

Confusion in Teaching Interaction Genetics

Very few instructors in Genetics can distinguish on a classical level, dominance from epistasis, or concomitantly, alleles from non-alleles. Why does no one think this is reprehensible? It is not entirely the fault of instructors. The textbooks they learn from are basically deficient in this respect. You don't believe me? How can such simple things be not clear in texts? Try these crosses.

A white rabbit is crossed with a yellow rabbit, both of purebred stock. The F_1 is yellow and the F_2 has $3/4$ yellow and $1/4$ white. Who can doubt that yellow is dominant to white?

From purebred stocks a black chicken is crossed with a white chicken. The F_1 is all black. The F_2 consists of $3/4$ black and $1/4$ white. Who can doubt that white is recessive to black?

Try another concept. Yellow in rabbits is allelic to the agouti color. Chinchilla color in rabbits is allelic to the agouti color. Things (yellow and chinchilla) allelic to the same thing (agouti) must be allelic to each other -
- right!?

Now you want me to justify my doubts and "clarify" these seemingly faultless conclusions. As a step in the right direction. Suppose we use another model that most instructors are familiar with. From purebred stock cross a walnut comb chicken with a rose comb. The F_1 is walnut and the F_2 consists of $3/4$ walnut and $1/4$ rose comb. Who can doubt that rose comb is recessive to walnut? Most instructors can do so, since they likely have used this model and recognize that rose comb is a dominant to single comb and walnut comb is an interaction of pea comb and rose comb combination. The texts have this nearly correct. They might still fail to note that single comb is wild type. But that walnut comb and rose comb have something (a mutant rose comb) in common is recognizable, if given at all, in textbook material. And rose comb is not confused as being allelic to walnut.

The key is a standard type (= normal or wild type) for comparison with mutants. Appropriate analytical methodology recognizes the need to have a standard type in the F_2 , for example. Without it one is confined to the evident "monohybrid segregation" in the first two examples. But the mutant forms may be single mutants or multiple mutants, and might carry a mutant in common. Yes, alternatively they might be alleles. Standard type in the problem distinguishes. The white rabbit crossed with agouti (the wild type) gives an F_2 in sixteenths. $9/16$ are agouti, yellow and chinchilla each appear as $3/16$ classes, and $1/16$ are white. So white had yellow in common with the yellow stock, but had chinchilla also. It was white because the chinchilla mutant blocked the phaeomelanin (yellow) and the yellow mutant blocked the eumelanin (black). Both these independent mutants expressed phenotypically together blocked both melanins in the fur leaving white (colorless). So yellow is not dominant to white, but white is an interaction of yellow and chinchilla mutants.

The particular type of white chicken crossed with wild type ("black and red") would yield an all black F_1 and $3/16$ wild type in the F_2 along with $1/4$ white ($4/16$) and $9/16$ black. So this white is not recessive to black but shows recessive epistasis to the dominant black mutant.

Using the term dominant and recessive for both the gene and the character, as almost everyone does, may partly explain some confusion and, therefore, may not be wise. For example, in the Muscovy duck, $NN \rightarrow$ ash gray (silver), NN^+ (that is a superscript +) \rightarrow blue [N = Nero, Italian for black. The gene was probably named after the wild type, black]. The ash gray color is recessive, but the mutant gene controlling ash gray and blue is codominant. But it is the standard type concept that is necessary for appropriate analysis.

The allelic puzzle about things allelic to the same thing being allelic to each other is on the way to solution in the elucidation of the yellow and white rabbits explanation previously given. Yellow is a single mutant form. White is not. That is, yellow and chinchilla ($3/16$ each in the F_2) are obviously recessive independent single mutants and cannot be alleles. How can both be allelic to agouti?

Agouti is not a single thing. There is no such thing as the agouti gene. It is successful phenotypic expression of normal (wild type) genes at all (perhaps 50?) loci in the biochemical chain of pigment and pattern production. Therefore, "normal" (= wild type) is allelic to any mutant! It is only the single locus mutant forms that can be tested for allelism versus non-allelism in classical usage. Single mutant relationships are "transitive". But normal, or interaction mutants break the logical rule of transitive relationships. They are non-transitive.

The classical test of allelism, then, with single mutant forms is to cross them. If a monohybrid result in the F_2 is obtained, then they are alleles, and wild type will not appear. If the F_2 yield dihybrid results, they are non-alleles and will show one of the classes with "reversion to wild type". Should both single mutants be recessive, then the F_1 is sufficient to determine allelism. Recessive allelic forms will yield a mutant phenotype in the F_1 , while recessive non-alleles will show reversion to wild type in the F_1 . This is the original forerunner to complementation tests.

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