Homework # 4b

Linkage Round 2

The Homework #4b score can be used to replace the Homework #4 score

Consider the data presented on just the 10 OWBs.

1. Each column of allele data (a haplotype for each of the 10 OWBs) shows only 1 allele per locus because each column is for a doubled haploid plant: it would be redundant to show the two identical alleles at each locus.
	1. T
	2. F
2. It was correct for each of the 10 groups (each group representing 1 OWB plant) to choose alleles at vrs1 that matched alleles at the adjoining loci because it is very unlikely that there would be double crossovers between co-segregating loci.
	1. T
	2. F
3. The allele type at vrs1 is independent of the allele types at GBSS-1, nud and lks2 because vrs1 is in one chromosome (2H) and the other three loci are in another chromosome (7H).
	1. T
	2. F
4. The GBSS-1 and nud loci are 86 cM apart and are therefore expected to show independent assortment. The parental vs. non-parental data for this small sample suggest that the two are linked. This is due to small sample size and the “incorrect” assignment of crossover (non-parental) types to parental classes.
	1. T
	2. F
5. There is evidence that the nud and lks2 loci are linked, even in this small sample size.
	1. T
	2. F
6. It is useful to show where and how crossovers occurred using a small sample size of 10 but a larger sample size of 82 is more likely to provide better data.
	1. T
	2. F

Consider the full data set on the 82 OWBs

1. The apparent recombination value between vrs1 and GBSS-1 of 48.78 and the conversion of this to 109 cM is a “false fact”. In fact, these loci show independent assortment, as is apparent from a chi square test.
	1. T
	2. F
2. The apparent recombination value between GBSS-1 and nud of 37.80 cM and the conversion of this to 49 cM is also a “false fact”. In fact, these loci show independent assortment, as is apparent from a chi square test. The apparent excess of parental types is due to the number of double crossover events that occurred for the 82 doubled haploids between GBSS-1 and nud.
	1. T
	2. F
3. The nud and lks2 loci do not show independent assortment. Therefore they are linked. This is a fact.
	1. T
	2. F
4. The distance between nud and lks-2 is calculated by dividing the number of non-parental combination of alleles as the two loci (12) by the total population size (82).
	1. T
	2. F
5. In the case of nud and lks-2, the cM value is slightly larger than the % recombination value in order to adjust for the double-crossover types that lead one to classify crossover types as parental types.
	1. T
	2. F
6. If there were no recombination in barley, there would be 7 “super-loci”.
	1. T
	2. F
7. Experiential meiosis and recombination – there is nothing like it!
	1. T
	2. F