Simulation Suggests that One-Off Simple Supplementation from the Wild into Captive Population May Not Increase Captive Genetic Diversity

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Abstract

Loss of genetic diversity in captive population due to inbreeding is a concern to commercial farming. Supplementation from the wild, which is deemed to be more genetically diverse, into captivity has been proposed as a method to increase genetic diversity in inbred captive populations. Here, we examine the possibility of a one-off supplementation by maintaining the increased captive population size for the period of one generation after supplementation using computer simulations on 50 markers of 10 equally proportioned alleles each. Our results suggest that one-off supplementation is not likely to increase the genetic diversity of captive population and we also observed that the genetic diversity of captive population may reduce proportional to supplementation ratio.

Keywords: *Captive Population; Inbreeding; Genetic Diversity; Supplementation; Computer Simulations*

Introduction

Inbreeding in captive population is of constant concern in many areas [1], spanning across conservation biology [2,3] to commercial farms [4]. Studies had demonstrated higher degree of inbreeding in captive population compared to wild population. For example, the average number of alleles and allelic richness in pikeperch [5] and Atlantic salmon [6] were significantly lower in farm stocks as compared to the wild population. This is likely to be the result of founder effect where a subset of the population form a new colony, leading to an alteration of allele frequency is altered and potential decrease in genetic diversity [7]. This is more pronounced in small isolated populations [8,9]. However, this trend is commonly seen in aquaculture where cultured fish often cross-fertilize without any inflow of new broodstock [10-12], leading to multiple detrimental effects [13].

Although inbreeding is also possible in wild populations [14-16], it is generally deemed to be more genetically diverse compared to captive populations. This led to suggestions to supplement captive from the wild [17] to increase genetic diversity, leading to lowered inbreeding. However, this requires further study [15].

In this study, we examine the effects of one-off simple supplementation from the wild into captive population in terms of genetic diversity using computer simulations, which are commonly used in the study of inbreeding [18-20] and evolution [21-24]. Our simulation results suggest that one-off simple supplementation while keeping population size constant is unlikely to increase genetic diversity. Moreover, genetic diversity may be inversely proportional to supplementation ratio.

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Methods

Genetic diversity is simulated using the software, Island [25], which had been used in a previous study [15]. Three captive sizes (500, 5000, and 50000 organisms) of five replicates, total of 15 populations, were generated with 50 genetic markers. Each marker had 10 alleles of equal proportion. For each population, 20 generations were simulated with population size kept constant throughout the simulation. Chi-square statistic was calculated for each generation using the uniform allelic frequency as expected while the allelic frequencies in the population for each generation were used as observed values [26-28]. To compare results from different simulations, normalized Chi-square value was calculated from Chi-square statistic as a quotient of Chi-square statistic and the degrees of freedom. A population of 1 million organisms was generated using the same allelic frequencies (50 marks of 10 alleles of equal proportions) as wild population. A sample equivalent to 10%, 17.5%, or 25% of the captive sample size were randomly selected from the population and supplemented to the captive population at generation 5 and simulated for another 15 generations. The captive population size remains constant and kept at that of pre-generation 5 for the subsequent supplemented generations.

Results and Discussion

Number of organisms tested is critical in measuring the degree of inbreeding

Our initial results suggest inbreeding in all 3 sample sizes (500, 5000, and 50000) throughout 20 generations (Figure 1A) as the mean normalized Chi-Square value increased in a linear line, which is similar to that in previous study [15]. However, Chi-Square statistic is known to be sensitive to large sample size [29]. To illustrate, we consider an example of 49% tea drinkers versus 51% coffee drinkers in the population and testing against the null hypothesis of equal preference. 100 participants will give a non-significant Chi-Square statistic of 0.04 (p-value = 0.841) while 10000 will give a significant Chi-Square statistic of 4.0 (p-value = 0.0455).

Hence, it may be plausible that the estimated inbreeding is a result of large sample size (500 organisms vs 50000 organisms). As such, we selected a random sample of 50 (typical experimental capacity of a single researcher) from each generation regardless of population size to evaluate for inbreeding. Our results suggest that only the smallest population size (n = 500) show significant inbreeding throughout the 20 generations (Figure 1B); hence, a suitable case to evaluate the effects of one-off naïve supplementation. This is consistent with small population size demonstrating higher inbreeding and lower genetic diversity compared to larger populations [30]. However, the relationship between population size and sample size requires further studies.
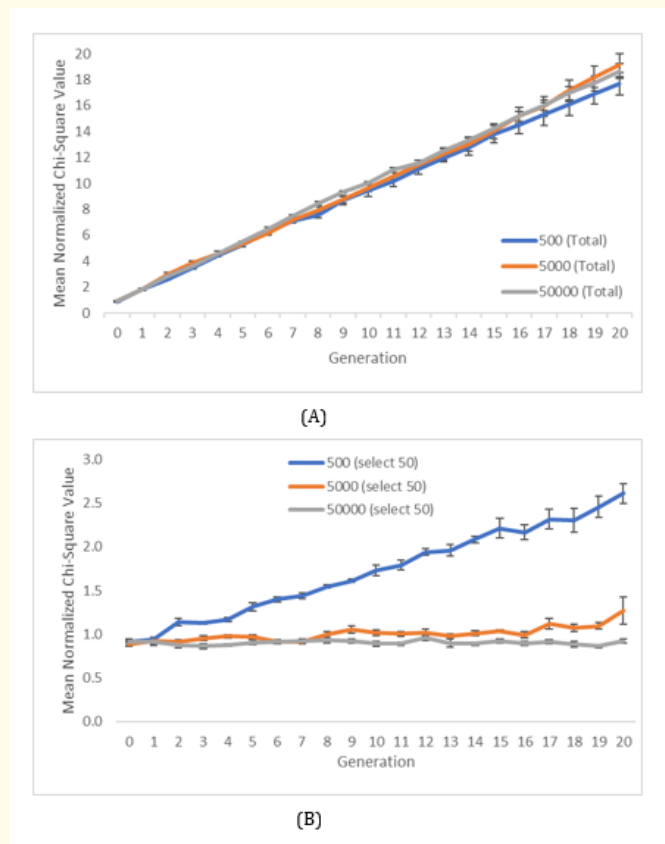

Figure 1: *Effects of sample size on estimated inbreeding. Panel A shows the degree of inbreeding by testing the entire population while Panel B show the degree of inbreeding by testing on a sample of 50 organisms regardless of population size. Error bar represents standard error.*

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One-off simple supplementation may reduced genetic diversity

Using the populations of 500 organisms, we examined whether can simple one-off supplementation at the 5th generation can reduce inbreeding from the 6th generation. The simpleness is due to population size where the population increases immediately after supplementation but was reverted to 500 from the 6th population. In practice, this is like supplementing an inbred fishpond with wild population, allowing to mate and kept the population constant at pre-supplementation. If one-off simple supplementation can reduce inbreeding, we expect to see a significant decline in the slope of mean normalized Chi-Square value from generation 6 to 20 leading to an overall decline in mean normalized Chi-Square value.

Our results no significant difference (Figure 2; t = 1.437, p-value = 0.162) between no supplementation (slope = 0.0837) and 10% supplementation (slope = 0.0884), suggesting that one-off simple 10% supplementation is unable to reduce inbreeding. However, it may be plausible that increasing supplementation ratio may reduce inbreeding. Yet, our results show that 17.5% supplementation increases the slope (slope = 0.147) significantly (t = 13.5, p-value = 3.089E-13) rather than the expected decrease, and 25% supplementation also increases the slope (slope = 0.227) significantly (t = 25.0, p-value = 1.020E-19). Moreover, there is also a significant increase in slope (t = 12.6, p-value = 1.370E-12) between 17.5% and 25% supplementation. This suggests that one-off simple of higher supplementation ratios (17.5% or 25%) are unable to reduce inbreeding. More importantly, the degree of inbreeding may increase proportionally with supplementation ratio.
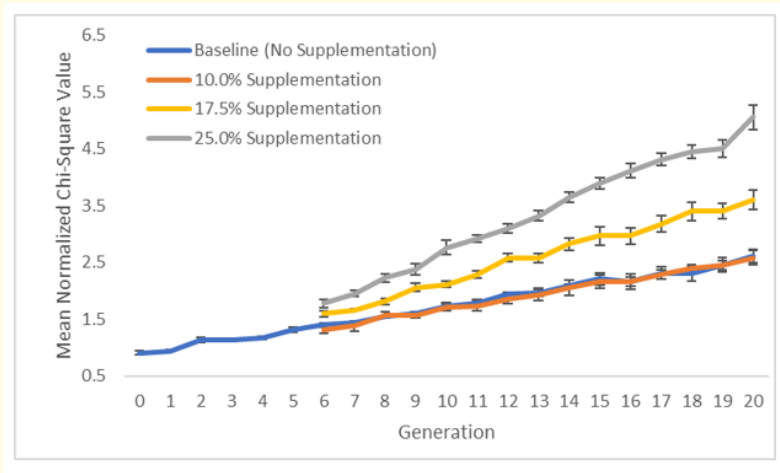

Figure 2: *Degree of inbreeding is inversely proportional to supplementation ratio. 10%, 17.5%, and 25% represents 50, 88, and 125 organisms supplemented into the 5th generation of 500 organisms. Error bar represents standard error.*

Hence, our results suggest that one-off simple supplementation from the wild is unlikely to increase genetic diversity of captive populations. Moreover, it may unexpectedly reduce genetic diversity. However, repeated supplementation [31] or more elaborate genetic rescue schemes [32-34] may work but this requires further studies. Despite so, our results can act as baseline to evaluate other methods to reduce inbreeding in captive populations.

Conclusion

Our results suggest that one-off naïve supplementation while keeping population size constant is unlikely to increase genetic diversity in captive populations. In fact, our results suggest a possibility of genetic diversity is inversely proportional to supplementation ratio.

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Supplementary Materials

Data files for this study can be downloaded at http://bit.ly/GeneticDriftB.

Conflict of Interest

The authors declare no conflict of interest.

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Volume 6 Issue 7 July 2021