

Dominant mutations

Why mutations are recessive

If assume for a pigmentation gene:

null = 0

wild type =100

Then, we almost always see

0/0 no color

100/100 color

100/0 (50) color

What does that say? Most wild type genes are expressing at least twice as much gene product as they need. That's why we observe mutations that are recessive.

Since alleles can theoretically occupy any level of expression, we can determine when the level of expression is low enough to affect expression.

Take a 50% allele, do you see pigment? (etc.)

50/50 full color

50/0 (25) ?

For the maize bronze gene 0.5 - 1 % of wild type is all that is necessary

For the maize waxy gene its ~10%

Its only at the level when the gene product is limiting for the particular phenotype that you can see incomplete dominance (remember the four-o'clocks).

Codominance

Only possible when both gene products are visible

Allozymes in plants. Indicate that many enzymes function as dimers or sometimes tetramers

All genes are codominant at the level of gene expression. In fact the distinction between recessive and codominant is arbitrary: depends on where you look.

Dominant mutations

If all genes are essentially codominant, how can you get truly dominant mutations?

Haploinsufficient. There are a few examples in plants, which may related to haploid phase i.e. one gene always HAS to be enough.

Overexpression. There are examples but all have been from transgenic overexpression experiments. One example is the overexpression of the Flowering Locus C (FLC, a MADS box transcription regulator) gene in Arabidopsis (Michaels and Amasino, Plant Cell 11, 949-956, 1999).



Landsberg erecta (Ler) and constitutively expressed FLC in the Ler background

Gain of function. A gene expressed in the wrong place or wrong time. E.g. Ac, Spm etc. where there is no normal allele. Other examples are maize Knotted and its homologs in other organisms, as discussed in Wednesday's paper.

Dominant negative. "gums up the works"

- might be expected with gene products that function as dimers or tetramers - one bad subunit kills the whole complex
- an example are RNAi constructs
- another example is C-I

We can often interpret which it is by knowing the function of the gene and the sequence of the dominant alleles, as illustrated in our papers. Another way to tell is to vary gene dosage, as shown below.

In a simple world where **** = most severe phenotype:

	haploinsufficient	overexpression	gain of function	dominant negative
D/D	****	****	****	****
D/-	****	**	****	****
D/+	**	***	****	**
D/++	+	****	****	*

Often cannot get all dosages, but even a series of three can help.

-In maize: B-A translocations or endosperm (as in upcoming C-I paper) can be used.

-In Arabidopsis: it has been done using triploids (here can't get the D/- treatment).

For the dominant *Arabidopsis axr2* mutation; auxin levels required for 50% inhibition of root growth (gain of function). Wilson and Estelle, 1994, *Genetics* 138, 1239-1249

Genotype	IAA (μM)	2,4-D (μM)
+/+	0.03 \pm 0.02	0.02 \pm 0.01
axr2/+	1.40 \pm 0.07	0.21 \pm 0.01
axr2/axr2	1.30 \pm 0.50	0.20 \pm 0.01
+/+/+ (only two individuals)	0.03; 0.02	0.04; 0.02
axr2+/+ (only two individuals)	2.00; 1.20	0.12; 0.20