5.6 Test mating, statistical tests

When a smaller material is pointing at Mendelian segregation, there would often be alternative hypotheses, which cannot be excluded. The segregation can, as mentioned earlier, also be caused by simulated genetics (phenocopies) or threshold inheritance, where the segregation can resemble simple Mendelian inheritance. If a given hypothesis is to be accepted, test mating is in many cases simply waiting for more offspring to be born, in which the results are predictable. If the results deviate, a new hypothesis, which can be tested, has to be formulated.

How much data material is needed for a given test to give a final answer?

This is one of the important questions that have to be answered before the initiation of test mating.

Test mating of a bull, which is a suspected carrier, can be done by mating the bull with known affected cows, known carriers or the bull's own daughters. Taking these cases into consideration, how many normal offspring does the bull have to produce before he can be declared unaffected? The probability that one normal offspring is born in the three cases is respectively 1/2, 3/4 and 7/8. By applicating the multiplication rule for probabilities in mating with known carriers, the probability of getting one normal offspring is $(3/4)^n$. By means of this formula and a limit of significance of 0.05, 0.01 and 0.001 n can be determined to meet the classic probability criteria.

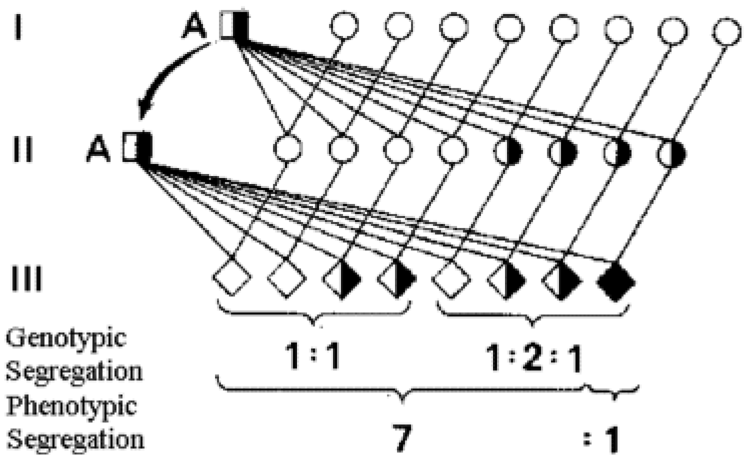
Number of normal offspring (n) which is needed to exclude a bull as carrier

Exclusion of bull as carrier by test mating with	Probability			Formula
	0,05	0,01	0.001	$(x)^n$ less than
Knowingly recessive	5	7	10	x=1/2
Known carrier	11	16	24	x=3/4
Own daughters	23	35	52	x=7/8

For normal offspring of a heterozygotic individual by father/daughters mating the probability is 7/8, as can be derived from Figure 5.6. The number of offspring needed to declare the father non-carrier on the 5% level is $(7/8)^n = 0,05$ corresponding to $n*\ln(7/8) = \ln(0,05)$, which rounded is n=23.

Mating with own daughters also has the advantage that the bull is tested as carrier of all possible recessive genes, not only the one he is suspected of having.

Figure 5.6 Theoretical segregation of recessive genes in test mating with own daughters.



Chi-square tests

By testing for segregation ratios for known mating a Chi-square test can be utilized. The test for mating with known carriers resembles the test for H-W equilibrium, but here the expected numbers are in the ratios 1:2:1 for co-dominant and 3:1 for dominant cases. The expected numbers are calculated by multiplying the expected frequencies (ratios) with N, as shown in the table below.

Segregation by test mating of Aa x Aa, codominant inheritance.

Genotype	AA	Aa	aa	Total

Numbers, obs	30	51	39	= 120 = N
Frequency, exp	1/4	1/2	1/4	= 1,00
Numbers, exp	30	60	30	= 120
Deviation	0	-9	9	
Chi-squared	0	1.35	2.70	= 4.05

Df = 3-1 = 2, since the material only supplies the parameter N to the calculation of expected numbers. The Chi-square value is less than the H_0 test value of 5.99, which means that there is no statistical significant deviation from a 1:2:1 segregating on the 5% level.

Segregation by test mating of Aa x Aa, dominant inheritance

Genotype	AA+ Aa	aa	Total
Numbers, obs	81	39	= 120 = N
Frequency, exp	3/4	1/4	= 1,00
Numbers, exp	90	30	= 120
Deviation	-9	9	
Chi-squared	1.00	2.70	= 3.70

Df = 2-1 = 1, since the material only supplies the parameter N to the calculation of expected numbers. The Chi-square value is just below the H_0 test value of 3.84, which means that there is no statistical significant deviation from a 3:1 segregation on the 5% level.