MCDB 1A Genetics Problem-Solving Tips

How do I start analyzing a genetics problem?

1. Note all information that you are given. Adjectives that are used can give vital information. "Pure-breeding" means homozygous; "rare" human traits mean that you don't expect outsiders marrying into the family to be carriers.
2. If it's a human pedigree, write down the pedigree and assign all genotypes that are immediately obvious.
3. If males and females from a cross have different phenotypes, at least one of the genes involved is probably sex-linked. If there is a human pedigree, assign sex chromosomes to each individual.
4. Look at the ratios that arise. If you only see variations on 1:2:1 (e.g. 3:1 or 1:2:1) then one gene is involved. If you see variations on 9:3:3:1, at least two genes are involved. If you see other ratios, then perhaps two genes are linked, or three or more genes are involved. If you see 2:1 ratios and the inability to produce a pure-breeding line, suspect a recessive lethal allele for one of the genes involved.
5. Define symbols for each allele of each gene. If only one gene is involved (only variations on 3:1 or 1:1 ratios), is there evidence for multiple alleles, such as lots of different phenotypes showing up?
6. Based on what you came up with in 1-5 above, come up with a tentative model explaining the results. e.g., if variations of a 9:3:3:1 ratio are seen, then the parents are likely to be dihybrids. Assign genotypes, and see if the results agree with what you would expect. Genetics problem-solving often requires a trial-and-error approach, where you rapidly test out various models and eliminate them, finally focusing on the correct model.
7. If your model explains some of the results, then continue to assign genotypes to explain the remaining results.
8. If the numbers don't really look right, test for linkage with Chi-square.
9. If linkage is indicated, you MUST remember how recombination frequency is defined (freq. of haploid products of meoisis that are different from the gametes giving rise to the meiocyte). If the organism is haploid or a test cross is involved, you can directly compute the RF. If not, can you use some tricks to figure out what the RF is (look at the double recessive class and work backward; look at the males if the genes are sex-linked; in Drosophila, remember that there is no recombination in males)?

Recombination

1. Recombination frequency is *defined* as (# recombinant gametes/total # gametes).
2. Percent recombination = recombination frequency x 100 = map units = centimorgans
3. ~0% recombination = Genes very tightly linked.
4. 50% Recombination = unlinked genes (either >50 map units apart on the same chromosome or on different chromosomes).

Mapping Sex Linked Genes

1. Sex linked genes are usually on the X-chromosome for flies and humans.
   The two largest phenotype classes of the male offspring are likely to be the genotypes of the X-chromosome from the female parent.
2. To estimate the frequency of crossovers on the X-chromosome use the data from the males only. For three sex-linked genes, alleles of the two least frequent phenotypes of the male offspring are used to indicate gene order.

Mapping genes from an F1 dihybrid cross

1. In an F1 cross involving autosomal linked genes, focus on the double homozygous recessive class to estimate recombination frequency. Take the square root of that phenotypic class to determine the frequency of the gametes that gave rise to that class.

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