

3. Below is a table of complementation and recombinations results from studies of phage mutants.

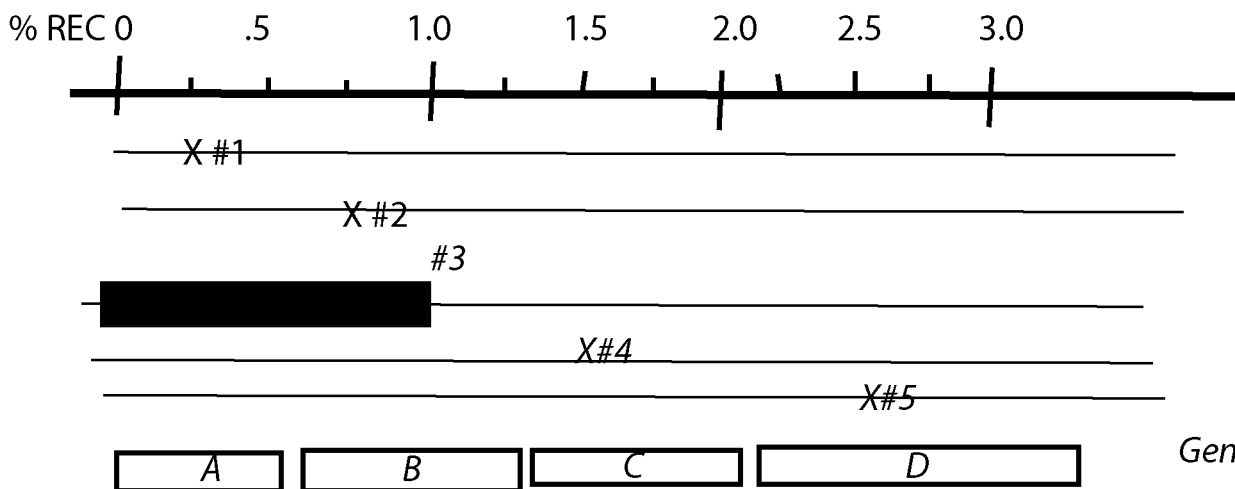
In the space below the table indicate where the mutations reside. Mutation #1 is given and is present on the far left side of the map. The map is given in % recombination. For example, mutation #2 crossed with mutations #1 gave 0.5 % wildtype recombinants, so the two are 0.5% apart.

Indicate point mutations with an "X", and a deletion with a black bar.

B. below the diagram indicate the likely positions of genes consistent with the data. (You may not know exactly where genes end and begin, but you know where they must be different.)

Cross	Complementation	Recombination	% Recombination
1x1	-	-	0
1x2	+	+	0.5
1x3	-	-	0
1x4	+	+	1.25
1x5	+	+	2.25
2x3	-	-	0
2x4	+	-	0.75
2x5	+	+	1.75
3x4	+	-	0.5
3x5	+	+	1.5
4x5	+	+	1.0

should both be +



Genes A, B, C, D