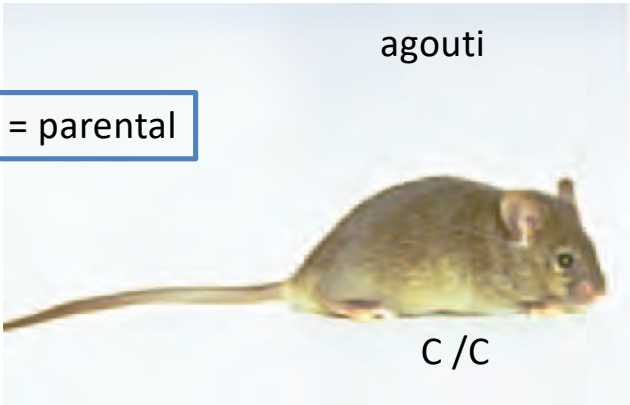


Gène tyrosinase

P = parental



X
↓

F1
100 % agoutis
C / c



X
↓



F2
1/4 C/C } 3/4
2/4 C/c }



1 gène :
3 : 1



Question :

Mâle :
taille normale
albinos

Femelle :
naine
agouti



X
↓

F₁
100% taille normale
100% agouti



2 gènes :
9 : 3 : 3 : 1

F₁ X F₁

↓

F₂ : ??

2 gènes non liés



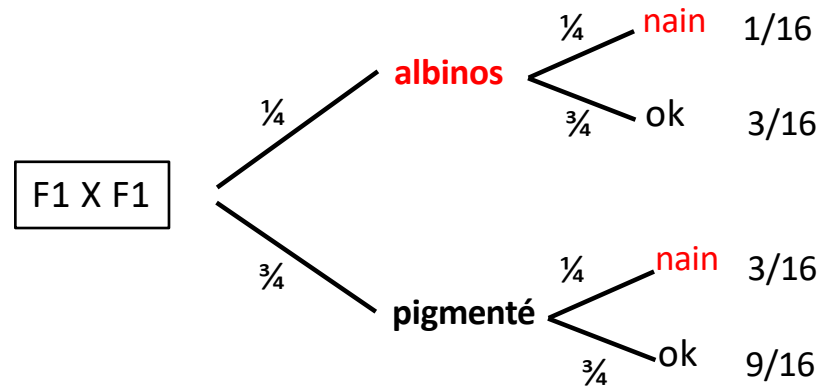
F2



9 : 3 : 3 : 1



Dihybridisme :



Dans le dihybridisme
F1 X F1 donne
4 génotypes.
(sans épistasie)

2 gènes :
9 : 3 : 3 : 1



Question :

Mâle :
taille normale
albinos

Femelle :
naine
agouti



X
↓

F₁
100% taille normale
100% agouti



2 gènes :
9 : 3 : 3 : 1

F₁ X F₁

↓

F₂ : ??

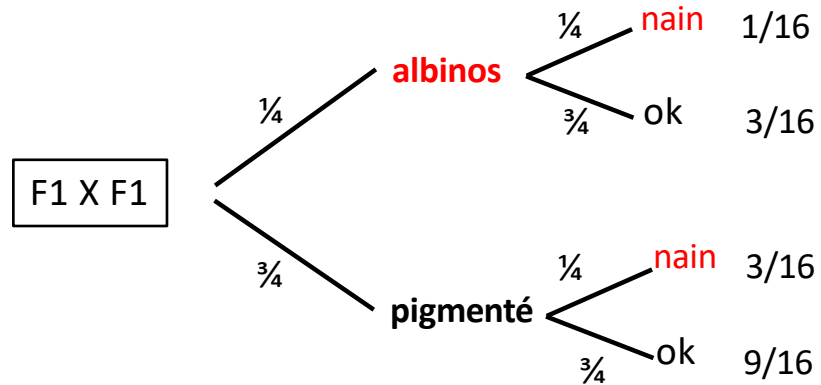
2 gènes totalément liés
= voisins



F2

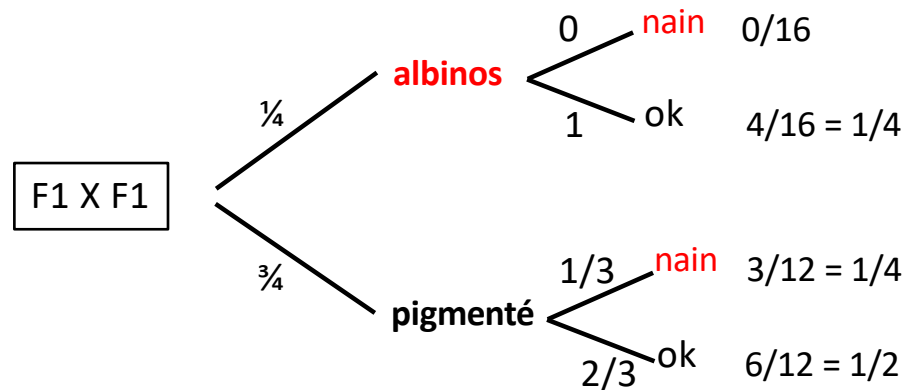


Dihybridisme :



Dans le dihybridisme
F1 X F1 donne
4 génotypes.
(sans épistasie)

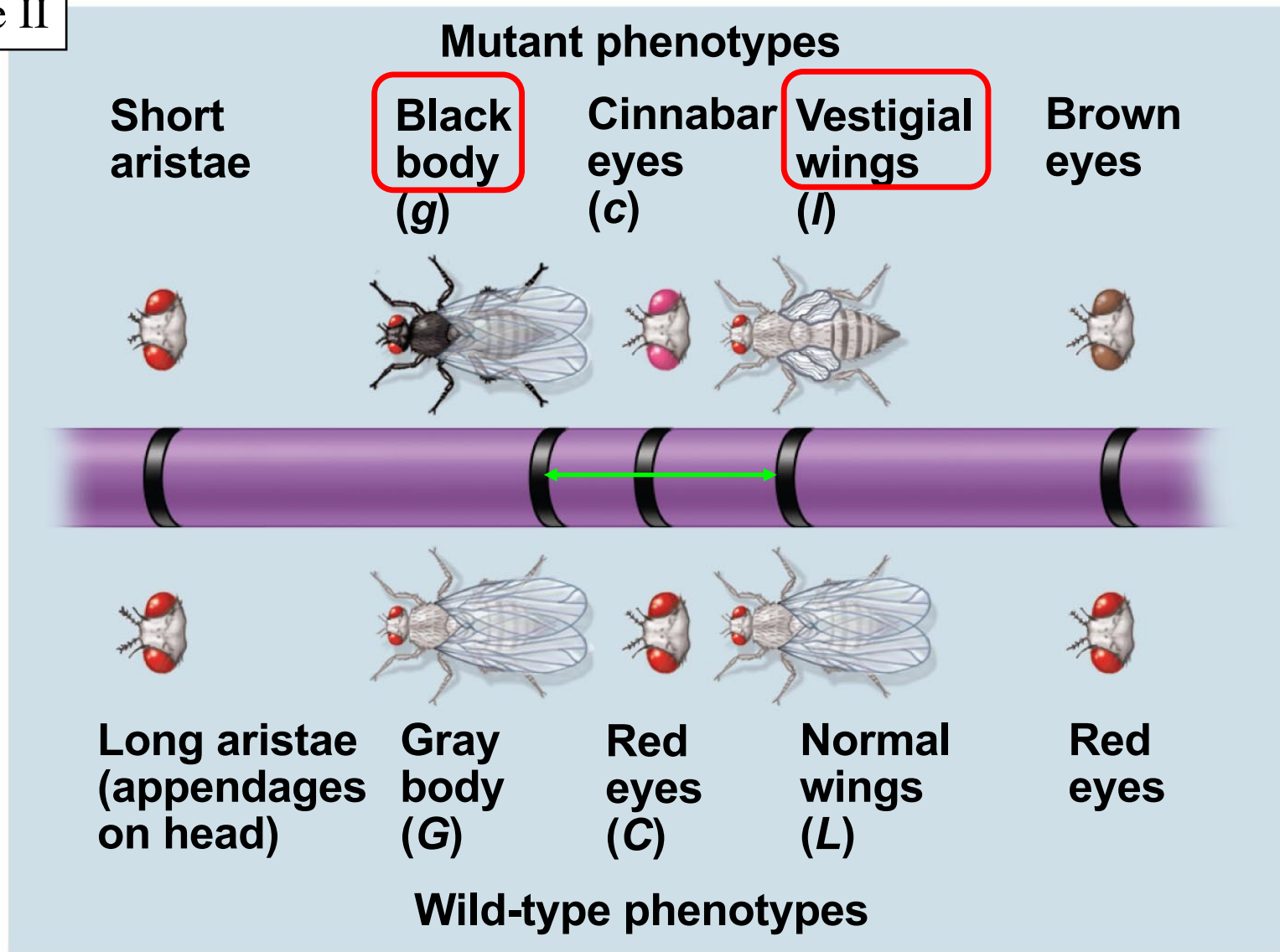
2 gènes :
9 : 3 : 3 : 1



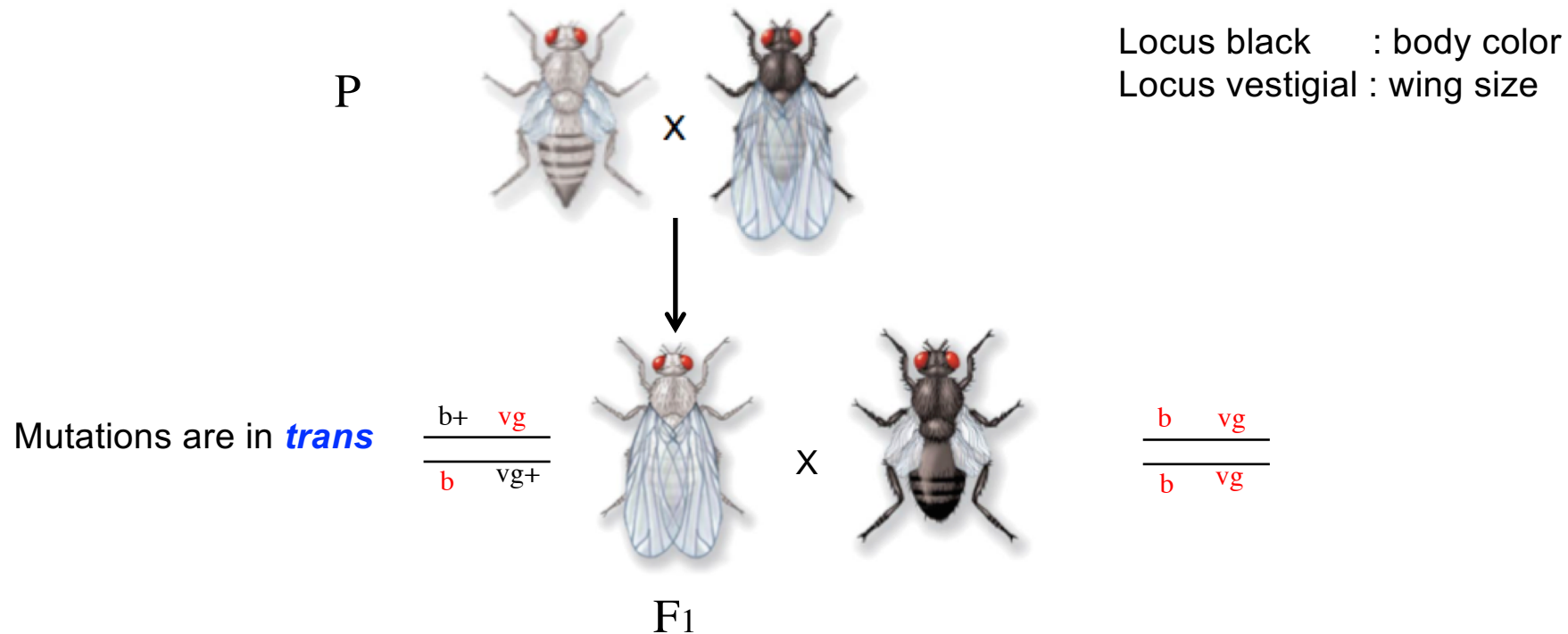
	p T	P t
p T	pp	
P t		tt

Chromosome II

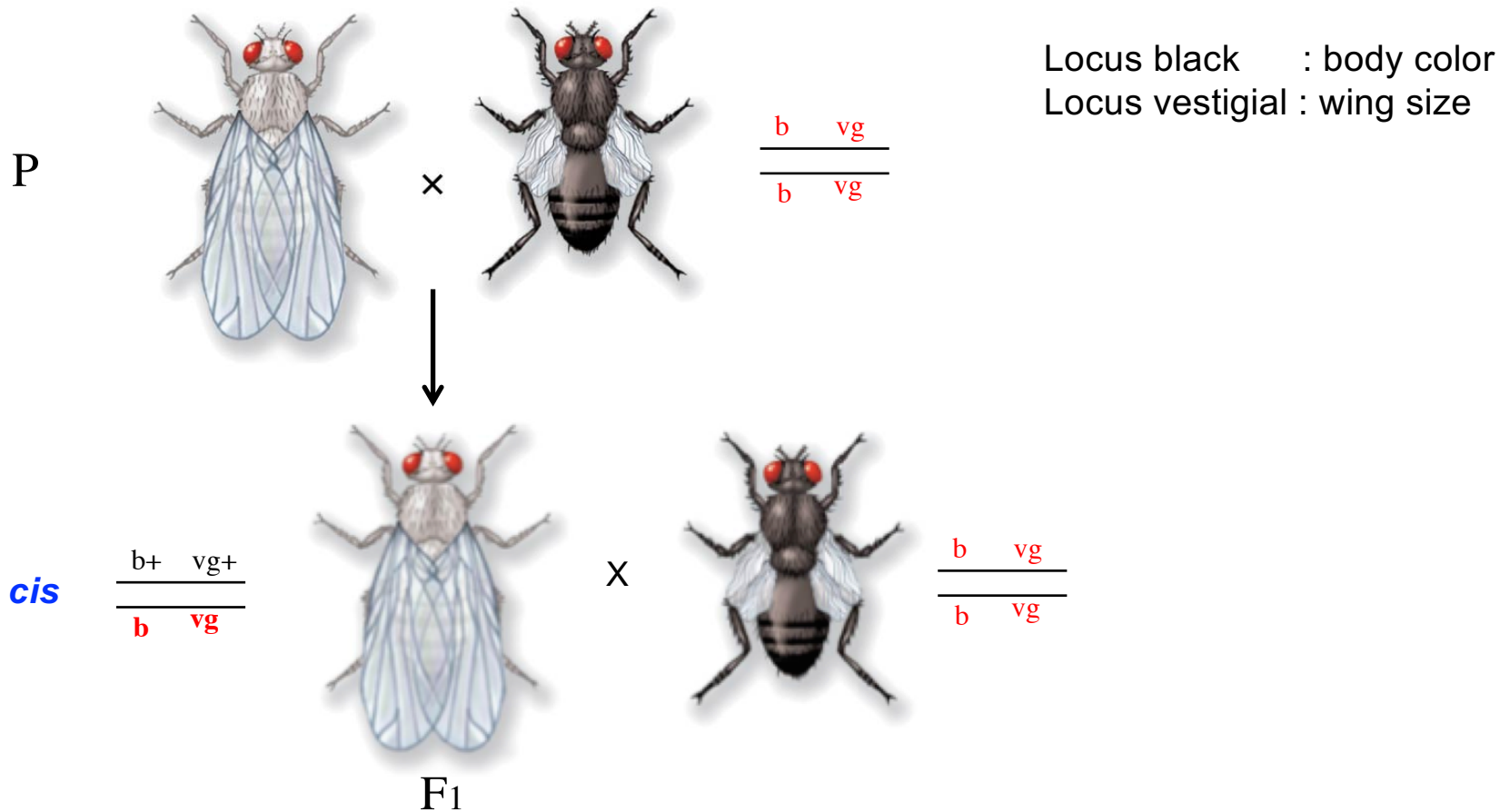
Question :
What is the **genetic distance** between the **black locus** and the **vestigial locus** ?



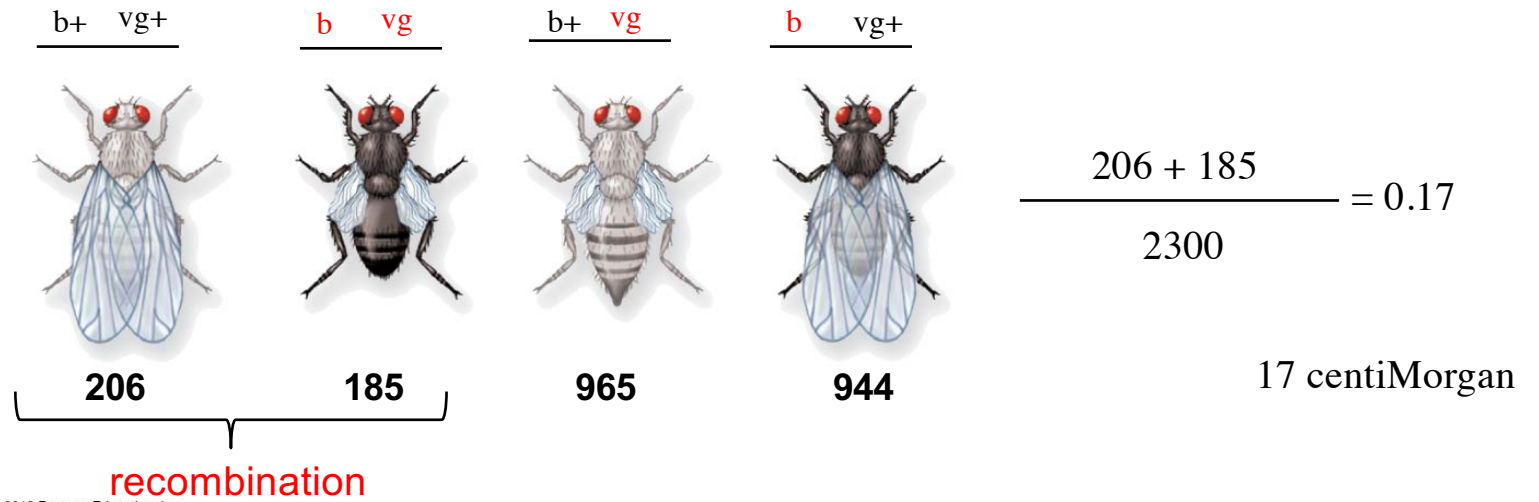
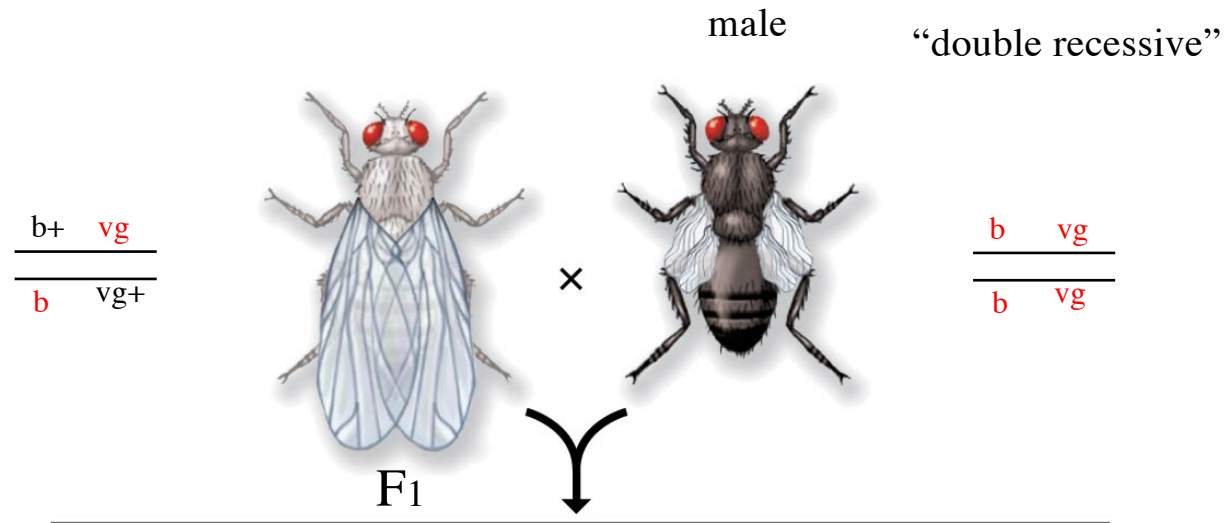
Measuring the genetic distance between 2 loci:



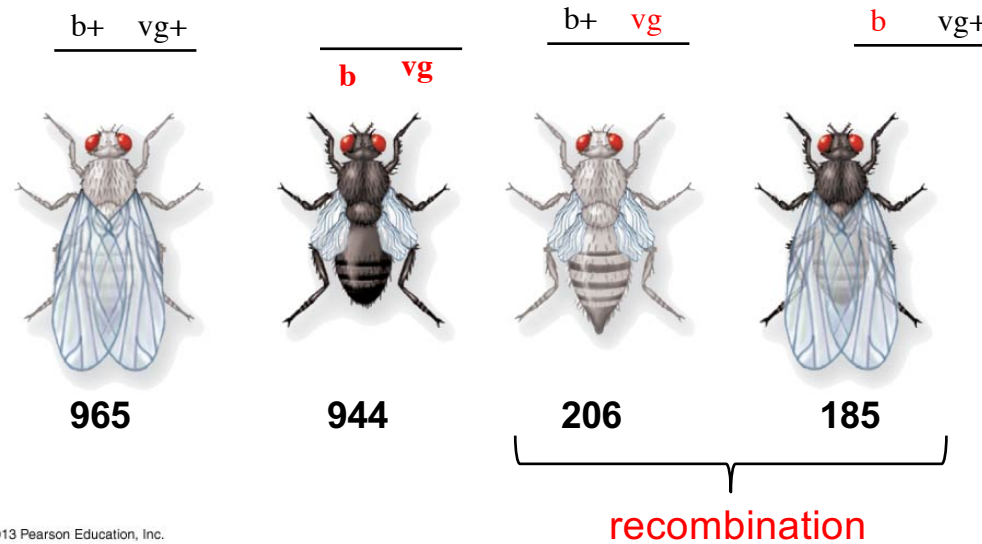
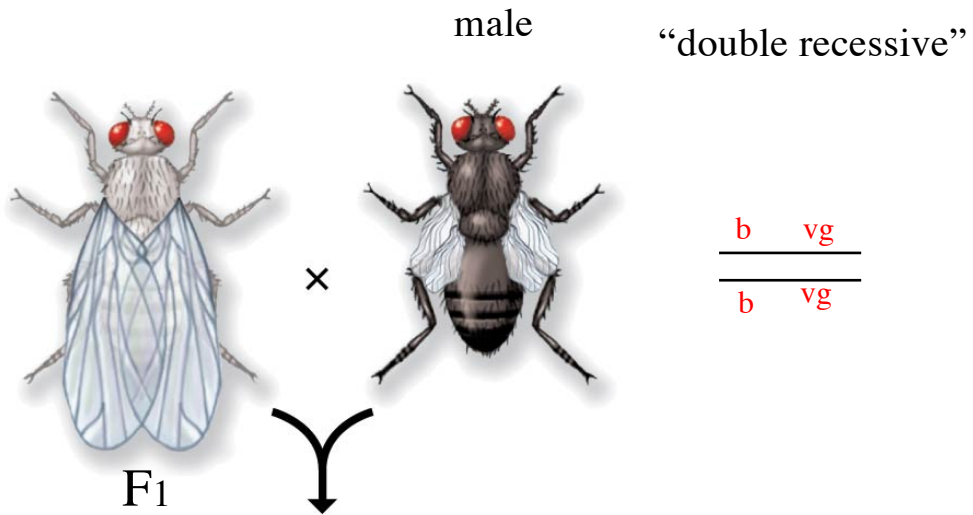
Measuring the genetic distance between 2 loci:



Mutations are in *trans*



Mutations are in *cis*

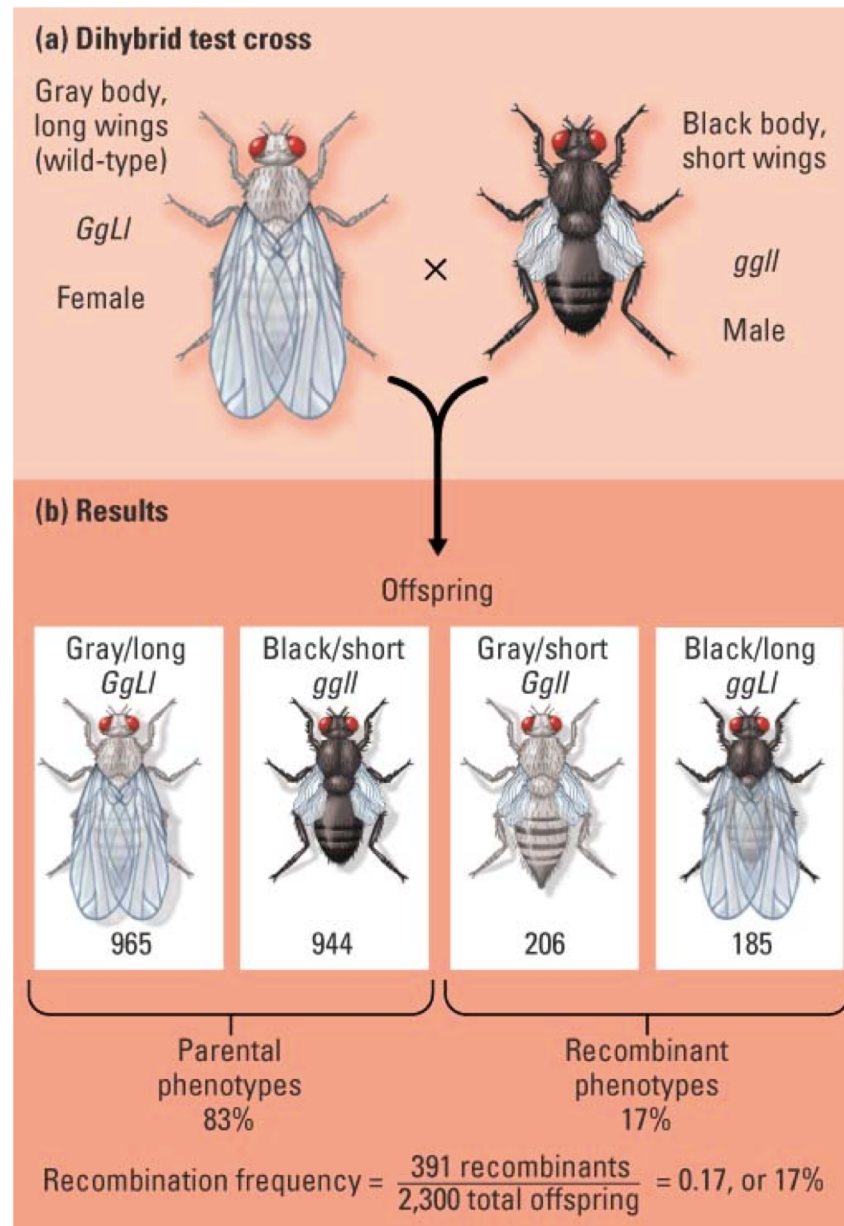
$$\frac{b^+ \quad vg^+}{b \quad vg}$$


$$\frac{206 + 185}{2300} = 0.17$$

17 centiMorgan

In textbooks, the mutations are in *cis*.

The case with mutations in *trans* is omitted.

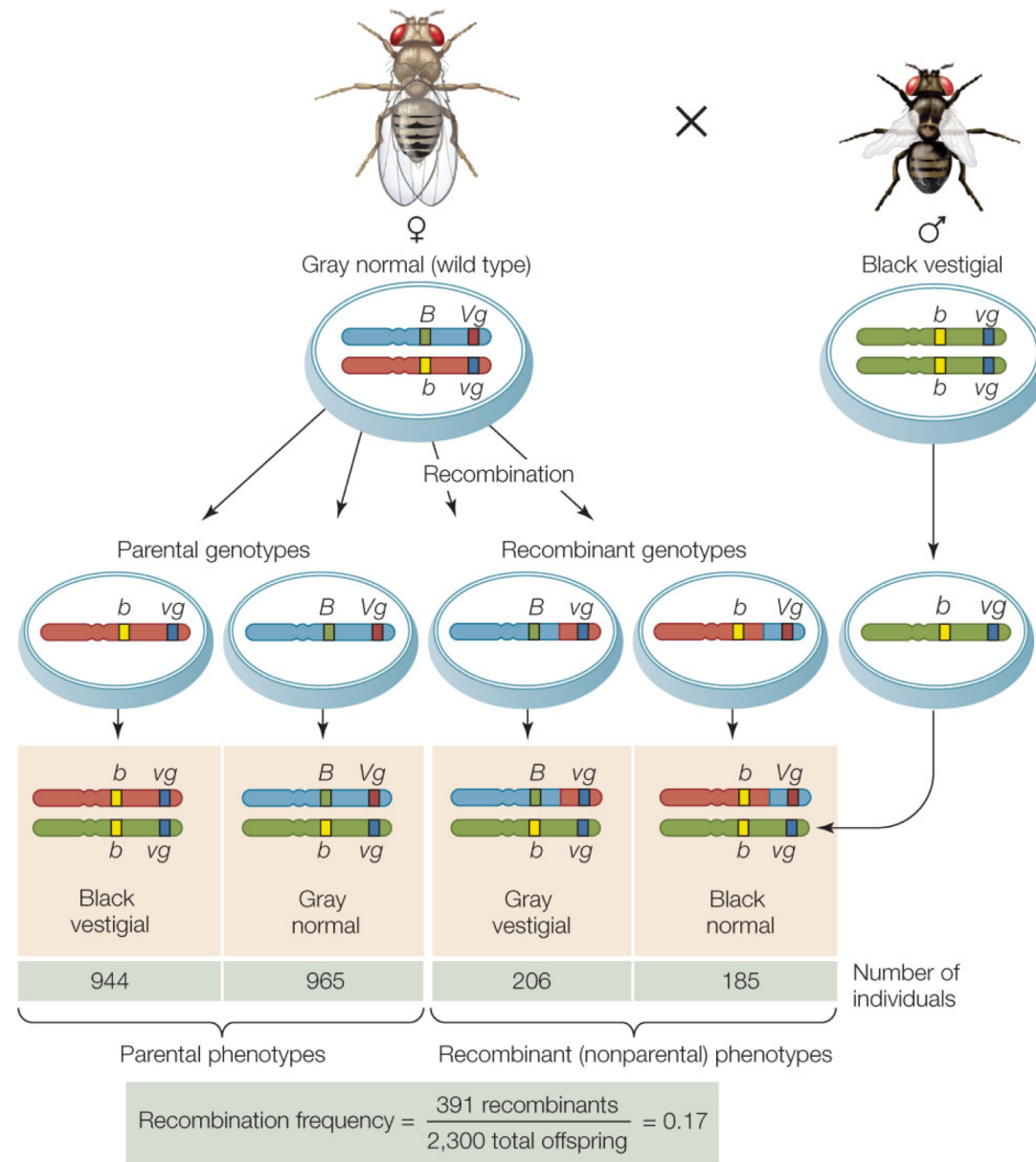


Essential Biology
Fig 9.24

Hillis, chapter 8

We observe crossovers during meiosis in the female. The female produces 4 types of gametes.

The phenotype of the offspring reflects the genetic information transmitted by the mother.



Ce mâle est double récessif

The male produces only 1 type of gametes

What is expected from you :

1. Given the genetic distance between the 2 loci and the number of offspring you should be able to calculate the expected numbers for all 4 phenotypes.
2. Given the numbers for all 4 phenotypes among the offspring you should be able to calculate the genetic distance between the 2 loci.

Remarkable cases :

$d < 50\text{cM}$ Detection of linkage

$d = 50\text{ cM}$ $\frac{25 + 25}{25 + 25 + 25 + 25} = 0.5$

The loci behave as if they were not linked

$d > 50\text{ cM}$ The genetic distance cannot be deduced from one single cross; several crosses are needed to measure the genetic distance.