EUKARYOTIC MAPPING PRACTICE PROBLEMS

1.   In <u>Drosophila</u> the genes *A B D* are linked. You cross a strain that is homozygous for *d* with a strain that is homozygous for *ab.* Below are the phenotypes and progeny of a test cross. Outline the cross and determine the map for the genes. Calculate the coefficient of coincidence and the interference.

Phenotype	Number
ABd	389
abD	413
ABD	60
abd	68
aBd	29
AbD	34
Abd	3
aBD	4

2.   In <u>Drosophila</u> the genes *X Y Z* are linked. You cross a strain that is homozygous for *x z* with a strain that is homozygous for *y.* Below are the phenotypes and progeny of a test cross. Outline the cross and determine the map. Calculate the coefficient of coincidence and the interference.

Phenotype	Number
Xyz	13
XYZ	220
XyZ	2480
xyZ	170
xYz	2429
XYz	178
xYZ	19
xyz	233

3.   In Tasmanian devils, three recessive mutations are *h* (hairy nostrils), *r* (rat tail), and *f* (short fang).   Outline a test cross between a devil with hairy nostrils and rat tail with a devil with short fangs. From the data below, calculate the map, the coefficient of coincidence, and the interference.

Phenotype	Number
HRF	73
hrf	63
Hrf	96
hRF	110
HrF	2
hRf	2
hrF	306
HRf	348

4. You are conducting genetic research on rare Tasmanian fuzz puppies. To your dismay, you find that your arch rival, an unscrupulous geneticist at the University of Rochester has just published a genetic map of the very same mutants that you are studying. Her genetic map is as follows:

Rd — 10.4 — Bt — 6.2 — Fz

Rd is a mutation that gives fuzz puppies blood-shot eyes. Bt is a mutation that produces black tongues. Fz is a mutation that causes the fuzzy hair on their ears to be straight. All mutations are recessive. You decide to repeat her experiment and cross a wild-type strain with a strain that is homozygous recessive for all traits. The results of your cross is below. Is her map consistent with yours?

Phenotype	Number
rd bt fz	310
RD BT FZ	328
RD bt fz	40
rd BT FZ	44
rd bt FZ	35
RD BT fz	37
rd BT fz	4
RD bt Fz	4

5. Three Drosophila genes map as follows:

A — 15.7 — B — 3.9 — D

Using the map, calculate the expected F2 progeny for the cross
ABD x *abd* in which a test cross was performed with the F1 progeny. Assume a coefficient of 1.0. and a total of 3000 progeny. How would the numbers change if the coefficient of coincidence was 0.8? Determine whether the data below is consistent with your map.

Phenotype	Number
ABD	1121
abd	1139
aBD	257
Abd	266
ABd	87
abD	112
AbD	8
aBd	10

6. You cross a dihybrid cross with a strain of flies that is *a* and a strain that that is *b*. The results of the F2 are given. Use X^2 to help you determine if *a* and *b* are linked.

Phenotype	Number
AB	1757
Ab	583
aB	605
ab	225

7. You cross a dihybrid cross with a strain of flies that is **a** and a strain that that is **b**. The results of the F2 are given. Use X^2 to help you determine if **a** and **b** are linked.

Phenotype	Number
AB	1827
Ab	424
aB	386
ab	298

EUKARYOTIC MAPPING PRACTICE PROBLEMS - SOLUTIONS

1.   P 1   ABd/ABd x abD/abD

            F 1   ABd/abD x abd/abd

Test Cross

Phenotypes	Number		
ABd	389	highest number	
abD	413	= nonrecombinants	
ABD	60	intermediate number	
abd	68	= single XO	
aBd	29	intermediate number	
AbD	34	= single XO	
Abd	3	smallest number	
aBD	4	= double XO	

In the double XO's, B is the gene that has changed linkage. Therefore, the sequence is -- A - - - B - - - D - - .

A - B = [(29 + 34 + 3 + 4) / 1000] x 100 = **7 cM**

B - D = [(60 + 68 + 3 + 4) / 1000] x 100 = **13.5 cM**

A   7.0 B   D   13.5

|________|________________|

20.5

Coef. Coinc = obsvd 2XO's / exp 2XO's

            = (7/1000) / (.007 x .135)

            = **0.74**

interference = 1 - coef. coinc. = 1 - 0.74 = **0.26** = pos interf.

2.   P1   xYz/xYz x XyZ/XyZ

            F1   xYz/XyZ x xyz/xyz

Test Cross
  Phenotypes   Number
      xYz   2429   highest number
      XyZ   2480   = nonrecombinants
      xyZ   170   intermediate number
      XYz   178   = single XO
      XYZ   220   intermediate number
      xyz   233   = single XO
      Xyz   13 smallest number
      xYZ   19   = double XO

In the double XO's, Z is the gene that has changed linkage. Therefore, the sequence is   --
X - - - Z - - - Y - - .

X - Z = [(170 + 178 + 13 + 19) / 5742] x 100 =_6.62 cM_

Z - Y = [(220+ 233 + 13 + 19) / 5742] x 100 =_8.45 cM_

             X   Z   Y
                     6.6   8.45
             ├────────────────────┼──────────────────┤
                           15.05

Coef. Coinc = obsvd 2XO's / exp 2XO's

            = (32 /5742) / (.066 x .0845)

            = _1.0_

interference = 1 - coef. coinc. = 1 - 1.0 = _0_= no interf.

3. P 1   hrF/hrF   x HRf/Hrf

    F 1   hrF/HRf   x   hrf/hrf

        Test Cross
        Phenotypes   Number
            HRF   73   intermediate number
            hrf   63   = single XO
            Hrf   96   intermediate number
            hRF   110   = single XO
            HrF   2   smallest number
            hRf   2   = double XO
            hrF   306   highest number
            HRf   348   = nonrecombinants

In the double XO's, His the gene that has changed linkage. Therefore, the sequence is   --
F - - - H - - - R - - .

H - F = [(73 + 163 + 12 + 2) / 1000] x 100 =_14 cM

F - R = [(96 + 110 + 2 + 2) / 1000] x 100 =_21 cM

            F   H   R
        |_____14_____|_____21_____|
                        36

Coef. Coinc = obsvd 2XO's / exp 2XO's

            = (4 /1000) / (0.14 x 0.21)

            = 0.136

interference = 1 - coef. coinc. = 1 - 0.136 = 0.864 = pos interf.

4.   When comparing results of two experiments, you must compare data, not maps. Therefore, you must calculate the data you would have expected based on your competetors map. These numbers become your expected values, and your numbers become your observed values in a X^2 test.

Of 802 progeny, 10.4% should show a recombination event between Rd and Bt:

802 x 0.104 = 83.4 = single + double recombinants

6.2% should show a recombination event between Bt and Fz:

802 x 0.062 = 49.7 = single + double recombinants

The double recombinants will be

802 x 0.104 x 0.062 = 5.2

The Rd - Bt single recombinants will be

83.4 - 5.2 = 78.2

The Bt - Fz single recombinants will be

49.7 - 5.2 = 44.5

Finally, the nonrecombinants will be

802 - 78.2 - 44.5 - 5.2 = 674.1

Now we are ready to set up the X2 table. But don't forget that each of the four classes of phenotypes that you have calculated are actually 8 pairs of reciprocals. Therefore, you must take the numbers and divide them in half, one for one of the pair, and one for the other.

PHENOTYPE	OBSERVED	EXPECTED	O - E	$(O - E)^2$	DIV EXPT
rd bt fz	310	337.05	-27.05	731.70	2.17
RD BT FZ	328	337.05	-9.05	81.90	0.24
RD bt fz	40	39.10	0.90	0.81	0.02
rd BT FZ	44	39.10	4.90	24.01	0.61
rd bt FZ	35	22.25	12.75	162.56	7.31
RD BT fz	37	22.25	14.75	217.56	9.78
rd BT fz	4	2.60	1.40	1.96	0.75
RD bt Fz	4	2.60	1.40	1.96	0.75

$$X^2 = 21.64$$

degrees of freedom = 7   probability = 0.05   Crit. X^2 =14.067

H_O = there is no significant difference between observed and expected values

$$X2 = 21.64 > 14.067$$

Therefore, reject the H_O. Your data does not agree with your competetor's map. But who is correct?????

5.   Of 3000 progeny, 15.7% should show a recombination event between A and B:

    3000 x 0.157 = 471 = single + double recombinants

3.9% should show a recombination event between B and D:

    3000 x 0.039 = 117 = single + double recombinants

The double recombinants will be

    3000 x 0.157 x 0.039 = 18

The A - B single recombinants will be

    471- 18 = 453

The B - D single recombinants will be

    117 - 18 = 99

Finally, the nonrecombinants will be

    3000 - 453 - 117 - 18 = 2430

Now we are ready to set up the X2 table. But don't forget that each of the four classes of phenotypes that you have calculated are actually 8 pairs of reciprocals. Therefore, you must take the numbers and divide them in half, one for one of the pair, and one for the other.

PHENOTYPE	EXPECTED	EXPECTED	OBS - EXP	$(O - E)^2$	DIV BY EXP
ABD	1121	1215.0	-94.00	8836.00	7.27
abd	1139	1215.0	-76.00	5776.00	4.75
aBD	257	226.5	30.50	930.25	4.11
Abd	266	226.5	39.50	1560.25	6.89
ABd	87	49.5	37.50	1406.25	28.41
abD	112	49.5	62.50	3906.25	78.91
AbD	8	9. 0	-1.00	1.00	0.11
aBd	10	9.0	1.00	1.00	0.11

$X^2 =$ 130.57

degrees of freedom = 7   probability = 0.05   Crit. X^2 =14.067

H_O = there is no significant difference between observed and expected values

            X2 = 130.57> 14.067

Therefore, reject the H_O. Your data is inconsistent

If the coefficient of coincidence is 0.8, that means you are only seeing 80% of the double recombination that you expect. Therefore, the double recombinants will be

    0.8 x [3000 x 0.157 x 0.039] = 0.8 x 18 = 14

You then subtract 14 instead of 18 from the other classes of recombinants.

6. If the two genes are _unlinked_ then they would segregate in a 9:3:3:1 ratio. If they were linked, then there would be a substantial departure from this ratio, but without knowing their distance, we could not predict the phenotype numbers. Therefore, we will test to see if they are unlinked.

Phenotype	Observed	Expected	O - E	$(O - E)^2$	/ Exp
AB	1757	1782.9	-25.90	670.81	0.38
Ab	583	594.4	-11.40	129.96	0.22
aB	605	594.4	10.60	112.36	0.19
ab	225	198.1	26.90	723.61	3.65
				$X^2 =$	4.44

degrees of freedom = 3   probability = 0.05   Crit. X^2 = 7.815

H_O = there is no significant difference between observed and expected values

$$X2 = 4.44 < 7.815$$

Therefore, accept the H_O. The genes are unlinked

7. If the two genes are _unlinked_ then they would segregate in a 9:3:3:1 ratio. If they were linked, then there would be a substantial departure from this ratio, but without knowing their distance, we could not predict the phenotype numbers. Therefore, we will test to see if they are unlinked.

Phenotype	Observed	Expected	O - E	$(O - E)^2$	/ Exp
AB	1827	1651	176.00	30976.00	18.76
Ab	424	550	-126.00	15876.00	28.87
aB	386	550	-164.00	26896.00	48.90
ab	298	183	115.00	13225.00	72.27
				$X^2 =$	168.80

degrees of freedom = 3   probability = 0.05   Crit. X^2 = 7.815

H_O = there is no significant difference between observed and expected values

$$X^2 = 168.8 > 7.815$$

Therefore, reject the H_O. The genes are probably linked with some degree of recombination between them.