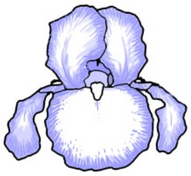
Basic Genetics 2—Dominant and Recessive, Tetraploid Version

In tetraploid plants, each parent gives *two* alleles to each of its seedlings, not just one. This changes the usual ratios seen in diploid seedlings, and also opens more possible combinations of alleles.

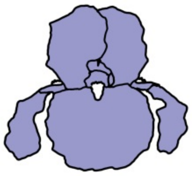
The sections that follow revisit the types of crosses discussed in “Basic Genetics 1—Dominant and Recessive”, which should be read first. If you do not have an appetite for the details that follow, the big takeaway is this: it is much harder to recover recessive phenotypes when working with tetraploids.

Crossing Two Parents with Different Traits (F1 Generation)

Consider crossing a tetraploid plicata with a tetraploid violet self that is not a plicata carrier.



x



The plicata has *four* plicata alleles *plplplpl* and the self has *four* nonplicata alleles ***PlPlPlPl.*** Each gives *two* alleles to the seedlings, so the genotype of all the F1 seedlings is *__PlPl__plpl.* These will all appear as violet selfs, just as in the example with diploids. All are carriers of two copies of *pl.*

Crossing Siblings (F2 Generation)

Now things start to get interesting. Each F1 seedling will give two alleles to its own seedlings, but which ones? There are three possibilities: ***PlPl, Pl****pl,* and *plpl.* What are the probabilities of each of these pairs? The basic operation is to pick one of the four alleles at random, then pick another one at random from the remaining three. What is the chance of a particular pair, say ***PlPl****?* The chance of picking a ***Pl*** from the original four is ½. (There are two ***Pl***’s and two *pl*’s, so the odds are even.) But now to get a second ***Pl,*** we must select it at random from the *three* remaining alleles, ***Pl,*** *pl,* and *pl.* The odds of getting that second ***Pl*** are thus 1/3. Combining the ½ chance of getting the first ***Pl*** with the 1/3 chance of getting the second one gives an overall change of ½ x 1/3 = 1/6. Obviously, then, the probability of getting *plpl* is also 1/6. The probability of getting *__Pl__pl* is the remaining 4/6, or 2/3.

> Note: At this point, it is necessary to state a caveat. Chromosomes actually divide into two copies before they are selected to go off into a gamete for delivery to the seedlings. So one is not really selecting two alleles out of four, but rather two out of eight. This possibility can change the probabilities a little under some circumstances, but the differences are not usually large enough to be noticed unless the number of seedlings grown is huge. In this introductory discussion, these differences will not be taken into account.

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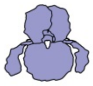
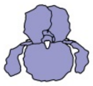
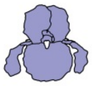
So here is the Punnett square for our cross:

		pollen parent, genotype **PlPl***plpl* 		
	allele given to offspring	1/6 **PlPl**	2/3 **Pl***pl*	1/6 *plpl*
pod parent, genotype **PlPl***plpl* 	1/6 **PlPl**	1/36 **PlPlPlPl** 	1/9 **PlPlPl***pl* 	1/36 **PlPl***plpl* 
	2/3 **Pl***pl*	1/9 **PlPlPl***pl* 	4/9 **PlPl***plpl* 	1/9 **Pl***plplpl* 
	1/6 *plpl*	1/36 **PlPl***plpl* 	1/9 **Pl***plplpl* 	1/36 *plplplpl* 

Now we have to gather together the different cells in the table that have the same genotype. For example, there are two cells that have **PlPlPl***pl.* Here are the results:

1/36 (2.8%) **PlPlPlPl**

2/9 (22.2%) **PlPlPl***pl*

4/9 (44.4%) **PlPl***plpl*

2/9 (22.2%) **Pl***plplpl*

1/36 (2.8%) *plplplpl*

Only the seedlings in the last group (*plplplpl*) will be plicatas. So whereas with the diploid F2 generation, we could expect 25% plicatas, with tetraploids there will be less than 3%! For the hobbyist, these are abysmal odds. You could raise 100 seedlings from a sib cross and only get a few plicatas, or perhaps none at all.

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Backcrossing

You might expect more plicatas from backcrossing the F1 seedlings to the plicata parent (or another unrelated plicata), and indeed this is true, although the odds are not as good as the 50% expected with diploids.

		pollen parent, genotype *plplplpl* 
	allele given to offspring	all *plpl*
pod parent, genotype ***PlPl***_plpl_ 	1/6 ***PlPl***	1/6 ***PlPl***_plpl_ 
	2/3 ***Pl***_pl_	2/3 ***Pl***_plplpl_ 
	1/6 *plpl*	1/6 *plplplpl* 

So we can expect 1/6 plicata seedlings from the backcross, or about 17%. Not a great percentage, but enough to have several to select from if you raise a good number of seedlings. Notice that most of the self seedlings from this backcross carry three *pl* alleles. When backcrossed again to a plicata, these are expected to give 50% plicata seedlings. So it has taken us two generations of backcrossing to get to a place similar to what one generation gave us with diploids.

Test Crosses and Inferring an Unknown Genotype

We can use test crosses to check for carriers. Now, however, there are three different types of carriers: those with one, two, or three copies of the recessive allele. A carrier with three copies of *pl* is expected to give 50% plicatas when crossed with plicatas, one with two copies should give 17%, and one with only one copy should not give any. (However, because of the “two out of eight” instead of “two out four” possibility mentioned above, one may get a plicata anyway, on rare occasions.)

Summary of Mendelian Ratios for Tetraploids

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. I have only included crosses with more than a negligible chance of recovering the recessive trait.

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AAaa x *AAaa*	1:35	2.8%
AAaa x *Aaaa*	1:11	8.3%
AAaa x *aaaa*	1:5	17%
Aaaa x *Aaaa*	1:3	25%
Aaaa x *aaaa*	1:1	50%
aaaa x *aaaa*	1:0	100%

Tom Waters
Iris Hybridizing *Facebook group*
2018.Mar.11

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