# Drosophila melanogaster

ASSIGN BUSTER

**Autosomal**

Inheritance of Wrinkled and black Mutations in Drosophila melanogaster Abstract Homozygous Wrinkled virgin females and homozygous black male Drosophila melanogaster, were crossed. Mutations were located on chromosomes two and three respectively. The F1 generation, all Wrinkled and black, was inbred yielding and F2 generation. A phenotypic ratio of hypothesized with wrinkled wings and wild type body: wrinkled wings and black body: wild type wings and body wing: wild type wings and black body correspondingly. A p-value <0. 01 was obtained from a? 2= 23. 24 thus rejecting the hypothesis.

Observed data gave a 5: 3: 2: 1 phenotypic ratio of wrinkled wings: wrinkled wings and black body: wild type wings body: black body respectively yielding these values. A BLAST search on the black mutant gene alignment gave an E-value of zero when compared to Anopheles Gambia. A BLASTn search on the Wrinkled gene sequence produced an E-value of 2 x 10-18 when compared to Anastrepha Ludens. Search results concluded the biological relevance and homology of these genes.

Results

A parental cross of black male mutants and Wrinkled female mutants yielded an F1 generation of all Wrinkled and black flies. The F1 generation was self crossed then F2 generation scored and hypothesized to give a 9: 3: 3: 1 phenotypic ratio. In experiment three parental viles with virgin females were made. Two vials contained two male Wrinkled flies and two female black flies, and one vile with two male black flies and two female Wrinkled flies.

The F1 generation survived in two of the three viles all yielding the wrinkled wings and black body phenotype. The F1 flies were then self-crossed into three separate files yielding an F2 generation. Only the F2 files from the original black male and wrinkled female parents survived. The Wrinkled mutation sequence’s top hit was Anastrepha ludens, or more commonly known as theMexicanfruit fly, with an E= 2 x 10-18 (BLAST 2012). The black mutation sequence’s top hit was Anopheles Gambiae, the African malaria mosquito, with an E= zero. The hypothesis p-value was less than 0. 01, which was much lower than the 0. 05 requirements thus rejecting the hypothesis. The hypothesis could have been rejected do to human and mechanical error, and epistasis. More parental Drosophila could have been used to eventually lead to a larger sample population to give better results. Up-to-date and powerful microscopes could also have been used to help sex-flies.

A different media also may yield a better survival: death ratio. To determine where the expression of one gene depended on the presence of a modifier gene a test cross could have been performed. If the reciprocal cross had been conducted the same results would have been obtained. Had the mutations been sex-linked rather than both autosomal a reciprocal cross would be useful to determine the influence of each parental sex on the inheritance patterns. Mutant alleles were located on chromosomes two, and three therefor the sex of the fly would not determine the phenotypic ratio. A BLASTn search was done to establish homology of genes and helped determine the function of the wild type Wrinkled and black genes.

The black gene encodes a component of an amine pathway that is involved in melanization and crosslinking. The black phenotype shows aspartate decarboxylase activity is reduced in adults, and at pupa formation. The mutation is a frame shift, and flies with this phenotype do not have the black/DGAD2 protein. This protein is expression in glial cells of the first optic ganglion. Black mutants are deficient in B-alanine, if the larvae are injected with this amine they develop with normal pigmentations. B-alanine is conjugated to dopamine to form NBAD. NBAD is a product of the ebony gene, and has a storage/transport function, that inactivates two toxic amines. NBADH a product of the tan locus hydrolyses NBAD back to its original amines, concluding that ebony, black and tan genes are all part of the same pathway. The black mutation showed homology to the DNA sequence of Anopheles Gambiae with an E-value equal to Zero suggesting biological relevance. In Drosophila, the wrinkled mutant gene is referred to as hid. Hid stands for, head involution defective. Hid is a gene in the region which encodes for a regulator of programmed cell death. The mutant embryos have lower cell death and have extra cells in the head. This gene encodes for a 410 amino acid protein and the mRNA is expressed in regions where cell death occurs. The wrinkled phenotype can be suppressed by expression of anti-apoptotic p35 protein. The ability of hid to kill cells appears in the same pathway as the reaper function. Both functions are independent of each other. The hid phenotype results from decreased levels of PCD. The Wrinkled mutation showed homology to the DNA sequence of Anastrepha ludens with an E-value of 2 x 10-18 suggesting biological significance.

In summary a 9: 3: 3: 1 ratio of Wrinkled: Wrinkled and black: wild type: black was not obtained, however different precautionary methods may have been taken, such as using more up-to-date microscopes which could alter the  2 value and not reject the hypothesis. The DNA sequences of both mutations are relevant in homology with other organisms, and the genes share the same chemical pathways as other mutations. Literature Cited

# Reference

1. Abler M. , L. Baines, F. Ellis, A. Galbraith, and R. Werren 2013.
2. Genetics Laboratory Manual. University of Wisconsin La Crosse, La Crosse, WI, USA. 22 BLAST 2012.
3. Accessed February 2013.
4. Grether M. E. , J. M. Abrams, J. Agapite, K. White, and H. Steller 1995.
5. The head involution defective gene of Drosophila melanogaster functions in programmed cell death Genes & Development 9: 1694-1708 Phillips A. M. , R. Smart, R. Strauss, B. Brembs, and L. E. Kelly 2005.
6. The Drosophila black enigma: The molecular and behavioural characterization of the black1 mutant allele : 131-142.