Lecture 7, BIOL 2030, Fall, '09 (Ch. 5: 28, 31-34a,b, 35)

I. Review
- A. Detecting linkage (P > R)
- B. Map distance between two genes = 100 x R/(P + R)
- C. Three-pt. testcross procedure
  - i. organize into 8 reciprocal classes
  - ii. most frequent are P
  - iii. least frequent are dco
  - iv. determine gene order from dco
  - v. map distance = 100 x (sco in interval + dco)/total
- D. 50% is maximum detectable frequency of recomb. because
  - i. x-over at 4-strand stage (after repl., before MI)
  - ii. double x-over occurs without chromatid interference
    (freq. of 2 str. = 3 str. = other 3 str. = 4 str.)
- E. By knowing these rules we can:
  - i. determine frequency of different meiotic events that produced observed progeny
  - ii. predict frequency of different meiotic events that will produce a given map
  - iii. determine map distances based on the frequency of different meiotic events

II. Yeast tetrad mapping
- A. Saccharomyces cerevisiae
  - i. single-celled, grown on Petri dishes in lab
  - ii. can be haploid or diploid
- B. Nutritional mutants are frequently used (auxotrophs)
  - i. prototrophs grow on minimal media (simple carbon and nitrogen)
  - ii. auxotrophs require additional factors, e.g. amino acids
  - iii. phenotype determined by replica plating
- C. sex = mating type (two alleles of one gene)
  - i. haploids fuse (mate) to become diploid
    - a. forced matings by selection for prototrophy
    - b. COMPLEMENTATION – critical concept!!
  - ii. diploids can sporulate (meiosis) to become haploid
  - iii. all 4 products of a single meiosis can be recovered
- C. Tetrad analysis – analyzing genotypes of single meiotic event (=tetrad)
- D. Rules of tetrad analysis (analyze two genes at a time)
  - i. three types possible: P, N, T
  - ii. random assortment gives 1P, 1N, 4T (T = 2/3 of total)
  - iii. if P = N, then genes are unlinked
    - a. if unlinked, determination of sum of gene-centromere distances may be possible (if T < 2/3 or total), sco between one gene and its centromere produces T (1/2 R spores)
    - b. sum of gene-cen. distances = 100 x (T/2)/total
  - iv. if P > N then genes are linked
  - v. N and T have recombinant spores
    - a. E0 meioses produce P (none are R)
    - b. E1 meioses produce T (1/2 are R)
    - c. E2 meioses produce 1P, 2T, 1N (all are R)
  - vi. distance is 100 x (all exchanges)/total
    formula is m.d. = 100 x (T/2 + 3N)/total