“ Molecular Genetic Analyses of Polytene Chromosome Region 72A-D in Drosophila melanogaster Reveal a Gene Desert in 72D ”

Monica T. Cooper, James A Kennison

Student Name

Polytene Summary Essay

Within the scientific community, model organisms are invaluable, *Drosophila Melanogaster* is one such model organism. A model organism is one that we use to study a particular portion or branch of genetics. Within this journal article we take a closer look at some of the functions and abilities found within each genome of *Drosophila Melanogaster*, a subject that despite being a model organism, not much information is available to geneticist.

The primary goal that Cooper and Kennison were working towards was to be able to identify and apply characteristics to the essential genes within the 22 polytene chromosome bands within the subsections 72A to 72D on the third chromosome and from these genes we estimated that 57 of them would be a particular type of protein-coding gene. In total Cooper and Kennison, investigated 300 kb of genomic DNA, a kb is one kilobyte. It is important to understand what a polytene chromosome is in order to gain a better understanding of what we will be looking at within this study; a polytene chromosome is an enlarged chromosome, found within the salivary glands of *Drosophila Melanogaster.* In addition it is important to understand the ability of "complementation" to restore a normal phenotype, knowing this in order to find and isolate these areas representatives from each complementation group Cooper and Kennison crossed both representatives into overlapping deletions. These crosses are illustrated within Figure 1, those deletions with molecularly characterized breakpoints are outlined in red.

After completeing tandem gene duplication, there were 6 different gene groups that were created as a direct result. These groups ended up having approximately 17 out of the 57 of the estimated protein- coding genes. In addition to this for, all of the gene groups the rate of related gene groups was considerably higher than the rate that was expected per the data from the rate of the first genome. It is possible that the high rate of tandem gene may be able to help explain or

perhaps may even be the cause of why the estimations on the total number of essential genes by mutational analysis was a lot lower than the number of genes found through the process of molecular analysis.

Now, understanding the prior knowledge it begs the question, " How many mutations does it take for a gene to begin to demonstrate the mutant phenotypic allele?". Upon reaching the conclusion of the experiment Cooper and Kennison had a total of 130 mutations, which is the equivalent of 1 mutation for every 2.26 base pairs. In addition to this, that ratio is also the estimation for mutations that cause the lethal mutant phenotype. In order to create mutants within the experiment, the male flies were fed "EMS" or Ethyl methane sulfonate and then mated with virgin females. It was found that certain gene regions within the polytene chromosome, in this case CG5151 and CG5018, were very alike to gene deserts the very same that are common in mammals. A gene desert is a large swath of DNA that is devoid of protein encoding sequences as well as serves no visible biological function.