Genetics Review

Terms:

The main terms have been identified in the online quiz. Here is a good list.

1. Gene
2. Locus
3. Allele
4. Heterozygous
5. Homozygous
6. Genotype
7. Phenotype
8. Dominant
9. Recessive
10. incomplete dominance
11. Pleiotropic
12. Multi-gene trait
13. epistatic/epistasis
14. true-breeding (see 5)
15. trisomy
16. Hardy-Weinberg equilibrium

Chapters:

The bulk of this is from chapters 13-15. However, there will be no specific questions about meiosis. So, most of 13 is for review. In addition, there is the **limited** amount of Hardy-Weinberg equilibrium as indicated below.

The idea of a gene:

How are the various ways "gene" has been defined? We have used either "unit of inheritance;" "a stretch of DNA that encodes a protein and its regulatory sequences" most of the time. But, what about genes that encode tRNAs or the small nuclear RNAs? They don't encode proteins, but certainly could have alleles that result in phenotypes. So, gene could be any DNA that results in a phenotype that is inherited. Why are some alleles "recessive" and others "dominant?"

Crosses

Data will be similar to those seen in VGL (but maybe not identical). Questions like the online quiz in which you need to do a Punnet square to answer a multiple choice will be there. You should be able recognize in a cross whether a trait is dominant, recessive or shows incomplete dominance. You should also recognize sex-linked. To do this, you should know the sorts of ratios expected for a cross (1:2:1 for genotype, 3:1 for phenotype if simple dominance; 1:2:1 for both genotype *and* phenotype if incomplete dominance). Examples:

	R	**W**
R	RR	RW
W	RW	WW

Incomplete dominance:

True-breeding Red flower by true-breeding white flower gives all pink flowers in the F1. F1 cross depicted below:
The RR is red, ww is white, RW is pink (1:2:1)
Neither allele is dominant
Reds and whites are each always true-breeding
Pinks give 1:2:1 when bred to each other
Red by pink gives 50% each RR (red) and RW (pink)
Same for white by pink.
If, say, red were dominant, ¾ of the flowers would be red.

Co-dominance:

Really closely related to incomplete dominance and kind of a semantic difference. It's when both traits are seen. A/B blood type could fit this. But, stick with incomplete dominance most of the time.

X-linked:

Red male X white female	**X^r**	**Y**
X^w	**X^rX^w**	**X^wY**
X^w	**X^rX^w**	**X^wY**

white male X red female	**X^w**	**Y**
X^r	**X^rX^w**	**X^rY**
X^r	**X^rX^w**	**X^rY**

The small sex chromosome *does not* have the same genes as the large. So, our "Y" chromosome will not have alleles that can cover up mutant recessive alleles. Since males only have one X (or females only have one "W" in birds), Recessive traits are seen far more often in the "heterogametic" sex (XY in humans). Also, for sex-linked traits, it matters whether the mother or father has the trait in question. Males get there lone X from their mother.
Consider white-eyed male by red-eyed female fly:
The F1 looks normal, with white-eyes being recessive.
If I had done it with a white-eyed female and a red-eyed male, I would get:

All the males are white-eyed.
All the females are red-eyed heterozygotes.
You might want to practice filling out the squares for the expected F1 cross for each of these cages (X^rX^w by X^rY and X^rX^w by X^wY).

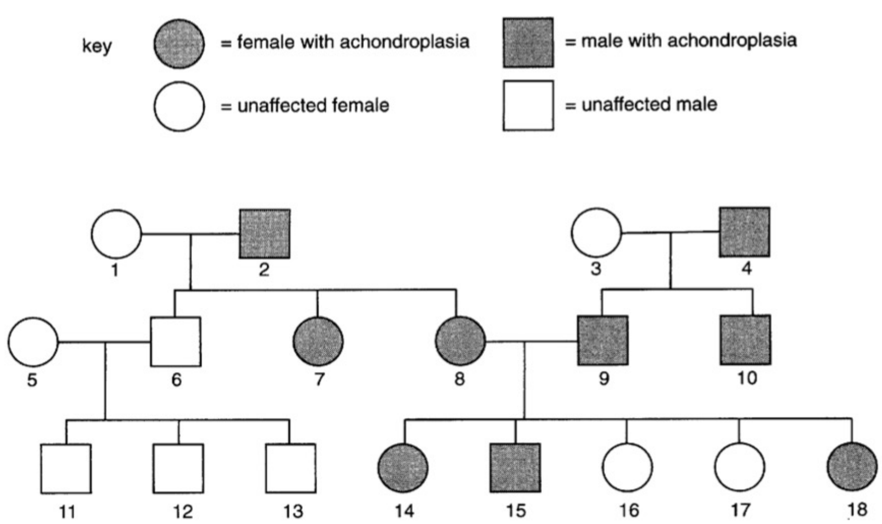
Dihybrid:

You should be able to recognize the patterns expected for both a dihybrid (9:3:3:1) and test cross (1:1:1:1) and perform a chi-square to assess if there is likely linkage (test the null hypothesis that any deviation is random fluctuation). Equations will be provided. The blog has examples of these.

DON'T BE SHOCKED if a cross combines components of these (eg, a sex link in a dihybrid cross).

Pedigree:

They will be simple. The key thing to look for is any parents that have one trait ("A") and have offspring with the other trait ("B"). B is therefore recessive since it was covered up in the parents. It doesn't matter whether "A" or "B" were considered the mutant trait (or "affected").Below is a pedigree for achondroplasia (a form of dwarfism). Look at individuals 8



and 9. They are both dwarfs and have unaffected offspring (16 and 17). Thus, this form of dwarfism is dominant and individuals 8&9 are heterozygous.
For X-linked, you see a recessive show up far more in males, as before. But, you never see passage from father to son, as you would for a very rare Y-linked.

Karyotype:

Again, simple. Look for trisomy (three copies of one chromosome). Look for whether the individual is XY or XX. The chromosomes will be aligned for you, if there is a karyotype.

Chi-squared

You will be given example data and all the equations necessary. You should know how to write a null hypothesis (i.e. "This is just random fluctuations from the expected pattern") and test whether the data are a good fit for that hypothesis. Be sure you know what you can and **cannot** claim based on your result. That is, you cannot say "I proved the distribution is random because the p-value was not significant." A non-significant p-value could mean you don't have enough data yet…or the distribution may be random. If you get a significant p-value, you can claim that random distribution is disproved to that level of confidence (eg. 0.01, if that's the p-value).

Hardy Weinberg:

You will **NOT** be asked questions on types of speciation. You will be asked to figure out "p" and "q" from data using the two forms of the equation (provided). Remember:

- You cannot directly use the percent of the dominant phenotype because that includes both homozygous and heterozygous individuals. If you get "40% have the dominant phenotype," the work flow looks like this:
- frequency of homozygous recessive is $q^2 = 1 - 0.4 = 0.6$
- $q = \sqrt{0}.6 = 0.77$
- $p = 1 - q = 0.33$

You should know the significance of a population being in H-W equilibrium (no **net** selective pressure). Given data, you should be able to assess whether a population is in H-W equilibrium.