The Effect Of Violations Of Hardy-Weinberg Equilibrium Conditions On The Allele Frequency Of Drosophila Melanogaster Populations Essay, Research Paper

Introduction

The interaction between genetic variation and natural selection is one of the most important concepts in modern biology. The product of this interaction, evolution, which is a change in a population?s allele frequency, is responsible for the great complexity and diversity of life seen on earth today.Allele frequencies of a non-evolving population (one in which the allele frequencies are not changing) can be elegantly modeled using the Hardy-Weinberg theorem. For a population to be at equilibrium, five conditions must be met: 1) large population size, 2) random mating, 3) no mutation, 4) no migration, and 5) no natural selection. Violation of these conditions can produce a change in the allele frequencies of the population under study. Our purpose is to examine the effects of small population size and of natural selection. In this experiment, we will use populations of Drosophila melanogaster to model the Hardy-Weinberg theorem. Drosophila populations are ideal for modeling evolutionary dynamics for two reasons: they are inexpensive, to both buy and maintain, and, more important, have a brief reproductive cycle, allowing several generations to be studied in a short length of time. We will be working with two populations of Drosophila, designated A and B. Population A will be used to examine the effects of a small population (the founder effect). Natural selection will be studied using population B. We hypothesize that the violation of a single Hardy-Weinberg equilibrium condition present in each population will give rise to a specific change in allele frequency in that population. We hypothesize that the allele frequencies of the two A sub-populations will diverge over time, due to genetic drift magnified by sampling error in the A-Small population. We hypothesize that the frequency of the Cy allele will decrease in population B, due to natural selection. In order to test our hypotheses, we will be scoring Drosophila for several generations (F2, F3, and F4). We will then be able to calculate allele frequencies within the different populations. These frequencies will be compared to determine if the populations are in Hardy-Weinberg equilibrium and if their allele frequencies are changing.

Materials and Methods

For a complete listing of Materials and Methods (including the procedures for anesthetizing and identifying Drosophila), see the Biology 220W Lab Manuel.

Population A is comprised of wild-type Drosophila and those marked with one of two mutant traits: eyeless (ey) or sparkling-polished (sp). Each mutation is indicative of a Drosophila that is homozygous for that allele. Heterozygous flies show the wild-type phenotype. The Drosophila in population A are first randomly divided in two groups: a small group, containing 10 flies, and a large group, containing all other flies from population A. Note that the population A-Small must contain at least 2 flies from each sex. The number of Drosophila of each phenotype is determined for both the A-Small and the A-Large. The second and third generations are also scored in this manner.Population B is comprised of the F2 generation of a cross between wild type and curly winged (Cy) Drosophila. All flies with the curly winged phenotype are assumed to be heterozygous, as the Cy mutation is homozygous lethal. The number of flies of each phenotype is determined; this is done for each of three generations.In both parts of the experiment, phenotype frequencies are used to determine allele frequencies. Allele frequencies are used to determine if the populations are in Hardy-Weinberg equilibrium. They are also compared across generations to determine if they are changing. In both parts of the experiment, the independent variable is the small population size (i.e. the violation of Hardy-Weinberg equilibrium) and the dependent variable is the change in allele frequencies.ResultsTable 1 presents all data for sub-populations A-Small and A-Large. It shows a total number of Wild-type flies in week 5 as 666. Table 2 presents the results of x2 tests performed to test for the existence of Hardy-Weinberg equilibrium within the Drosophila populations. It shows most populations to be far out of Hardy-Weinberg equilibrium. However, all Small sub-populations are in Hardy-Weinberg equilibrium in week 1, at a 0.005 level of confidence. Table 3 shows the tests for shifts in phenotype (which is indicative of shifts in allele frequencies) across generations. x2 tests show changes in phenotype in almost every population. Graphs 1 and 2 show Populous simulations for sub-populations A-Small and A-Large. The are indicative of the possible result of running this experiment out to 100 generations. Notice that the allele frequencies of sub-population A-Small fluctuate greatly before fixation, and that the frequencies of A-Large shift only gradually.Table 4 shows the raw data for population B. It shows a steadily decrease in the frequency of Cy and a steady increase in the frequency of Cy+. Table 4 shows the results of the x2 test on this change in frequency. At the 0.05 level of confidence, it shows a change in frequency in all but one population. Graph 3 show a Populous simulation representative of population B, if the experiment had been taken out to 100 generations. Note the quick drop in the frequency of the Cy allele, but that it was always maintained at a low frequency.Discussion In general, the data from population A supports our hypotheses. Both A sub-populations showed a shift in allele frequencies. They were both gradual though, probably due to the fact that A-Small was constrained to 10 flies for only the first experimental cross. A procedure more indicative of the effects of small population size might have culled the population back to 10 flies at each generation. Of note is the fact that the original samplings in the Small sub-population were at Hardy-Weinberg equilibrium. This is probably due to sampling error. The data from population B also supports our hypothesis. There is an obvious drop in the frequency of the Cy allele. Natural selection constrains the expression of the Cy allele (i.e. homozygous genotype results in death) so Cy alleles are weeded out of the population.Unfortunately, our results are not particularly meaningful. With only 3 generations to look at, it is difficult to infer patterns in shifts in allele frequencies. An obvious extension of this experiment would be one in which the fly populations were followed for many generations.