BIR572 Exam Questions from Joel Huberman, February 28, 2005

1. It's summertime in Buffalo. You're feeling too hot, so you decide to take a vacation in Antarctica. There you discover a new fission yeast species, *Schizosaccharomyces frigidiae*. Since you're passionately fond of yeast genetics, you decide to carry out some preliminary characterization of this new species. Since *Schizosaccharomyces frigidiae* seems to grow very well at low temperatures, such as 0°C, you decide to try to isolate temperature-sensitive mutants that can grow at 0° but not at 25°C.

You quickly discover that *Schizosaccharomyces frigidiae* has two mating types, which you call Plus and Minus, and you discover variants of Plus and Minus cells that are heterothallic (cannot switch mating types). By mutagenizing one of the heterothallic Plus strains and then selecting for growth at 0° but not at 25°C, you isolate 26 temperature-sensitive mutants. You backcross each of these mutants several times to wild-type heterothallic Minus cells. Then you carry out complementation tests. You find that all of the mutants are recessive, and they form just seven complementation groups.

Next, you carry out tetrad analyses to find out whether the seven complementation groups correspond to seven separate genes and to create a preliminary genetic map. You cross each of the complementation groups (termed **A–G**) with each of the other complementation groups, and you score about 60 tetrads from each cross. This is hard work, because you have to check each temperature-sensitive spore colony by complementation with appropriate tester strains to find out whether it displays a mutant phenotype due to mutation in just one of the complementation groups (and, if so, which one) or due to mutation in both complementation groups. Fortunately, there's not much else to do in Antarctica, and you're relieved to be free of the heat and humidity of Buffalo in the summertime, so you're in no rush to leave.

The following table (which extends onto the next page) summarizes the results that you obtain:

Cross	PD	NPD	T	Cross	PD	NPD	T
AxB	10	12	39	**CxD**	13	12	46
AxC	40	3	12	**CxE**	14	16	35
AxD	11	10	41	**CxF**	28	4	27
AxE	29	30	5	**CxG**	11	9	41
AxF	16	5	42	**DxE**	13	12	48
AxG	12	11	41	**DxF**	10	11	39
BxC	9	8	37	**DxG**	27	6	30

Cross	PD	NPD	T	Cross	PD	NPD	T
BxD	26	5	28	**ExF**	11	13	47
BxE	12	13	49	**ExG**	9	11	41
BxF	10	9	40	**FxG**	12	10	49
BxG	63	0	0				

1. (15 points). For each of the 21 crosses in the above table, state whether the two genes involved in the cross are genetically linked to each other or not. Also state whether one or both of the genes is linked to a centromere. In cases where you think that one or both of the genes is centromere-linked, briefly state your reasons for thinking so. Please do *not* state your reasoning in cases where you think that neither gene is centromere-linked.

2. (5 points). Do the results suggest that each of the seven complementation groups represents a specific gene, or is there evidence for intragenic complementation?

3. (15 points). Based on the results in the above table, please create a preliminary genetic map of *Schizosaccharomyces frigidiae*. On this map, indicate the genes that are linked to centromeres. Also indicate which genes are linked to each other, and indicate the order of those genes along their chromosomes. Also indicate which genes, if any, are *not* linked to any other of the tested genes. If multiple genes are linked to the same centromere, indicate which are closest to and which farthest from the centromere. **Hint: the mapping formula that we learned in class is *not* relevant to this problem; you do not need to calculate map distances; the answers to most of the parts of this question should be obvious from your responses to question 1.**