

Dominant and recessive alleles experiment



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DiscussionPart A

The number of dominant genes was constant from one generation to the next. It remained at a number of 50 alleles considering that all Bengal tigers with the dominant allele (H), survived to pass on the gene. On the other hand, the frequency of the dominant allele increased over the ten generations. The frequency of the dominant allele during the first generation was 0.50, but by the tenth generation, the frequency increased to 0.93. This was because all the offspring with the homozygous recessive genotype weren't able to survive. As generations passed by, the gene pool grew smaller, the number of the recessive alleles also decreased, however the number of dominant alleles remained the same; resulting in an increase of the "H" allele frequency.

The number of recessive genes generally decreased from one generation to the next. However, there were a few cases where it stayed the same; if no offspring with the homozygous recessive genotype was produced in that generation. In generation one, the number of recessive alleles was 50, but by the tenth generation, the number decreased significantly to only 4. Similarly, the frequency of the recessive allele decreased as well, considering that only the homozygous recessive cubs died while the homozygous dominant cubs survived to reproduce. In the beginning, the frequency number was 0.50, by the tenth generation the number was to 0.07. The frequency of the recessive allele would be zero permanently for all future generations, if the recessive gene became extinct. All members of the population would be homozygous dominant in the absence of the recessive allele; hence the <https://assignbuster.com/dominant-and-recessive-alleles-experiment/>

frequency would be zero as there would be no chance of producing heterozygous or homozygous recessive offspring within the population. In this case, the dominant allele would be considered as a fixed allele with a consistent frequency of one (“Fixed Allele,” 2014).

As emigration and immigration came into play, the gene frequency of “H” and “h” in the tiger population either increased or decreased. As the population accepted new members, the frequency of the alleles increased considering that additional genes were being added to the existent gene pool. Moreover, as members of the population left the group, the frequencies decreased considering that as the size of a population decreased; its gene pool would shrink.

Part B

According to the Hardy-Weinberg principle, it was expected that the derived population would contain equivalent proportions of the dominant allele (red candy) and the recessive allele (green candy). Considering that the frequency of the dominant and the recessive allele were the same, 0.50; ($p + q = 1$), the two alleles should have equal probability of getting chosen to be a part of the derived population. Therefore in a population of 20 genes, 10 should be dominant and 10 should be recessive, while in a population of four genes, two should be dominant and the other 2 recessive.

The actual results differed from the expected results. It was predicted that in the smaller populations, there would be equal amounts of the dominant and recessive alleles considering that the two started off equally with the same frequency number; equal potential of getting chosen. However, the actual

results revealed that it was impractical for the number of the dominant and recessive alleles to be equal in the smaller populations. Out of eight derived populations of 20 genes, only two consisted of equal amounts of “ H” and “ h” alleles. Furthermore, out of the eight derived populations of four genes, only one had the expected result with two dominant and two recessive alleles. In all the small populations of 20 genes, the amount of dominant to the amount of recessive were fairly close to each other (ex. 8: 12), if not precisely the same. However, for the small populations of four genes, there were two extreme outcomes where either the dominant or recessive allele was absent in the population resulting in the presence of a fixed allele (ex: 0: 4).

The expected results or the theoretical probability of the allele frequencies was only an effective method of estimating the results based on the given information. It was a calculation derived from a theory, and therefore it did not always represent the actual results. However, it did provide an idea of the likelihood for a situation to occur. For example, the subject would know that the allele frequencies for the majority of the derived populations should be close to 0. 50.

It could be possible for a small population to produce a large population in one generation, however highly unlikely, also it would depend on the kind of organism. In this case, the life span of a tiger was approximately 20 years old and it took about 16 weeks for cubs to be born. Furthermore, tigers did not have a fixed mating season and females could produce one to seven cubs per litter (“ Tiger Reproduction,” 2014). Therefore, it was possible for a small population to produce a large number of offspring, however not all will

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survive. The more cubs the females would have to take care, the higher the mortality rate of the offspring. Hence, it would be extremely improbable for all the offspring produced to survive long enough to reproduce.

A population bottleneck would present similar fluctuations as a genetic drift. A bottleneck effect could be defined as a drastic decrease in the size of a population due to human activities, an inability to reproduce offspring fit enough to survive, or natural disasters such as earthquakes, floods, and droughts (“ The Genetic Variation,” 2013). This would further limit the variation in the gene pool of the population and could even cause the population to become extinct, considering that the smaller the population, the higher the chance for inbreeding to occur in the population. The process of inbreeding would result in the accumulation of the hidden, unwanted and harmful alleles in the population. Furthermore, the population’s ability to adapt to fluctuating environments and new selection pressures would decrease due to the loss of genetic variation within the population (“ Population Bottleneck,” 2014). Another form of the bottleneck effect is the founder effect; where a small group from a population decided to establish a new population separated from the main population resulting in a great loss of genetic variation (“ Population Bottleneck,” 2014). Hence, it would be extremely difficult for a small population to be able to produce a large population in a few generations.

Part C

The percentage of each allele gave a better idea of the genetic make-up of a population considering that it simplified the total number to 100. Therefore,

a percent could be defined as a portion of every 100, knowing that the total number would always be constant; it'd be easier to visualize the genetic make-up in one's mind. For example, the use of a pie charts. Furthermore, percentages were comparable; the higher number always showed that certain gene dominated a large portion of the population and approximately how large (ex. $\frac{1}{2}$ of the population). On the other hand, the numbers of each allele did not give the observant much immediate information about the genetic make-up of the population. The subject would have to calculate the total number of alleles first, in order to achieve a vague idea of which gene was the most frequent in the population. However, when comparing the genetic make-up between the original population and after the bottleneck effect, the use of percentages gave a lot more information than the numbers of allele considering that the total number of alleles differed in the two scenarios.

For most of the alleles, the allelic frequency increased after the bottleneck effect, while for others, it decreased. The alleles that experienced an increase in their allelic frequency were orange, red, blue, pink and purple. The alleles that showed a decrease were white and green. The allelic frequency for yellow stayed the same considering that the allele was extinct.

The alleles left in the bottle were wiped out of the population and weren't included in the small population. The small group could have been geographically separated from the main population or the few survivors of the population after a catastrophe such as an earthquake.

The death of a small number of individuals in the large population would have little effect on the gene pool of the population. However, if those certain individuals possessed a specific gene that was rare in the population, then it would have a larger effect on the gene pool and the allelic frequencies of that population. For example, the rare gene could gradually become extinct since it was already low in quantity in the population.

A few long-term consequences of the bottleneck effect on a population included; an increased chance of becoming extinct, a loss of genetic variation, a loss of rare alleles, a greatly limited gene pool, and lastly a reduced potential to adapt to new environments or new selection pressures such as climate changes and a change in resource abundance (“ Population Bottleneck,” 2014).

Conclusion

It could be concluded that gene frequencies and the size of the gene pool of a population could have a huge influence on evolution and the survival probability of the population. Gene frequencies of a population are greatly affected by environment pressures. Over time, the environment pressures would cause the favoured gene to increase in frequency and the disfavoured to decrease or in rare cases, become extinct. This would result in the formation of a population that has been adapted to the new environment and became more physically fit to survive in the new environment. Furthermore, the gene pool of a population is significantly affected by genetic drift and the bottleneck effect of a population. It was proven in the lab that the resulting number of genes after a genetic drift was in fact by

chance. The bottleneck effect was characterized by a drastic decrease in a large population. Hence in both situations, the gene pool of the population would experience a sharp reduction in size. This could lead to the extinction of the population due to the lack of genetic variation caused by inbreeding. Though it could be possible for the small population to produce a large population, it would be highly likely.

Error

An error that had occurred while conducting the experiment was that the candies and gumballs may not have been mixed properly. A few times, the subject forgot to shake the bag of candies before drawing out two alleles. This could have produced biased results as more of one type of candy might have ended up on the top, which increased its chance of being chosen. Additionally the percentage of the alleles did not add up to 100% after the bottleneck effect. This was because the whole percentage weren't taken into account as all the results were rounded to only two decimal places.