Non-sister chromatid exchange

* Leads to significant addition and losses of genetic information
* Is one the principal causes of genome expansion (the C-value paradox)
* Does not lead to the loss or addition of chromatin
* Occurs in both mitosis and meiosis

Assuming that there is no loss or gain of chromatin with sister chromatid exchange, there will no consequences in terms of meiosis generating new combinations of alleles at linked loci.

* T
* F

Which meiotic phenomenon would you hypothesize to be most related to the synaptonemal complex?

* Spindle fiber formation
* Cytokinesis
* Alignment of paired homologous chromosomes at Metaphase I
* Crossing over

If you calculate a recombination value of 30% between two loci and convert this value to centiMorgans (Haldane or Kosambi)

* The cM value will be larger than the % recombination value
* The cM value will be smaller than the % recombination value
* The cM value will be the same as the % recombination value

If you calculate a recombination value of 3% between two loci and convert this value to centiMorgans (Haldane or Kosambi)

* The cM value will be larger than the % recombination value
* The cM value will be smaller than the % recombination value
* The cM value will be the same as the % recombination value

A cM value can be converted to Mb of DNA using the following formula (cM\*360)/3.14

* T
* F

Regions around the centromere are generally heterochromatic and therefore will have, on average, more Mb/cM than euchromatic regions with higher recombination rates.

* T
* F

Assuming you have sufficient markers to generate a medium density linkage map with an average spacing of 3 cM in a species that is 2n = 2x = 30, how many linkage groups would you expect?

* 10
* 15
* 20
* 30

Significant segregation distortion, as describe in the assigned reading by Cistue et al., would lead you to:

* Reject a chi square hypothesis of 1:1 segregation of alleles at a locus in a doubled haploid population
* Under-estimate the coefficient of coincidence
* Give up on trying to make a linkage map
* Conclude that the phenotype controlled by these alleles show quantitative rather than qualitative inheritance

In linkage maps based on different crosses within the same species, locus orders will usually be consistent but estimates of distance will vary

* T
* F

2 strand double crossovers, 3 strand double crossovers, and 4 strand double crossovers will lead to different outcomes in terms of parental and non-parental combinations of alleles at linked loci

* T
* F

Which of the following are the best examples of utility of linkage maps for plant geneticists?

* Gene discovery
* Measuring transcription rates of specific genes
* Understanding syntney
* Measuring DNA replication rates during the S phase
* All of the above
* None of the above
* A and C

DNA-based markers, as opposed to phenotypic markers, are preferred for linkage mapping because:

* DNA markers are more abundant
* DNA markers are usually assayed more accurately
* Phenotypic markers never show linkage
* A and B above
* A and C above
* All of the above

Alleles at loci on different chromosomes should always show independent assortment: if they do not, one should very carefully check the data.

* T
* F

Loci “far enough” apart on same chromosome show independent assortment – due to “sufficient” crossovers between the loci in a population of individuals.

* T
* F

Molecular marker linkage maps are often sufficiently dense (e.g. <10% recombination) that the usual assumption is complete interference.

* T
* F