

Basic Genetics 1—Dominant and Recessive

Many traits of interest to plant breeders are inherited in a “yes or no” fashion. The plant either shows the trait or it does not. How this works was first worked out by Gregor Mendel in the 1860s, although his work was not noticed until about 1900.

The basic idea is that many traits are the result of a single hereditary unit, a **gene**. In more precise modern terminology, we say there is a **locus** (a particular spot on a particular chromosome), where different bits of DNA, or different “versions” of the gene may be present. These different versions are called **alleles**. The word “gene” is imprecise, because it may refer to a locus, or to a particular allele at that locus.

Inheritance is easiest to understand in diploid organisms. A **diploid** has two full sets of chromosomes, one inherited from each of its parents. So there are two copies of any locus, which may have the same or different alleles.

Crossing Two Parents with Different Traits (F1 Generation)

Consider the diploid tall bearded iris ‘Swerti’. This is a plicata. It has two copies of the plicata allele *pl*. A typical clone of the species *Iris pallida* is a violet self. It has two copies of the nonplicata (self) allele ***Pl***. What happens when we cross these two irises?



X



Each parent gives one of its alleles (selected at random) to the seedling. Since ‘Swerti’ has only *pl* alleles, it will always give one *pl* to its seedlings. Similarly, *I. pallida* will always give one ***Pl***. So every single seedling will have one of each allele, ***Plpl***. (These first-generation seedlings are called **F1**, for “first filial generation”, *filius/filia* being Latin for son/daughter.)

What do the seedlings look like? Are they plicatas like ‘Swerti’, violet selves like *I. pallida*, or something in between?


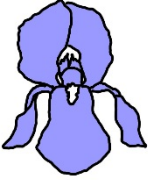
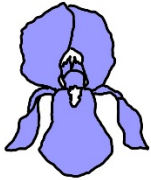

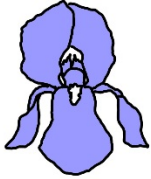

The answer is that they are all selves like the *I. pallida* parent. They all have one *pl* allele, but it has no effect on how the irises appear. This is what it means to say that ***Pl*** is **dominant** and *pl* is **recessive**. Both alleles are present, but one controls how the plant looks (its **phenotype**) and the other does not.

All the seedlings are selfs, but they are **carriers** of the plicata allele *pl*. This suggests that the plicata trait might reappear in future generations, which is indeed the case.

Crossing Siblings (F2 Generation)

What happens if we cross these seedlings amongst themselves, sibling to sibling? (This is called the **F2** generation.) Since each seedling has the **genotype** (assortment of genes) *Pipl*, each can give either a ***PI*** allele to its offspring, or a *pl* allele. Which of these it provides is entirely random, so half the time it should provide ***PI*** and half the time *pl*.

So what are the possible gene combinations for the seedlings? They are ***PIPI*** (each parent gives ***PI***), *plpl* (each parent gives *pl*), or ***Pipl*** (one parent gives ***PI***, the other gives *pl*). To keep track of these combinations, we can use a diagram called a **Punnett square**:


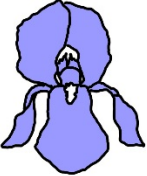
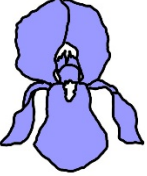
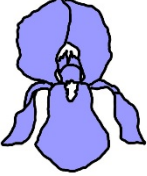
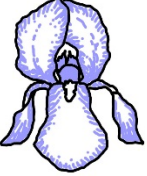
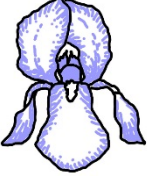
		pollen parent, genotype <i>Pipl</i>	
			
	allele given to offspring	$\frac{1}{2} PI$	$\frac{1}{2} pl$
	$\frac{1}{2} PI$	$\frac{1}{4} PIPI$ 	$\frac{1}{4} Pipl$ 
	$\frac{1}{2} pl$	$\frac{1}{4} Pipl$ 	$\frac{1}{4} plpl$ 

(By convention, the dominant allele is written first, ***Pipl***, regardless of which parent it comes from). So we can see that $\frac{1}{4}$ of the seedlings will be ***PIPI***, like *I. pallida*, $\frac{1}{4}$ will be *plpl*, like 'Swerti', and $\frac{1}{2}$ ($\frac{1}{4} + \frac{1}{4}$) will be ***Pipl***, like the F1 seedlings. Only the *plpl* seedlings will show the plicata pattern. The rest will be selfs, but those with genotype ***Pipl*** are plicata carriers, just like the F1 seedlings.

So if I raise 100 seedlings from this cross, I can expect about 25 plicatas and 75 selfs, 50 of which will be plicata carriers. This 3:1 ratio of the dominant phenotype to the recessive phenotype in the F2 generation is a classic **Mendelian ratio**, which applies for any trait determined by a single gene with one dominant and one recessive allele. Because the alleles given to the offspring are chosen at random, the ratio is only an approximation. A count of real seedlings will give a different ratio, but it should be close to the predicted 3:1, especially if many seedlings are raised.

Backcrossing

What happens if instead of crossing the F1 seedlings amongst themselves, we cross them with one of the original parents, a **backcross**? Here is the Punnett square for crossing an F1 seedling to its plicata parent 'Swerti':

		'Swerti' pollen parent, genotype $plpl$ 	
		$\frac{1}{2} pl$	$\frac{1}{2} pl$
F1 pod parent, genotype $Pppl$ 	$\frac{1}{2} Pl$	$\frac{1}{4} Pppl$ 	$\frac{1}{4} Pppl$ 
	$\frac{1}{2} pl$	$\frac{1}{4} plpl$ 	$\frac{1}{4} plpl$ 

Now 'Swerti' always gives the recessive pl allele to its seedlings. The F1 pod parent gives Pl half the time and pl half the time. So half the resulting seedlings are $Pppl$ (plicata-carrying selfs) and half are $plpl$ (plicatas). The backcross gives us twice as many plicatas (50%) as the F2 sib-cross (25%).

Following the same reasoning, you can deduce that backcrossing an F1 seedling to the *I. pallida* parent will give 100% selfs, half of which will be plicata carriers.

Test Crosses and Inferring an Unknown Genotype

In these examples, we assumed that we always know the genotype of each parent. This is true for irises showing the recessive trait, plicata pattern in this case. Only p/pl will have the plicata phenotype, so any plicata we see must be p/pl . If the iris is a self, however, we cannot be sure if it is a plicata carrier or not. How can we tell, since we cannot see the genes themselves?

The answer is to make a test cross. We saw that the F1 plicata carriers, backcrossed to a plicata, will give 50% plicata seedlings. A noncarrier, with genotype **PIPI**, like our original *I. pallida* parent, will give no plicata seedlings at all. This difference in progeny should be clear, if you raise enough seedlings. Crossing an iris with unknown genotype to an iris showing the recessive trait of interest will tell you if the first iris is a carrier for that trait or not.

You can also learn something of an iris's genotype from its parentage. If one parent is a plicata, the seedling *must* be a plicata carrier. (Think of the F1 generation in our earlier example. All these seedlings are carriers, because all of them received one $p/$ allele from their plicata parent.) However, you cannot draw any certain conclusion from more remote ancestors. Our F2 generation, for example, have two plicata grandparents, but some of them are **PIPI**, carrying no plicata alleles at all.

Summary of Mendelian Ratios for Diploids

Here we are using the symbol A for any dominant allele and a for its recessive counterpart. The ratios given are the proportion of seedlings showing the recessive trait to those that do not show it. The percentages are the fraction of seedlings showing the recessive trait.

$AA \times AA$	0:1	0
$AA \times Aa$	0:1	0
$AA \times aa$	0:1	0
$Aa \times Aa$	1:3	25%
$Aa \times aa$	1:1	50%
$aa \times aa$	1:0	100%

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Iris Hybridizing Facebook group
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