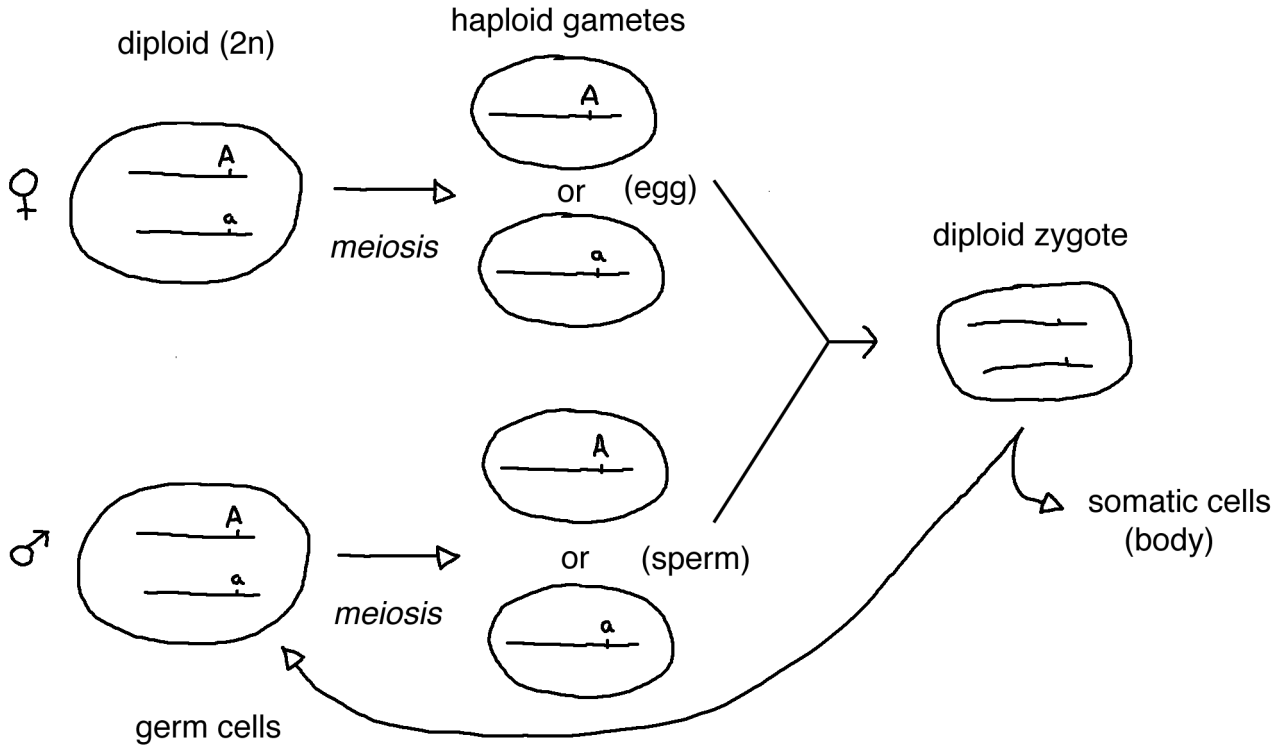
Lecture 3

Now let's consider diploid organisms:



The genotype of the zygote will depend on which alleles are carried in the gametes.

Allele in gamete		sperm **A**	sperm **a**
egg	**A**	**A/A**	**A/a**
	a	**a/A**	**a/a**

Zygote

When heterozygotes mate their offspring will have different phenotypes: If **A** is dominant to **a**, the two possible phenotypes will be the phenotype of **a/a** or the phenotype of **A/A** and **A/a**.

When we do breeding experiments it is important to know the genotypes of the parents. But as you can see from the example above individuals with the dominant trait could be either **A/A** or **A/a**. A method to control this type of variation is to start with populations that we know to be homozygous. One way to do this is to keep inbreeding individuals until all crosses among related individuals always produce identical offspring. This is known as a true-breeding population and all individuals can be assumed to be homozygous.

True Breeding: homozygous for all genes

Say we have a true breeding line of shibire flies these flies are paralyzed and have genotype **shi$^-$/shi$^-$**.

First, we can test to see whether the shibire allele is dominant or recessive.

shi$^-$/shi$^-$ **x** (wild type) **shi$^+$/shi$^+$**

↓

all are **shi$^-$/shi$^+$**

(The offspring from a cross of two true breeding lines is known as the F_1 or first filial generation). The F_1 flies appear like wild type therefore **shi$^-$** is recessive (not expressed in heterozygote)

Say we have isolated a new paralyzed mutant that we call **par**.

We start with a true breeding **par$^-$** strain that we mate to wild type. We find that the mutation is not expressed in the F_1 heterozygotes and therefore is recessive.

To find out whether **par$^-$** is the same as **shi$^-$** we can do a complementation test since both mutations are recessive. For this test, we cross a true breeding **par$^-$** strain to a true breeding **shi$^-$** strain.

par$^-$/par$^-$ **x** **shi$^-$/shi$^-$**

↓

F_1 (these flies must inherit both **shi$^-$** and **par$^-$**)

Possible outcome	Complementation?	Explanation	Inferred genotype
F_1 not paralyzed	**shi$^-$** and **par$^-$** complement	**par$^-$** genotype can supply function missing in **shi$^-$** and vice versa	**par$^-$/par$^+$** **shi$^+$/shi$^-$**
F_1 paralyzed	**shi$^-$** and **par$^-$** do not complement	**par$^-$** has lost function needed to restore **shi$^-$**	**shi$^-$/shi$^-$**

Let's look more carefully at gene segregation in a cross between F_1 flies.

shi$^-$/shi$^+$ **x** **shi$^-$/shi$^+$**

What is the probability of a paralyzed fly in the next (F_2) generation?

Definition: $p(\mathbf{a}) = \frac{n_a}{N}$ n_a = number of outcomes that satisfy condition **a**

N = total number of outcomes (of equal probability)

Probability problems can be solved by accounting for every outcome, but usually it is easier to combine probabilities.

p(paralyzed F_2 fly) = p(inherit **shi$^-$** from mother and inherit **shi$^-$** from father)

Product rule: p(**a** and **b**) = p(**a**) x p(**b**)

(note the product rule only applies if **a** and **b** are independent which is the case here since the allele from mother does not affect the allele from the father)

p(**shi$^-$** from mother) = $^1/_2$

p(paralyzed) = $^1/_2$ x $^1/_2$ = $^1/_4$

p(not paralyzed) = 1 – $^1/_4$ = $^3/_4$

Thus in the F_2 generation the phenotypic ratio will be, 1 paralyzed : 3 not paralyzed

A 1 : 3 phenotypic ratio among the F_2 in a breeding experiment shows that alleles of a single gene are segregating.

This actually constitutes a third definition of a gene. Historically, this was the first definition of the gene developed by Gregor Mendel in the 1860s. Mendel was able to detect single genes segregating in pea plants because he looked at simple traits and started with true-breeding strains.

Let's see how these ideas can be applied to a very interesting problem in the evolution of corn. Domestic corn is derived from wild progenitor Teosinte. There is no historical record of how the breeding was done to produce Maize but there is a genetic record of the differences between Teosinte and Maize recorded the genomic differences between these two species. Maize and Teosinte can be crossed to give viable progeny.

Teosinte x Maize

↓

F_1 all same and unlike either parent

↓

F_2 50,000 plants

~$^1/_{500}$ look like Teosinte and ~$^1/_{500}$ look like Maize

How many genes contribute to the differences between the two kinds of plants?

Let's designate the genes that differ as **A**, **B**, **C**, **D ...**

For each gene there are two alleles: the allele present in Teosinte and the allele present in Maize.

For the **A** gene we will designate these alleles A_T and A_M respectively. For the **B** gene there will be alleles B_T and B_M and so on for all the genes that differ.

Let's follow the **A** gene through the cross between Maize and Teosinte

$$A_T/A_T \times A_M/A_M$$

F_1 : A_T/A_M

Because the F_1 don't look like either parent, let's assume that the alleles are codominant.

Codominant: heterozygote different than either homozygote.

Incomplete dominance: heterozygote expresses the traits of both homozygous parents.

(Alternatively, the genes that differ could have a mixture of dominant and recessive alleles)

F_2:	A_T/A_T		A_T/A_M		A_M/A_M
	1	:	2	:	1

$^1/_4$ will look like Teosinte.

For two genes that differ: A_T/A_T B_T/B_T

$^1/_4 \times {}^1/_4 = {}^1/_{16}$ will look like Teosinte.

Similarly, for three genes the probability will be $^1/_{64}$. For four genes it will be $^1/_{256}$, and for five genes it will be $^1/_{1024}$.

Since ~1/500 look like Teosinte the conclusion is that 4–5 genes differ between wild corn (Teosinte) and domestic corn (Maize). Using modern methods, it has been confirmed that there are about five significantly different alleles and several of these have been located using mapping methods.