

E1. A. We first need to calculate the standard deviations for height and weight, and then the covariance for both traits:

Height: variance = 140.02; standard deviation = 11.8

Weight: variance = 121.43; standard deviation = 11.02

Covariance = 123.3

$$r_{(x,y)} = \frac{CoV_{(x,y)}}{SD_x SD_y}$$

$$r_{(X,Y)} = (123.3)/(11.8)(11.02)$$

$$r_{(X,Y)} = 0.948$$

B. With 8 degrees of freedom, this value is statistically significant. This means the association between these two variables occurs more frequently than would be expected by random sampling error. It does not necessarily imply cause and effect.

E2. To calculate the mean, we add the values together and divide by the total number.

$$\text{Mean} = \frac{1.9 + 2(2.4) + 2(2.1) + 3(2.0) + 2(2.2) + 1.7 + 1.8 + 2(2.3) + 1.6}{15}$$

$$\text{Mean} = 2.1$$

The variance is the sum of the squared deviations from the mean divided by $N - 1$. The mean value of 2.1 must be subtracted from each value, and then the square is taken. These 15 values are added together and then divided by 14 (which is $N - 1$).

$$\begin{aligned}\text{Variance} &= \frac{0.85}{14} \\ &= 0.061\end{aligned}$$

The standard deviation is the square root of the variance.

Standard deviation = 0.25

E3.

$$\begin{aligned}n &= \frac{D^2}{8V_G} \\ n &= \frac{(514 - 621)^2}{8(382)} \\ n &= 3.7\end{aligned}$$

So there would be a minimum of about 4 genes that cause weight to vary among these two varieties of cattle.

E4. The results are consistent with the idea that there are QTLs for this trait on chromosomes 2 and 3 but not on the X chromosome.

E5. The heritability reflects the amount of genetic variation that influences a trait. In the strain with seven QTLs, there are at least seven different genes that exist in two or more alleles that are influencing the outcome of the trait. In the other strain, there are the same types of genes, but three of them are monomorphic and therefore do not contribute to the variation in the outcome of the trait.

E6. When we say that an RFLP is associated with a trait, we mean that a gene that influences a trait is closely linked to an RFLP. At the chromosomal level, the gene of interest is so closely linked to the RFLP that a crossover almost never occurs between them.

Note: Each plant inherits four RFLPs, but it may be homozygous for one or two of them.

Small: 2,700 and 4,000 (homozygous for both)

Small-medium: 2,700 (homozygous), 3,000, and 4,000; or 2,000, 2,700, and 4,000 (homozygous)

Medium: 2,000 and 4,000 (homozygous for both); or 2,700 and 3,000 (homozygous for both); or 2,000, 2,700, 3,000, and 4,000

Medium-large: 2,000 (homozygous), 3,000, and 4,000; or 2,000, 2,700, and 3,000 (homozygous)

Large: 2,000 and 3,000 (homozygous for both)

- E7. These results suggest that there are (at least) three different genes that influence the size of pigs. This is a minimum estimate because a QTL may have two or more closely linked genes. Also, it is possible that the large and small strains have the same RFLP band that is associated with one or more of the genes that affect size.
- E8. Let's assume that there is an extensive molecular marker map for the rice genome. We would begin with two strains of rice, one with a high yield and one with a low yield, that greatly differ with regard to the molecular markers that they carry. We would make a cross between these two strains to get F_1 hybrids. We would then backcross the F_1 hybrids to either of the parental strains and then examine hundreds of offspring with regard to their rice yields and molecular markers. In this case, our expected results would be that six different markers in the high-producing strain would be correlated with offspring that produce higher yields. We might get fewer than six bands if some of these genes are closely linked and associate with the same marker. We also might get fewer than six if the two parental strains have the same marker that is associated with one or more of the genes that affect yield.
- E9. This answer assumes that a mouse must be homozygous for all the sensitive alleles in order to be susceptible to the leukemia virus. Let's call the viral-resistance genes $V1$, $V2$, $V3$, etc. $V1$ is a resistant allele and $v1$ is an allele of the same gene that confers sensitivity. $V2$ is an allele of a different gene compared to $V1$, and $V2$ confers resistance while $v2$ confers sensitivity. With these ideas in mind, we can calculate the probability that an F_2 mouse would be homozygous for all of the sensitivity alleles.

If there are two genes involved, the parental cross is

$$V1V1V2V2 \times v1v1v2v2$$

This cross produces F_1 offspring that are $V1v1V2v2$.

If you construct a Punnett square, there is a $1/16$ chance that an F_2 offspring will be $v1v1v2v2$. Or, we can use the product rule. The chances of an F_1 parent passing a recessive allele at each gene to their offspring is $1/2$. The chances of an offspring inheriting all four recessive alleles is: $1/2 \times 1/2 \times 1/2 \times 1/2 = 1/16$

$$\text{Expected number of viral-sensitive } F_2 \text{ offspring} = 1/16 \times 120 = 7.5$$

We can follow this same approach to determine the likelihood that offspring will be homozygous for all the recessive alleles if three or more genes are involved.

$$\text{For three genes: } 1/2 \times 1/2 \times 1/2 \times 1/2 \times 1/2 \times 1/2 = 1/64$$

$$\text{Expected number of sensitive } F_2 \text{ offspring} = 1/64 \times 120 = 1.9$$

$$\text{For four genes: } 1/2 \times 1/2 \times 1/2 \times 1/2 \times 1/2 \times 1/2 \times 1/2 \times 1/2 = 1/256$$

$$\text{Expected number of sensitive } F_2 \text{ offspring} = 1/256 \times 120 = 0.5$$

For 120 offspring, we expect about two mice that would be sensitive to the virus if three genes are involved. Therefore, three genes would appear to be the most likely number of genes. If we had not obtained any sensitive mice, we would probably conclude that four or more genes are involved. It would be unlikely to have no sensitive mice if three genes or less were involved.

E10. A. If we assume that the highly inbred strain has no genetic variance:

$$V_G \text{ (for the wild strain)} = 3.2 \text{ g}^2 - 2.2 \text{ g}^2 = 1.0 \text{ g}^2$$

B. $H_B^2 = 1.0 \text{ g}^2 / 3.2 \text{ g}^2 = 0.31$

C. It is the same as H_B^2 so it also equals 0.31.

E11.

$$h_N^2 = \frac{R}{S}$$

$$R = \bar{X}_o - \bar{X}$$

$$S = \bar{X}_p - \bar{X}$$

In this problem:

\bar{X} equals 1.01 (as given in the problem)

\bar{X}_o equals 1.11 (by calculating the mean for the parents)

\bar{X}_p equals 1.09 (by calculating the mean for the offspring)

$$R = 1.09 - 1.01 = 0.08$$

$$S = 1.11 - 1.01 = 0.10$$

$$h_N^2 = 0.08 / 0.10 = 0.8 \text{ (which is a pretty high heritability value)}$$

E12. A

$$h_N^2 = \frac{\bar{X}_o - \bar{X}}{\bar{X}_p - \bar{X}}$$

$$0.21 = (26.5 \text{ g} - 25 \text{ g}) / (27 \text{ g} - 25 \text{ g})$$

$$\bar{X}_o - 25 \text{ g} = 2 \text{ g} (0.21)$$

$$\bar{X}_o = 25.42 \text{ g}$$

B.

$$0.21 = (26.5 \text{ g} - 25 \text{ g}) / (\bar{X}_p - 25 \text{ g})$$

$$(\bar{X}_p - 25 \text{ g})(0.21) = 1.5 \text{ g}$$

$$\bar{X}_p = 32.14 \text{ g parents}$$

However, since this value is so far from the mean, there may not be 32.14 g parents in the population of mice that you have available.

E13. In this problem, you need to set up Punnett squares based on genotypes.

A. Let's call the alleles $A1$ and $A2$. The F_1 would be genotypically $A1A2$. The F_2 results would be a $1 A1A1 : 2 A1A2 : 1 A2A1$. Since $A1A1$ and $A2A2$ plants produce 1 lb fruit and $A1A2$ produce 2 lb fruit, this would yield a phenotypic ratio of 50% 2 lb : 50% 1 lbs.

B. Let's call the alleles A and a and B and b and assume they contribute additively. The F_1 offspring will be $AaBb$. The F_2 ratio will be

$$1 AABB (2 \text{ lb}) : 2 AABb (2 \text{ lb}) : 1 AAbb (1.5 \text{ lb}) :$$

$$2 AaBB (2 \text{ lb}) : 2 Aabb (1.5 \text{ lb}) : 4 AaBb (2 \text{ lb}) :$$

$$1 aaBB (1.5 \text{ lb}) : 2 aaBb (1.5 \text{ lb}) : 1 aabb (1 \text{ lb})$$

The phenotypic ratio would be 9 (2 lb) : 6 (1.5 lb) : 1 (1 lb).

C. Let's call the alleles $A1$ and $A2$ and $B1$ and $B2$ and assume they contribute additively. The F_1 offspring will be $A1A2B1B2$. The F_2 ratio will be

$$1 A1A1B1B1 (1 \text{ lb}) : 2 A1A1B1B2 (1.5 \text{ lb}) : 1 A1A1B2B2 (1 \text{ lb}) : 2 A1A2B1B1 (1.5 \text{ lb}) : 2 A1A2B2B2 (1.5 \text{ lb}) : 4 A1A2B1B2 (2 \text{ lb}) : 1 A2A2B1B1 (1 \text{ lb}) : 2 A2A2B1B2 (1.5 \text{ lb}) : 1 A2A2B2B2 (1 \text{ lb})$$

The phenotypic ratio would be 4 (1 lb) : 8 (1.5 lb) : 4 (2 lb), which can be reduced to a 1:2:1 ratio.

D. You cannot calculate a precise ratio. As the number of genes increases, it becomes more unlikely to be heterozygous at all of the loci so it becomes less likely to produce 2 lb fruit. With a very large number of genes, most of the F₂ offspring would be in the intermediate (1.5 lb) range.

E14. We first need to calculate a and b . In this calculation, X represents the height of fathers and Y represents the height of sons.

$$b = \frac{144}{112} = 1.29$$

$$a = 69 - (1.29)(68) = -18.7$$

For a father who is 70 in tall,

$$Y = (1.29)(70) + (-18.7) = 71.6$$

The most likely height of the son would be 71.6 in.

E15. If we assume that this correlation coefficient is statistically significant, and if we assume that all the genetic variance is due to the additive effects of alleles, then

$$h_N^2 = r_{\text{obs}}/r_{\text{exp}}$$

In this problem, the r_{obs} is 0.15 and the expected correlation for siblings is 0.5. Therefore

$$h_N^2 = 0.15/0.5 = 0.3$$

E16. The identical and fraternal twins, which probably share very similar environments, but who differ in the amount of genetic material they share, are a strong argument against an environmental bias. The differences in the observed correlations (0.49 vs 0.99) are consistent with the differences in the expected correlations (0.5 vs 1.0).

E17. A. After six or seven generations, the selective breeding seems to have reached a plateau. This suggests that the tomato plants have become monomorphic for the alleles that affect tomato weight.

B. There does seem to be heterosis since the first generation has a weight of 1.7 lb, which is heavier than Mary's and Hector's tomatoes. This partially explains why Martin has obtained tomatoes that are heavier than 1.5 lb. However, heterosis is not the whole story; it does not explain why Martin obtained tomatoes that weigh 2 lb. Even though Mary's and Hector's tomatoes were selected for heavier weight, they may not have all of the "heavy alleles" for each gene that controls weight. For example, let's suppose that there are 20 genes that affect weight, with each gene existing in a light and heavy allele. During the early stages of selective breeding, when Mary and Hector picked their 10 plants as seed producers for the next generation, as a matter of random chance, some of these plants may have been homozygous for the light alleles at a few of the 20 genes that control weight. Therefore, just as a matter of chance, they probably "lost" a few of the heavy alleles that affect weight. So, after 12 generations of breeding, they have predominantly heavy alleles but also have light alleles for some of the genes. If we represent heavy alleles with a capital letter, and light alleles with a lowercase letter, Mary's and Hector's strains could be the following:

Mary's strain: *AA BB cc DD EE FF gg hh II JJ KK LL mm NN OO PP QQ RR ss TT*

Hector's strain: *AA bb CC DD EE ff GG HH II jj kk LL MM NN oo PP QQ RR SS TT*

As we see here, Mary's strain is homozygous for the heavy allele at 15 of the genes but carries the light allele at the other 5. Similarly, Hector's strain is homozygous for the heavy allele at 15 genes and carries the light allele at the other 5. It is important to note, however, that the light alleles in Mary's and Hector's strains are not in the same genes. Therefore, when Martin crosses them together, he will initially get

Martin's F₁ offspring: *AA Bb Cc DD EE Ff Gg Hh II Jj Kk LL Mm NN Oo PP QQ RR Ss TT*

If the alleles are additive and contribute equally to the trait, we would expect about the same weight (1.5 lb), because this hybrid has a total of 10 light alleles. However, if heterosis is occurring, genes (which were homozygous recessive in Mary's and Hector's strains) will become heterozygous in the F₁ offspring, and this may make the plants healthier and contribute to a higher weight. If Martin's F₁ strain is subjected to selective breeding, the 10 genes that are heterozygous in the F₁ offspring may eventually become homozygous for the heavy allele. This would explain why Martin's tomatoes achieved a weight of 2.0 pounds after five generations of selective breeding.

E18. $h_N^2 = r_{\text{obs}}/r_{\text{exp}}$

The value for r_{exp} comes from the known genetic relationships.

Mother/daughter	$r_{\text{obs}} = 0.36$	$r_{\text{exp}} = 0.5$	$h_N^2 = 0.72$
Mother/granddaughter	$r_{\text{obs}} = 0.17$	$r_{\text{exp}} = 0.25$	$h_N^2 = 0.68$
Sister/sister	$r_{\text{obs}} = 0.39$	$r_{\text{exp}} = 0.5$	$h_N^2 = 0.78$
Twin sisters (fraternal)	$r_{\text{obs}} = 0.40$	$r_{\text{exp}} = 0.5$	$h_N^2 = 0.80$
Twin sisters (identical)	$r_{\text{obs}} = 0.77$	$r_{\text{exp}} = 1.0$	$h_N^2 = 0.77$
			0.75

The average heritability is 0.75.

E19. A.

$$h_N^2 = \frac{\bar{X}_o - \bar{X}}{\bar{X}_p - \bar{X}}$$

$$h_N^2 = \frac{269 - 254}{281 - 254} = 0.56$$

B.

$$0.56 = \frac{275 - 254}{\bar{X}_p - 254}$$

$$\bar{X}_p = 291.5 \text{ lb}$$

E20. These data suggest that there might be a genetic component to blood pressure, because the relatives of people with high blood pressure also seem to have high blood pressure themselves. Of course, more extensive studies would need to be conducted to determine the role of environment. To calculate heritability, the first thing to do is to calculate the correlation coefficient between relatives to see if it is statistically significant. If it is, then you could follow the approach described in the experiment of figure 24.9. You would determine the correlation coefficients between genetically related individuals as a way to determine the heritability for the trait. In this approach, heritability equals $r_{\text{obs}}/r_{\text{exp}}$. It would be important to include genetically related pairs that were raised apart (e.g., uncles and nieces) to see if they had a similar heritability value compared to genetically related pairs raised in the same environment (e.g., brothers and sisters). If their values were similar, this would give you some confidence that the heritability value is due to genetics and not due to fact that relatives often share similar environments.