Chapter 13

Quantitative Aside 13.1--Genetic Mapping Using 3-Point Crosses

Mapping with 3-point crosses allows us to do two things: (1) determine the correct order of three genes, which may not be possible from a series of 2-point crosses, and (2) correct for the effect of double crossovers on longer distances (allows them to be detected between the outside markers).

Consider the data set below from *Drosophila melanogaster* using the genes purple eye (*pr*), black body (*b*), and vestigial wing (*vg*). First wild-type flies are crossed to the triple mutant to produce an F_1 that appears all wild type. This F_1 is test crossed to homozygous recessive to generate an F_2 that is shown in tabular form. Since the homozygous recessive tester strain only produces *b vg pr* gametes, only genotypes derived from the F_1 test parent are shown. Note that since the gene order is unknown when we begin this process, the order in which the markers are written is arbitrary.

Parents: $b^+ vg^+ pr^+/b^+ vg^+ pr^+ \times b\ vg\ pr/b\ vg\ pr$

F_1 $b^+ vg^+ pr^+/b\ vg\ pr$ (appears all wild type)

Test cross to homozygous recessive:

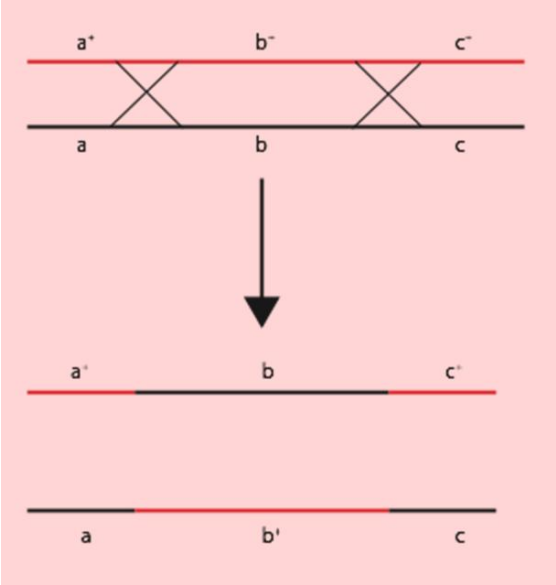
$b^+ vg^+ pr^+/b\ vg\ pr \times b\ vg\ pr/b\ vg\ pr$

Genotype	Number of Progeny
b vg pr	1779
$b^+ vg^+ pr^+$	1654
$b\ vg^+\ pr$	252
$b^+\ vg\ pr^+$	241
$b^+\ vg\ pr^+$	132
$b\ vg^+\ pr$	118
$b\ vg\ pr^+$	13
$b^+ vg^+ pr$	9

To analyze these data we use the following logic: the probability of a crossover is relatively low, so the probability of having two crossovers in the same interval would be the product of the two individual low probability events and therefore this double crossover class would be the least frequent class in the progeny. The most frequent class would be the parents (no crossovers). This second fact would actually allow us to identify the parental genotypes, even if we didn't know them (as we did in this case).

We then use these two classes to determine the order of genes. If we compare the parental with the double recombinant, we can determine which gene is in the

middle, as it will be recombinant, whereas the two flanking markers will be parental (see a general diagram below with three genes or figure 13.9).



If we take the parental and compare them with the recombinant, we can see that the purple gene must be in the middle:

Parental: *b* *pr* *vg*
b$^+$ *pr*$^+$ *vg*$^+$

Double recombinant:

b *pr*+ *vg*
b$^+$ *pr* *vg*$^+$

Using this information, we can reorder the data set to produce data that allow us to see each category of progeny: parental, recombinant between *b* and *pr*, recombinant between *pr* and *vg*, and double recombinant:

Genotype		Number of Progeny
Parental:	*b pr vg*	1779
Parental:	*b*$^+$ *pr*$^+$ *vg*$^+$	1654
Recombinant *pr vg*:	*b pr vg*$^+$	252
Recombinant *pr vg*:	*b*$^+$ *pr*$^+$ *vg*	241
Recombinant *b pr*:	*b*$^+$ *pr*$^+$ *vg*	132
Recombinant *b pr*:	*b pr vg*$^+$	118
Double recombinant:	*b pr*$^+$ *vg*	13
Double recombinant:	*b*$^+$ *pr vg*$^+$	9
Total		4197

We can then calculate the distance between *b* and *pr* and between *pr* and *vg* by adding the single crossovers in each region, plus the double recombinants (recombinant in each region) and multiplying by 100 to generate percent recombinant progeny:

Dist. *b*-*pr* = $((132+118+13+9)/4197) \times 100 = 6.4$ m.u.

Dist. *pr*-*vg* = $((252+241+13+9)/4197) \times 100 = 12.3$ m.u. (or 12.3 cM)