Multiple alleles, incomplete dominance, and co-dominance

In the real world, genes often come in many versions (alleles). Alleles aren't always fully dominant or recessive to one another, but may instead display co-dominance or incomplete dominance.

Introduction

Gregor Mendel knew how to keep things simple. In Mendel's work on pea plants, each gene came in just two different versions, or alleles, and these alleles had a nice, clear-cut dominance relationship (with the dominant allele fully overriding the recessive allele to determine the plant's appearance).

Today, we know that not all alleles behave quite as straightforwardly as in Mendel’s experiments. For example, in real life:

Allele pairs may have a variety of dominance relationships (that is, one allele of the pair may not completely “hide” the other in the heterozygote). There are often many different alleles of a gene in a population.

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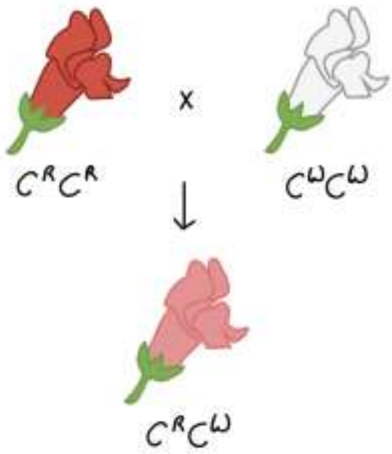
In these cases, an organism's genotype, or set of alleles, still determines its phenotype, or observable features. However, a variety of alleles may interact with one another in different ways to specify phenotype.

As a side note, we're probably lucky that Mendel's pea genes didn't show these complexities. If they had, it’ s possible that Mendel would not have understood his results, and wouldn't have figured out the core principles of inheritance—which are key in helping us understand the special cases!

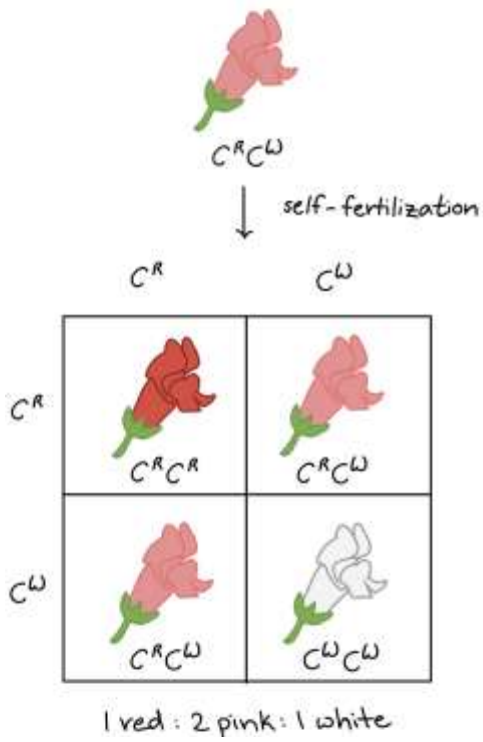
Incomplete dominance

Mendel's results were ground-breaking partly because they contradicted the (then-popular) idea that parents' traits were permanently blended in their offspring. In some cases, however, the phenotype of a heterozygous organism can actually be a blend between the phenotypes of its homozygous parents.

For example, in the snapdragon, Antirrhinum majus, a cross between a homozygous white-flowered plant ($C^W C^W$) and a homozygous red-flowered plant ($C^R C^R$) will produce offspring with pink flowers ($C^R C^W$). This type of relationship between alleles, with a heterozygote phenotype intermediate between the two homozygote phenotypes, is called incomplete dominance.



We can still use Mendel's model to predict the results of crosses for alleles that show incomplete dominance. For example, self-fertilization of a pink plant would produce a genotype ratio of 1 $C^R C^R$:2$C^R C^W$:1 $C^W C^W$ and a phenotype ratio of 1:2:1 red:pink:white. Alleles are still inherited according to Mendel's basic rules, even when they show incomplete dominance.



Co-dominance

Closely related to incomplete dominance is co-dominance, in which both alleles are simultaneously expressed in the heterozygote.

We can see an example of co-dominance in the MN blood groups of humans (less famous than the ABO blood groups, but still important!). A person's MN blood type is determined by his or her alleles of a certain gene. An L^M allele specifies production of an M marker displayed on the surface of red blood cells, while an L^N allele specifies production of a slightly different N marker.

Homozygotes ($L^M L^M$ and $L^N L^N$) have only M or an N markers, respectively, on the surface of their red blood cells. However, heterozygotes ($L^M L^N$) have both types of markers in equal numbers on the cell surface.

As for incomplete dominance, we can still use Mendel's rules to predict inheritance of co-dominant alleles. For example, if two people with $L^M L^N$ genotypes had children, we would expect to see M, MN, and N blood types and $L^M L^M$, $L^M L^N$, and $L^N L^N$ genotypes in their children in a 1: 2: 1 ratio (if they had enough children for us to determine ratios accurately!)

Multiple alleles

Mendel's work suggested that just two alleles existed for each gene. Today, we know that's not always, or even usually, the case! Although individual humans (and all diploid organisms) can only have two alleles for a given gene, multiple alleles may exist in a population level, and different individuals in the population may have different pairs of these alleles.

As an example, let's consider a gene that specifies coat colour in rabbits, called the C gene. The C gene comes in four common alleles: C, c^{ch}, c^{h}, and c:

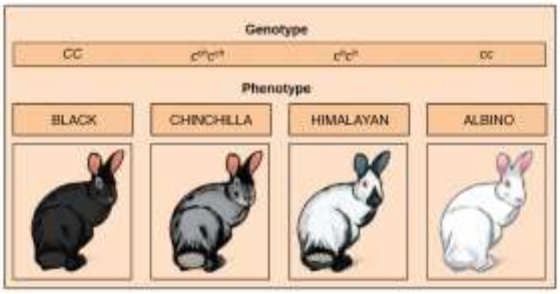
A C C rabbit has black or brown fur

A c^{ch} c^{ch} rabbit has chinchilla coloration (greyish fur).

A c^{h} c^{h} rabbit has Himalayan (colour-point)

patterning, with a white body and dark ears, face, feet, and tail

A cc rabbit is albino, with a pure white coat.



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Multiple alleles makes for many possible dominance relationships. In this case, the black C allele is completely dominant to all the others; the chinchilla c^{ch} allele is incompletely dominant to the Himalayan c and albino c alleles; and the Himalayan c^{h} allele is completely dominant to the albino c allele.

Rabbit breeders figured out these relationships by crossing different rabbits of different genotypes and observing the phenotypes of the heterozygous kits (baby bunnies).