Analysis of Lethal Recessive Alleles in Petroica traversi

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*Abstract*

Black robins are an endangered species that were wiped out when mammals were introduced by humans on the Chatham Islands in New Zealand. The population declined rapidly and was moved to the Mangere Island where they began to thrive again. However, inbreeding in the population began to increase and lethal recessive alleles became significant in offspring survival. Three populations of black robins were observed and analyzed using RStudio to determine the effects of inbreeding. The frequency of these lethal recessive alleles showed to be higher in the ancestors of the black robin population than in the new offspring.

*Introduction*

The *Petroica traversi*, or known as the black robin, is a highly inbred population located in the Chatham Islands of New Zealand. Based on available data from free-living bird populations, this population has the highest degree of shared relatedness ever recorded at this time. (Kennedy, 2013). The development of inbreeding was led by the arrival of humans to the island bringing a variety of mammalian predators, such as cats and rats (Kennedy, 2013; Lawrence, 2017; Massaro, 2017 & 2018). Sturnus vulgaris, or starlings, are competitors of black robins who destroy nests, break eggs, and kill chicks (Lawrence, 2017; Massaro, 2018). These predators and competitors preyed on the black robins causing the population to rapidly decline until in 1893 when the black robins had been moved to Little Mangere Island (Lawrence, 2017; Massaro, 2018). In 1893 the black robins were moved to Little Mangere Island where the remaining population was managed and given access to more suitable conditions (Kennedy, 2013).

Homozygosity is increased as a result of inbreeding which increases the risk of recessive or deleterious traits being transmitted to offspring. The result is a temporary decline in the biological fitness of a population, called inbreeding depression, which is its ability to survive and reproduce. This includes lethal recessive alleles being inherited throughout generations. Lethal recessive alleles contribute to the increased risk of premature death of organisms who inherit them. The hypothesis of this paper is the frequency of lethal recessive alleles will increase from ancestors to new offspring.

*Methods*

The analysis done in this study was focused on the survival of offspring with lethal recessive alleles. The authors created a pedigree of 1,345 individuals whose inbreeding goes back to at least their grandparents. By analyzing the proportion of fledglings that survive one year of age, they were able to examine the effects of inbreeding on the survival of first yearlings using a generalized linear mixed model, which shows estimated fixed and random effects. The amount of inbreeding is expressed as the number of lethal equivalents, which is the number of deleterious genes per haploid genome whose cumulative effect is equivalent to one lethal gene. Lethal equivalents were calculated using slopes of regressions on survival and recessive lethal allele frequencies were measured.

In this paper the frequency of lethal recessive alleles in the offspring’s ancestors and the offspring are compared to determine if the lethal recessive alleles continue to increase in frequency throughout generations. The paper’s data was downloaded from the paper “Severe Inbreeding Depression and No Evidence of Purging in an Extremely Inbred Wild Species—the Chatham Island Black Robin”, saved as a Microsoft Excel file and then the recessive allele frequency data of the offspring and ancestors were read into RStudio. After reading the data in RStudio a linear regression graph was created to compare the frequencies of lethal recessive alleles in ancestors and offspring data sets together. The data was taken from three generations the grandparents, the parents, and offspring from all three original sites. A correlation test was used to determine a relationship between the number of lethal recessive alleles in ancestors and offspring.

*Results*

The ancestors maintained higher lethal recessive allele frequencies than the offspring did (Fig. 3). As the lethal recessive allele frequencies get higher in the offspring the presence of these alleles decreases, whereas the ancestors show to have higher presence of lethal recessive allele frequencies. The correlation results showed a negative correlation between ancestor and offspring (t = -17.321, p < 2.2e-16). This futher supports that the figure below as one variable decreases (offspring) as another increases (ancestors). The p value is lower than 0.05 therefore showing this relationship is significant. Therefore, inbreeding is playing some role in the inheritance of these lethal reccessive alleles. However, these new results may infer that inbreeding isn’t the only significant factor in inheriting these lethal reccessive alleles. As genertations continue you would expect to see more offsrping having higher frequencies of lethal reccessive alleles if inbreeding played a higher role.

Chart, scatter chart

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*Figure 3*. The frequency of ancestor lethal recessive alleles and offspring lethal recessive allele frequency.

*Discussion*

Three populations of black robins were observed, and their data was run through simulations in RStudio to determine the effects inbreeding has on the offspring. The more inbreeding, the more lethal recessive alleles were thought to be passed down in generations. However, the data showed these lethal recessive alleles were increasing as generations continued. The ancestors maintained higher lethal recessive alleles than the offspring did (Fig. 3). This did not support my hypothesis as I thought the lethal recessive alleles would increase in newer generations due to the rapid inbreeding in the populations. As stated, before inbreeding decreases heterozygosity which would increase more homozygous alleles being expressed. This provides us with further information that there is more involvement in increasing lethal allele frequency than passing on these alleles in a highly inbred population. Therefore, when going into future populations of inbred species researchers can focus on other factors that affected the rise of lethal recessive alleles than inbreeding itself.

The reason the results turned out this way could be because of having two generations being compared to total ancestral lethal recessive allele frequency instead of having more generations tested in the populations. There also could’ve been unrecorded migration that rook place before and during sampling. To further this study, one could compare the different generations to each other to see exactly how much the lethal recessive allele frequency goes increases or decreases between generations. This could give a better idea of how inbreeding is affecting these lethal recessive alleles.

*References*

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