

Colten Palkon

11/30/2022

Fly Lab

Introduction

Fruit flies scientifically known as *Drosophila melanogaster* have been one of the most genetically studied organisms. Used first 100 years ago by Thomas Hunt Morgan, *Drosophila* were studied to characterize the “passing down” of physical traits. His work with these insects started modern genetics (Torres1). *Drosophila* made good test subjects due to their “short lifecycle of 2 weeks and ease of care in the laboratory” (Nezrick). Each allele on *Drosophila* had distinct traits that were easy to distinguish. The dominant red eyed wild type were crossed with the recessive white eyed mutant. The type of eyes inherited was sex linked. This meant that on the X chromosome genes could code for red or white eyes. The mother *Drosophila* would pass down its allele to her offspring. When the recessive allele such as white eyes was also paired with a dominant allele in a female *Drosophila* the dominant would be the phenotype observed. This also would allow for the male offspring to get the recessive allele since they only had one X chromosome. Independent assortment like sex linked was genetically based. But instead of being due to the sex chromosome, other non sex determining chromosomes had pairs. In the experiment that studied independent assortment it was the random combinations of the alleles on chromosomes that determined what phenotype a *Drosophila* showed. The wing shape of dumpy or normal as well as sepia eyed *Drosophila* were due to independent assortment. The homologous chromosomes that made up each *Drosophila* were randomized for each individual, but a certain trend was followed. A 9:3:3:1 ratio was followed where the most populous was normal wing, normal eye. Then the dumpy wing and normal eye and normal wing and sepia eye

were both 3. The rarest phenotype was the sepia eye, dumpy wing which held two recessive traits. The Punnett squares below gave the predicted phenotype for the F2 generation of *Drosophila*. Sex linked inheritance and independent assortment were to follow the general trend of these squares and give comparable phenotype ratios.

Figure 1: Chromosome 3 and sex linked loci

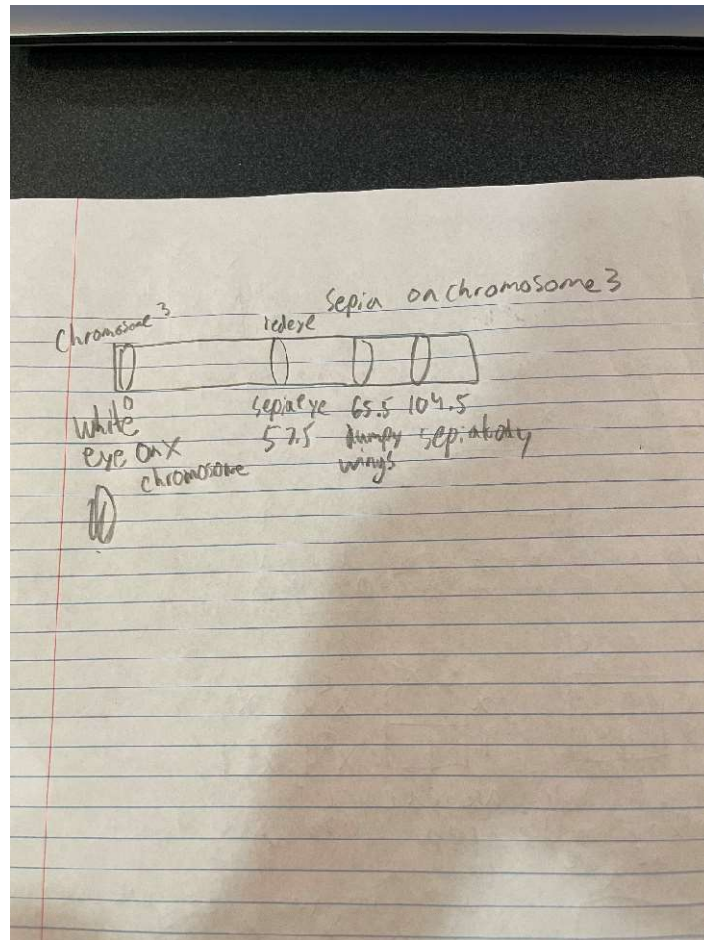
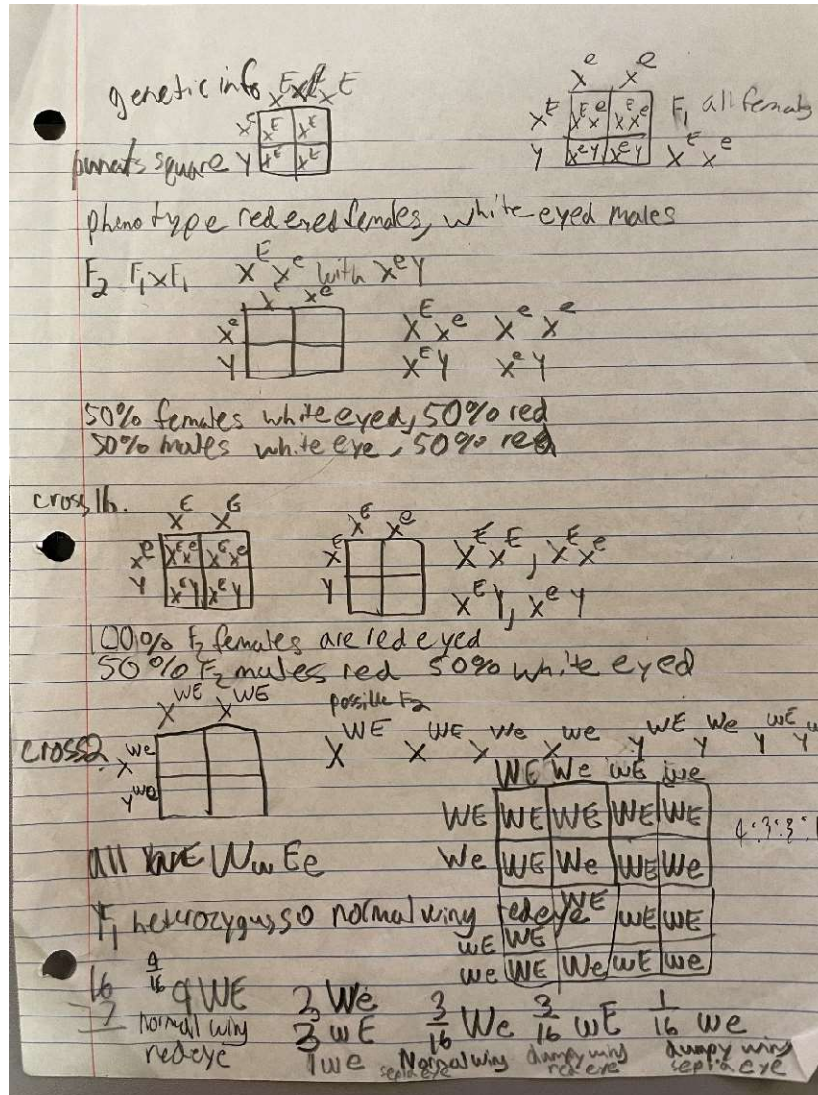


Figure 2: Punnett square for all 3 experiments



Materials and Method

Counting took place with anesthetic to put the flies to sleep as well as microscopes to view the specimens better. Each Cross was put into a vial with potato pieces, yeast and water. Dead specimens were tossed into the morgue.

Cross 1a was initially made from virgin female white eyed EZ flies and male EZ wild type. These fly strains were "procured from Carolina Biological Supply Company"(Nezrick). The cross was then left to breed and maggots to spawn for two weeks on a heating pad. From there the F1 generation pupated and hatched. On 10/26 there were plenty of pupa and maggots.

On 10/28 the female flies were separated and dominant ones with red eyes killed so that the F2 generation would yield recessive traits. The male flies were then left to breed with the females. Two weeks later after the F2 maggots had turned into flies, all flies were counted according to sex and eye color.

Cross 1b was initially made from female red eye EZ flies and male EZ white eye. These fly strains were “procured from Carolina Biological Supply Company”(Nezrick). The cross was then left to breed and maggots to spawn for two weeks on a heating pad. From there the F1 generation pupated and hatched. On 10/26 there were plenty of pupa and maggots. On 10/28 the flies were separated and all males had white eyes while all females had heterozygous red eyes. These flies were then observed and then left to breed. Two weeks later after the F2 maggots had turned into flies, all flies were counted according to sex and eye color.

Cross 2 was initially made from Female wild type normal wing flies crossed with recessive sepia eye dumpy winged males. These flies were left for two weeks to breed, maggot spawn, and hatch the F1 generation. On 10/28 all flies were observed and left for the process to repeat for the F2 generation. Once the F2 generation hatched all flies were counted according to wing shape and eye color.

Data

Class Data

Cross 1a	Jack	Orlando	Andrew	Madison	Colten	Rylen	Grace	Brian	Lea	Zach	Allele Total
Female Red Eye	48	29	62	85	22	46	115	91	80	43	621
Female White Eye	35	8	88	83	22	54	110	82	72	28	582
Male Red Eye	43	63	36	53	23	53	112	77	86	40	586
Male White Eye	35	42	46	63	24	50	98	56	83	33	530
Total Flies	161	142	232	284	91	203	435	306	321	144	2319
Cross 1b	Jack	Orlando	Andrew	Madison	Colten	Rylen	Grace	Brian	Lea	Zach	Allele Total
Female Red Eye	75	92	140	21	66	76	102	121	63	117	873
Female White Eye	0	6	0	0	0	9	3	0	0	0	18
Male Red Eye	15	193	83	19	39	56	78	65	96	52	696
Male White Eye	24	67	69	12	40	57	38	42	73	50	472
Total Flies	114	358	292	52	145	198	221	228	232	219	2059
Cross 2	Jack	Orlando	Andrew	Madison	Colten	Rylen	Grace	Brian	Lea	Zach	Allele Total
Red Eye, Normal Wing	35	38	59	113	29	137	168	29	237	131	976
Sepia Eye, Normal Wing	19	10	35	29	12	32	38	23	67	41	306
Red Eye, Dumpy Wing	21	4	41	24	10	37	42	150	69	31	429
Sepia Eye, Dumpy Wing	23	1	51	10	3	25	10	10	14	15	162
Total Flies	98	53	186	176	54	231	258	212	387	218	1873

Personal Data

Cross 1a	Colten
Female Red Eye	22
Female White Eye	22
Male Red Eye	23
Male White Eye	24
Total Flys	91
Cross 1b	Colten
Female Red Eye	66
Female White Eye	0
Male Red Eye	39
Male White Eye	40
Total Flys	145
Cross 2	Colten
Red Eye, Normal Wing	29
Sepia Eye, Normal Wing	12
Red Eye, Dumpy Wing	10
Sepia Eye, Dumpy Wing	3
Total Flys	54

Results

Each result includes the prediction, number gathered, percent allele from total, phenotype ratio for each sex if applicable, and the calculated χ^2 (the calculations were done on calculator)

Cross 1a: Predicted, 50% white eyed females, 50% red eyed females 1:1 phenotype

50% white eyed males, 50% red eyed males 1:1 phenotype

Personal Results:

91 total flies, 22 Red female(24.2% of tot), 22 while female (24.2% of tot)= female Phenotype ratio: 1:1 $\chi^2 = 0$

23 Red males (25.3% tot), 24 white males (26.4% tot) = male Phenotype ratio: 0.49:0.51

$\chi^2 = 0.0004$

Class results:

2319 total flies, 621 Red female(26.78% of tot), 582 white female (25.10% of tot)= female
Phenotype ratio: 0.516:0.484 $\chi^2 = 0.0010$

586 Red males (25.27% tot), 530 white males (22.85% tot) = male Phenotype ratio:
0.525:0.475 $\chi^2 = 0.0025$

Cross 1b: Predicted, 100% females red eyes 0% females white eyes 1:0 phenotype

50% males red eyes 50% males white eyes 1:1 phenotype

Personal Results:

145 total flies, 66 Red female(45.5% tot), 0 white female(0% tot) 1:0 phenotype $\chi^2 = 0$

39 Red males (26.9% tot), 40 White males (27.6% tot) 0.494: 0.506 phenotype
 $\chi^2 = 0.000144$

Class Results:

2059 total flies, 873 Red female(42.4% tot), 18 white female(0.87% tot) 0.98:0.02 phenotype
 $\chi^2 = 0.0008$

696 Red male (33.8% tot), 472 white male (22.9% tot) 0.596:0.404 phenotype
 $\chi^2 = 0.037$

Cross 2: Predicted, 9/16 normal wing red eye, 3/16 normal wing sepia eye, 3/16 dumpy wing red eye, 1/16 dumpy wing sepia eye.

Personal Results:

54 total flies, 29 normal wing red eye (53.7%), 12 normal wing sepia eye(22.2%), 10 dumpy wing red eye (18.5%), 3 dumpy wing sepia eye (0.056%). 0.54:0.22:0.19:0.06 phenotype
 $\chi^2 = 0.0067$

Class Results:

1873 total flies, 976 normal wing red eye (52.1%), 306 normal wing sepia eye(16.3%), 429 dumpy wing red eye (22.9%), 162 dumpy wing sepia eye (8.65%) 0.52:0.16:0.23:0.087 phenotype
 $\chi^2 = 0.0265$

Conclusion

The experiments with *Drosophila* went very well. The personal results were very close to the ideal. This most likely happened due to a lot of underdeveloped or damaged flies having to be thrown out. This led to taking of time and the numbers turned out how they were supposed to be. The class results also went well. Although there were some outliers like the white females in cross 1b. This was probably due to contamination or bad counting. In the future things like this could be avoided by using a microscope or not letting preprogenated females into the experiment. The ratios collected were not whole numbers which was expected, but when converting the theoretical values into decimal form the Chi squared could be calculated. The Chi squared yielded extremely low numbers. This added to the credibility of the phenotype ratios and the results followed the probability. There was no significant critical values which meant the data from the experiment matched the expected. The cross two had the largest Chi squared but this was expected since it had a larger degree of freedom. When that is taken into account cross two experiment outperformed the other two. Overall the experiments for all went great.

Works cited

Nezrick, Tiana. "Lab 10- Exploring Genetics Using *Drosophila melanogaster*."(p.143-148).
Torres, Isabel. "Why do scientists study fruit flies." *Prettysmartscience.com*. 19 January 2019.