Population of drosophila melanogaster

Purpose:

Determining the effect of selection on a recessive allele in a population of Drosophila melanogaster by using different types in a population cage. Observations were obtained, which gave the outcome of what happened when flies exhibiting different traits were placed in a container and allowed to reproduce.

Results:

In the experiment, 25 male and female Drosophila melanogaster of both the wild-type and winged mutant were collected and placed in a cage. After sample one had been created and reproduction was allowed to take place, 149 wild-type and 5 winged mutant flies were scored and removed from the population. After sample two had been created and reproduction was allowed to take place, 32 wild-type and 2 winged mutant flies were scored and removed from the population. After sample three had been created and reproduction was allowed to take place, 29 wild-type and 7 winged mutant flies were scored and removed from the population. At the end of the experiment, the final flies were scored and removed. In the final sample, 130 wild-type and 12 winged mutant flies were obtained and scored. The initial ratio for the different alleles p and q were even, due to the fact that even amounts of mutants and wild-type flies were originally in the population. The allele frequencies for the p allele and q allele were obtained for sample one and they were: p = 0. 968 and q = 0. 032. The allele frequencies for the p allele and q allele were obtained for sample two and they were: p = 0. 941 and q = 0. 059. The allele frequencies or the p allele and q allele were obtained for sample three and they were: p = 0. 806 and q = 0. 194. The

allele frequencies for the p allele and q allele were obtained for the final sample and they were: p = 0. 916 and q = 0. 084. The selection coefficient was calculated from q(initial) = 0. 5 and q(1) = 0. 194, which were obtained from the original Drosophila melanogaster in the population and those scored from sample three. The selection coefficient was 1. 25.

Table 1: Total count for flies in each sample.

	Initial	Sample 1	Sample 2	Sample 3	Final Sample
Total Number of Flies	25wt 25wm 50total	149wt 5wm 154total	32wt 2wm 34total	29wt 7wm 36total	130wt 12wm 142total

Table 2: Allele frequencies, gene frequencies, and selection coefficient values for each sample.

	Initial	Sample 1	Sample 2	Sample 3	Final

Allele Frequency	p = 0. 5 q = 0. 5	p = 0. 968 q = 0. 032	p = 0. 941 q = 0. 059	p = 0. 806 q = 0. 194	p = 0. 916 q = 0. 084
Genotypic Frequency	p^2 = 0. 25 2pq = 0. 25 q^2 = 0. 125	p^2 = 0. 937 2pq = 0. 002 q^2 = 0. 001	p^2 = 0. 885 2pq = 0. 005 q^2 = 0. 003	p^2 = 0. 65 2pq = 0. 05 q^2 = 0. 038	p^2 = 0. 839 2pq = 0. 117 q^2 = 0. 007
Selection coefficient	S = (q(initial)-q(sample 3))/q(initial) ²(1-q(sam				

	ple 3)) =(0. 5-0. 194)/(0. 5)²(1- 0. 194) = 1. 25	

Graph 1: Depiction of allele frequency over time for each sample.

Discussion:

In the experiment, all steps followed the experiment design described in Laboratory Exercises in Genetics by M. Beck, Fall 2009 pp. 10-14. Originally, 25 Drosophila melanogaster displaying both the wild-type genotype and the winged mutant genotype were placed in a population cage to allow reproduction to take place.

The original hypothesis (null) was that the flies entered the population cage in Hardy-Weinberg equilibrium and the final count at the end of the experiment should remain constant. The only ways that the original hypothesis could be wrong the population somehow deters from equilibrium includes the possibility of selection occurring, migration, or mutation within the population of Drosophila melanogaster.

After several weeks, the first sample of adult flies was removed, scored and discarded. Table 1 provides categorized data for the counts in each sample. There were 154 flies obtained from sample one. Of the 154 flies, 149 were wild-type and 5 were winged mutant. The allelic frequencies were obtained for sample one by dividing the total number of winged mutant flies observed by the total number of flies in the population cage at that time. The allelic frequency for p (dominant) was 0. 968 and the allelic frequency for q (recessive) was 0. 032, which can be viewed for all samples in Table 2. The genotypic frequency for p (homozygous dominant) was calculated to be 0. 937. The genotypic frequency for pq (heterozygous) was calculated to be 0. 002. The final genotypic frequency for sample one, which was for q (homozygous recessive) was calculated to be 0. 001.

Then, several weeks after sample one had been observed, scored, and discarded, the adults from sample two were removed and recorded. The total amount of flies removed during the checking of sample two was 34. Of the 34 flies, 32 were wild-type and 2 were winged mutant. The allelic frequencies were obtained for the flies in sample two and the value for p (dominant) was 0. 941 and q (recessive) was 0. 059. The genotypic frequencies for the flies in sample two were calculated and for p (homozygous dominant) the value was 0. 885, for pq (heterozygous) the value was 0. 005, and for q (homozygous recessive) the value was 0. 003.

In the next couple of laboratory meetings, the flies within the population cage were allowed to reproduce. Then, sample three adults were removed, scored, and discarded. The total amount of flies removed during the checking of sample three was 36. Of the 36 adult flies removed, 29 were

wild-type and 7 were winged mutant. The allelic frequencies were obtained for the flies in sample three and the value for p (dominant) was 0. 806 and the value for q (recessive) was 0. 194. The genotypic frequencies for the flies in sample three were also calculated and the values were as follows: p (homozygous dominant) = 0. 65; pq (heterozygous) = 0. 05; q (homozygous recessive) = 0. 038.

On the final collection of data for the flies in the population cage, all adults were removed, scored, and discarded. This has been denoted as the final count, or it could be assumed to be sample four. The total amount of flies removed for the final count was 142. Of the 142 flies removed, 130 were wild-type and 12 were winged mutant. The allelic frequencies for both alleles in the fly population were calculated and the value for p (dominant) was 0. 916 and the value for q (recessive) was 0. 084. The genotypic frequencies for the flies in the population were then calculated using the values from the determined allelic frequencies. The values for each genotypic frequency include: p (homozygous dominant) = 0. 839; pq (heterozygous) = 0. 117; q (homozygous recessive) = 0. 007.

Finally, once all of the different frequencies had been calculated for the different samples obtained, the selection coefficient was able to be determined. The value for the selection coefficient was calculated to be 1. 25. This unusually high number indicates that the allele for the recessive phenotype was nearly wiped out from the population. This would infer that the population within the population cage did not remain in Hardy-Weinberg equilibrium.

The original amount of flies added was equal in both representation of the phenotypic wild-type flies and the phenotypic winged-mutant flies. Had the population remained in Hardy-Weinberg equilibrium, the population ratios at the end of the experiment would have shown approximately the same 50-50 relationship for both the recessive and dominant phenotypes and genotypes. That was not the case for the experiment, which is shown in Graph 1. Problems that could have occurred during the experiment include selection, which was clearly evident among the flies, migration, due to faulty structural restrictions of the cage, and mutation may have occurred to cause the recessive allele to be almost entirely removed from the population.

To add an interesting note about why selection may have taken place that inevitably diminished the recessive allele's presence in the population is that wing size plays a secondary role in mating for the flies. As explained by experimental data recorded by Janice McDonald, " selection for the wing vibration component of courtship in the Oregon-R stock of D. melanogaster was practiced for 44 generations. Selection was successful, indicating that there is genetic variation for the trait in the Oregon-R stock" (McDonald 1979). The data provided shows a relationship between the size of the wings, vibrations produced (song), and the selection of males as mating partners. This would account for the selection against the smaller, vestigial wings of the recessive phenotype.

Overall, the experiment proved that over time, the dominant, preferred characteristics will be the predominant phenotype expressed. This experiment was a short glimpse to evolution occurring that causes the fittest

genes within a population to be more readily passed from generation to generation.

References

Beck, Melvin. 2009. Laboratory Exercises in Genetics. 10-14.

McDonald, Janice. 1979. Genetic Analysis of Lines Selected for Wing Vibration in Drosophila melanogaster. Behavioral Genetics 9: 579-584.