CHAPTER 5 Answers to Problems

Problem 5.1.

Genotype	Observed	Expected	Chi-square
150/150	9	($\hat{p}^2N$ = 8.27)	0.64
150/154	5	(2 $\hat{p}\,\hat{q}N$ = 6.47)	0.33
154/154	2	($\hat{q}^2N$ = 1.26)	0.43
Total	16	(16.0)	0.83

Estimated frequency of *A* = $\hat{p}$ = [(2x9)+5]/32 = 0.719

Estimated frequency of *A'* = $\hat{q}$ = [5 + (2x2)]/32 = 0.281

Degrees of freedom = 1

The calculated X^2 of 0.83 is less than the critical value for P<0.05 with 1 d.f. of 3.84 (Table 5.1). Therefore we would accept the null hypothesis that the sampled population was in Hardy-Weinberg proportions at this locus.

Problem 5.2. Chromosome 2 is out of Hardy-Weinberg proportions in both populations because the chi-square values are greater than the critical value of 3.84 with 1 df. Chromosome 9 is in Hardy-Weinberg proportions in both populations (P>0.05).

	Chromosome 2					Chromosome 9				
	BB	*SB*	*SS*	f(*B*)	X^2	*CC*	*CR*	*RR*	f(*C*)	X^2
Wild born	51	0	41	0.55	92.00	67	22	3	0.85	0.49
	(28.3)	(45.5)	(18.3)			(66.1)	(23.7)	(2.1)		
Zoo born	90	44	82	0.52	75.67	71	34	3	0.81	0.20
	(58.1)	(107.9)	(50.1)			(71.7)	(32.6)	(3.7)		

Problem 5.3.

	Genotypes						Allele frequencies							
Locus	*11*	*12*	*22*	*13*	*23*	*33*	*1*	*2*	*3*	X^2	df	Prob	H_o	H_e
GPI-2	81	2	0	--	--	--	0.988	0.012	0.000	0.01	1	P>0.05	0.024	0.024
LDH-A	77	6	0	--	--	--	0.964	0.036	--	0.12	1	P>0.05	0.072	0.070
PGD	7	30	39	3	1	3	0.283	0.657	0.060	29.24	3	P<0.001	0.410	0.485
PGM-1	55	26	2	--	--	--	0.819	0.181	--	0.28	1	P>0.05	0.313	0.296
TPI-1	67	16	0	--	--	--	0.904	0.096	--	0.94	1	P>0.05	0.193	0.174
29 loci	83	--	--	--	--	--	1.000	--	--	--	--	--	0.000	0.000

$P = 5 / 34 = 0.15$

$$H_o = \frac{(0.024 + 0.072 + 0.410 + 0.313 + 0.193)}{34} = 0.030$$

$$H_e = \frac{(0.024 + 0.070 + 0.485 + 0.296 + 0.174)}{34} = 0.031$$

Problem 5.4. The simplest model of inheritance is that pale is recessive to dark because all progeny from pale X pale matings are pale. Let's call the dominant allele *D*, and the recessive allele *d*.

We can estimate the frequency of the *d* allele using expression 5.5 where N_{22} is the number of pale progeny and *N* is the total number of progeny:

$$\hat{q} = \sqrt{\frac{N_{22}}{N}} = \sqrt{\frac{106}{106 + 326}} = 0.495$$

And therefore, $\hat{p} = (1 - \hat{q}) = 0.505$.

Three independent events must occur simultaneously for a pale chick to be produced by a dark X dark mating. First, the mother must be heterozygous (not *DD*), second the father must be heterozygous (not *DD*), and finally both heterozygous parents must pass on the *d* allele.

Some dark parents are heterozygous *Dd* and some are homozygous *DD*. The proportion of dark individuals that are expected to be heterozygous with this model is the expected frequency of heterozygotes ($2pq$) divided by the total expected frequency of dark individuals ($p^2 + 2pq$):

$$\frac{2pq}{p^2 + 2pq} = \frac{2(0.505)(0.495)}{(0.505)^2 + 2(0.505)(0.495)} = \frac{0.500}{0.255 + 0.500} = 0.662$$

That is, nearly two-thirds of all dark individuals are expected to be heterozygous with this model of inheritance if the population is in Hardy-Weinberg proportions.

If both parents are heterozygous (*Dd*), then we expect one-quarter (0.25) of all progeny to be pale (*dd*) based upon Mendelian inheritance.

The probability that all three of these events occurs is the product of their independent probabilities:

(Prob mother *Dd*) x (Prob father *Dd*) x (Prob progeny *dd* from *Dd* x *Dd*)

= 0.662 x 0.662 x 0.25 = 0.110

Therefore, we expected 29.1 (0.110 x 265) of the 265 progeny from dark x dark matings to be pale. We cannot use our standard chi-square test for fit to Hardy-Weinberg proportions in this situation. Nevertheless, the observed (25) and expected (29.1) numbers of pale progeny from matings between dark parents are in close agreement.

Problem 5.5.

(a)

Locus *5*	freq(*108*)=0.673	chi-sq=1.23, 1 df	NS, accept null hypothesis
Locus *82-2*	freq(*136*)=0.753	chi-sq=0.84, 1 df	NS, accept null hypothesis

Locus *Fu2* freq(*210*)=0.707 chi-sq=1.43, 3 df NS, accept null hypothesis
freq(*222*)=0.173
freq(*228*)=0.129

(b)

Locus	H_e historical	H_e extant
5	0.39	0.44
82-2	0.46	0.37
Fu2	0.90	0.45
13	0	0
31	0.05	0
46-1	0	0
89	0.04	0
107	0.68	0
140	0	0
Fu1	0.45	0
Mean	0.30	0.13

Problem 5.6. (a) Let freq (*a*) = *q*

$$\hat{q}^2 = 7/50 = 0.14$$

$$\hat{q} = \sqrt{0.14} = 0.37$$

$$\hat{p} = 1 - \hat{q} = 0.63$$

(b) Two independent events must occur simultaneously for a white bear to be produced by a black X white mating. First, the black parent must be heterozygous, and, second, this heterozygous parent must pass on the *a* allele.

The proportion of black individuals that are expected to be heterozygous is the expected frequency of heterozygotes (2*pq*) divided by the total expected frequency of black individuals (p^2+ 2*pq*):

$$\frac{2pq}{p^2 + 2pq} = \frac{2(0.63)(0.37)}{(0.63)^2 + 2(0.63)(0.37)} = \frac{0.47}{0.40 + 0.47} = 0.54$$

We expect a heterozygous individual to transmit the recessive allele one-half of the time based upon Mendelian expectations.

The probability both these events occur is the product of their independent probabilities:

$$(0.54)(0.50) = 0.27$$

Therefore, there is a 27% probability that the first progeny born to a mating between a black and a white bear this population will be white.

Problem 5.7. The simplest (and best) estimate of the frequency of the *r* allele is simply the frequency of black females since females will be hemizygous at this locus (*R*W or *r*W). Therefore, $q = 0.802$. We therefore expect q^2 or 64.3% of the males to be black; this is very close to the observed proportion of 68.3%. Thus, the observed frequencies are compatible with the proposed model.

Problem 5.8. Estimated frequency of the null allele is 0.215.

Problem 5.9. These data would suggest that there is something unusual about this population sample that produced a tendency for an excess of heterozygotes. We will see in Section 6.6 that there is a tendency for an excess of heterozygotes in small populations.