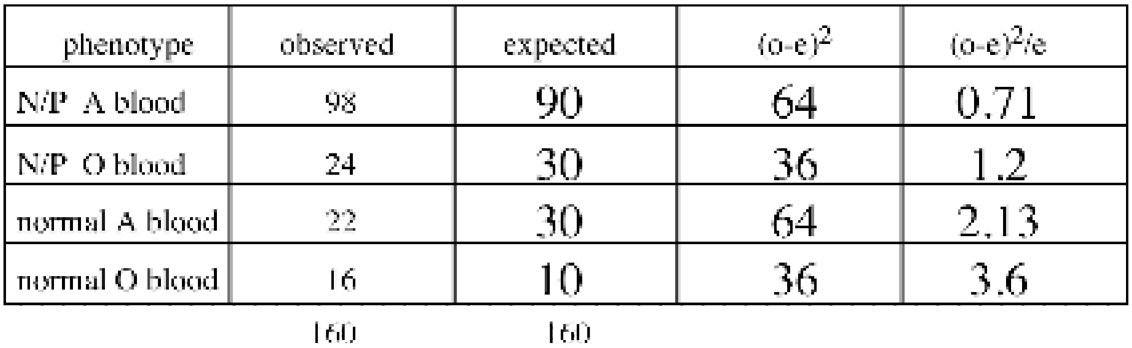
Genome 371
Fall 2003
Berg/Brewer

KEY to Nail Patella Problem using X^2 analysis to test hypotheses

A. The hypothesis being tested is that in this dihybrid cross that both traits are segregating properly (giving a 3:1 ratio for each trait) AND that the segregation of alleles at one locus aren't influencing the segregation of the other locus. To be more specific the gametes from each dihybrid will be in a ratio of 1:1:1:1 for the four possible types and that random fertilization of those gametes by gametes from a second dihybrid will result in a 9:3:3:1 ratio in the offspring. The "null" hypothesis is that the data above are no different from a 9:3:3:1 ratio.

B.



phenotype	observed	expected	$(o-e)^2$	$(o-e)^2/e$
N/P A blood	98	90	64	0.71
N/P O blood	24	30	36	1.2
normal A blood	22	30	64	2.13
normal O blood	16	10	36	3.6
	160	160		

What is the X^2 value? 7.64

How many degrees of freedom are there? 3

What is the P value? 0.1 to 0.05

Do you accept or reject the null hypothesis? accept--but only barely

Are you feeling good about the data? no

Maybe you would want to look at the individual traits ? okay

C. The X^2 analysis on the two separate traits.

	blood type	nail/patella
Observed ratios:	120:40	122:38
Expected:	120:40	120:40
X^2 values?	0	0.13
Degrees of freedom ?	1	1
What is the P value?	>0.995	>0.9
Accept or reject	accept	accept

D. The data for the single traits are just about as perfect as one could hope for. So why are the data for the dihybrids so bad?

The Chi-squared analyses on the single traits are only looking at Mendel's law of segregation. Indeed the two genes are segregating just as Mendel predicted. The Chi-squared analysis on the dihybrid data is measuring the goodness of fit between the data and both of Mendel's laws simultaneously. Since we can show that the alleles at each locus are actually segregating properly , it must be the case that they are failing to segregate INDEPENDENTLY: In particular, failure to adhere to the law of independent assortment is responsible for this poor fit of the data to the expected values. These genes are probably NOT independently assorting.