

A new species of fly was discovered on an island in the South Pacific. Several different crosses were performed, each using 100 females and 100 males. The phenotypes of the parents and the resulting offspring were recorded.

Cross I: True-breeding bronze-eyed males were crossed with true-breeding red-eyed females. All the F_1 offspring had bronze eyes. F_1 flies were crossed, and the data for the resulting F_2 flies are given in the table below.

F_2 Phenotype	Male	Female
Bronze eyes	3,720	3,800
Red eyes	1,260	1,320

Cross II: True-breeding normal-winged males were crossed with true-breeding stunted-winged females. All the F_1 offspring had stunted wings. F_1 flies were crossed, and the data for the resulting F_2 flies are given in the table below.

F_2 Phenotype	Male	Female
Normal wings	1,160	1,320
Stunted wings	3,600	3,820

Cross III: True-breeding bronze-eyed, stunted-winged males were crossed with true-breeding red-eyed, normal-winged females. All the F_1 offspring had bronze eyes and stunted wings. The F_1 flies were crossed with true-breeding red-eyed, normal-winged flies, and the results are shown in the table below.

Phenotype	Male	Female
Bronze eyes, stunted wings	2,360	2,220
Bronze eyes, normal wings	220	300
Red eyes, stunted wings	260	220
Red eyes, normal wings	2,240	2,180

- What conclusions can be drawn from cross I and cross II? **Explain** how the data support your conclusions for each cross.
- What conclusions can be drawn from the data from cross III? **Explain** how the data support your conclusions.
- Identify** and **discuss** TWO different factors that would affect whether the island's fly population is in Hardy-Weinberg equilibrium for the traits above.

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- (a) What conclusions can be drawn from cross I and cross II? **Explain** how the data support your conclusions for each cross. **(4 points maximum)**

Conclusion for cross I (1 point maximum)	Possible explanations for cross I (1 point maximum)
<ul style="list-style-type: none"> Bronze dominant/red recessive Autosomal (non-sex-linked) 	<ul style="list-style-type: none"> All F_1 /heterozygotes express dominant trait (bronze). F_2 shows 3:1 ratio (bronze:red/dominant:recessive). Equal distribution of F_2 phenotypes for both genders.
Conclusion for cross II (1 point maximum)	Possible explanations for cross II (1 point maximum)
<ul style="list-style-type: none"> Stunted dominant/normal recessive Autosomal (non-sex-linked) 	<ul style="list-style-type: none"> All F_1 /heterozygotes express dominant trait (stunted). F_2 shows 3:1 ratio (stunted:normal/dominant:recessive). Equal distribution of F_2 phenotypes for both genders.

- (b) What conclusions can be drawn from the data from cross III? **Explain** how the data support your conclusions. **(4 points maximum)**

Conclusion for cross III (1 point per bullet; 2 points maximum)	Explanation for cross III (1 point per bullet; 2 points maximum)
<ul style="list-style-type: none"> Genes linked Crossing over Genes 10 map units apart 	<ul style="list-style-type: none"> Not a 1:1:1:1 ratio (as predicted by independent assortment). Not a 1:1 ratio/two recombinant phenotypes (unexpected). Frequency of recombinant phenotypes was 10 percent (setup equation OK)/parental phenotypes (bronze/stunted and red/normal) are represented in 90 percent of offspring.

- (c) **Identify** and **discuss** TWO different factors that would affect whether the island's fly population is in Hardy-Weinberg equilibrium for the traits above. **(4 points maximum)**

Identification (1 point per bullet; 2 points maximum)	Discussion of effect (1 point per bullet; 2 points maximum)
<ul style="list-style-type: none"> Large population Random mating 	<ul style="list-style-type: none"> Minimized genetic drift. No gene pool change due to mate preferences.
<ul style="list-style-type: none"> No mutation No immigration/emigration/migration (no gene flow) 	<ul style="list-style-type: none"> No new alleles in population. No gene pool change by addition/loss of alleles.
<ul style="list-style-type: none"> No natural selection 	<ul style="list-style-type: none"> No alleles favored or disfavored by environment.