The impact of habitat loss and population fragmentation on genomic erosion

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Abstract

Habitat loss and population fragmentation pose severe threats to biodiversity and the survival of many species. Population isolation and the decline in effective population size lead to increased genetic drift and inbreeding. In turn, this reduces neutral diversity, and it also affects the genetic load of deleterious mutations. Here, we analyse the effect of such genomic erosion by designing a spatially explicit, individual based model in SLiM, simulating the effects of the recorded habitat loss in Mauritius over the past ~ 250 years. We show that the loss of neutral diversity (genome-wide heterozygosity) was barely noticeable during the first 100 years of habitat loss. Changes to the genetic load took even more time to register, and they only became apparent circa 200 years after the start of habitat decline. Although a considerable number of deleterious mutations were lost by drift, others increased in frequency. The masked load was thus converted into a realised load, which compromised individual fitness and population viability after much of the native habitat had been lost. Importantly, genomic erosion continued after the metapopulation had stabilised at low numbers. Our study shows that historic habitat loss can pose a sustained threat to populations also in future generations, even without further habitat loss. The UN's Decade on Ecosystem Restoration needs to lead to transformative change to save species from future extinction, and this requires the urgent restoration of natural habitats.

Introduction

The loss and degradation of habitat is the leading driver of global biodiversity decline (Rands et al. 2010; IPBES 2018a, b). Habitat loss leads to a dramatic reduction of population sizes and fragmentation of populations, hindering the connectivity of individuals between habitat patches (Haddad et al. 2015; Newbold et al. 2015). The Kunming-Montreal

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Global Biodiversity Framework has four long-term goals for the 2050 Vision for biodiversity (CBD 2022). Goal A stipulates that the connectivity of ecosystems is maintained or restored to conserve the genetic diversity within populations, thereby safeguarding their adaptive potential (CBD 2022). Within ecosystems, individual species face various threats that are reported in the Red List of the International Union for Conservation of Nature (IUCN). The Red List reports 11 defined threats that affect the viability of populations, and presently, these are recorded for 150,388 species (IUCN Red List 2022–2). At least five of these threat categories (Threats 1, 2, 3, 6 and 7) directly reduce the amount of suitable habitat that is available to species. Some threats cause population sizes to decline (e.g., Threats 5 and 9), whilst others reduce the population connectivity (e.g., Threat 4) (see IUCN Red List 2022–2). These threats can lead to Allee effects, resulting in a reduction in individual fitness with the decline in population density, which increases the extinction risk (Berec et al. 2007). In addition, the threats recorded in the Red List also lead to genomic erosion, which might not be immediately visible due to a time-lag between the cause

of decline and the evolutionary genetic effects. Conservation scientists are aware that we may underestimate the long-term threat to species survival, which is acknowledged by terms such as the "extinction debt" (Tilman et al. 1994; Kuussaari et al. 2009).

The reduction in effective population size and the lack of gene flow between isolated subpopulations increase both genetic drift and the level of inbreeding (Lacy 1987; Stevens 2018). Both processes exacerbate each other's effects, making declining populations in fragmented habitats particularly vulnerable to genomic erosion and extinction (Saccheri et al. 1998; Van Oosterhout et al. 2000; Heinrichs et al. 2016; Niskanen et al. 2020). Genomic erosion is the damage inflicted to a species' genome or gene pool, for example, due to a loss of genetic diversity, an increase in expressed genetic load, and maladaptation (Oosterhout et al. 2022). The genetic load of deleterious variation represents a pervasive, long-term threat to the viability of declining populations (Bertorelle et al. 2022; Kyriazis et al. 2022; Oosterhout et al. 2022). It is pervasive because in nature, sexually reproducing species possess a considerable amount of deleterious variation that can cause genetic disorders, infertility, and mortality if they become expressed by inbreeding (Ralls et al. 1988; Barrett and Charlesworth 1991; van Oosterhout et al. 2000; Launey and Hedgecock 2001; O'Grady et al. 2006; Lynch 2016; Smeds and Ellegren 2022). These mutations tend to be (partially) recessive and rare in ancestral populations because they are kept at low frequency in a mutation-selection equilibrium (Bataillon and Kirkpatrick 2000). This means that a single healthy wildtype allele at the same locus renders heterozygotes (nearly) as fit as individuals without the mutation. During population decline, genetic drift and inbreeding can increase the frequency of these rare mutations and make them homozygous. However, because these mutations are initially rare, and depending on the severity of population size decline, this process can take many generations. Fundamentally, this explains why the threat of the genetic load is not immediately apparent, and why it constitutes a pervasive, long-term threat to declining populations. The time-lag of evolutionary genetic change during population size decline is sometimes referred to as the "drift debt" (Gilroy et al. 2017).

While some deleterious mutations are lost during population decline by either drift or selection (Glémin 2003) some other mutations accumulate or increase in frequency (Grossen et al. 2020; Femerling et al. 2023; Dussex et al. 2023). Hence, even though the number of loci with deleterious mutations reduces during population decline due to drift and purging, the total number of loci that are homozygous for such mutations typically increases (Mathur and DeWoody 2021; Ochoa and Gibbs 2021; Bertorelle et al. 2022; Dussex et al. 2023) (see Box 1). In addition, during metapopulation decline and population fragmentation, the rate of inbreeding increases, which reduces heterozygosity even further (Box 2). Consequently, the deleterious fitness effects of recessive mutations can become expressed even before these mutations reach a high frequency in the total population. This process may be particularly pertinent in fragmented populations (or metapopulations) because of localised inbreeding in small or isolated subpopulations. Hence, the fitness loss during metapopulation size decline in a fragmented habitat might be even worse than that of a declining population in a continuous habitat where mating is random. Understanding the conversion of the genetic load during population size decline and habitat fragmentation would help us better understand how species will respond to habitat degradation.

Here, we study the spatiotemporal dynamics of the genetic load and its components, i.e., the masked load (or inbreeding load) and the realised load (or expressed load) (Bertorelle et al. 2022). We design a spatially explicit model in SLiM for a hypothetical threatened species that experiences population fragmentation and decline, based on the well-documented habitat degradation in the island of Mauritius (Mauremootoo et al. 2003a) responsible of pushing several species to the brink of extinction, including the pink pigeon (*Nesoenas mayeri*) (Jackson 2022), the echo parakeet (*Psittacula echo*) (Raisin et al. 2012), the Mauritius kestrel (*Falco punctatus*) (Groombridge et al. 2001), and others (Cheke and Hume 2008; Florens 2013). We model habitat loss and fragmentation based on historic forage coverage data in Mauritius dating back to 1773, and we forecast the impact on the genetic load and neutral genetic diversity 200 years into the future.

Box 1—The impact of genetic drift on the genetic load and realized load

Assume a large population of a diploid sexually reproducing species with 10,000 loci that carry deleterious mutations. Each mutation has a frequency $q = 0.01$, it is completely recessive ($h = 0$), and it reduces the fitness by 2% ($s = 0.02$). If this population is in Hardy–Weinberg equilibrium, an individual is expected to be homozygous for on average one of these loci (q^2 times the number of loci), and hence, its fitness would be 98% of that of a perfect individual without any genetic load.

However, if extreme drift eroded all variation so that all loci became fixed, the individuals in this population would be homozygous for deleterious mutations at circa 100 loci. (Here we assume that the mutations drift neutrally so that the probability of fixation is equal to their initial allele frequency of $q = 0.01$.) The fitness of individuals in this drifted population would then be $w = (1$

$-0.02)^{100} \cong e^{-2} \cong 13.5\%$ that of an unloaded individual (Bertorelle et al. 2022).

However, the genetic load expressed in lethal equivalents (LE) is identical in both populations. In the large population, the genetic load equals $\Sigma qs = 10{,}000 \times 0.01 \times 0.02 = 2$ LE. The genetic load in the fixed population equals $\Sigma qs = 100 \times 1 \times 0.02 = 2$ LE. Yet, despite carrying the same genetic load, the fixed population has lost fitness because drift converted the masked load into a realised load.

In natural populations, selection would be operating against these deleterious mutations, and purging is likely to cause fewer loci to become fixed (Dussex et al. 2023). Nevertheless, unless purging is perfectly efficient, the drifted population is expected to have a lower fitness than the large population.

Box 2—The impact of inbreeding on the genetic load and realized load

In addition to genetic drift, inbreeding also changes the composition of the genetic load by altering the genotype frequencies. Inbreeding reduces the frequency of heterozygotes by $(1 - F)$, where F is the inbreeding coefficient or fixation index.

Assuming that the population was initially in Hardy–Weinberg equilibrium, the expected proportion of heterozygotes equals $2(1 - F)\,q_i(1 - q_i)$ after inbreeding, where q_i is the frequency of the allele at locus i. At the same time, inbreeding increases the frequency of homozygotes by $(1 - F)q_i^2 + Fq_i$. These equations show that as F approaches unity, the population loses all heterozygotes. Furthermore, the second equation shows that the probability of fixing the allele q in homozygous state is equal to its initial allele frequency

The change in genotype frequencies due to inbreeding also affects the realised load in the population:

$$\text{Realised load} = \left\{ \sum_{i=1}^{L} (1 - F)q_i^2 s_i + Fq_i s_i \right\} + \left\{ 2(1 - F) \sum_{i=1}^{L} q_i[1 - q_i]h_i s_i \right\}$$

In this equation, the first term shows the effect of inbreeding on the realised load present in homozygous individuals in the population, and the second term the realised load of all heterozygotes (Bertorelle et al. 2022). During inbreeding, the deleterious fitness effects of recessive mutations can become expressed even if the mutations are still at low frequency in the population. This may be particularly important in structured or fragmented populations with localised inbreeding. In other words, the genetic load and inbreeding depression pose a particularly high threat for species with declining populations in a fragmented habitat.

Materials and methods

Forward-in-time, individual-based modelling was performed using spatial, non-Wright-Fisher simulations in SLiM 3.0 (Haller and Messer 2019). Our model uses reconstructed landscape data to build a scenario that covers the deforestation of Mauritius from 1773 to 1993 (Mauremootoo et al. 2003a). In our model, individuals exist in a geographically explicit landscape, and they are affected by conditions at the local scale, following the method developed by Battey et al. (2020). We thus simulated a spatially realistic metapopulation (see Supplementary Information 1). The simulation moves in discrete time steps, and each step is equivalent to one actual year. The average generation time was 3.6 years. At each step, fitness effects are applied to the individual level, based on intraspecific competition within a radius and the quality of habitat the individual occupies (see Supplementary Information 1). The potential for mate selection, reproduction, death, and offspring dispersal occurs within a bounded radius (see Supplementary Information 2). This creates 'demes' or subpopulations in the metapopulation, which have census population size that is an emergent property of the model and its parameter settings. Depending on the dispersal ability of the offspring, habitat fragmentation leads to (partial) reproductive isolation between the subpopulations.

The genomic region modelled is based on the chromosome 23 of the collared flycatcher (*Ficedula albicolli*; (Kawakami et al. 2017)) to incorporate a realistic distribution of genomic elements and recombination map. While we do not possess a recombination map for the pink pigeon, using one from another species is a valid proxy given that bird recombination landscapes are generally conserved (Singhal et al. 2015). Three genomic regions were assigned, with mutations arising differently in each. In the intron and exon region, the ratio of neutral: deleterious mutations were 3:2 (Huber et al. 2017), with only neutral mutations in the intergenomic non-coding regions. Deleterious mutations had a dominance coefficient (h) drawn from a normal distribution with mean = 0.246, and variance = 0.134, and a selection coefficient (s) drawn from a Gamma distribution of $\alpha = 0.186$, $\beta = 0.013$. All mutations arise at a set rate $\mu = 1e{-}8$ per nucleotide per generation. These simulation parameters are comparable to those used in recent studies (e.g., Bertorelle et al. 2022; Kyriazis, Robinson and Lohmueller, 2022; Dussex et al. 2023). While our simulations incorporate realistic genomic dynamics along one chromosome, the downside of simulating a relatively small genomic region (8Mb) is that we are underestimating the total amount of load in the genome. This means that we cannot examine the effects of population size decline and

habitat fragmentation on genetic Allee effects, population viability and the extinction risk. Nevertheless, we opted for this model because of computational limitations of simulating a high load, and because it avoids population extinction. By avoiding extinction, we are better able to examine the dynamics of the genetic load (and neutral genetic variation) during habitat fragmentation and population size decline.

The ancestral population is assumed to be in mutation-drift equilibrium, which was simulated by a burn-in of 80,000 generations and modelling the habitat in its initial state at full carrying capacity. At this point, the census population size equalled N = 6255, which is somewhat smaller than the ancestral population size of the pink pigeon population (Jackson 2022). The simulated equilibrium nucleotide diversity equalled $\pi = 0.00013$. The expected nucleotide diversity for a population with Ne = 6255 equals: theta = $4Ne\mu = 0.00025$, which is almost twice the value of the simulated π. Based on the simulated π, the effective population size of the simulated ancestral population equals Ne = 3250, approximately half the census size of simulated birds (Ne/N = 0.5). This is higher than the typical Ne/N ratio, possibly because our simulated populations were close to an ideal population, e.g., with regards to the distribution of the number of offspring per breeding pair, and little background selection due to the low genetic load. Note that the ancestral population was in a mutation-drift equilibrium. Hence, the relatively high Ne/N ratio cannot be explained by the relatively inflated nucleotide diversity (compared to the census population size) observed in threatened species (e.g., Wilder et al. 2023).

Switching from the burn-in to replicate-runs caused a simulation artefact that increased the population size. To correct for this artefact, each replicate had 1000 years of stability to allow mutation-drift equilibrium to re-settle. After this period, the 40 replicates were simulated with 380 years of a stable population of size N = 10,000 ($\pm$1000), followed by 220 years of population decline. The latter period represents deforestation of Mauritius from 1773 to 1993. Furthermore, the model simulated 200 years into the future, examining the long-term impact of small, fragmented population size. Summary statistics (genetic load, masked load, realised load, heterozygosity, nucleotide diversity, and inbreeding coefficient) were calculated every ten years (Supplementary Information 3). The inbreeding coefficient (F) was estimated by identifying the percentage of an individual's genome that was comprised of runs of homozygosity greater than 100kB in a sample of 20 individuals. The realised load, masked load and genetic load were calculated using equations in Bertorelle et al. (2022).
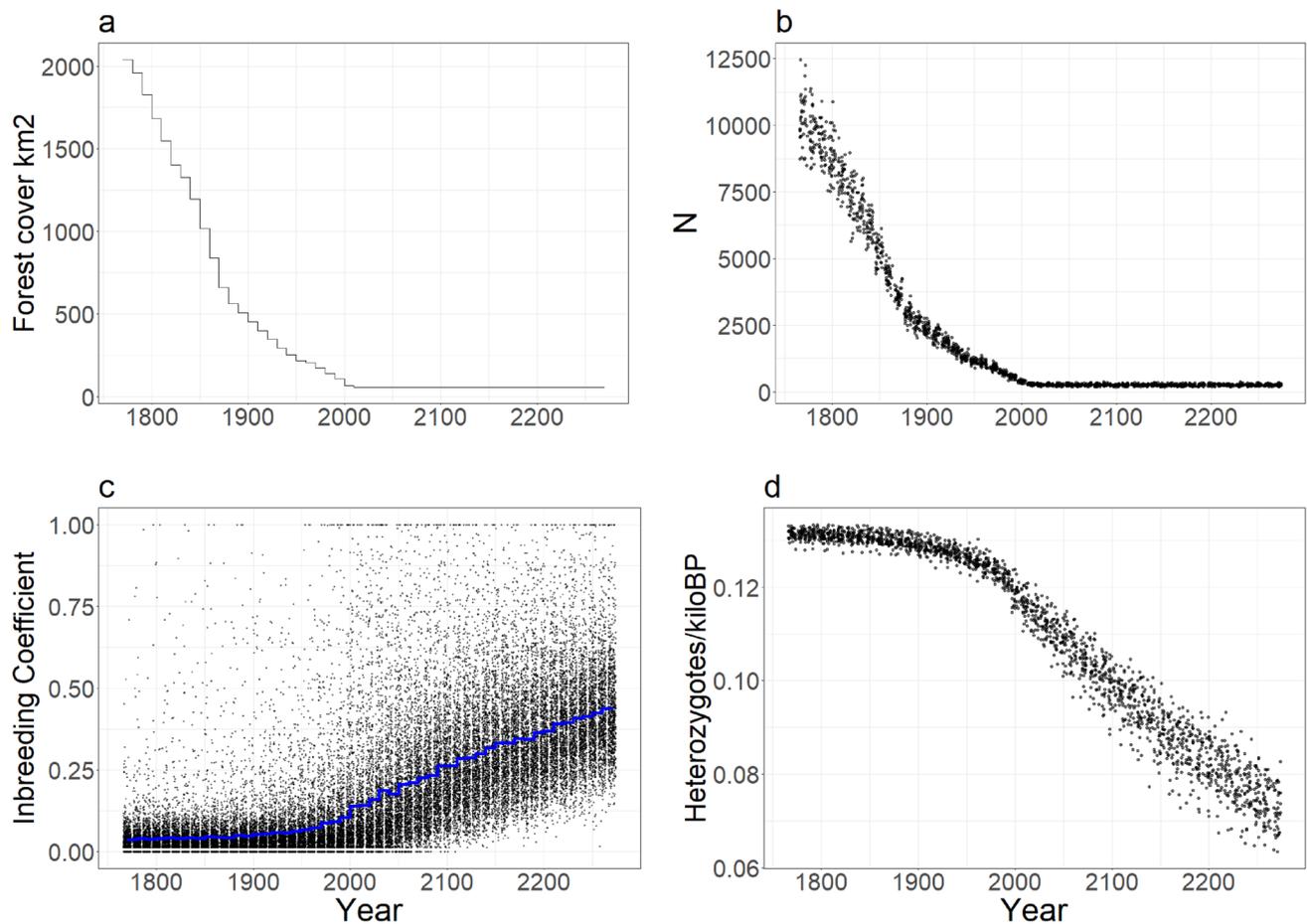
Results

The census population size (N) reduces nearly linearly with the amount of habitat loss (Fig. 1 and 2). In contrast, the inbreeding coefficient (F) and heterozygosity showed little or no change for more than 100 years of habitat loss, until the year 1900, approximately (Fig. 2). At that time, the total amount of suitable habitat was only circa 25% of the native undisturbed forest (500 km^2), and the census population size had dropped to approximately N = 2000 individuals, which is ~20% of the ancestral population size.

Interestingly, the effect of habitat loss and population fragmentation on the genetic load appeared to be slightly more delayed compared to the loss of neutral diversity (Figs. 2 and 3). The change in the genetic load is delayed because the frequency of deleterious mutations tends to be lower than that of neutral variants. Consequently, deleterious mutations that increase in frequency due to genetic drift are likely to have started from a low initial allele frequency compared to neutral alleles. Only once these deleterious alleles
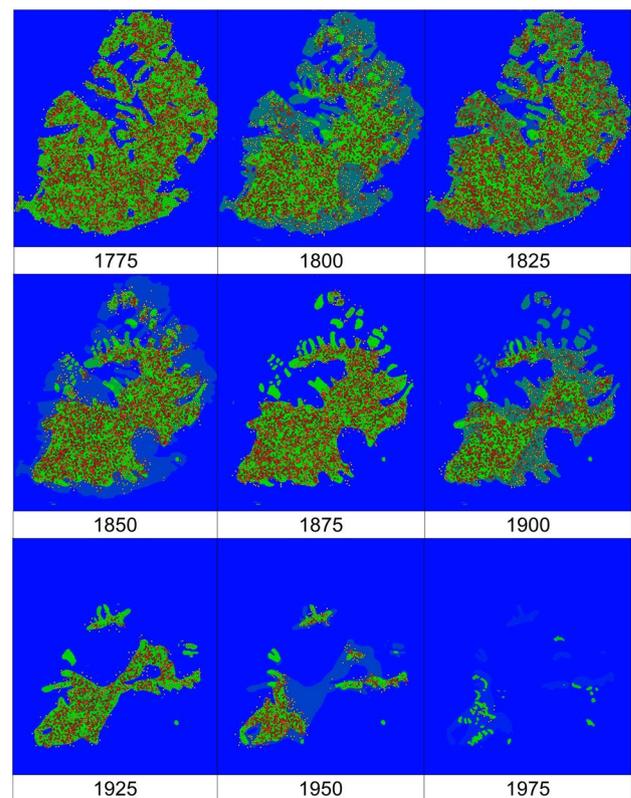
Fig. 1 Simulated habitat loss and census population size in years 1775–1955, based on forest coverage data on Mauritius (Mauremootoo et al. 2003b). The receding forested habitat is shown in shades of green, with lower quality habitat in fainter green, and uninhabitable habitat in blue. Individuals are simulated with red dots (see data repository and https://www.youtube.com/watch?v=rDm-sOzOI8g for video)

Fig. 2 **A** Habitat covered by forest, **B** census population (per replication), **C** inbreeding coefficient (individuals, blue line represents mean across replicates) and **D**) neutral heterozygosity (individuals). The simulation results are based on 40 replicates

have increased to appreciable frequencies do we observe the effects of purging (i.e., a decline in the genetic load due to purifying selection, see Dussex et al. 2023). Not until the year 2000, approximately, did we see a noticeable effect of purging (Fig. 3). The population had then reached a census population size of less than 500 birds (N = 500), and the suitable habitat was ~ 50 km², around 2.5% of that of the native forest. Around the same time, there was a marked increase in the realised load that resulted in inbreeding depression, which negatively affected individual fitness and (sub)population viability. However, because we simulated an extremely low genetic load of less than 0.1 lethal equivalents, the population managed to survive.

Discussion

In this computer simulation study, we examine the time-lag effect of habitat loss and population fragmentation on both the neutral genetic diversity and the genetic load of

deleterious mutations. We show that the loss of neutral genetic variation (i.e., heterozygosity) only becomes visible after more than 100 years of habitat loss. Furthermore, the impact of habitat loss on the genetic load only was noticeable after approximately 200 years. The difference in the time-lag between neutral and deleterious genetic variation is likely caused by the differences in their initial frequencies. If the ancestral population is in a mutation-selection-drift equilibrium, deleterious mutations occur at very low frequencies (Crow & Kimura 1970). Hence, it takes many generations of genetic drift for these mutations to increase to appreciable frequency. Consequently, the purging of the genetic load by purifying selection is also delayed relative to the loss of neutral variation.

Recently, Sachdeva et al. (2022) analysed the impact of migration, drift, and demographic stochasticity on the genetic load in peripheral populations, highlighting the importance of genetic Allee effects. In our study, we simulated a very low genetic load of less than 0.1 lethal equivalents. The simulated load is > 30 times smaller than values
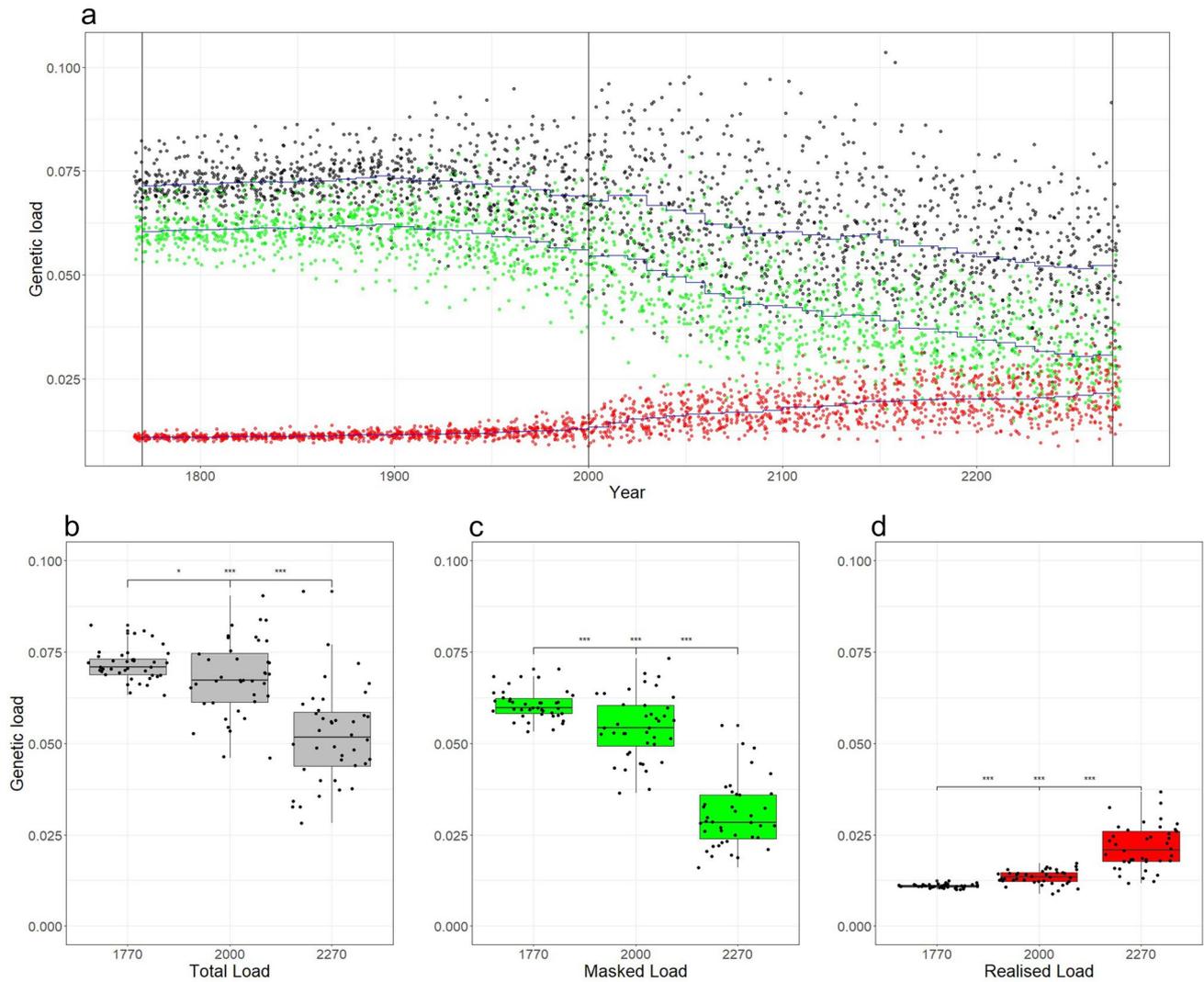
Fig. 3 a The components of genetic load measured in lethal equivalents (LEs). The genetic load is shown in grey, the masked load in green, and realised load in red. Comparison of the time-steps marked with vertical lines (years 1770, 2000, and 2270). Panel B shows that the genetic load decreases due to effective purging. Similarly, panel C shows that the masked load decreases because part of it is converted into the realised load. Although part of the genetic load is purged by selection, the realised load nevertheless increases due to increased homozygosity and the fixation of deleterious mutations. Bars between boxes represent significant differences (Welch's two sample t-test, p < 0.001, n = 80). The simulation results are based on 40 replicates

observed in captive mammals (Ralls et al. 1988), ~ 120 times smaller than the average in wild animals (O'Grady et al. 2006), and ~ 150 times smaller than the genetic load estimated for the pink pigeon in the island of Mauritius (Jackson et al., 2022). This avoids genetic Allee effects and extinctions, and it thereby also avoids the problem of generating simulation runs without data that are unusable to assess genomic erosion. Our model is simplified to ensure feasible computational times and implementation, but we acknowledge there are a number of caveats.

First, we simulated a genetic load that is under hard selection (i.e., resulting in death), whereas in nature, a proportion of the genetic load experiences soft selection, which only reduces the relative fitness (Wallace 1975). Second, we did not simulate pre- or post-zygotic selection, which is likely to play an important role in how populations cope with their genetic load (van Oosterhout et al. 2022b). Third, simulating a much higher genetic load will lead to rapid extinction of the modelled populations, yet we know that the natural population of the pink pigeon has not gone extinct despite harbouring a high genetic load of circa 15 lethal equivalents (Jackson et al., 2022). Altogether, this implies that a substantial part of the genetic load is under soft selection. In other words, if we had also simulated soft selection, we might have been able to model a more realistic genetic load. For future development of models, a significant advance can be

made by also simulating pre- and/or post-zygotic selection, and soft selection.

Although we simulated an (unrealistic) low genetic load, theoretically, the rate of load conversion due to inbreeding is independent of the magnitude of the genetic load (see equation in Box 2, and Bertorelle et al. 2022). In addition, the loss of load due to purging is also relative and unaffected by the size of the load (Dussex et al. 2023). This assumes free recombination between deleterious alleles and a sufficient excess of offspring that can be scrutinised by selection (i.e., little background selection). Given that we simulated an entire (albeit small) chromosome with realistic recombination landscape, we believe that the patterns we observed in our simulations are likely to hold true for more realistic load scenarios. Of course, real genomes and evolutionary processes are considerably more complex than those simulated here, and further research in the dynamics of the genetic load in spatially explicit populations is certainly needed. Despite these various caveats, our aim was to investigate the spatiotemporal dynamics of the components of genetic diversity in response to habitat loss and fragmentation. Accordingly, we believe we have successfully replicated the patterns predicted by population genetic theory. In particular, our spatially-explicit simulations show: (1) the stochastic loss of rare deleterious alleles by drift, (2) the purging of the genetic load by purifying selection, and (3) the conversion of the masked load into a realised load (e.g., Bertorelle et al. 2022). In addition, our simulations indicate that the impacts of some of these processes (i.e., points 2 and 3) may only become visible long after the initial habitat decline.

The genetic load is increasingly being recognised as a pervasive, long-term threat to the viability of declining populations (van Oosterhout 2020; Mathur and DeWoody 2021; Ochoa and Gibbs 2021; Bertorelle et al. 2022; Oosterhout et al. 2022; Kyriazis et al. 2022; Dussex et al. 2023). Changes in the genetic load only became visible circa 200 years after the start of habitat decline, which is much later than the observed loss in heterozygosity of neutral variation. Furthermore, the realised load continued to increase after the population had stabilised. Our simulations show that during population decline and fragmentation, genetic drift and inbreeding increase the frequency of initially rare mutations, making them homozygous, which increased the realised load. We parametrised our model based on the highly mobile pink pigeon. Species with less-mobile individuals are likely to suffer more from the effects of localised inbreeding (Sachdeva et al. 2022). This could accelerate the conversion of the masked load into a realised load and facilitate purging. Localised inbreeding in species with strong population structuring may also result in a less pronounced time-lag between habitat degradation and changes in the genetic load.

Jackson et al. (2022) also found that the pink pigeon population in Mauritius continued to lose genetic diversity, even during its population size recovery. Despite a rapid loss of genetic variation, the species was down listed twice in the Red List, from critically endangered to vulnerable. These observations highlight the discordance between the temporal genomic data and the ecological evaluation according to criteria A to D in the Red List assessment. In our simulations, the time-lag was substantial for neutral variation, and not until circa 75% of the native undisturbed forest had been destroyed, did we observe a decline in neutral diversity. Restoring declining populations in habitats that suffered extensive fragmentations is very challenging when they surpass a sensitivity threshold (Schrott et al. 2005). This threshold is a measure of the sensitivity of species' responses to habitat loss, and it is a function of the population growth rate relative to the rate of habitat loss, see Schrott et al. (2005). Here we identified a possible genetic mechanism (i.e., genomic erosion) underlaying the sensitivity thresholds and highlight the value of monitoring and managing genetic diversity during habitat loss. These findings are also relevant to spatial conservation prioritisation (see Andrello et al. 2022) by showing the inertia of evolutionary genetic change, which stresses the need for urgent habitat restoration.

In summary, our simulation study shows that genomic erosion should be considered a long-term threat to population viability, alongside the immediate threats that are presently recorded on the IUCN Red List. Although efficient purging reduced the genetic load (Dussex et al. 2023), a significant proportion of the deleterious mutations became expressed in our declining metapopulation. This elevation of the realised load occurred relatively late after the onset of habitat loss. However, it continued to pose a threat to the population also in future generations, even without any further habitat loss. In addition, the metapopulation continued to lose neutral genetic variation. Assuming that neutral diversity is a reasonable indicator for adaptive genetic variation (García-Dorado and Caballero 2021; Willi et al. 2022), the evolutionary potential of the population is also likely to become increasingly undermined (Kardos et al. 2021; van Oosterhout et al., 2022a). The fact that these processes continued to cause genomic erosion emphasises the urgent need of habitat and ecosystem restoration. We are in the UN's Decade on Ecosystem Restoration, and our study shows that we need to urgently restore habitat, which will help save species from future extinction.

Declarations

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