

A Simulation Study on the Effects of Founding Population Size and Number of Alleles Per Locus on the Observed Population Genetic Profile: Implications to Broodstock Management

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Abstract

Loss of genetic variability in small population, known as founder effect, is commonly seen in aquaculture, where broodstocks are not routinely supplemented from the wild, leading to detrimental effects. Yet, the relationship between founding population size and observed population genetic profile is not clear. Here, the effects of founding population size and number of alleles per locus on the observed population genetic profile across multiple generations were examined using simulation. Our results suggest that the number of alleles per locus (p-value = 1.2E-102) and generation counts (p-value < 1E-240) are significant factors in genetic drift but not founding population size (p-value = 0.12). This suggests that genetic drift occurs regardless of population sizes, which may have implications in broodstock management to constantly minimize the impact of genetic drift regardless of broodstock population.

Keywords: Genetic Variability; Founder Effect; Broodstock Population; Alleles Per Locus

Introduction

Evolution is the change of genetic variations and allele frequencies in a biological population over generations, giving rise to the variety of phenotypes [1]. The main driving forces are natural selection, biased mutation, gene flow and genetic drift [2], which are dependent on the existing variations within the population [3]. Natural selection is the adaptation of suitable phenotypes to the environment leading to improved survival and reproduction [4]. Mutation is the change in genetic sequences, which may give rise to new phenotypes [5,6]. Gene flow is the transfer of alleles, which are alternative forms of the same gene, from one population to another [7]. Genetic drift is the random change in the frequencies of existing alleles in a population [8,9] and its effect of genetic drift is the greatest in small populations [10].

There are two crucial types of genetic drift [11] - bottleneck and founder effect. Bottleneck occurs when the size of a population severely is decreased leading to a change in allelic frequencies in the survivor population, leading to potential further loss of phenotypic variation in the survivor population [12]. Founder effect occurs when a subset of the population form a new colony, leading to an alteration of allele frequency is altered and potential decrease in genetic diversity [13]. Both bottleneck and founder effect are result of small initial population size as genetic drift is more pronounced in small populations [14]. This is commonly seen in aquaculture where cultured fish often cross-fertilize without any inflow of new broodstock [15-17], leading to multiple detrimental effects [18].

However, the relationship between founding population size and observed population genetic profile is not clear. Computer simulations have been commonly used in the study [19-23] and teaching [24] of genetic drift and evolution. Hence, the study aims to examine the effects of different population size and different number of alleles per locus on the population genetic profile across multiple generations using simulation. Our results suggest that genetic drift occurs regardless of population size.

Methods

Genetic drift is simulated using the software, Island [25]. Diploid organisms each containing fifty loci with uniform allelic frequencies were simulated. The number of alleles per locus ranged from 2 to 10, resulting in allelic frequencies at each locus to be 50% to 10%. Eight population sizes (1000, 2000, 4000, 8000, 16000, 32000, 64000 and 128000) were generated for each allelic frequency, resulting in 72 populations in total (8 population sizes of 9 allelic frequencies). For each population, 10 generations were simulated. The population size was kept constant during 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. 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.

Results and Discussion

Our simulation results show that the normalized Chi-square value increases over generations regardless of the number of alleles per locus or the population size (Figure 1). Importantly, the degree of genetic drift is not proportional to population size. This suggests that genetic drift is likely regardless of population size of up to 128 thousand organisms, which is supported by Kvie., *et al.* [26] showing genetic drift in relatively large wild populations of Norwegian wild reindeer. This may imply that a null hypothesis of no genetic drift, which is equivalent to normalized Chi-square value of zero, may not be suitable. Instead, a simulated genetic drift of a sufficiently large population may be better suited as null hypothesis.

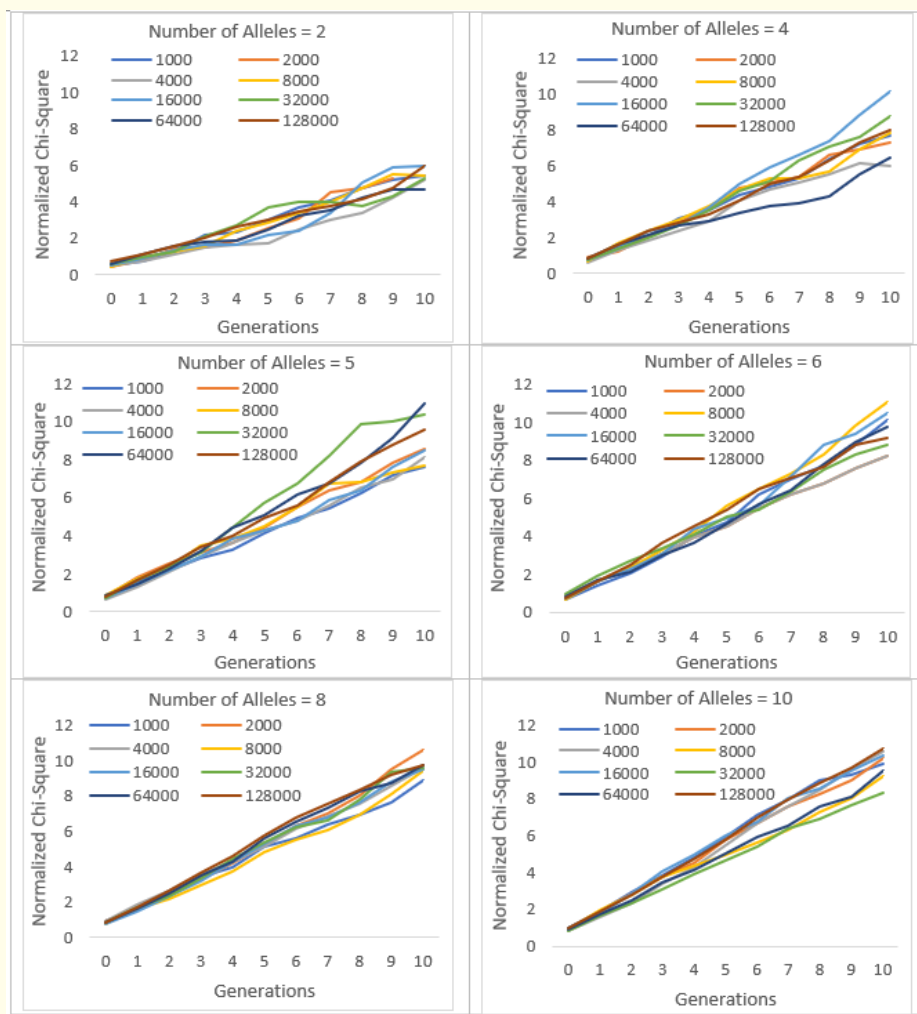


Figure 1: Normalized chi-square values for varying population sizes with different number of alleles per locus.

Regression analysis shows that the normalized Chi-Square value is significantly correlated (R-square = 0.9166, F = 2887, p-value < 1E-240) to all three regressors; namely population size, number of alleles per locus, and generation; yielding the regression model, normalized Chi-Square = 1.077E-6 (Population Size) + 0.2706 (Number of Alleles per Locus) + 0.7887 (Generation) - 0.9476. However, only number of alleles per locus (t = 25.1, p-value = 1.2E-102) and generation count (t = 89.6, p-value < 1E-240) are significant but the population size is not significant (t = 1.60, p-value = 0.12). This is consistent with our findings that genetic drift is likely to occur despite large population size. More importantly, our result highlights the impact of allelic richness in terms of the number of alleles per locus on genetic drift.

Taken together, our results suggest that genetic drift is a reality in broodstock management. This is supported by studies showing population genetic differences between domesticated and wild populations. For example, An., *et al.* [27] examined 233 black rockfish across 10 microsatellite loci in a hatchery facility in South Korea and found significant genetic differences between the parent and offspring populations. Molnár., *et al.* [28] average number of alleles and allelic richness in pikeperch were significantly lower in the pond cultured stocks as compared to the wild population. Similar trends had been observed between farmed and wild Atlantic salmon [29]. This has led to suggestions to routinely supplement broodstock from the wild [30] to reduce the impact of genetic drift in captive populations. However, this requires further studies. Importantly, our results suggest the need to monitor broodstocks for genetic drift regardless of the size of broodstocks.

Conclusion

The results from this study imply that allelic richness and population count have more significant impact on genetic drift than population size. Moreover, genetic drift is likely to occur regardless of population size, which calls for constant monitoring in broodstock management.

Data Availability

The data files for this study can be downloaded at <https://bit.ly/GeneticDriftA>, which is a zip file containing a folder; Parameter Files, where each parameter file contains the allelic frequencies to generate a population, and an Excel file containing the tabulated results from simulation.

Conflict of Interest

The authors declare no conflict of interest.

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