 36310 Vigo, Spain

² Departamento de Genética, Fisiología y Microbiología, Facultad de Biología, Universidad Complutense, 28040 Madrid, Spain

Fig. 5 Percentage of surviving populations through generations. Different rows of panels give results under a different migration scenario: one unique migration event; two migrations with an interval of five generations; periodic migrations every five generations; “one migrant per generation” strategy. Different columns are for different $N_1 - N_2$

demographic scenarios, coded as in Fig. 3 panels. Light dashed lines give the percentage of surviving populations under no rescue program while solid lines give results under the rescue program. Number of migrants per event as explained in Box 1

Fig. 6 Mutational models. **a** Probability density function (PDF) of the homozygous deleterious mutational effects multiplied by the deleterious mutation rate. Red line: Model inferred from evolutionary genomic analysis by Kim et al. (2017) (best fit model for the 1000 genomes data: mutation rate per gamete and generation 0.314, homozygous effect s gamma distributed with shape parameter 0.186 and mean 0.0161, predicted equilibrium inbreeding load $B=3.07$ for effective size 10^4). Black line: Model used in our simulations (mutation rate per gamete and generation 0.2, s gamma distributed with

shape parameter 0.33 and mean 0.2, predicted equilibrium inbreeding load $B=6.3$ for effective size 10^4); the lethal class generated in this model by assigning $s=1$ to s values above 1 is represented in the [0.99–1] interval. **b** The black thick line gives the average inbreeding coefficient as a function of s assumed in our simulations, where h is uniformly distributed between 0 and the thin black line (extracted from García-Dorado and Caballero 2000 and García-Dorado 2003). The red line gives the h values used by Kyriazis et al. (2020) simulations, which are constant for each value of s

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will

need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>.

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.