* Notation for Crosses with Linkage
  + Must know genotype and arrangement of genes on chromosomes.
  + Lines represent one of two homologous chromosomes
  + Genes on same side of line are on same chromosome
  + Opposite sides of line are on different chromosomes
* Complete Linkage Compared with Independent Assortment
  + Linkage: very close together on same chromosome, no crossing over
  + Testing done with testcross
  + Heterozygous produces two types of gametes
  + Nonrecombinant gametes: gametes that contain only original combinations of alleles present in parents (aka parental gametes)
  + Nonrecombinant progeny: progeny display original combinations of traits present in P generation (aka parental progeny)
  + Recombinant gametes: gametes with new combination of alleles
    - With independent assortment, nonrecombinant and recombinant gametes produced in equal proportions
  + Recombinant progeny: progeny with new combinations of traits formed from recombinant gametes
* Crossing Over with Linked Genes
  + Theory
    - Takes place during prophase I
    - Single crossover means two chromatids that did not take place in crossing over are nonrecombinant and other two are recombinant
    - In closely-linked genes, crossing over doesn’t occur every meiosis
    - Most number of recombinant genes for single crossing over is 50%, so frequency of recombinant gametes is half frequency of crossing over, max proportion of recombinant gametes 50%
  + Application
    - Most gametes are nonrecombinants
    - Testcross for two independently assorted genes is expected to produce 1:1:1:1 phenotypic ratio
    - Progeny don’t do this, so suspect that genes do not assort independently
* Calculating Recombination Frequency
  + Recombination frequency = number of recombinant prgeny / total number of progeny \* 100%
* Coupling and Repulsion
  + Linked gene crosses need to know arrangement of alleles to determine cross outcome
  + Coupling configuration / cis configuration: wild-type alleles found on one chromosome, mutants found on other
  + Repulsion configuration/trans configuration: each chromosome contains one wild-type and one mutant allele
* Evidence for the Physical Basis of Recombination
  + Stevens & Wilson’s discovery that sex associated with specific chromosomes in
  + Creighton & Clintock evidence of recombination result of physical exchange between chromosomes
    - Two traits on chromosome 9
    - Confirmed chromosomal theory of inheritance
  + Stern study on *Drosophilia* also confirmed
* Predicting the Outcomes of Crosses with Linked Genes
  + To determine proportions of types of offspring, need to know recombination frequency
* Testing for Independent Assortment
  + Calculate expected probability of each progeny type, assuming independent assortment, use chi-squared to evaluate whether deviation is significant
    - Problem: significant result can come from violation of assumption that genes are linked or not
    - Solution: do a series of chi-square tests, first for inheritance of genotypes at each locus separately and then for independent assortment
    - Faster solution: Chi-Square test of independence
  + The Chi-Squared Test of Independence
    - Carry out testcross
    - Table of traits is constructed
    - Genotypes for one locus along top
    - Other locus along side
    - Numbers of each genotype placed in cells, row, column, totals computed
    - Expected numbers of progeny, assuming independent assortment calculated
    - Chi-square value calculated
    - Probability less than 0.05, difference between numbers of observed and expected probably not due to chance
* Gene Mapping with Recombination Frequencies
  + Genetic maps: ghromosome maps calculated by using genetic phenomenon of recombination
  + Physical maps: chromosome maps calculated by uing physical distances along chromosome
  + Map units: distance on genetic maps (m.u.)
    - 1 mu = 1% recombination
    - Aka centiMorgans
* Constructing a Genetic Map with the Use of Two-Point Testcrosses
  + Two-point testcross: testcross between two genes
  + Helps in constructing genetic map