

Individuals of *Drosophila melanogaster* (a species of fruit fly) were collected from a wild population. A random sample of wild females were mated with males from a laboratory raised population that was homozygous at both loci (ab/ab). The phenotypes of the resulting progeny were scored. A is the dominant allele for red (wild type) eyes and a is recessive for peach eyes. B is the dominant allele for long wings (wild type) and b is recessive for short wings. The following phenotypes were observed:

A. In the space below give the genotype for each phenotype and the corresponding gamete haplotype from the wild population.

		Genotype	female gamete
Red eyes, long wings	330	AB//ab	AB
peach eyes, short wings	320	ab//ab	ab
Red eyes, short wings	200	Ab//ab	Ab
peach eyes, long wings	150	aB//ab	aB

Note that ALL male gametes are ab and should not count toward allele frequencies. The mating design samples gametes from the wild population so that we can estimate D.

B. Now estimate the allele frequencies, showing your work.

Allele frequencies: a: 0.47 A: 0.53 b: 0.52 B: 0.48

$$F(A) = (330 + 200)/1000 = 0.53 \quad \text{therefore } f(a) = 1 - f(A) = 0.47$$

$$F(B) = (330 + 150)/1000 = 0.48 \quad \text{therefore } f(b) = 1 - f(B) = 0.52$$

C. Calculate the actual and HWE expected gamete frequencies.

Gamete	Observed	obs gamete freq (P11, P22, P12, P21)	HWE exp gamete freq (p1, p2, q1, q2)	HWE exp # gametes
AB	330	0.33	$(0.53)(0.48) = 0.2544$	254.4
ab	320	0.32	$(0.47)(0.52) = 0.2444$	244.4
Ab	200	0.20	$(0.53)(0.52) = 0.2756$	275.6
aB	150	0.15	$(0.47)(0.48) = 0.2256$	225.6
				total = 1000.0

D. Use a χ^2 test to determine whether the gamete genotypes are in the ratio expected under gametic equilibrium (be sure to show all calculations for χ^2 including the degrees of freedom). Also check this result by using the χ^2 test shortcut (see Interact Box 2.4). Further, see PopGeneS² for a module that can be used to verify your calculations. Are the two loci in gametic equilibrium?

$$\text{AB gamete: } \frac{(330 - 254.4)^2}{254.4} = 22.47$$

$$\text{ab gamete: } \frac{(320 - 244.4)^2}{244.4} = 23.39$$

$$\text{Ab gamete: } \frac{(200 - 275.6)^2}{275.6} = 20.74$$

$$\text{aB gamete: } \frac{(150 - 225.6)^2}{225.6} = 25.33$$

df = 4 – 2 (for allele freq estimates) – 1 (chi-square test) = 1
Chi-squared value = 91.93 with p <<< 0.01

There is gametic disequilibrium in this population. The chi-square test shows us that the deviation from independent assortment (predicted by Mendel's 2nd law given the allele frequencies in this population) is greater than expected by chance alone.

Using Interact Box 2.4 method:

$$\frac{(0.0756)^2 1000}{(0.47)(0.53)(0.52)(0.48)} = 91.8 \text{ with a result and interpretation identical to above.}$$

Which gametes are coupling and which are repulsion if mating is random? Why? Using the observed gamete frequencies (same as the P11, P22, P12, P21) calculate the amount of observed gametic disequilibrium or \hat{D} .

By definition, the less frequent gametes are “repulsion” and the more frequent gametes are “coupling” when $r < 0.5$. AB and ab are more frequent and therefore coupling gametes. aB and Ab are less frequent and are therefore repulsion.

$$\hat{D} = (0.330)(0.320) - (0.20)(0.15) = 0.0756$$

Using your estimated allele frequencies (same as the p1, p2, q1, q2) now calculate the theoretical minimum and maximum gametic disequilibrium (D_{\min} and D_{\max}) for these data.

$$D_{\min} \text{ larger of } -p_1q_1 \text{ or } -p_2q_2 \\ -(0.53)(0.48) \text{ or } -(0.47)(0.52) \\ -0.2544 \text{ or } -0.2444$$

$$D_{\max} \text{ smaller of } p_1q_2 \text{ or } p_2q_1 \\ (0.53)(0.52) \text{ or } (0.47)(0.48) \\ 0.2756 \text{ or } 0.2256$$

$$D_{\min} = -0.2444 \text{ (use when } D < 0)$$

$$D_{\max} = 0.2256 \text{ (use when } D > 0)$$

How close is \hat{D} to its maximum?

$$\hat{D}/D_{\max} = 0.0756/0.2256 = 0.335 \text{ or } 33.5\% \text{ of the maximum gametic disequilibrium with these allele frequencies.}$$

What is the recombination rate (r) observed in these data? How many map units is this? How much gametic disequilibrium would be observed after additional ten generations assuming random mating?

r = the frequency of recombination or the combined frequency of the repulsion gametes.

$$r = (200 + 150)/1000 = 0.35$$

One map unit = 1% recombination frequency. So these two loci are apparently 35 map units apart (assuming gametic disequilibrium is caused only by physical linkage).

After 10 generations

$$D_{10} = (1 - 0.35)^{10}(0.0756) = 0.001$$

There will be no gametic disequilibrium after 10 generations assuming that no process is acting in opposition to recombination.