Mapping Unknown Mutations Of Mutant Strain U5914 D Essay, Research Paper

Abstract Unknown mutant strain U5914 Drosophila malanogaster with 3 mutated phenotypes: white eyed, dark body color, and incomplete longitudinal vein II and IV. This mutant strain was crossed with wild-type strain and marker strains to study the genetic characteristics of these 3 mutant genes. The results showed that dark body color is an autosomal recessive mutation (db) located on chromosome II. Incomplete longitudinal vein is also an autosomal recessive mutation (v) located on chromosome II. White-eyed phenotype is, however, controlled by 2 genes with one gene (w) masking over the expression of another gene (o); therefore, the genotype for eye color of the unknown mutant strain is ww,oo or ww,o+o. Due to the low number of offspring produced from male backcross of Cross II, we were unable to construct the chromosome map for body color and wing venation genes. However, we were able to calculate the distance between these two genes, which is 38.47m.u. The locations for eye-color genes are on X-chromosome at position 0, and 39.24. The chromosome map of these genes is : w—-16.27—-cv—–22.97—–o—–17.70—-fIntroduction Drosophila has been well studied, and commonly used as lab organism in variety of science fields because it has a short life cycle, easy to handle, and cheap to grow and store in large numbers. In this experiment, we will use Drosophila for the purpose of studying how to map unknown mutations on the genetic map. The experiment were carried out with an unknown mutant strain carrying 3 visible mutations (white eyed, dark body color, and incomplete longitudinal vein II and IV). This mutant strain was crossed with wild type flies (red eyed, light body color, and complete longitudinal veins) and marker strains that carried known mutations. By analyzing the data obtained from F1 and F2 progenies, we are able to determine how many genes are involved in controlling a certain phenotypic expression, how the genes are inherited, on which chromosome are the genes located, and their relative distances from the known genes. Materials and MethodsExperimental organism:A culture of unknown strain (U5914), a culture of Ore-R wild type, and 3 cultures of marker stock Drosophila malanogaster were obtained from Professor Jeyabalan. Marker stock M-1 carries recessive mutations on the sex chromosome with crossveinless wings and bent bristles phenotype (cv f). Marker stock M-2, however, carries dominant mutations on chromosome II with short thin bristles, lobed eyes, and curly wings phenotype (Bl L/Cy). Marker stock M-3 also carries dominant mutations, but the mutations are on chromosome III, and the phenotype is glued eyes, and short blunt bristles (Gl Sb/LVM). Crosses:To figure out the pattern of inheritance, 2 crosses were made: 1) Cross A: unknown virgin females X wild type males2) Cross B: wild type virgin females X unknown malesTo make a genetic map of the mutant traits, 7 crosses were made:1) Cross I: unknown virgin females X marker I males 2) Cross II: unknown virgin females X marker II males3) Cross III: unknown virgin females X marker III males4) F1 X F1 cross of A5) F1 X F1 cross of B 6) F1 X F1 cross of I7) Male backcross of II : F1 of cross I males X unknown virgin females8) Male backcross of III: F1 of cross II males X unknown virgin femalesFor each cross, flies were anesthetized with CO2 or fly nap (refer to lab manual pages 4-6 for procedure and techniques). 10 to 15 anesthetized flies from each sex were selected and placed into a plastic container with food. Then flies were allowed to mate for a period of time, and the offspring were collected and scored (procedure for making crosses, collecting, and scoring is described in lab manual pages 19-25).

Results and Discussion (refer to attachment for tables and data) The inheritance pattern for dark body color, and incomplete longitudinal wing venation of U5914 strain is autosomal recessive because all the progenies showed wild type phenotype for these traits and the traits were distributed equally between the males and the females (Table 2, and 4). The inheritance pattern for white eye, however, is sex-linked recessive because the mutant was only observed in the male progenies (Table 2). The alleles of body-color gene were equally segregated with an observed ratio very close to the expected ratio of 3:1 (df=1, χ2 = 0.073) (Table 8). The alleles of wing-venation gene, however, did not segregated equally (df=1, χ2 = 5.93) (Table 9). Despite these results, the alleles of wing-venation gene may have been equally segregated. The reason is that there were a numbers of wings got torn when we tried to separate the flies from sticking to each other; therefore, we may have miss-scored a numbers of flies. The analysis for the relationship between body-color and wing-venation genes showed that these genes are linked (df=3, χ2 = 141.56) (Table 10). The calculated genetic map distance between these genes is 38.47 m.u. The locations of these genes were found to be on chromosome II because the mutant traits for both of these genes did not show up with the marker traits on chromosome II (Table 13). Cross III confirmed that neither of these genes was on chromosome III because both mutant traits showed up with the marker traits (Table 14). The attempt to map the location for these eye-color genes on chromosome II, however, was failed due to the low number of progeny (8 flies) collected from the male backcross of II (Table 13). This low offspring production may due to the fact that F1 males of cross II are relatively weak and most of them died before they are able to mate. Unlike body-color and wing-venation genes, eye color seems to be controlled be 2 genes because there were 3 different eye-colors were observed in the F2 generation of crosses A and B (Table 11). We hypothesized that one gene must have been epistatic over the other gene for the result of 3 eye-colors phenotype. Further analysis, we can conclude that these genes were linked because if they were unlinked there would be more eye colors observed in the female progenies than just red. Since eye-color genes are sex-linked recessive, the progenies from cross I F1 X F1 allow us to locate the location of these 2 eye-color genes on the genetic map. From the data collected, the calculated distance between cv and f is 34.93 m.u., which constitutes 18% error compared to the actual value of 43 m.u. (see attachment p. 9). Since the distances that we calculated were based on the small sample size, we can not fit the values that we obtained onto the actual map; therefore we constructed a new map with w located at 0 and o located at 39.24 (see attachment p. 9). Summary White eyed, dark body, and incomplete longitudinal venation traits of mutant strain U5914 are all recessive mutation. Mutations for body color and wing venation are located on chromosome II. The mutation for eye color, however, is located on X-chromosome and there are 2 genes involved in the control of eye color expression. Since one of the genes is epistatic over the other, the genotype for the white-eyed observed in the unknown mutant strain is ww,oo or ww,o+o. Reference Lab manual pages 3-25Appendixχ^2 = ∑ ((observed number expected number)^2 / expected number)