

Genetic Aspects of Populations

The plant breeder (plant evolutionist) alters the genetic composition of crop populations by selection.

From Allard (1999): The breeder's task is to assemble within populations (optimal) **combinations of alleles of many genetic loci** that lead to **superior multi-locus genotypes** that result in **superior phenotypes in the environment envisioned** for the potential new variety.

Direct selection vs. indirect selection – Phenotypic vs. genotypic selection

From Allard (1999):

Genotype = *the genetic constitution of an organism as distinguished from its appearance (phenotype).*

Phenotype = *the observable properties of an organism brought about by its genotype in concert with the environment in which the organism develops.*

The phenotype is the end result of a course or track taken in expression of that trait. Some variability is genetic, some is due to environment. The genotype is the genetic constitution that determines the potential for development of a certain trait.

The terminology of allelic substitution (at a single locus):

Allele – Any one among many possible variant forms of genes that result from mutations (or transposon insertions.)

Pea example – P. Rhodes and L. Vodkin et al. The insertion of a transposable element into the gene governing expression of a starch metabolic enzyme blocked normal starch synthesis resulting in an accumulation of sugars – hence sweeter peas.

Major genes

- Major gene substitutions are recognized because they have sharp, consistently identifiable phenotypic effects.
- Their *relative* expression is little affected by environment so the phenotype is closely and consistently related to the genotype.

An example of a major gene (chlorophyll-a content): it confers a readily observable and hence scorable trait.

-- It is not quite as clear as the starchy vs. sugary peas used by Mendel however.

From Simmonds and Smartt (1999) pg. 63

Table 4.1 A major gene in wheat.. chp-a content

Material	Constitution	No. pl.	Mean cpl-a	Std. d.
P1 Capitole	hh	19	2.6	0.084
P2 Rouge De Bord.	HH	20	3.4	0.069
F1 P1 X P2	Hh	20	3.2	0.068
F2 low	hh	13	2.6	0.118
F2 high	HH/Hh	37	3.2	0.165
BC low	hh	24	2.5	0.111
BC high	H_	26	3.3	0.150

The *h* gene controls the level of chlorophyll-a content of the flag leaf in wheat.

- It can be classified visually by looking at the chaff color (why not the flag leaf?).
- The homozygote HH and the heterozygote (Hh) both display high chlorophyll content and the recessive hh displays lower content.
- The trait is said to have an “environmental element” or component of the variation.
- It tends to show some variation, even in homozygous pure lines. The authors refer to the increased variability in expression of the trait in segregating populations as being due to a genetic “background effect.”

See graphs in Simmonds and Smartt on pages on pages 64 and 65.

Three components of variation (according to Simmonds and Smartt):

- 1) due to the major gene effect – responsible for the large difference between the means of parental genotypes
- 2) an environmental effect apparent within homogeneous families
- 3) another genetic effect apparent only as enhanced variability in segregating families (F₂ plants are not families by the way – he may be referring to scorable classes)

No. 3 restated - The expression of the parental genotype (hh) is not exactly the same in each F₂ plant as in the parent. There appears to be a “background effect” resulting from the diverse backgrounds (bi-parental origin) of the individual F₂ plants.

The variability is due not only to environmental effects put also to some undefined genetic heterogeneity (“background”) effects.

Imagine if the unknown environmental and genetic background effects combined to increase their effect on the observed variability twofold.

Please note dashed lines in figures. Note that ambiguity in classification occurs at the middle of the phenotypic distribution.

In figure 4.2 we can see the quantitative variation of the major gene controlled trait (chl-a content). This would be termed a qualitative trait but we can see how the phenotypic distributions can become blurred for both genetic and environmental reasons.

If one can pick the different genotypes Hh, hh, Hh etc. with some certainty based on the phenotype, then the trait is said to be highly 'heritable.'

Gene expression

(Context of phenotypic trait expression)

Any single locus can exist with certainty only if at least two alleles with distinguishable phenotypic expressions have been shown by segregation tests to be responsible for the phenotypic expressions of the locus.

From Allard (1999):

Dominance – An allele is said to be fully dominant when the phenotype of one homozygote (e.g. a_1a_1) and the heterozygote (e.g. a_1a_2) are indistinguishable from each other phenotypically.



Gregor Mendel demonstrated dominance and recessive gene action in his landmark paper.

Codominant – Both are distinguishable in the heterozygote e.g. molecular marker fingerprints

Partially dominant – heterozygote is intermediate between the parental types e.g. pink flowers from red by white parents

Overdominance (Overdominant) – the phenotype of the heterozygote exceeds that of either parent. e.g. red x white flowering parents gives very dark red F1. Probably rare (and actually due to pseudo-overdominance)

Pseudo-overdominance -- (linked loci a and b interact epistatically and essentially create a new phenotypic effect that looks to be the result of a different gene (c_1) such that $c_1 = a_1 b_2$; $c_2 = a_2 b_1$ and $c_1 c_1 < c_1 c_2 > c_2 c_2$)

Recessive – an allele that does not produce a phenotypic effect when heterozygous with the dominant allele

An allele is said to show dominance, partial or full, if the heterozygote diverges from the mid homozygote (midparental) expression. A partial dominant shows an intermediate, not a median, expression. Many prefer the idea of median or 'additive' expression vs. degrees of dominance.

Phenotypic expression says nothing about gene expression *per se*. How we measure gene expression is a matter of scale and that choice is an arbitrary one. We can change the 'expression' of a gene merely by changing the scale used to measure it.

References:

- Allard, R.W. 1999. Principles of Plant Breeding. (2nd Edition), Academic Press. p. 254.
Hartl, D. 2000. A Primer of Population Genetics. Sinauer Press. pp. 221.
Lewontin, R. The Problems of Population Genetics (*In: Evolutionary Genetics*, Singh, R.S. and Krimbas, C.B. Ed.) 2000. Cambridge University Press. pp. 702
Simmonds, N.W. and J. Smartt. 1999. Principles of Crop Improvement (2nd Edition), Blackwell Science.