

ER 7, # 20

23 & 24. Three genetically linked genes are B, I and O (mutations are dominant). An individual heterozygous for all 3 loci was crossed with another individual homozygous for all three wild type traits (wild type is recessive). The following phenotypes and numbers are seen. Use this data to answer questions 23 & 24. NO particular gene order is implied in the data - you must determine the gene order for #23.

B ⁺ I ⁺ O ⁺	50
BIO	50
BIO ⁺	5
B ⁺ I ⁺ O	5
BI ⁺ O ⁺	125
B ⁺ IO	125
B ⁺ IO ⁺	320
BI ⁺ O	320

12. (4 pts) A student scientist studying wing length in fruit flies discovers a mutant fly with short wings. They generate a true breeding line of flies for this mutation, named short wings (later revised to short wings 1). While tasting maple syrup in Vermont they discover a short winged fruitfly and they bring it back to their apartment. They generate a second true breeding line for this mutation, named short wings 2. They take the two true breeding lines and mate them. ALL of the F1 progeny have normal wings. They find that fascinating. They then take one of the F1 flies and mate it to a fly from a population that is true breeding for both mutations. They find 25% of these offspring have normal wings and 75% have short wings. What hypothesis best describes these two mutations?

- A) short wings 1 and short wings 2 are mutations in the same genetic locus. The mutations are recessive to wild type alleles.
- B) short wings 1 and short wings 2 are mutations in the same genetic locus. The mutations are dominant to wild type alleles.
- C) short wings 1 and short wings 2 are mutations in different genetic loci. The two loci are genetically linked and separated by 20 centimorgans.
- D) short wings 1 and short wings 2 are mutations in different genetic loci. The two loci are genetically unlinked.
- E) short wings 1 and short wings 2 are mutations in different genetic loci. The two loci are genetically linked and separated by 75 centimorgans.

18. A male fruit fly with a striped abdomen and normal legs was crossed with a female fruit fly with a striped abdomen and 8 legs. She came from a population that was true breeding for 8 legs but NOT for striped abdomen. The phenotype and number of each progeny type is shown below. Determine the genotype of both the male and female fruitfly.

	Female	Male
Striped abdomen, extra legs (8)	601	599
Striped abdomen, normal leg # (6)	599	601
Normal abdomen, extra legs (8)	199	201
Normal abdomen, normal leg # (6)	201	199

Work space:

13. (5) A male fruit fly is mated to a female fruit fly. The male fly has normal shaped eyes and normal wings. The female has normal shaped eyes and normal wings. The offspring show the phenotypes as shown below.

Phenotype	# of Female Offspring	# of Male Offspring
Normal shaped eyes, divergent wings	0	376
Normal shaped eyes, normal wings	750	374
Bubble shaped eyes, divergent wings	0	123
Bubble shaped eyes, normal wings	250	127

1000 Total

1000 Total

Use correct fruit fly notation and show your work. A legend would be helpful!

(2) What is the genotype of the female parent?

(2) What is the genotype of the male parent?

b. (1) Calculate the map distance if the two traits are genetically linked. If the traits are genetically unlinked, then clearly state the traits are genetically unlinked.

Answers

23 & 24. Three genetically linked genes are B, I and O (mutations are dominant). An individual heterozygous for all 3 loci was crossed with another individual homozygous for all three wild type traits (wild type is recessive). The following phenotypes and numbers are seen. Use this data to answer questions 23 & 24. NO particular gene order is implied in the data - you must determine the gene order for #23.

B ⁺ I ⁺ O ⁺	50		I ⁺ B ⁺ O ⁺	50	
BIO	50		IBO	50	
BIO ⁺	5	dr	IBO ⁺	5	
B ⁺ I ⁺ O	5	dr	I ⁺ B ⁺ O	5	
BI ⁺ O ⁺	125		I ⁺ BO ⁺	125	
B ⁺ IO	125		IB ⁺ O	125	
B ⁺ IO ⁺	320	P	IB ⁺ O ⁺	320	
BI ⁺ O	320	P	I ⁺ BO	320	

The double recombinants (listed dr) represent the lowest frequency. The allele in them that appears different from the parental type chromosome (listed as P) is the one that is in the middle. From this you can tell B is in the middle. NOW rewrite them in the correct order. Note that the parent is IB⁺O⁺/I⁺BO. A recombinant between I and B loci would yield IBO or I⁺B⁺O⁺. The numbers are 50 + 50 for a total of 100. You must also include the 10 from the double recombinants since they also represent a crossover between the I and B loci. Thus 110/1000 is about 11 map units.

12. Initially you only know the two populations have the same phenotype but that could be due to the fact that the two mutations are at the same loci or at different loci that produce the same effect (for example a defect in either of several steps of a multi-step pathway may produce the same phenotype). From the F1 data you know the mutations represent different loci because the F1 flies have normal wings. You also know the mutant alleles are recessive to wild type. Go back and rewrite the correct genotypes of population 1 and 2. The notation below assumes the traits assort independently, we could also write them as if they assorted dependently.

Independently assorting (Case A)

Population 1 = $\frac{sw1}{sw1}; \frac{sw2^+}{sw2^+}$ Population 2 = $\frac{sw1^+}{sw1^+}; \frac{sw2}{sw2}$ F1 = $\frac{sw1}{sw1^+}; \frac{sw2^+}{sw2}$

Dependently assorting (Case B)

Population 1 = $\frac{sw1sw2^+}{sw1sw2^+}$ Population 2 = $\frac{sw1^+sw2}{sw1^+sw2}$ F1 = $\frac{sw1sw2^+}{sw1^+sw2}$

The two give very different ratios of gametes.

In the problem a F1 offspring is mated to a fly that is homozygous recessive for both mutations. Punnet squares are presented for both Case A and B. The boxes are not filled in with genotype, only the phenotype. Don't forget to have normal wings you must have at least one wild type allele at each locus. For Case A each box going down is 25%, and thus each box for offspring is 25%. In case B the percentage is P for parental and r for recombinant percentage. Case A matches are data.

