Research Article
Open Access
CrossMark

Differential fecundity in natural populations of *Drosophila Melanogaster from Mexico*

Abstract

Samples from six natural populations of Drosophila melanogaster were collected and their genetic composition was analyzed. The chromosomes obtained from each population were later exposed to irradiation and examined further. From these experiments, offspring production, which represents fecundity, was measured. For our analysis, chromosomes from each population were classified into different categories according to the percentage of offspring produced. A total of 36 two-tailed statistical tests were conducted to compare the population means and evaluate their similarities and differences. Among these, 15 tests compared normal genes with normal genes between populations, 15 tests compared deleterious genes with other deleterious genes, and 6 tests compared normal genes with deleterious genes. The frequencies of different gene categories-lethal, semilethal, subvital, subnormal, quasinormal, normal, and supernormal- were estimated for each population. The results showed clear differences in the distribution of these gene categories, confirming that the six populations are genetically distinct.

Volume 11 Issue 1 - 2026

Victor M Salceda
Departamento de Biología, Instituto Nacional de Investigaciones Nucleares, Mexico

Correspondence: Victor M Salceda, Departamento de Biología, Instituto Nacional de Investigaciones Nucleares, Mexico

Received: February 20, 2026 | **Published:** March 13, 2026

Introduction

One of the most extensively studied adaptive traits is fecundity, which is interpreted here as the capacity of an organism to produce a greater or lesser number of offspring. This trait has been widely investigated in species of the genus Drosophila, both in natural and experimental populations, as well as in strains with different characteristics, including lines carrying specific chromosome types or originating from different geographic regions.

Several important studies have contributed to the understanding of this trait. Early work by Bruce Wallace and Jack King[1] examined irradiated populations of Drosophila melanogaster. This research was later expanded by Wallace[2–4] and by Wallace and Madden,[5] who investigated different aspects of fecundity, including experimental approaches and methodology. Similarly, Baker[6] analyzed fitness in several strains of *D. melanogaster*, and later[7] conducted studies in experimental populations of Drosophila pseudoobscura.

Additional contributions include the work of Band and Ives,[8] who analyzed the genetic load of a population. Band[9] also introduced the possibility of comparing the genetic effects in heterozygous and homozygous individuals. Further research by Francisco J. Ayala[10,11] examined biomass and productivity in natural and irradiated populations of *Drosophila serrata*.

Later studies continued to expand this field. Kitagawa[12] investigated interactions among lethal genes in heterozygous conditions when studying viability. Meanwhile, Antonio Rodrigues da Cunha[13] and Hampton L Carson[14] examined natural populations of *D. melanogaster*. Related analyses include the work of Falk[15] on the adaptive value of heterozygotes and the study by Sánchez and collaborators,[16] who analyzed several components of adaptive value in *D. melanogaster*.

More recent studies include those of Yamasaki,[17] who investigated six experimental populations, and Fowler et al.,[18] who analyzed genetic variation related to total adaptive value. Subsequent research by Gardner et al.[19] and Barnes et al.[20] compared feeding behavior, fecundity, and lifespan in female flies. Additional studies include Reuser et al.,[21] who examined the evolution of late-life fecundity, and Curtsinger,[22] who analyzed fecundity in long-lived populations of *D. melanogaster*. Environmental influences were also explored by Abolhasan,[23] who compared the effects of different temperatures on viability and fecundity.

Considering these previous studies, the present work aims to analyze fecundity in six natural populations of *D. melanogaster*. After irradiation experiments, lethal and deleterious genes were identified through the analysis of genetic load. These genes, together with normal genes, were classified into seven fecundity categories (Table 1), which allowed comparisons among the populations examined in this study.

Table 1 Criteria for determining the different fertility categories

% of Decendents	Category
0 – 14	Lethal
15-29	Semilethal
30-49	Subvital
50-69	Subnormal
70-85	Quasinormal
86-114	Normal
115 or more	Supernormal

Materials and methods

The following populations were analyzed:

A. Coyoacán "A", 19°21′N and 99°6′W, 2243 m asl.

B. Col. del Valle, 19°22′N and 99°09′W, 2243 m asl.

C. Mixcoac, 19°21′N and 99°11′W, 2243 m asl.

D. Tuxtla Gutiérrez, 16°45′N and 93°7′W, 534 m asl.

E. Coyoacán "B", 19°18′N and 99°12′W, 2243 m asl.

F.- The Nopalera in Chapingo, 19°24′N and 98°53′W, 2750 m above sea level.

After this study the original offspring was irradiated at 6000r and the resulting descendency was incorporated to the study. For gene extraction and characterization, the cross known as CyL, initially

described and used by Wallace (1956) was employed. These are schematically represented as follows:

P: 3 CyL/Pm females x 1 1+/2+ male

F1: 3 CyL/Pm females x 1 CyL/1+ male

F2: 5 CyL/1+ females x 5 CyL/1+ males

F3 test generation with the following offspring:

1 homozygous CyL/CyL that dies; 2 heterozygous CyL/1+ individuals; 1 homozygous 1+/1+ individual the last term is a chromosome extracted from the population, and its fertility is characterized according to Table 1.

All cultures were maintained in a culture medium based on corn flour, brewer's yeast, and sugar, supplemented with propionic acid and Tegosept as fungicidal and bactericidal agents. They were kept at a constant temperature of 25±1°C and a relative humidity of 60%. The data obtained were used to construct different tables to facilitate statistical analysis using Student's t-tests.

Results

The study analyzed 1,162 second chromosomes extracted from six populations, representing a total of 416,290 individuals. From these, the average offspring values for each chromosome were calculated—first by population and chromosome type (normal or lethal), and then across all six populations, including their irradiated offspring. These values were subsequently used to construct the tables containing the data of interest for our analysis. The first step involved quantifying, for each population, the number of normal chromosomes (n) and the number of chromosomes carrying lethal genes (l), which we generally refer to as lethal chromosomes. The counts for each population were as follows: Coyoacán "A": 135 n, 56 l, Colonia del Valle: 102 n, 54 l, Mixcoac: 140 n, 46 l, Tuxtla Gutiérrez: 184 n, 17 l, Coyoacán "B": 140 n, 45 l, Nopalera: 183 n, 59 l

Next, the average offspring values for each chromosome type whether normal or lethal were calculated by population: Coyoacán "A": 356.18 n, 255.55 l, Colonia del Valle: 271.43 n, 193.46 l, Mixcoac: 474.46 n, 353.26 l, Tuxtla Gutiérrez: 376.91 n, 257.29 l, Coyoacán "B": 472.45 n, 347.21 l, Nopalera: 340.71 n, 252.54 l

The average fecundity across all six populations was also determined, corresponding to 373.19 individuals for normal chromosomes and 276.55 individuals for chromosomes carrying lethal genes. These results are summarized in Tables 2, 3, and 4. Another aspect considered in this study involves dividing fertility into different categories, as shown in Table 1, which presents the percentages corresponding to each category on which the study is based. The results of this categorization are presented in Tables 5 & 6.

From the analysis of the data in Tables 2–4, the first step was to determine whether chromosomes free of lethal genes are better adapted than chromosomes carrying lethal genes, measured in terms of the number of offspring. These comparisons within populations are summarized in Table 2. Similarly, comparisons between the different populations were performed, with the observed differences shown in Table 3.

The study also considered the fractionation of fertility into categories based on the number of offspring per isolated chromosome. This approach allowed the determination of gene frequencies within each category, following the methodology employed by Wallace and Madden (1953). The distribution of these classes is presented in Table 1.

Discussion

The analysis of the data presented in Tables 2 & 3 shows that, in all comparisons, the control populations exhibit better adaptability than the irradiated populations when considering chromosomes free of lethal genes (Table 3). The same is observed for chromosomes carrying lethal genes, as shown in Table 4.

Table 2 Inter-population comparison of average fecundities, given 2 at a time for normal genes

Population	No. Chrom.	Means	Deviation. vs. Dev..	Dev. "t"	"t"
A vs. B	135 vs. 102	356.185 vs. 271.431	153.596 vs. 237.619	131.729	4.904
A vs. C	135 vs.140	356.185 vs. 474.464	153.237 vs. 237.619	201.548	-4.665
A vs. D	135 vs 184	356.185 vs. 376.918	153.596 vs. 166.869	161.894	-1.130
A vs. E	135 vs. 140	356.185 vs. 472.457	153.596 vs. 237.128	201.251	-4.750
A vs. F	135 vs.183	356.185 vs. 340.715	153.596 vs. 146.874	150.238	0.908
B vs. C	102 vs. 140	271.431 vs. 474.464	93.564 vs. 237.619	181.461	-8.146
B vs. D	102 vs. 184	271.431 vs. 376.918	93.564 vs. 166.869	145.550	-5.871
B vs. E	102 vs. 140	271.431 vs. 472.457	93.564 vs. 237.128	191.105	-8.080
B vs. F	102 vs. 183	271.431 vs. 340.715	93.564 vs. 146.874	130.785	-4.287
C vs. D	140 vs. 184	474.464 vs. 376.918	237.619 vs. 166.869	201.148	4.324
C vs. E	140 vs. 140	474.464 vs. 472.457	237.619 vs. 237.128	238.226	0.070
C vs. F	140 vs. 183	474.464 vs. 340.715	237.619 vs. 146.874	192.155	6.990
D vs. E	184 vs. 140	376.918 vs. 472.457	166.869 vs. 237.128	200.896	-4.240
D vs. F	184 vs. 183	376.918 vs. 340.715	166.869 vs. 148.874	1587.647	2.200
E vs. F	140 vs. 183	472.457 vs. 340.715	237.128 vs. 140.874	191.891	6.114

Citation: Salceda VM. Differential fecundity in natural populations of *Drosophila Melanogaster from Mexico*. *MOJ Biol Med.* 2026;11(1):16–20. DOI: 10.15406/mojbm.2026.11.00265

Table 3 Inter-population comparison of average fecundities, given 2 at a time for lethal genes

	No. Chrom.	Means	Deviation. vs. Dev.	Dev. "t"	"t"
A vs. B	56 vs 54	255.553 vs. 193.463	111.572 vs. 77.367	97.198	3.349
A vs. C	56 vs. 46	255.553 vs. 353.260	111.571 vs.164.162	139.168	-3.528
A vs. D	56 vs. 17	255,553 vs. 257.294	111.571 vs.130.181	117.796	-0.053
A vs. E	56 vs. 46	255.553 vs.347. 217	111.571 vs.160.271	137.065	-3.361
A vs. F	56 vs. 59	255.553 vs. 252.542	111.571 vs. 118.696	116.297	0.139
B vs. C	54 vs 46	193.463 vs. 353.260	77.367 vs. 164.162	125.016	-6.181
B vs. D	54 vs. 17	193.463 vs. 257.294	77.367 vs. 130.181	94.127	-2.438
B vs. E	54 vs. 46	193.463 vs. 347.217	77.367 vs. 160.271	123.984	-6.184
B vs. F	54 vs. 59	193.463 vs. 252.542	77.367 vs. 118.696	101.984	-3.076
C vs. D	46 vs. 17	353.260 vs. 257.294	164.162 vs. 130.181	158.238	2.136
C vs. E	46 vs. 46	353.260 vs. 347.217	164.162 vs. 160.271	164.022	0.177
C vs. F	46 vs. 59	353.260 vs. 252.294	164.162 vs. 118.696	141.796	3.611
D vs. E	17 vs. 46	257.294 vs. 347.217	130.181 vs. 160.271	155.221	-2041
D vs. F	17 vs. 59	257.294 vs.252.542	130.181 vs. 118.696	122.984 139.984	0.140 154
E vs. F	56 vs 54	255.553 vs. 193.463	111.572 vs. 77.367	97.198	3.349

Table 4 Intra-population comparison of average fecundities for normal genes (n) versus detrimental genes (d)

Population	Num. Chrom.	Mean.	Dev. Mean.	Dev. "t"	"t"
A n vs. A d	135 vs. 56	356.18 vs. 255.55	153.59 vs. 114.57	143.31	4.418
B n vs. B d	140 vs.46	472.45 vs. 347.21	237.12 vs. 160.27	221.82	3.322
C n vs. C d	102 vs. 54	271.43 vs. 193.46	93.56 vs. 77.36	88.86	5.213
D n vs. D d	140 vs. 46	474.46 vs. 353.26	237.61 vs. 164.16	222.931	3.199
E n vs. E d	183 vs. 59	340.71 vs. 252.54	146.87 vs. 118.69	141.111	4.174
F n vs. Fd	184 vs. 17	376.91 vs. 257.29	166.86 vs. 130.18	164.906	2.862

When comparing normal chromosomes to lethal chromosomes (Table 2), higher adaptability was consistently observed for chromosomes carrying normal genes, regardless of whether they were products of irradiation. This finding contrasts with Wallace,[3,4] who reported that both chromosomes carrying and not carrying lethal genes showed better adaptability when derived from irradiated populations. However, studies by Falk and Ben-Zeev[15] and Salceda[24] reported a decrease in adaptability in irradiated populations, while Mukai et al. (1966) observed only a slight advantage for chromosomes from irradiated populations. All these studies employed the same CyL/Pm technique used here, allowing for direct comparison of results (Table 3).

Other studies, such as Ayala,[11] show that radiation initially favors better adaptation, measured in terms of offspring number. This effect was not observed in our study. A possible difference is that Ayala used a different methodology, employing demographic measurements and using other species, namely *D. serrata* and *D. birchii*. (Table 4)

The results presented in Table 5 refer to the fractionation of average fecundities into the different categories indicated in Table 1. These results are consistent with those in Table 3 and show the relative frequencies of each chromosome type according to its fecundity, compared with the average fecundity of the corresponding population. The upper part of Table 5 represents the frequencies for normal chromosomes (free of lethal genes), while the lower part represents chromosomes carrying lethal genes.

Table 5 Frequency distribution by category for normal genes

Pop..	Type		Semilet	Subvit.	Subnor.	Quasin	Normal	Supern	Total.
A	F	%	6 4.44	13 9.63	19 14.07	10 7.07	44 32.59	43 31.85	135
B	F	%	0 0	8 7.54	12 11.32	18 16.98	34 32.07	34 32.07	106
C	F	%	12 8.57	16 11.42	16 11.42	11 7.85	28 20.0	57 40.71	140
D	F	%	5 2.71	19 10.32	22 11.95	33 17.93	44 23.91	61 33.15	184
E	F	%	12 8.58	16 11.42	17 12.14	10 7.14	28 20.0	57 40.71	140
F	F	%	8 4.37	17 9.28	22 12.09	19 10.38	54 29.50	63 34.42	183

In the case of normal chromosomes, when comparing the control population with the irradiated populations, the frequencies across the different categories are generally very similar, particularly in the supernormal category. For the remaining five categories, no consistent pattern emerges when comparing each irradiated population to the control. Chromosomes carrying lethal genes exhibit a similar lack of pattern. This variability in response can be attributed to minor pleiotropic effects of different genes, which, by chance, confer greater or lesser adaptive responses to their carriers. From these observations, we can conclude that within-population comparisons, regarding the

Citation: Salceda VM. Differential fecundity in natural populations of *Drosophila Melanogaster from Mexico*. *MOJ Biol Med.* 2026;11(1):16–20.
DOI: 10.15406/mojbm.2026.11.00265

presence or absence of lethal genes, show significant differences favoring chromosomes free of lethal genes, as shown in Table 2.

Comparisons between populations (Tables 3 & 4) indicate that population "C" is the least adapted. In this population, as well as in populations "B" and "D," the observed differences are attributable to pleiotropic effects. At the time of the study, despite a relaxation period, these populations had not yet reached equilibrium. When examining the relative frequencies of the different fertility categories (Table 5), deviations are observed in all populations relative to the control. For chromosomes free of lethal genes (top of the table), differences are seen in the supernormal category. In the normal category, frequencies are lower in populations "B" and "D"; in the quasinormal category, there is an excess in populations "B" and "C"; in the subnormal category, frequencies are higher in populations "B" and "D." In the subvital category, a gradient is observed, which may reflect differences in dosage ratios.

When examining chromosomes carrying lethal genes in the three irradiated populations, differences were observed in the frequencies of supernormal chromosomes. For normal chromosomes, population "D" stands out, exhibiting a notably high frequency. A similar pattern is seen for quasinormal chromosomes, while for subnormal chromosomes, all three populations show elevated frequencies. In the case of subvital chromosomes, population "D" exhibits a low frequency, whereas population "B" shows a high frequency (Table 6).

Table 6 Frequency distribution by category for lethal genes

Pop.	Type		Semilet		Subvit.		Subnor.		Quasin		Normal		Supern		Total.
A	F	%	0	0	11	19.64	5	8.92	9	16.07	9	16.07	22	39.28	56
B	F	%	0	0	2	3.70	10	18.51	11	20.37	14	25.92	17	31.48	54
C	F	%	2	4.34	6	13.04	7	15.21	4	8.64	9	19.56	18	39.13	46
D	F	%	0	0	3	17.64	4	23.52	1	5.88	1	5.88	8	47.05	17
E	F	%	2	4.34	6	13.04	6	13.04	4	8.69	8	17.39	20	43.47	46
F	F	%	0	0	7	11.85	13	22.04	5	8.47	12	20.34	22	37.28	59

We interpret these differences as resulting from internal and independent adjustments within each experimental population. These adjustments tend toward an equilibrium relative to the control or ancestral population; however, achieving this equilibrium requires varying periods of readaptation. The duration of this readjustment depends on the interactions among different mutations, all of which act pleiotropically and undergo a process of selection and adaptive stabilization.

Acknowledgments

I wish to express my gratitude to the ININ Authorities for their support during the development of my activities.

Conflicts of interest

The authors declare that there are no conflicts of interest.

References

1. Wallace B, King JC. Genetic changes in populations under irradiation. *Am Nat.* 1951;85:209–222.
2. Wallace B. The estimation of adaptive values of experimental populations. *Evolution.* 1952;6:333–341.
3. Wallace B. Studies on irradiated populations of *Drosophila melanogaster*. *J Genet*. 1956;54:280-293.
4. Wallace B. The viability effects of spontaneous mutations in *Drosophila melanogaster*. *Am Nat*. 1965;99:335–348.
5. Wallace B, Madden C. The frequencies of sub and supervitals in experimental populations of *Drosophila melanogaster*. *Genetics.* 1953;38(5):456–470.
6. Baker JSF. The estimation of relative fitness of Drosophila populations. III. The fitness of certain strains of *Drosophila melanogaster*. *Evolution*. 1962;17:138–146.
7. Baker JSF. The estimation of fitness of Drosophila populations. IV. Experiments on *Drosophila pseudoobscura. Genetics.* 1965;51(5):747–759.
8. Band HT, Ives PT. Genetic structure of populations. I. On the nature of the genetic load in South Amherst population of *Drosophila melanogaster*. *Evolution.* 1963;17(2):198–215.
9. Band HT. Genetic structure of populations. II. Viabilities and variances of heterozygotes in constant and fluctuating environments. *Evolution.* 1963;17:307–319.
10. Ayala F. Evolution of fitness in experimental populations of *Drosophila serrata. Science.* 1965;150(3698):903–905.
11. Ayala F. Evolution of fitness. III. Improvement of fitness in irradiated populations of *Drosophila serrata. Proc Natl Acad Sci U S A.* 1967;58(5):1919–1923.
12. Kitagawa O. Interaction in fitness between lethal genes in heterozygous condition in *Drosophila melanogaster*. *Genetics*. 1967;57(4):809–820.
13. da Cunha AB. Maintenance of lethal and detrimental genes in natural populations. In: *Proceedings of the XII International Congress of Genetics*. 1968;2:162–163.
14. Carson HL. Maintenance of lethal and detrimental genes in natural populations. *Jpn J Genet*. 1969;44(Suppl 1):225–227.
15. Falk R. Fitness of heterozygotes in Drosophila. Mutat Res. 1967;4(6):805–819.
16. Sánchez PJL, Salceda VM, Molina J. Effecto de genes letales recesivos en posición trans en el cromosoma II de *Drosophila melanogaster* (Meigen) sobre algunos componentes de valor adaptativo. Agrociencia. 1974;16:75–82.
17. Yamazaki T. Measurement of fitness and its components in six laboratory strains of *Drosophila melanogaster*. Genetics. 1984;108(1):201–211.
18. Fowler K, Semple C, Barton NH, et al. Genetic variation for total fitness in *Drosophila melanogaster*. *Proc R Soc Lond B Biol Sci.* 1997;264(1379):191–199.
19. Gardner MP, Fowler K, Barton NH, et al. Genetic variation for total fitness in *Drosophila melanogaster*. Genetics. 2005;169(3):1553–1571.
20. Barnes AL, Neghy S, Borne JM, et al. Feeding, fecundity and lifespan in female *Drosophila melanogaster*. *Proc R Soc B Biol Sci.* 2008;275(1643):1875–1883.

21. Reuser CL, Tieney JJ, Gunion SM, et al. Evolution of late life fecundity in *Drosophila melanogaster*. *J Evol Biol.* 2016;19(1):289–301.
22. Curtsinger JW. Fecundity for free? Enhanced oviposition in longevous populations of *Drosophila melanogaster*. *Biogerontology.* 2019;20(4):397–404.
23. Abolhasan R. The effect of different temperatures on viability and fertility of *Drosophila melanogaster*. *Egypt Acad J Biol Sci*. 2012;5(1):81–87.
24. Salceda VM. Viability effect of lethal and non-lethal II chromosomes of irradiated *Drosophila melanogaster* populations. *Arh Biol Nauka*. 1985;37(1-4):27–32.

Citation: Salceda VM. Differential fecundity in natural populations of *Drosophila Melanogaster from Mexico. MOJ Biol Med.* 2026;11(1):16–20.
DOI: 10.15406/mojbm.2026.11.00265