1. Backcrossing is an important strategy in agriculture for introducing a new locus into the genome of an otherwise desirable strain. In the rice example in lecture, the authors introduced the submergence tolerance locus from a tolerant strain T into the crop strain Swarna (S). What proportion of the genome originated from the T strain in:

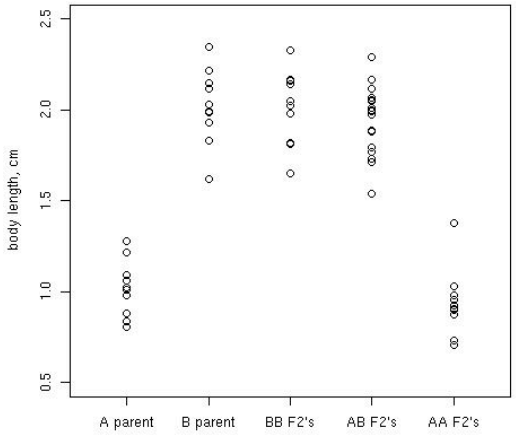
(a) The F1 generation?

(b) The B1 generation?

(c) The B2 generation?

(d) The B12 generation?

2. A study of body length in millipedes was launched to dissect the genetic basis of the difference in body length between two homozygous lines A and B, which are on average 1 and 2 cm in length, respectively. The lines were crossed to generate F2's, and F2's were genotyped at a number of markers; researchers mapped a single locus that was completely responsible for the variation in length. The phenotypes of 10 genetically identical lines of each parent strain, and 40 genetically distinct F2's split out by genotype at the marker, are shown below.



(a) What single-locus genetic model best explains the data?

(b) What is the expected average phenotype across all F2's?

(c) What is the expected average phenotype across all measurements of BOTH parents?

(d) For what kind of single-locus genetic model would the answers to (b) and (c) be the same? Draw a picture to illustrate.

(e) Heritability is the ratio of the estimate of genetic variance across genetically diverse individuals and the total variance across these individuals. To get genetic variance, we estimate the environmental/error variance from replicate measurements of genetically identical individuals, and subtract this from the total variance. For this calculation, when we have replicate measurements for BOTH parents, the usual tactic is to calculate the variance for each and then take the average over these two variances. Write down an expression for the heritability using all the information you have here, including means; you will not be able to calculate a numerical value.

3. You are studying the rate of blinking in humans and want to understand the genetic basis of the variation between people in how frequently they blink. You collect pairs of twins raised apart and use a Blink-O-Meter™ to measure the blinks per minute for each individual. Your data look like this:

	Twin 1	Twin 2	Mean
Twin pair 1	10.2	15.6	12.9
Twin pair 2	12.8	15.3	14.05
Twin pair 3	9.7	10.4	10.05
Twin pair 4	13.4	9.1	11.25

(a) Based on these data, the heritability for this trait is quite low. Explain how you would have a sense for this just from looking at the data, without doing a calculation.

(b) Imagine that there is a genetic locus varying in the population with a modest, but real, effect on blink frequency. In other words, the heritability of this trait should be appreciable, yet in the data above it is not. (Imagine that the trends were recapitulated over many more twin pairs than what you see here!) Propose a hypothesis to explain the discrepancy, and describe what you would do to test your idea.

4. Imagine that, by sequencing DNA from fossils, it is possible to take genetic snapshots of ginkgo species through evolutionary time. In single chromosomes isolated from unrelated samples from 150 million years ago, you see the following alleles at a region on chromosome 5:

	marker 1	marker 2	marker 3
Sample 1	G	C	C
Sample 2	G	T	G
Sample 3	A	A	A
Sample 4	G	T	G

From unrelated trees collected in modern Berkeley, you see:

	marker 1	marker 2	marker 3
Sample 5	A	A	A
Sample 6	G	A	A
Sample 7	G	A	A
Sample 8	T	A	C

(a) If these trends were borne out in much larger samples, what might you conclude about the evolutionary importance of the region around marker 2?

(b) Which marker, 1 or 3, would you expect to be closer to marker 2 on the basis of these data, and why?