

ANSWER KEY

Biology 164 Laboratory

Genetics and Chi-square (χ^2) Problem Set

Use the pedigree given below in the following situations:

- Individuals 5 and 14 in the third generation come to you and ask, "What is the probability that if we have a child, the child will be albino?"

The solution to this question has three parts. First, in order to have an albino child, parents having a normal phenotype must both be heterozygous. Thus, the probability of each parent being heterozygous must be calculated. Second, the probability of heterozygous parents producing an albino child must be calculated. Lastly, the probability of the parents producing an albino child will be the product of the three previously mentioned probabilities.

Since the sister of 5 is albino, we know that the parents of 5 are both heterozygotes. Thus we can calculate that the probability of 5 being a heterozygote is 2/3. (The probability is not 1/2 because we know by looking at the phenotype of 5 that he is not homozygous recessive.) The same reasoning applies to 14 because her brother is albino. The probability of two heterozygotes producing an albino is 1/4. Thus the probability of 5 and 14 producing an albino is

$$2/3 \times 2/3 \times 1/4 = 1/9$$

- Individuals 1 and 11 in the third generation come to you and ask, "What is the probability that if we have a child, the child will be albino?" Does the pedigree alone provide enough information for you to help this couple? Explain.

The general approach to here is similar to that of the first problem. The pedigree alone does not provide enough information to calculate a single probability because of insufficient information about the father of individual #1. However a range of probabilities can be calculated by making alternative assumptions about the genotype of individual #1's father.

If individual #1's father is not carrying the albino allele, the probability of 1 being heterozygous is 1/2, since we know that 1's mother is a carrier. If individual #1's father is also a carrier, then the probability of 1 being heterozygous increases from 1/2 to 2/3.

The probability of 11 being heterozygous is 1/1 because his mother was albino.

The probability of two heterozygotes producing an albino is 1/4. Thus the probability of 1 and 11 producing an albino ranges from $1/2 \times 1/1 \times 1/4 = 1/8$ to $2/3 \times 1/1 \times 1/4 = 1/6$

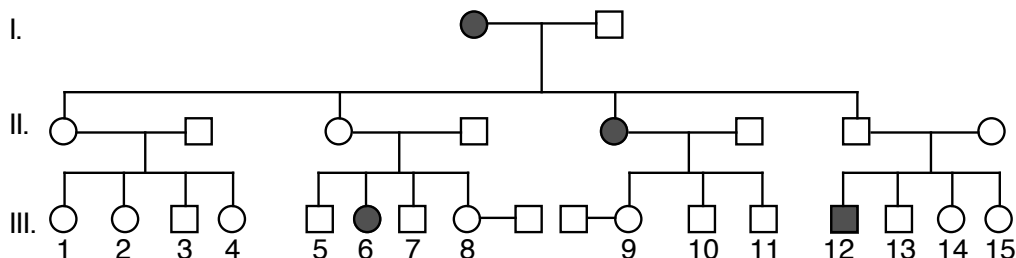


Figure 1. Human pedigree showing three generations. Circles represent females and squares represent males. Shaded areas represent albino individuals.

3. Two phenotypes appear in an experiment in the numbers 16:4.

A) How well does this sample fit a 3:1 ratio? Support your answer using Chi-square analysis.

Category	Observed	Expected	Deviation d	d ²	d ² / e
3/4	16	3/4 x 20 = 15	+1	1	1/15 = 0.067
1/4	4	1/4 x 20 = 5	-1	1	1/5 = 0.200
Total	20	20	0		$\chi^2 = 0.267$

Because .50 < p < .80, accept null hypothesis that data fits a 3:1 ratio.

B) Would a sample with the same proportional deviation fit a 3:1 ratio if it were
(i.) 10 times larger (i.e., 160:40)? Support your answer using Chi-square analysis.

Category	Observed	Expected	Deviation d	d ²	d ² / e
3/4	160	3/4 x 200 = 150	+10	100	100/150 = 0.67
1/4	40	1/4 x 200 = 50	-10	100	100/50 = 2.00
Total	200	200	0		$\chi^2 = 2.67$

Because .10 < p < .20, accept null hypothesis that data fits a 3:1 ratio.

(ii.) 20 times larger? Support your answer using Chi-square analysis.

Category	Observed	Expected	Deviation d	d ²	d ² / e
3/4	320	3/4 x 400 = 300	+20	400	400/300 = 1.33
1/4	80	1/4 x 400 = 100	-20	400	400/100 = 4.00
Total	400	400	0		$\chi^2 = 5.33$

Because .01 < p < .05, reject null hypothesis that data fits a 3:1 ratio.

4. In the garden pea, yellow cotyledon color is dominant to green, and inflated pod shape is dominant to the constricted form. Considering both of these traits jointly in self-fertilized dihybrids, the progeny appeared in the following numbers:

193 green, inflated
184 yellow constricted
556 yellow, inflated
61 green, constricted

Do these genes assort independently? Support your answer using Chi-square analysis.

Category	Phenotypic ratio	Observed	Expected	Deviation d	d ²	d ² / e
Grn, infl	3/16	193	3/16 x 994 = 186	+7	49	49/186 = .263
Yel, con	3/16	184	3/16 x 994 = 186	-2	4	4/186 = .022
Yel, infl	9/16	556	9/16 x 994 = 559	-3	9	9/559 = .016
Grn, con	1/16	61	1/16 x 994 = 62	-1	1	1/62 = .016
Total		994	994	0		$\chi^2 = 0.317$

Because .80 < p < .95, accept null hypothesis, therefore genes sort independently.

5. A dominant gene "A" governs the production of purple anthocyanin pigment in tomato stems and its recessive allele "a" produces green stem. A dominant gene "H" controls the development of hairy stems and its recessive allele "h" produces hairless stems. A dihybrid purple, hairy plant is **test crossed** (backcrossed with a parent recessive for both traits) and produces:

73 purple, hairy
 12 purple, hairless
 75 green, hairless
 9 green, hairy

- A) Is the purple:green ratio among the test cross progeny compatible with the expectation for segregation? Support your answer using Chi-square analysis.

Category	Phenotypic ratio	Observed	Expected	Deviation d	d ²	d ² / e
Purple	1/2	85	1/2 x 169 = 84.5	+0.5	.25	.25/84.5 = .003
Green	1/2	84	1/2 x 169 = 84.5	-0.5	.25	.25/84.5 = .003
Total		169	169	0		$\chi^2 = 0.006$

Because .80 < p < .95, accept null hypothesis, therefore genes segregate normally.

- B) Is the hairy:hairless ratio among the test cross progeny compatible with the expectation for segregation? Support your answer using Chi-square analysis.

Category	Phenotypic ratio	Observed	Expected	Deviation d	d ²	d ² / e
Hairy	1/2	82	1/2 x 169 = 84.5	-2.5	6.25	6.25/84.5 = .074
Hairless	1/2	87	1/2 x 169 = 84.5	+2.5	6.25	6.25/84.5 = .074
Total		169	169	0		$\chi^2 = 0.148$

Because .50 < p < .80, accept null hypothesis, therefore genes segregate normally.

- C) Do these genes assort independently? Support your answer using Chi-square analysis.

For a test cross, one would expect the four phenotypes to be found in equal numbers. Clearly, that is not the case. A chi-square analysis would result in a very large chi-square value, and hence a very low p-value resulting in a rejection of the null hypothesis. Thus, independent assortment is not occurring and the genes must be linked since they are segregating as expected.