Student name: **Code number:**

GENETICS

Lab 1

(2014 - 2015)

MENDELIAN GENETICS

Objectives

Upon completion of this lab, students should:

1. Understand the principles and terms used in Mendelian genetics.
2. Know how to complete a Punnett square to estimate phenotypic and genotypic ratios in offspring.
3. Be able to solve Mendelian inheritance problems.
4. Know how the results from mono and dihybrid corn crosses support Mendel's first and second laws using Chi square test.

MENDEL RULE AND LAWS

Please read and make sure you understand the following instructions and knowledge before you go on.

Revised from Lecture 1:

- All the genetic definitions
- All mendelian terms
- All the crosses performed (mono-,di-, and trihybrid crosses, test and back crosses)

In Mendelian inheritance:

1. The character is controlled by one gene only (**monogenic traits)**
2. Nuclear Inheritance
3. All units of inheritance are passed on to offspring unchanged
4. Based on Dominance/Recessive rule (**Complete dominance**)

Mendelian rule and Laws:

RULE OF DOMINANCE

Complete dominance occurs when only one allele (**dominant**) accounts for the phenotypic expression in heterozygotes. In heterozygotes, the unexpressed allele is called **recessive**.

Symbolism for Dominant and Recessive alleles

According to Mendel: Alphabetical letters were used as capital letter for dominant and small letter for recessive.

According to Bateson: The capital letter was derived from the name of the dominant and so, its small letter will represent the recessive.

According to Wild type System: The allele of the recessive will be signed with the letter of its name and that of wild type will be signed + alone or the letter of the recessive with + as superscript.

Note: If they can't determine the second allele in any pair they can again use "_" to signify that the allele could be Dominant or recessive, and that there isn't enough information to determine which it is or that don't matter.

Eg: (GG) and (Gg) genotypes are collectively designated as (G_) genotype.

MENDEL'S FIRST LAW (LAW OF SEGREGATION)

Law 1. states that every individual possesses a pair of alleles for any particular **trait** (assuming diploidy). Each parent passes a randomly selected copy (allele) of only one of these to its offspring. Interactions between alleles at a single locus influence how the offspring expresses that trait according to dominant and recessive rule (previously explained).

MENDEL'S SECOND LAW (LAW OF INDEPENDENT ASSORTMENT)

Law 2. states that different separate genes for different separate traits are passed independently of one another from parents to offspring during gamete formation. That is, the biological selection of a particular gene in the gene pair for one trait to be passed to the offspring has nothing to do with the selection of the gene for any other trait.

STATISTICAL TESTS FOR MENDELIAN INHERITANCE

Chi Square "Goodness of Fit Test"

- To determine if your data fit Mendelian Laws
- To determine if your data "good" or deviated from expected.
- To find out if probability are due to chance alone

As you know all too well by now, a valid test of your hypotheses, requires more than a mere visual inspection of the data. The investigator can make no claims about significance without first performing a statistical test on his/her data.

The Experiment:

Cross between "P" homozygous purple flowers and white flowers produce 100% heterozygous purple flowers"F_1". By self-crossing, the F_2 generation consists of 150 offsprings: 105 purple flowers and 45 white flowers (figure below).

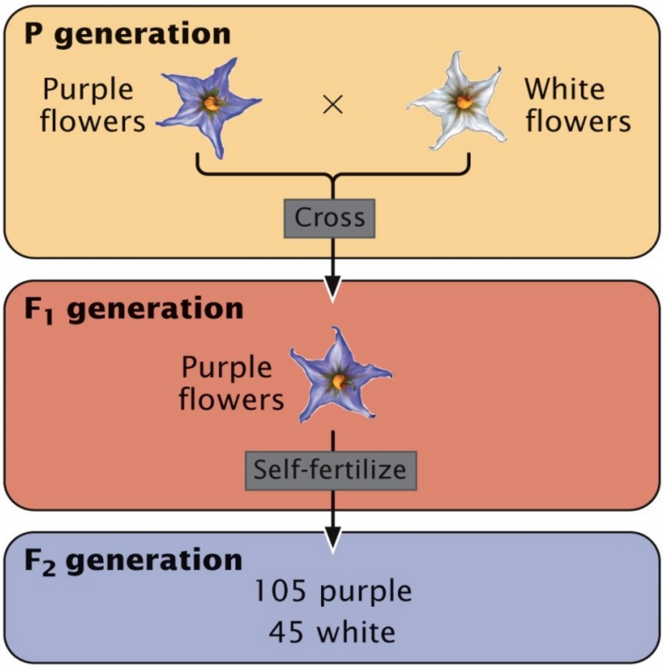


Fig_03-14-1 *Genetics, Second Edition* © 2005 W.H. Freeman and Company

Steps:

1. Perform the cross
2. Count and tabulate your results.
3. Determine whether the variation in phenotype frequency you counted is significantly different from the frequencies expected from each of the parental genotypes.
4. Before we count the offspring of each sample, we must ask whether the ratio of the phenotypes we actually count is likely to occur in a random sample produced by a mono- or di- or trihybrid cross.
5. In our case:

   Total offspring = 150

   The observed values: Purple flowers = 105 and White flowers = 45

   We have two phenotypes of the trait = purple and white for the color

   The genotype of the offspring = Pp, PP, pp

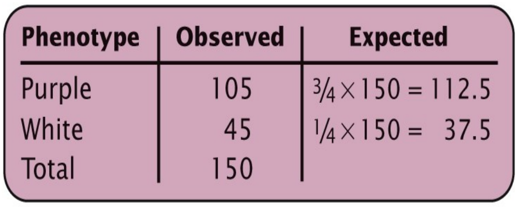
   The expected Mendelian ratio = 3:1

   Those data must be filled in the following table:

	Phenotype	**Genotype**	**Observed values**	**Expected ratios**	**Expected values**
Total:	----------	----------			

6. Calculate: the expected value of each phenotype as in table.

Expected values= total offspring x (expected ratio/total expected values)



Phenotype	Observed	Expected
Purple	105	¾×150 = 112.5
White	45	¼×150 = 37.5
Total	150	

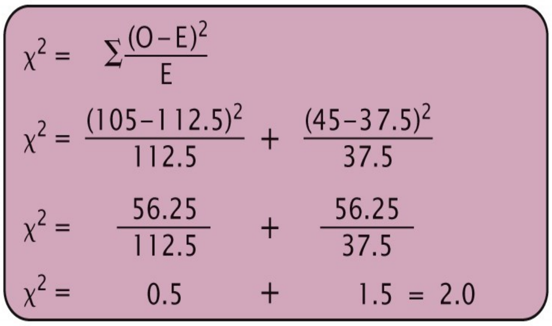
7. Calculate the **Chi square (X^2)** to determine whether our observed (counted) ratios of sample phenotypes are significantly different or deviated from the expected (from the known parental genotypes) ratios. The formula for this test is as follows:

$$X^2 = \sum \frac{(\text{Observed frequencies} - \text{Expected frequencies})^2}{\text{Expected frequencies}}$$

$$= \sum \frac{(Fo - Fe)^2}{Fe}$$

Where:

- Fo = the observed (counted) number of a particular phenotype
- Fe = the expected number of a particular phenotype.
- Σ represents the summation of X^2 values over every phenotypic category



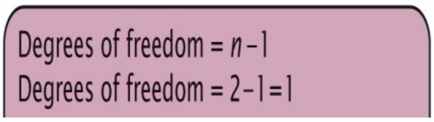
$$\chi^2 = \sum\frac{(O-E)^2}{E}$$

$$\chi^2 = \frac{(105-112.5)^2}{112.5} + \frac{(45-37.5)^2}{37.5}$$

$$\chi^2 = \frac{56.25}{112.5} + \frac{56.25}{37.5}$$

$$\chi^2 = 0.5 + 1.5 = 2.0$$

8. Calculate the degree of freedom:



Degrees of freedom = $n-1$

Degrees of freedom = $2-1=1$

Where n is the number of phenotype in the experiment

9. Use the probability table to determine whether the flower character is inherited according to Mendel's law or not.

   This will be by the values of both X^2 **and df.**

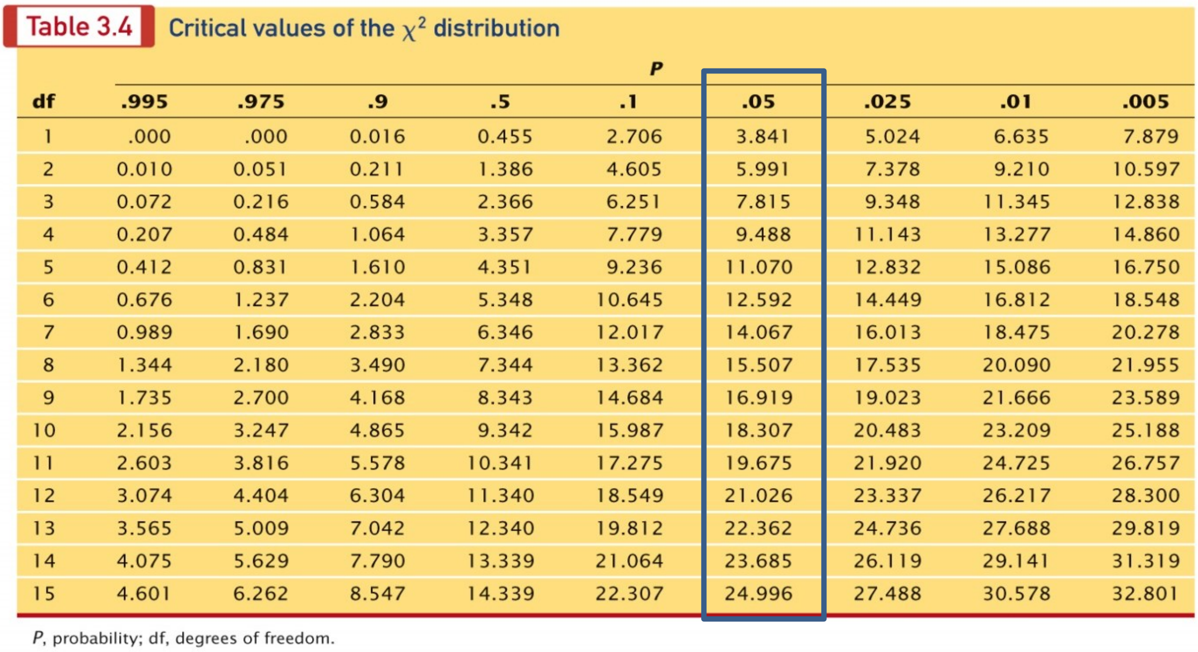


Table 3.4 Critical values of the χ^2 distribution

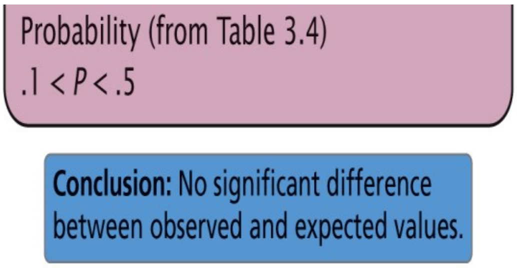
					P				
df	**.995**	**.975**	**.9**	**.5**	**.1**	**.05**	**.025**	**.01**	**.005**
1	.000	.000	0.016	0.455	2.706	3.841	5.024	6.635	7.879
2	0.010	0.051	0.211	1.386	4.605	5.991	7.378	9.210	10.597
3	0.072	0.216	0.584	2.366	6.251	7.815	9.348	11.345	12.838
4	0.207	0.484	1.064	3.357	7.779	9.488	11.143	13.277	14.860
5	0.412	0.831	1.610	4.351	9.236	11.070	12.832	15.086	16.750
6	0.676	1.237	2.204	5.348	10.645	12.592	14.449	16.812	18.548
7	0.989	1.690	2.833	6.346	12.017	14.067	16.013	18.475	20.278
8	1.344	2.180	3.490	7.344	13.362	15.507	17.535	20.090	21.955
9	1.735	2.700	4.168	8.343	14.684	16.919	19.023	21.666	23.589
10	2.156	3.247	4.865	9.342	15.987	18.307	20.483	23.209	25.188
11	2.603	3.816	5.578	10.341	17.275	19.675	21.920	24.725	26.757
12	3.074	4.404	6.304	11.340	18.549	21.026	23.337	26.217	28.300
13	3.565	5.009	7.042	12.340	19.812	22.362	24.736	27.688	29.819
14	4.075	5.629	7.790	13.339	21.064	23.685	26.119	29.141	31.319
15	4.601	6.262	8.547	14.339	22.307	24.996	27.488	30.578	32.801

P, probability; df, degrees of freedom.

10. A scientifically observed result is said to be statistically significant if there is less than or equal to a 5% ($P \leq 0.05$) probability that the phenomenon is due simply to random chance. Conversely, this means that there is a 95% chance that the phenomenon is due to some factor other than chance.

11. From the table $0.455 < X^2 = 2 < 2.706$

12. Probability $0.1 < P < 0.5$ i.e. 10% to 5%



Probability (from Table 3.4)
$.1 < P < .5$

Conclusion: No significant difference between observed and expected values.

13. If our count is not significantly different from the expected, we have no reason to reject it (null hypothesis, H_0) i.e. Obey's Mendel law.

However, if our number is significantly different from the expected, we conclude that there is very little probability of obtaining such a ratio by random chance, so it will be rejected (H_a) i.e. Doesn't obey's Mendel law. Some other factor must be at work here--one we must try to explain in terms of other genetic events such as gene linkage, lethal genes, etc….

Animation on Chi square:

https://www.youtube.com/watch?v=RAeAshXisKI

https://www.youtube.com/watch?v=yKr41Dzq6TI

YOUR LABORATORY INSTRUCTOR WILL TELL YOU WHAT YOU ARE TO TURN IN FOR THIS LAB EXERCISE.

WORK SHEET

1) Predict the ratio between the phenotypes resulted from crossing of a homozygous green seeded pea plant and a homozygous yellow seeded one, knowing that yellow color is the dominant phenotype. What is the ratio expected from back crossing of offspring with each parent**?**

2) What is the ratio between phenotypes resulted from self-pollination of heterozygous yellow seeded pea plant?

3) You are provided with the results observed following crossing of pea plants. Find the possible phenotypes of offspring and their parents.

a) Green X Yellow $\longrightarrow$ 100% yellow

b) Green X Yellow → 50% yellow and 50% Green.

c) Yellow X Yellow → 100% Yellow

d) Yellow X Yellow → 25% Green and 75% yellow.

e) Green X Green → 100% Green.

4) Predict the ratio between the phenotypes resulted from crossing of a homozygous green wrinkled seeded pea plant and a homozygous yellow rounded seeded one, knowing that yellow color and rounded shape are the dominant phenotypes. What is the ratio expected from back crossing of offspring with each parent?

5) What is the ratio between phenotypes resulted from self-pollination of heterozygous yellow rounded seeded pea plant?

6) You are provided with the results observed following crossing of pea plants. Find the possible genotypes of offspring and their parents.

a) Green wrinkled X Yellow rounded → 100% yellow rounded.

b)Green wrinkled X Yellow rounded → 50% yellow rounded and 50% Green wrinkled.

c) Yellow rounded X Yellow wrinkled → 50% Yellow rounded and
50% Yellow wrinkled.

d) Yellow rounded X Yellow wrinkled → 100% Yellow rounded.

e) Yellow rounded X Yellow wrinkled → 75% yellow rounded and 25% Green rounded.

f) Yellow rounded X Yellow rounded →

9 Yellow rounded, 3 Yellow wrinkled, 3 Green rounded and 1 Green wrinkled.

7. A scientist performed a series of crossing experiments to study the inheritance of flower color in *Bougainvillea glabra*. Two color phenotypes were observed, purple and yellow. He hypothesized that color was controlled by a single gene where the allele for purple was dominant (P) and the allele for yellow was recessive (p). He crossed the two heterozygous plants (Pp X Pp).

What is the expected genotypic ratio in the offspring?

8. Self-crossing was performed between two heterozygous elongated-smooth seeds of broad beans (*Vicia faba*), where elongated seeds (L) were dominant over rounded ones (l) and the smooth texture (S) were dominant over the wrinkled ones (s).

The offspring phenotypic results were:

315 Elongated-smooth seeds

108 Elongated-wrinkled seeds

101 Rounded-smooth seeds

32 Rounded-wrinkled seeds

Perform the cross than **Calculate** the Chi square (X^2) to determine whether the observed ratios were significantly different from the expected ratios for Mendel's law (use the previous statistical table).

	Phenotype	**Genotype**	**Observed values**	**Expected ratios**	**Expected values**
Total:	**----------**	**----------**			

Student name: **Code number:**

STUDENT'S ASSINMENT

Give it to your laboratory instructor

1. In tomato, yellow fruit color is recessive to red. **Deduce** the parental genotype(s) of red color, according to the following offspring data:

- Red X Red → 312 Red

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- Red X Yellow → 215 Red : 207 Yellow

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- Red X Red → 76% Red : 24% Yellow

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- Red X Yellow → All are Red

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2. Self-crossing was performed between two heterozygous elongated seeds of broad beans (*Vicia faba*), where elongated seeds (L) were dominant over rounded ones (l). The offspring phenotypic results were:

83 Elongated-seeds

26 Rounded seeds

Perform the cross than **Calculate the Chi square (X^2)** to determine whether the observed ratios were significantly different from the expected ratios for Mendel's law (use the previous statistical table).

3. A scientist performed a series of crossing experiments to study the inheritance of the flower colors in different plants:

In *Pisum sativum*

Purple x White → 50% Purple : 50% White

In *Solanum nigrum*

Yellow x Yellow → 100% Yellow

In *Bougainvillea glabra*

Orange x Orange → 25% White : 75% Orange

Find all the possible genotypes of these crosses indicating their dominant and recessive traits (when available).

4. Deduce the parental genotype (s) of *Pisum* seeds according to the following offspring ratios:

a. 372 wrinkled

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b. 123 Round : 42 wrinkled

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c. 288 Round

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5. A heterozygous trihybrid corn plant with Long stem, Rounded seed and Smooth stem was test crossed.

Note that: Long stem (A) is dominant while short stem (a) is recessive**,** Rounded seed (B) is dominant while wrinkled seed (b) is recessive **and** Smooth stem (C) is dominant while rough stem (c) is recessive.

Perform the cross and find the phenotype and genotype of the F_1 generation.