



Minimum number of generations to start detecting purging

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BACKGROUND

Minimum viable population (MVP) sizes have been proposed to determine whether endangered populations are likely to survive, e.g. the 100/1000 rule (Frankham et al. 2014). However these recommendations do not take into account genetic purging, which requires inbreeding (and time) to potentially reduce the inbreeding load, allowing for the survival of smaller populations.

How it was deduced

Ancestral inbreeding (F_a , Ballou 1997) indicates the fraction of the genome that has been exposed to inbreeding in the past, at least once in at least one ancestor, and can be used to detect purging.

Following López-Cortegano et al. (2018), it can be estimated as:

$$F_a = 1 - \left(1 - \frac{1}{2N}\right)^{\frac{1}{2}(k-1)}$$

This parameter increases exponentially with time as a function of t^2 . Thus, a narrow window of time where most purging occur is expected, before F_a reaches its asymptotic value at $F_a = 1$.

That time window correspond to the range of generations that make $F_a > 0$, being $F_a = \left(t - \frac{1}{2}\right) \left(F_a - 1\right) \log \left(1 - \frac{1}{2N}\right)$ the first derivative of F_a .

F_a has a maximum value that can be taken as a time point around purging is expected to occur faster, increasing the opportunity for it being detected, compared to previous generations. This maximum can be obtained by equating the second derivative of F_a to zero, being $F_a'' = 1 + \left(t - \frac{1}{2}\right)^2 \log \left(1 - \frac{1}{2N}\right)$.

Solving for the number of generations t :

$$t = \frac{1}{2} + \sqrt{\frac{1}{\log \left(1 + \frac{1}{2N} - 1\right)}}$$

Which can be approximated to:

$$t \approx \sqrt{2N}$$

Purging is expected to start becoming relevant at time:

$$t \approx \sqrt{2N_e}$$

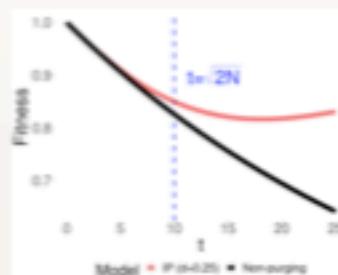
CONCLUSIONS

- Purging is not expected to become relevant before $t = \sqrt{2N_e}$ generations after a bottleneck.
- A complete evaluation of the viability of small populations should be made considering not only the population size alone, as time is important for both evaluating inbreeding depression and genetic purging.

Validation with alternative purging models

The inbreeding-purging model (IP, García-Oráñez 2012) allows to predict the decline of inbreeding load, as well as the change of fitness over time under inbreeding and purging selection, as a function of a purging coefficient (d) that equals Falconer's degree of dominance $d = \frac{1}{2}(1 - 2h)$.

Always that $d > 0$, a minimum value of fitness is predicted from where a partial recovery is expected. However, the recursive nature of the functions under the IP model do not allow to estimate the moment when that recovery is expected.

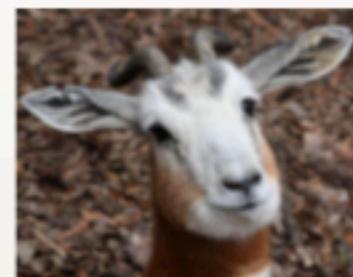


From evolution over time (t) in a simulated population of $N_e = 50$ and inbreeding load $\delta = 6$ following two models: a non-purging model (in black), and a purging model with $d = 0.25$ (in red). The blue dashed line indicates the minimum number of generations to observe purging.

The estimated minimum number of generations to start detecting purging fits well the time point when fitness is expected to be minimum (see Figure above), and the frequency of deleterious alleles in homozygosity is maximum. That observation holds for varying N_e and d .

Examples on real data

The expression $t = \sqrt{2N_e}$ helps explaining why some studies have failed detecting purging. For example, Bailes et al. (2007) did not find significant purging in a meta-analysis of 119 zoo populations, but in these the median N_e was 22.6, and the t was 3. On the other hand, fitness recovery was observed in a *Drosophila* experiment with $N_e = 43$ at $t = 20$ but not yet in $t = 10$ (López-Cortegano et al. 2018). Purging is also expected to be more efficient with slow inbreeding (López-Cortegano et al. 2018), although it delays more time to become apparent.



We are currently working on a inbreeding-purging analysis for four endangered species of ungulates, including the Dama gazelle (Nanger dama, picture above). These populations have extremely low sizes (e.g. $N_e = 9$ for *N. dama*).

Preliminary results show evidence of purging on records with 5-7 equivalents to complete generations (more than 40 years), changing our expectation on survival of these species.

There is hope for populations with extremely low population sizes, but enough records are required to properly measure purging.

References

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