Aiyanna Vaughan

Writing Assignment 3

Dissemination of genetic disorders is a major concern in domestic animal species. It has been recognized that genetic disorders of animals have a social as well as an economic impact on producers, consumers and owners. Once a disease has reached a high frequency within a breed, it is extremely complicated and expensive for breeders to eliminate it. The article “ *Mating practices and the dissemination of genetic disorders in domestic animals, based on the example of dog breeding*” highlights the investigation into simulations and genealogical data of ten dog breeds, three popular mating practices (popular sire effect, line breeding, close breeding) and their effects on the dissemination of genetic disorders. The main goal of this investigation was to investigate the effects of some common breeding practices on dissemination or purging of deleterious alleles, using several dog breeds as examples.

The first step into this investigation was to investigate the occurrence of the mating practices popular sire effect, line breeding, and close breeding in ten dog breeds raised in France. Then, by using computer simulations, the authors aimed to study the effects of such practices on the dissemination and possible purging of deleterious alleles and make statements about the currently unknown risk of popular breeding practices with regard to dissemination of unfavourable alleles. To do this they first started with ten breeds with different population sizes and origins chosen from the genealogical database of the French Kennel Club.

They started by simulating a single gene with two alleles, one of which was recessive and lethal, determining that homozygous affected individuals would die without reproducing. The conditions were one locus per animal and to set the initial frequency of the lethal allele in a base population to 2%, meaning that under random mating conditions, within 1000 births, 0.4 individuals would die and would therefore not be considered as potential parents. The dissemination risk was defined as the risk as the percentage of simulation runs in which the allele frequency of the lethal allele reached 5% in any generation, meaning that under random mating conditions, in every 1000 births, 2.5 individuals would die. To create the next generation, two lists, consisting of 800 potential dams and 400 potential sires, were randomly sampled from the base population. Effects of the three mating practices were then investigated separately, each simulation starting with a base population as described above, followed by one generation under random mating conditions.

After running a series of simulations, it was found that each of the three practices investigated seems to speed up the decrease in deleterious allele frequency in relation to an increase in the number of deaths/homozygous individuals during the first generation, with this number decreasing after some time. However, there were large differences between the ways each practice influenced the set parameters. It was also found that the increase in average number of deaths was more dramatic in the former generations of the close breeding simulations.  In comparison, the evolution of the three parameters under line breeding conditions was similar, but the evolution under close breeding conditions was more noticeable. It was confirmed that the popular sire practice leads to a dissemination of genetic disorders, contrary to line breeding and close breeding practices.

In light of this information it has been recommended that the overuse of certain reproducers should be limited. This goes for limiting the amount of litters of puppies sires can reproduce. It should also be noted that the practices of line and close breeding largely decrease the risk of dissemination.

References

Leroy, G., and R. Baumung. “Mating Practices and the Dissemination of Genetic Disorders in Domestic Animals, Based on the Example of Dog Breeding.” *Wiley Online Library*, John Wiley & Sons, Ltd, 11 Jan. 2011, onlinelibrary.wiley.com/doi/full/10.1111/j.1365-2052.2010.02079.x.