Cloning the Flying Gene: Molecular Genetic Analysis of the Hold Up (hup) Gene in Drosophila

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Past studies indicated that Drosophila (fruit flies) share 75% of the genes that cause diseases with humans. Thus by studying fruit fly genetics, one can learn about human genetics and possibly gain a better insight into diseases that affect both humans and fruit flies. Last year's project identified the general location on the chromosome of the gene known as 'hold up' (hup), which was found to affect the fruit flies' fertility and muscle structure. These findings are important because flies make muscles using similar genetic processes to those used in humans. However, the identity of the gene has not been determined. This year, the project focuses on locating the identity of the hup gene by cloning and sequencing its DNA and comparing its sequences with the wild type version of the gene to look for changes and to confirm the identity of the hup gene. To identify the gene that contains the hup mutation, fly crosses were conducted to test each of the genes for the hup phenotype found in the identified location. After locating the gene that may contain the hup mutation, PCR was performed to amplify the mutant DNA, and the amplified DNA was inserted into a plasmid. After insertion, large cultures of these bacterial cells were grown, and the cloned plasmid DNA was purified from the cultures. To perform DNA sequencing, a machine was used to illuminate the different colors of the nucleotides and provide the order of the nucleotides. Results of the fly crosses indicated that the gene named CG6700 is the likely candidate to contain the hup mutation. DNA sequencing also showed a change in the hup version of the sequence in comparison to the wild type version, revealing a short stopping in the production of proteins, which may explain the muscle defects caused by the mutation.

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