Codominance

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Glossary

Dominance The genetic phenomenon involving one locus with two alleles in which the two homozygotes differ in phenotype and the heterozygote has the same phenotype as one of the homozygotes.

Dominance heritability The portion of genetic variation due to dominance.

The terms codominance, dominance, and incomplete dominance all refer to the relative contribution of two alleles at a locus to phenotype. Both dominance and codominance can be unequivocally defined at the molecular level. The classical example of dominance is the garden pea used in Mendel's experiments, with one locus and two alleles. The 'white' allele does not produce any pigment, and the 'red' allele produces the red pigment. The red allele is dominant over the white allele as heterozygotes are all red. In general, a null allele that does not produce any gene product is recessive to the alternative allele that does.

Codominance occurs when two gene products, respectively, from the two alleles at a locus in a heterozygote exist in roughly equal amount, where gene products refer to different transcripts from the two alleles, different proteins from cellular processing of the transcripts, or different metabolites specifically associated with the enzymatic activity of the transcripts or proteins. The AB heterozygote at the classical blood type locus (the ABO locus) expresses both the A and B blood type antigens and has been considered as a classical case of codominance. The A and B antigens result from the enzymatic activities of the two different types of glycosyltransferases encoded, respectively, by the A allele and the B allele. Another example of codominance is the beta-thalassemia minor involving a mutant hemoglobin β-chain. The heterozygote ($\beta^o\beta$) exhibits codominance because both alleles produce roughly equal amount of their respective proteins.

In contrast to dominance and codominance, incomplete dominance cannot be clearly defined at the molecular level. The classical example of incomplete dominance is the plant snapdragon. In contrast to the garden pea where the white allele is a null allele that does not produce any pigment, the white and the red alleles in snapdragon produce white and red pigments, respectively, at roughly equal amount. They are, therefore, codominant at the molecular level in terms of pigment production. The heterozygotes have pink flowers, intermediate between the white and red flowers in the two homozygotes, respectively. Incomplete dominance is defined as the genetic phenomenon in which the two distinct gene products from the two codominant alleles blend to form an intermediate phenotype between those of the two homozygotes. This definition would fit snapdragon (in fact it is tailor-made for snapdragon) because the white pigment and the red pigment do blend to form an intermediate phenotype, the pink flower.

The definition of incomplete dominance above is awkward. Note that the blending of colors in the snapdragon heterozygotes does not occur at the molecular level, that is, the white and red pigments do not blend chemically to form a pink pigment. So the definition of incomplete dominance becomes scale-dependent, that is, at which resolution scale should we consider the blending to have occurred to warrant the use of incomplete dominance? At the fine scale, there is no blending as white pigments stay white and red pigments stay red. At the other extreme, a near-sighted person may see only pink in a plot with intermixed white and red snapdragon flowers. The definition of incomplete dominance is awkward because we need to specify the resolution scale at which the blending of the two pigments occurs.

To avoid confusion between codominance and incomplete dominance, I would suggest to restrict incomplete dominance in a very special situation when one allele (say a) does not generate any gene product and the other (say A) in a heterozygote (Aa) does not produce enough gene product for the heterozygote to fully exhibit the phenotype of the AA homozygote. For example, a locus could have a black allele (B) that produces black pigment and a white allele (b) that does not produce any pigment. The homozygote BB is fully black. The heterozygote (Bb), producing about half as much black pigment as the BB homozygote, is gray instead of fully black. In this particular case, the use of incomplete dominance is natural and intuitive, that is, B is incompletely dominant over b and not vice versa.

Codominance does not provide a quantitative description of the relative contribution of the two alleles to phenotype. It is for this reason that I have used 'roughly equal' in describing codominance of the two alleles in producing their respective gene products. Population geneticists typically would use a special type of regression to quantify the effect of the two alleles on the phenotypic trait. Suppose a locus with two alleles (A and a). We have characterized the genotype (GT) and the genotypic value (GV) for 13 individuals (Table 1). To quantify the dominance effect, we will create two additional variables X_1 and X_2, with X_1 being the number of allele A in each individual and X_2 being 1 for the heterozygote and 0 for the two homozygotes (Table 1). The squared correlation (r^2) between GV and X_1 is the additive heritability (h^2_A) and is equal to 0.7943 for data in Table 1. The regression of GV on both X_1 and X_2 will lead to the following linear relationship

$$\mathrm{GV} = b_0 + b_1X_1 + b_2X_2 = 2 + 4X_1 + 2X_2 \qquad [1]$$

Table 1 A fictitious data set for illustrating the regression technique for characterizing different degrees of dominance

GT	*GV*	X_1	X_2
aa	1	0	0
aa	3	0	0
aa	2	0	0
Aa	7	1	1
Aa	9	1	1
Aa	8	1	1
Aa	9	1	1
Aa	7	1	1
Aa	8	1	1
AA	10	2	0
AA	8	2	0
AA	12	2	0
AA	10	2	0

GT, genotype; GV, genotypic value.

For the aa genotype, X_1 and X_2 are 0 (Table 1), so the regression equation is reduced to GV = 2, which is the mean GV for the aa genotype. For the Aa heterozygote, both X_1 and X_2 are equal to 1 (Table 1), so GV for the Aa genotype is GV = 2 + 4 + 2 = 8, which is the mean GV for Aa individuals. Had there been no dominance effect, b_2 would be 0 and GV for Aa would be 6 instead of 8. For the AA genotype, $X_1 = 2$ and $X_2 = 0$ (Table 1), so its GV is $2 + (4 \times 2) = 10$. The squared correlation from the multiple regression is 0.8926 for data in Table 1, which is an estimate of the summation of additive heritability (h^2_A) and the dominance heritability (h^2_D). Therefore,

$$h^2_D = 0.8926 - h^2_A = 0.0982 \quad [2]$$

With the complete dominance, b_2 in eqn [1] would be either equal to b_1 (when GV is the same for Aa and AA) or $-b_1$ (when GV is the same for Aa and aa). If GV for Aa is exactly the average of GV for the AA and aa genotypes, we will have $h^2_D = 0$, $b_2 = 0$ and the regression model of $GV = a + b_1X_1$ will be just as good as that in eqn [1], with the squared correlation from the two models being identical. Finally, with overdominance, that is, when GV for the Aa genotype is greater than that for the AA genotype, b_2 will be greater than b_1, and h^2_D will typically account for most of the genetic variance, which implies that h^2_A will be small, and selection will be relatively inefficient against the aa genotype (if allele a is deleterious).

See also: Additive Genetic Variance; Alleles; Genetic Variation; Genotype; Heritability; Locus; Mendelian Genetics; Mutation.

Further Reading

Crow JF (1986) *Basic Concepts in Population, Quantitative, and Evolutionary Genetics*. New York: Freeman.

Hartl DL and Clark AG (2006) *Principles of Population Genetics*, 4th edn. Sunderland, MA: Sinauer Associates.