E1. Pea plants are relatively small and hardy. They produce both pollen and eggs within the same flower. Since a keel covers the flower, self-fertilization is quite easy. In addition, cross-fertilization is possible by the simple manipulation of removing the anthers in an immature flower and later placing pollen from another plant. Finally, peas exist in several variants.
E2. The experimental difference depends on where the pollen comes from. In self-fertilization, the pollen and eggs come from the same plant. In cross-fertilization, they come from different plants.
E3. Two generations would take two growing seasons. About 1 and $1 / 2$ years.
E4. According to Mendel's law of segregation, the genotypic ratio should be 1 homozygote dominant : 2 heterozygotes : 1 homozygote recessive. This data table considers only the plants with a dominant phenotype. The genotypic ratio should be 1 homozygote dominant : 2 heterozygotes. The homozygote dominants would be truebreeding while the heterozygotes would not be true-breeding. This 1:2 ratio is very close to what Mendel observed.
E5. In a monohybrid experiment, the experimenter is only concerned with the outcome of a single trait. In a dihybrid experiment, the experimenter follows the pattern of inheritance for two different traits.
E6. All three offspring had black fur. The ovaries from the albino female could only produce eggs with the dominant black allele (because they were obtained from a true-breeding black female). The actual phenotype of the albino mother does not matter. Therefore, all offspring would be heterozygotes $(B b)$ and have black fur.
E7. The data are consistent with two genes (let's call them gene 22 and gene 24) that exist in two alleles each, a susceptible allele and a resistant allele. The observed data approximate a 9:3:3:1 ratio. This is the expected ratio if two genes are involved, and if resistance is dominant to susceptibility.
E8. If we construct a Punnett square according to Mendel's laws, we expect a 9:3:3:1 ratio. Since a total of 556 offspring were observed, the expected number of offspring are
$556 \times 9 / 16=313$ round, yellow
$556 \times 3 / 16=104$ wrinkled, yellow
$556 \times 3 / 16=104$ round, green
$556 \times 1 / 16=35$ wrinkled, green
If we plug the observed and expected values into the chi square equation, we get a value of 0.51 . There are four categories, so our degrees of freedom equal $n-1$, or 3 . If we look up our value in the chi square table (see Table 2.1), it is well within the range of expected error if the hypothesis is correct. Therefore, we accept the hypothesis. In other words, the results are consistent with the law of independent assortment.
E9. No, the law of independent assortment applies to transmission patterns of two or more genes. In a monohybrid experiment, you are monitoring only the transmission pattern of a single gene.
E10. A. If we let $c^{+}$represent normal wings and $c$ represent curved wings, and $e^{+}$represents gray body and $e$ represents ebony body:

Parental Cross: $c c e^{+} e^{+} \times c^{+} c^{+} e e$.
$\mathrm{F}_{1}$ generation is heterozygous $c^{+} c e^{+} e$.
An $F_{1}$ offspring crossed to flies with curved wings and ebony bodies is

$$
c^{+} c e^{+} e \times c c e e .
$$

The $\mathrm{F}_{2}$ offspring would be a 1:1:1:1 ratio of flies.

$$
c^{+} c e^{+} e: c^{+} \text {cee }: \text { cce }^{+} e: \text { ссеe }
$$

B. The phenotypic ratio of the $\mathrm{F}_{2}$ flies would be a 1:1:1:1 ratio of flies.
normal wings, gray body : normal wings, ebony bodies : curved wings, gray bodies : curved wings, ebony bodies
C. From part B, we expect $1 / 4$ of each category. There are a total of 444 offspring. The expected number of each category is
$1 / 4 \times 444$, which equals 111 .

$$
\begin{aligned}
& \chi^{2}=\frac{(114-111)^{2}}{111}+\frac{(105-111)^{2}}{111}+\frac{(111-111)^{2}}{111}+\frac{(114-111)^{2}}{111} \\
& \chi^{2}=0.49
\end{aligned}
$$

With 3 degrees of freedom, a value of 0.49 or greater is likely to occur between 95 and $80 \%$ of the time. So we accept our hypothesis.

E11. We would expect a ratio of 3 normal : 1 long neck. In other words, there should be $1 / 3$ as many long-necked mice as normal mice. If we multiply 522 times $1 / 3$ the expected value is 174 . However, we observed only 62.
Therefore, it appears that $174-62$, or 112, mice died during early embryonic development; 112 divided by 174 gives us the percentage that died, which equals 0.644 , or $64.4 \%$.
E12. Follow through the same basic chi square strategy as before. We expect $3 / 4$ of the dominant phenotype and $1 / 4$ of the recessive phenotype.

The observed and expected values are as follows (rounded to the nearest whole number):

| Observed* | Expected | $\frac{(O-E)^{2}}{E}$ |
| :--- | ---: | ---: |
| 5,474 | 5,493 |  |
| 1,850 | 1,831 | 0.066 |
| 6,022 | 6,017 | 0.197 |
| 2,001 | 2,006 | 0.004 |
| 705 | 697 | 0.012 |
| 224 | 232 | 0.092 |
| 882 | 886 | 0.276 |
| 299 | 295 | 0.018 |
| 428 | 435 | 0.054 |
| 152 | 145 | 0.113 |
| 651 | 644 | 0.338 |
| 207 | 215 | 0.076 |
| 787 | 798 | 0.298 |
| 277 | 266 | 0.152 |
|  |  | 0.455 |

*Due to rounding, the observed and expected values may not add up to precisely the same number.

Because $n=14$, there are 13 degrees of freedom. If we look up this value in the chi square table, we have to look between 10 and 15 degrees of freedom. In either case, we would expect such a low value or higher to occur greater than $99 \%$ of the time. Therefore, we accept the hypothesis.

E13. This means that a deviation value of 1.005 or greater (between the observed and expected data) would occur $80 \%$ of the time. In other words, it is fairly likely to obtain this value due to random sampling error. Therefore, we accept our hypothesis.
E14. The dwarf parent with terminal flowers must be homozygous for both genes since it is expressing these two recessive traits: ttaa, where $t$ is the recessive dwarf allele, and $a$ is the recessive allele for terminal flowers. The phenotype of the other parent is dominant for both traits. However, since this parent was able to produce dwarf offspring with axial flowers, it must have been heterozygous for both genes: TtAa.
E15. Our hypothesis is that disease sensitivity and herbicide resistance are dominant traits and they are governed by two genes that assort independently. According to this hypothesis, the $\mathrm{F}_{2}$ generation should yield a ratio of 9 disease sensitive, herbicide resistant : 3 disease sensitive, herbicide sensitive : 3 disease resistant, herbicide resistant : 1 disease resistant, herbicide sensitive. Since there are a total of 288 offspring produced, the expected numbers would be

$$
\begin{aligned}
& 9 / 16 \times 288=162 \text { disease sensitive, herbicide resistant } \\
& 3 / 16 \times 288=54 \text { disease sensitive, herbicide sensitive } \\
& 3 / 16 \times 288=54 \text { disease resistant, herbicide resistant } \\
& 1 / 16 \times 288=18 \text { disease resistant, herbicide sensitive } \\
& \\
& \qquad \chi^{2}=\frac{(157-162)^{2}}{162}+\frac{(57-54)^{2}}{54}+\frac{(54-54)^{2}}{54}+\frac{(20-18)^{2}}{18} \\
& \\
& \chi^{2}=0.54
\end{aligned}
$$

If we look up this value in the chi square table under 3 degrees of freedom, the value lies between the 0.95 and 0.80 probability values. Therefore, we expect a value equal to or greater than 0.54 , at least $80 \%$ of the time, due to random sampling error. Therefore, we accept the hypothesis.

E16. Our hypothesis is that blue flowers and purple seeds are dominant traits and they are governed by two genes that assort independently. According to this hypothesis, the $\mathrm{F}_{2}$ generation should yield a ratio of 9 blue flowers, purple seeds : 3 blue flowers, green seeds : 3 white flowers, purple seeds : 1 white flower, green seeds. Since there are a total of 300 offspring produced, the expected numbers
would be
$9 / 16 \times 300=169$ blue flowers, purple seeds
$3 / 16 \times 300=56$ blue flowers, green seeds
$3 / 16 \times 300=56$ white flowers, purple seeds
$1 / 16 \times 300=19$ white flowers, green seeds

$$
\begin{aligned}
& \chi^{2}=\frac{(103-169)^{2}}{169}+\frac{(49-56)^{2}}{56}+\frac{(44-56)^{2}}{56}+\frac{(104-19)^{2}}{19} \\
& \chi^{2}=409.5
\end{aligned}
$$

If we look up this value in the chi square table under 3 degrees of freedom, the value is much higher than would be expected $1 \%$ of the time by chance alone. Therefore, we reject the hypothesis. The idea that the two genes are assorting independently seems to be incorrect. The $\mathrm{F}_{1}$ generation supports the idea that blue flowers and purple seeds are dominant traits.

