LECTURE 14

Polygenic Inheritance (cont.):

A. Experimental evidence (in wheat)

P_1 red kernels x white kernels
F_1 intermediate
F_2 normally distributed (ranging from red to white)

1. Classification by color intensity revealed that 1/16 of the F_2 was as red as P_1 and 1/16 were white; the remainder were intermediate but variable in color intensity

2. Of critical importance was the observation that the base number in the F_2 was 16; this indicated that there must be *two genes* segregating from a dihybrid F_1

3. Deductions of this experiment were

a) There must be two Mendelian genes, each with two alleles
b) One allele at each locus adds to phenotype, while one alleles does not (add to phenotype)
c) The "additive" effect is small but cumulative, and
d) There is no dominance or epistasis

4. This could be modeled as

P_1 AABB (4) x aabb (0)
F_1 AaBb (2)
F_2 Punnett square:

	AB	**Ab**	**aB**	**ab**
AB	AABB (4)	AABb (3)	AaBB (3)	AaBb (2)
Ab	AABb (3)	AAbb (2)	AaBb (2)	Aabb (1)
aB	AaBB (3)	AaBb (2)	aaBB (2)	aaBb (1)
ab	AaBb (2)	Aabb (1)	aaBb (1)	aabb (0)

4 doses, 0 doses 1/16 each
1 dose, 3 doses 4/16 each
2 doses 6/16

B. Sir Ronald A. Fisher, the "founding father" of quantitative genetics, developed these ideas and model. [Fisher also was one of the "founding fathers" of population genetics as well.]. Note that the "rounding-out" the distribution (i.e., making it appear "normal" or "bell-shaped") was hypothesized to be due to environmental effects. Thus, quantitative (polygenic) traits and the continuous variation produced were modeled as stemming from several genes with additive effects and from environmental effects. Environmental effects are considered as more-or-less random, meaning that the "average" environmental effect (over a population) is zero.

C. Another cross (Nilsson-Ehrle, also in wheat)

P_1	red x white	but, in F_2:	1/64 red like P_1
F_1	intermediate		1/64 white
F_2	continuous variation		62/64 intermediate (but variable)

1. Clearly, there must be three genes (AaBbCc) segregating in the F_1

Question: As the two crosses involved the same trait in the same species, how can the different results be explained under the same, simple hypothesis?

Answer: There are three genes, but one of the three was homozygous for a non-contributing allele in the first cross.

2. This illustrates point that one can estimate the *minimum* number of genes affecting a polygenic trait by, in effect, estimating the number of genes segregating in a given cross.

   a) Set the frequency of <u>one</u> of the extreme phenotypic classes in $F_2 = (1/4)^n$, where n = number of genes *segregating*

   b) Thus, 1/4 = one gene, 1/16 = two genes, 1/64 = three genes, 1/256 = four genes, etcetera

D. Transgressive variation

1. The polygene (multiple gene) hypothesis explained a phenomenon called transgressive variation where phenotypes in an F_2 population were more extreme than those observed in either P_1 parent.

2. An example might be where there are seven (7) polygenes for a trait in the following P_1 cross

   AAbbCCDDeeffGG x aaBBccddEEFFgg

E. Analysis of quantitative characters

1. In most cases, dealing with Mendelian genes that produce quantitative traits is a formidable task, in large part because the number of genes involved (even under a strictly additive model) is not small.

2. However, because most quantitative traits (or at least those of economic interest) are generally distributed normally, one can use “normal distribution statistics” (means, variances, etcetera); other statistics used are correlations, covariances, and regression [beyond the scope of GENE 301]

F. Heritability: The proportion of the variation in a trait due to genetic factors

1. A concept developed by Fisher that attempted to quantify the proportions of a the variation in a quantitative trait that were due to genetic differences among individuals and what proportion was due to environmental differences (influences).

   $P = G + E$ (phenotype = genotype plus environment)

2. Because one measures variance, $V_P = V_G + V_E$

   a) The proportion of the phenotypic variance due to genetic variance is $V_G/V_P = h^2$

      h^2 = broad-sense heritability

      h^2 because variance is measured in squared units

      broad-sense because all genetic variation included, i.e., variation due to dominance, epistasis, additive effects, etcetera

   b) Thus, $V_G = V_a + V_d + V_e$ V_a = additive genetic variance
      V_d = dominance variance
      V_e = epistatic variance

   c) The precision of predicting phenotypes based on genotypes depends on the amount of genetic variation due to additive effects (contributing or non-contributing alleles);thus, the *heritability* of interest in both estimating the proportion of variation that might be attributed to selection or that can be *artificially selected* is that due to additive genetics effects

      Thus, V_a/V_P = narrow-sense heritability

G. Quantitative Trait Loci (QTLs)

1. Genes responsible for quantitative traits are now called QTLs; finding (and mapping) QTLs is currently “big business” in universities and elsewhere

   a) There are, for example, large QTL identification and mapping research programs at TAMU, primarily in crop plants and domesticated “barnyard” critters

2. The basic premise is to saturate chromosomes with map locations of very highly polymorphic DNA markers that come in all sizes and shapes [minisatellites, microsatellites, AFLPs, to name a few]

3. The approach is to ask whether specific alleles at these highly polymorphic loci segregate or assort non-randomly with phenotypic variation in a characters of importance; the essence is that QTLs for such a trait map close to the polymorphic marker(s); thus, one can “select” for the polymorphic marker allele (and hence the appropriate QTLs),and (eventually) one can localize and sequence the QTL (to try to figure out what it does