Title: Corn Genetics

Purpose:

to determine the genetic makeup of gametes and offspring using a corn model
to use a statistical test (Chi-square: X^2) to determine match of theoretical and actual values

Materials:

starchy~waxy pollen   small petri dishes
starchy~waxy segregating corn   marker pins
(monohybrid)   sandpaper
purple~starchy: purple~sweet: iodine solution
yellow~starchy: yellow~sweet corn   pipettes
(dihybrid)

Procedure:

Work in pairs in groups of 4

Pollen Analysis

1. Obtain 4~5 drops corn pollen per pair
2. Put pollen in petri dish
3. Add 4 drops iodine solution to the pollen in the petri dish
   bluish-black indicates presence of starchy, reddish brown indicates waxy
4. Count and record in Table 1 the number of pollen grains of each type
   1 person counts and the other records
   You may want to set up a tally sheet to record the *raw* counts
5. Combine your data with that of other class members and record in Table 2 (actual count)
6. To determine the expected count, construct a Punnet square:
   Note: The pollen was collected from the F_1 generation of a cross between a homozygous starchy corn and a homozygous waxy corn. What proportion of the gametes would be starchy and what proportion would be waxy? Multiply these proportions by the total number of pollen grains counted to get the expected count.
7. Complete the X^2 analysis for the pollen grains. (see Table 6)

Monohybrid Cross

1. Obtain 1 ear of starchy~waxy corn (all yellow corn) per pair
2. Obtain small sandpaper square
3. Sand outer layer (aleurone) of all corn kernels, exposing the endosperm in a small area
4. When all kernels are sanded, place one drop of iodine solution on exposed endosperm
   bluish-black indicates presence of starchy, reddish brown indicates waxy
5. Count and record in Table 1 the number of kernels of each phenotype
   1 person counts and the other records
   You may want to set up a tally sheet to record the *raw* counts
6. Put a colored marker pin in the end of one row of kernels and count and record the phenotypes
   Put an uncolored row marker pin in the end of the next row and continue counting. After each row is completed, move the row marker pin to the next row until you return to the row marked by the colored pin.
7. Combine your data with that of other class members and record in Table 3
8. Indicate the dominant phenotype (HOW DO YOU KNOW?)
9. To determine the expected count construct a Punnet square
   The corn kernels are an F_2 generation resulting from a cross between homozygous starchy and homozygous waxy corn. Thus the parents of the F_2 were heterozygous starchy ~waxy. What proportion would be the dominant phenotype and what proportion recessive? Multiply these proportions by the actual count to obtain the expected count.

Results: Monohybrid Cross

Table 1: Monohybrid Cross

	Pollen			Corn Ears	
	Bluish-Black	Reddish-Brown		Bluish-Black	Reddish-Brown
Sample 1			Ear 1		
Sample 2			Ear 2		
Total 1 + 2					

Construct Punnet Squares Here: (Use Wx for starchy and wx for waxy)

Parents	F_1	F_2
WxWx x wxwx		

Table 2: X^2 Analysis Pollen (monohybrid) Class Data

$$X^2 = \frac{(a_1-e_1)^2}{e_1} + \frac{(a_2-e_2)^2}{e_2}$$

	Bluish-Black	Reddish-Brown	Total
Actual Number	a_1	a_2	
Expected Number	e_1	e_2	

Table 3: X^2 Analysis Corn Ears (monohybrid) Class Data

$$X^2 = \frac{(a_1-e_1)^2}{e_1} + \frac{(a_2-e_2)^2}{e_2}$$

	Bluish-Black	Reddish-Brown	Total
Actual Number	a_1	a_2	
Expected Number	e_1	e_2	

Dihybrid Cross

The purple color is produced by a pigmented layer within the grains. If the layer is not pigmented (colorless), the yellow color of an inner tissue shows through. Sweet corn grains can be recognized because they wrinkle upon drying while starchy grains remain smooth. Individual kernels may be purple and starchy, purple and sweet, yellow and starchy, or yellow and sweet.

1. Obtain one ear of purple~yellow corn per pair.
2. Count and record in Table 4 the number of kernels of each phenotype
   1 person counts and the other records
   You may want to set up a tally sheet to record the *raw* counts
3. Put a colored marker pin in the end of one row of kernels and count and record the phenotypes
   Put an uncolored row marker pin in the end of the next row and continue counting.
   After each row is completed, move the row marker pin to the next row until you return to the row marked by the colored pin.
4. Combine your data with that of other class members and record in Table 5
   To determine the expected count construct a Punnet Square:
   Multiply these proportions by the actual count to obtain the expected count.

Construct Punnet Squares Here: (Use Wx for starchy and wx for waxy)

Parents	F_1	F_2
Purple Starchy (PPSS) vs Yellow Sweet (ppss)	Purple Starchy (PpSs)	

Table 4: Dihybrid Cross

	Purple~Starchy	Purple~Sweet	Yellow~Starchy	Yellow~Sweet
Total Ear 1				
Total Ear 2				
Total 1 + 2				

Table 5: Analysis Corn Ears (dihybrid cross) Class Data

$$X^2 = \frac{(a_1-e_1)^2}{e_1} + \frac{(a_2-e_2)^2}{e_2} + \frac{(a_3-e_3)^2}{e_3} + \frac{(a_4-e_4)^2}{e_4}$$

	Purple~Starchy	Purple~Sweet	Yellow~Starchy	Yellow~Sweet	Total
Actual Number	a_1	a_2	a_3	a_4	
Expected Number	e_1	e_2	e_3	e_4	

Table 6: X^2 Values

d. f. *	.95	.90	.80	.70	.50	.30	.10	.05	.01
				P (probability)					
1	.004	.016	.064	.148	.455	1/03	2.71	3.84	6.64
2	.103	.211	.446	.713	1.38	2.41	4.60	5.99	9.20
3	.352	.584	1.00	1.42	2.37	3.66	6.25	7.82	11.30

*degrees of freedom   = 1 for monohybrid cross
                                  = 3 for dihybrid cross

X^2 Data from http://www.richland.cc.il.us/james/lecture/m170/tbl-chi.html
X^2 calculator: http://www.physics.csbsju.edu/stats/chi-square_form.html

You are looking for the difference to be INSIGNIFICANT!
P values above .05 are INSIGNIFICANT (not significant)
This means that actual values DO NOT differ from expected values.

Do not forget the Discussion, Conclusion, and Reflection
Please include background information on corn genetics.
Cite your sources!

For background on monohybrid and dihybrid crosses in corn, see
http://www.mtps.com/hs/faculty/kolchinskya/dihybrid.ppt

For background information on Mendelian genetics, see
http://www.biology.arizona.edu/mendelian_genetics/mendelian_genetics.html
http://www.ndsu.nodak.edu/instruct/mcclean/plsc431/mendel/

For lab grading guidelines go to:
http://www.jdenuno.com/PDFfiles/LabGuide1.PDF