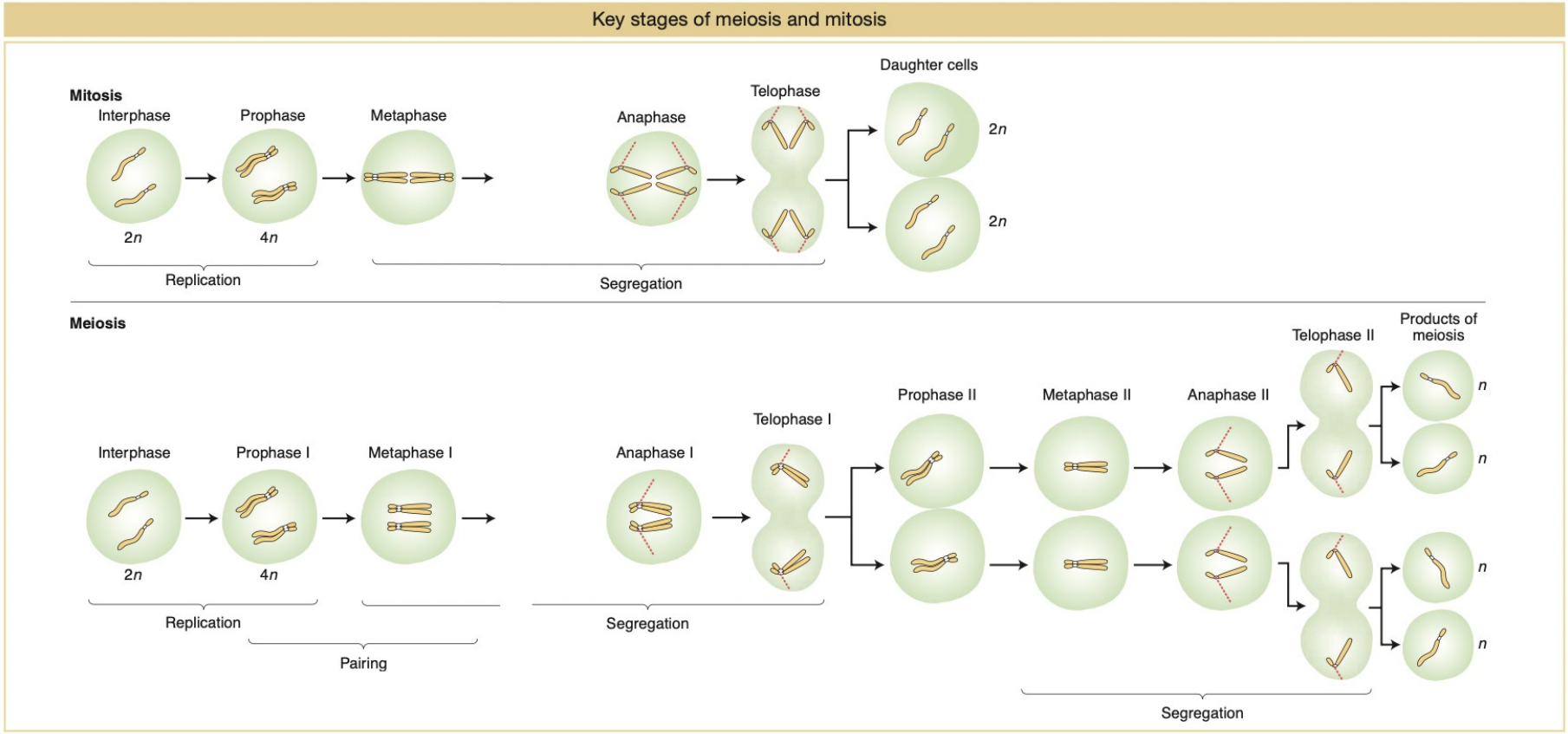
Bi 122 Midterm Review

By Abdullah, Emma, Indeever, and Cherise

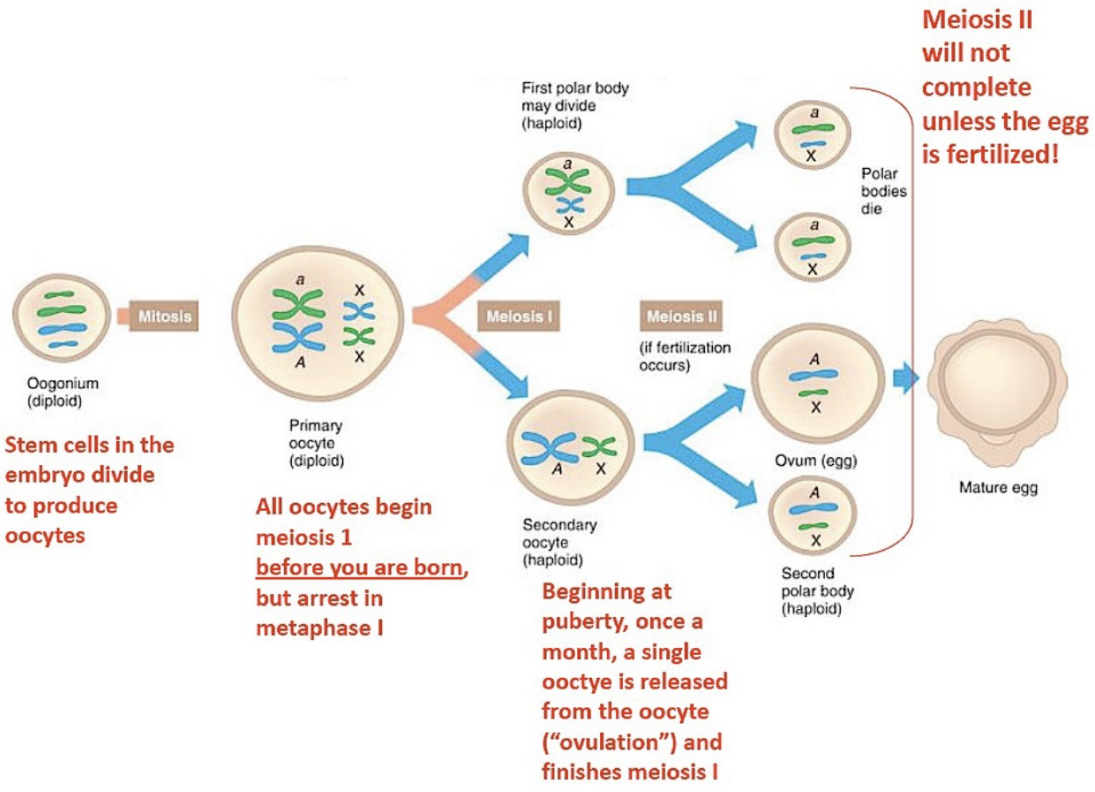
Exam Logistics

- Midterm exam (Sunday, 11/2 at 1 PM in Chen 100) will cover up to “Lecture 8” that was covered in PSet 4
- **Please arrive at 12:45pm**
- In-person exam is open note, open book; internet and other resources are prohibited, but clarification questions to the TAs are allowed
- Select 4 out of 6 questions to answer, with an optional 5th question for EC (within the 2 hour time limit)
- Breaks during the exam are allowed (i.e. bathroom breaks), but extra time to the exam will not be allotted
- Calculators allowed (you won’t need anything past arithmetic operations)

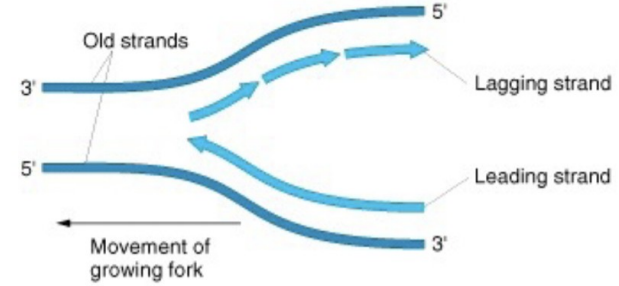
Mitosis and meiosis

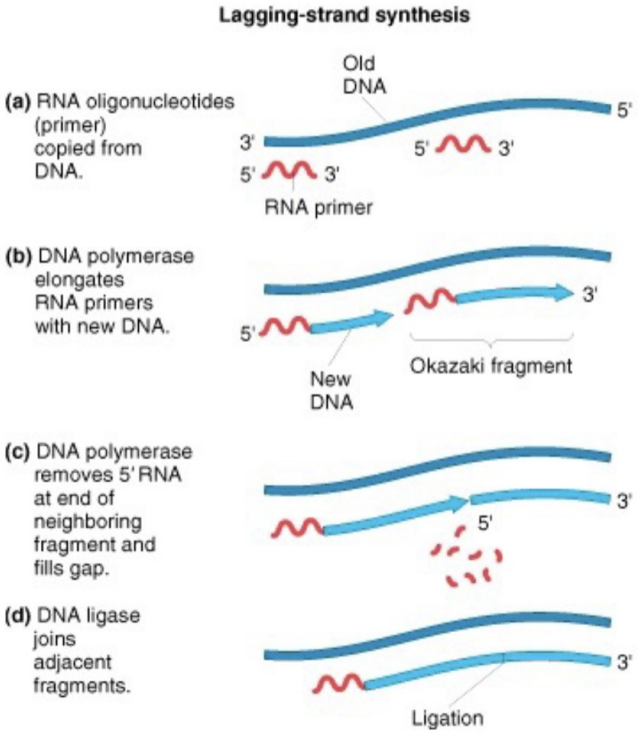


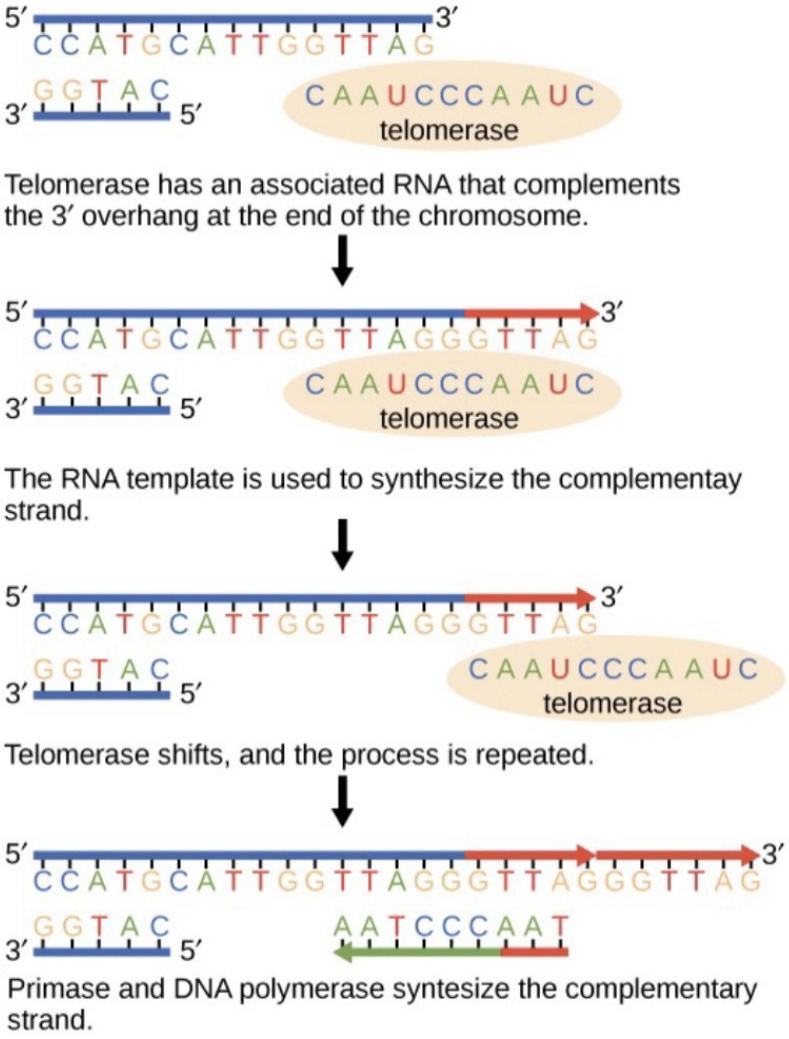
Polar bodies



Telomeres


Old strands
5′
3′
Lagging strand
Leading strand
Movement of growing fork

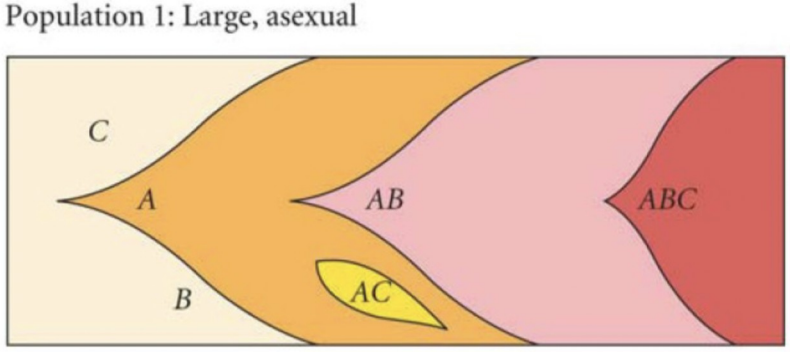

Lagging-strand synthesis
(a) RNA oligonucleotides (primer) copied from DNA.
Old DNA
RNA primer
(b) DNA polymerase elongates RNA primers with new DNA.
New DNA
Okazaki fragment
(c) DNA polymerase removes 5′ RNA at end of neighboring fragment and fills gap.
(d) DNA ligase joins adjacent fragments.
Ligation


5′ CCATGCATTGGTTAG 3′
3′ GGTAC 5′
CAAUCCCAAUC
telomerase
Telomerase has an associated RNA that complements the 3′ overhang at the end of the chromosome.
5′ CCATGCATTGGTTAGGGTTAG 3′
3′ GGTAC 5′
CAAUCCCAAUC
telomerase
The RNA template is used to synthesize the complementay strand.
5′ CCATGCATTGGTTAGGGTTAG 3′
3′ GGTAC 5′
CAAUCCCAAUC
telomerase
Telomerase shifts, and the process is repeated.
5′ CCATGCATTGGTTAGGGTTAGGGTTAG 3′
3′ GGTAC 5′
AATCCCAAT
Primase and DNA polymerase syntesize the complementary strand.

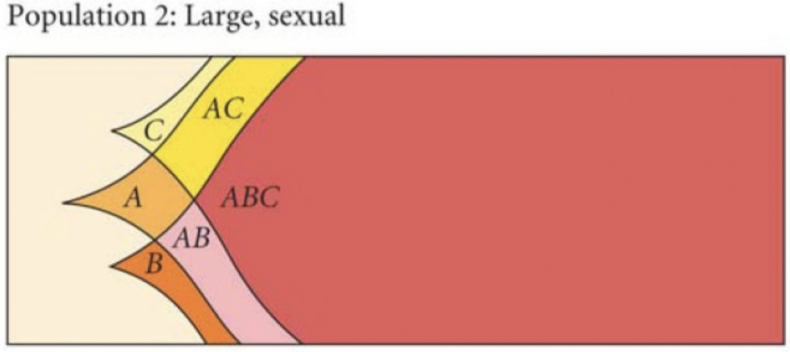
Asexual vs sexual reproduction

Sex and recombination bring together rare, advantageous gene combinations in the same individual

No sex and recombination

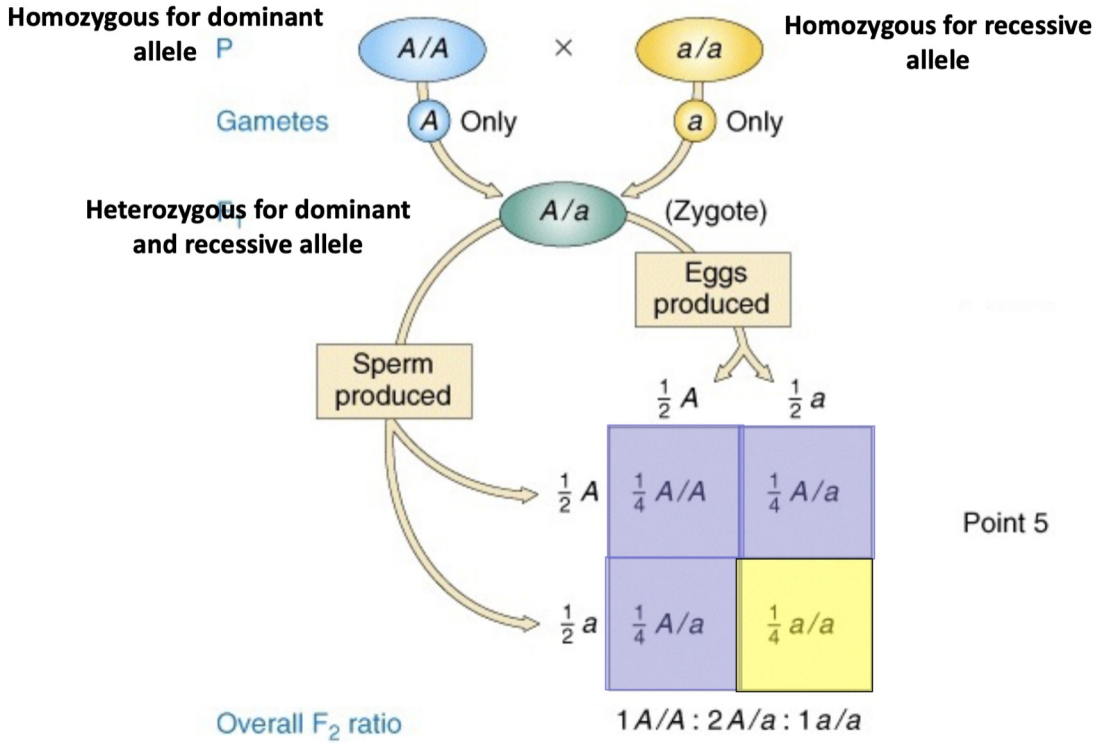


Sex and Recombination



Mendelian Genetics

Independent segregation of A/a locus alleles during meiosis

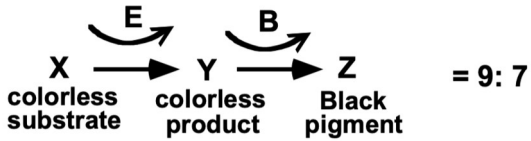


Point 5

Complementation

Complementary gene action

Dominant alleles from two different genes must be present to produce a particular phenotype.



= 9: 7

	BE	Be	bE	be
BE	BBEE (Black)	BBEe (Black)	BbEE (Black)	BbEe (Black)
Be	BBeE (Black)	BBee (Golden)	BbeE (Black)	Bbee (Golden)
bE	bBEE (Black)	bBEe (Black)	bbEE (Golden)	bbEe (Golden)
be	bBeE (Black)	bBee (Golden)	bbeE (Golden)	bbee (Golden)

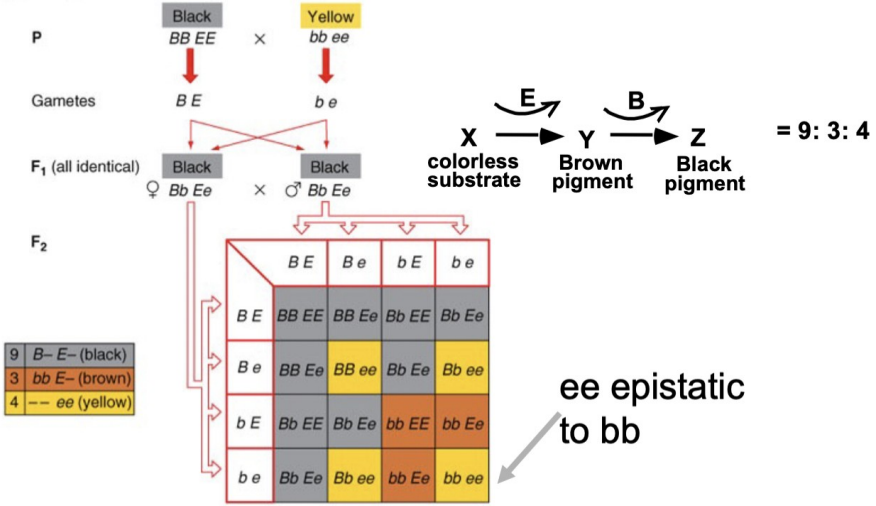
Notice that if we had a way to distinguish colorless product X from colorless product Y this would be an example of recessive epistasis.

Epistasis

In epistasis the genotype at one locus masks the ability to determine the genotype at a second locus. Epistasis relationships are often found in biochemical pathways.

Recessive epistasis

Disruption of an early step in the pathway blocks the ability to determine the genotype with respect to genes involved in later steps



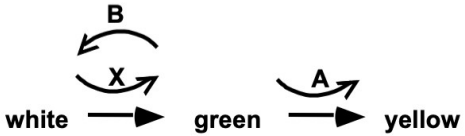
= 9: 3: 4

Dominant epistasis produces ratios of 12:3:1 or 13:3

12:3:1---A dominant allele in one gene, B, masks the contribution of a second gene, A, (blocks color formation) regardless of the A allele. Thus in bb individuals the A- and aa genotypes can express themselves, resulting in a total of three different phenotypes.

Dominant epistasis: one possible mechanism

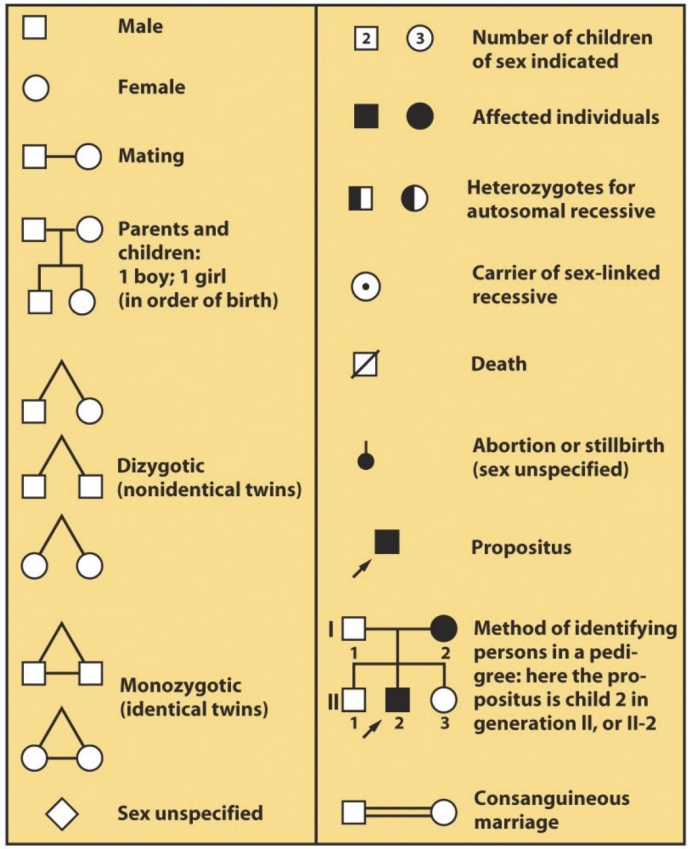
= 12 (white): 3(yellow): 1(green)

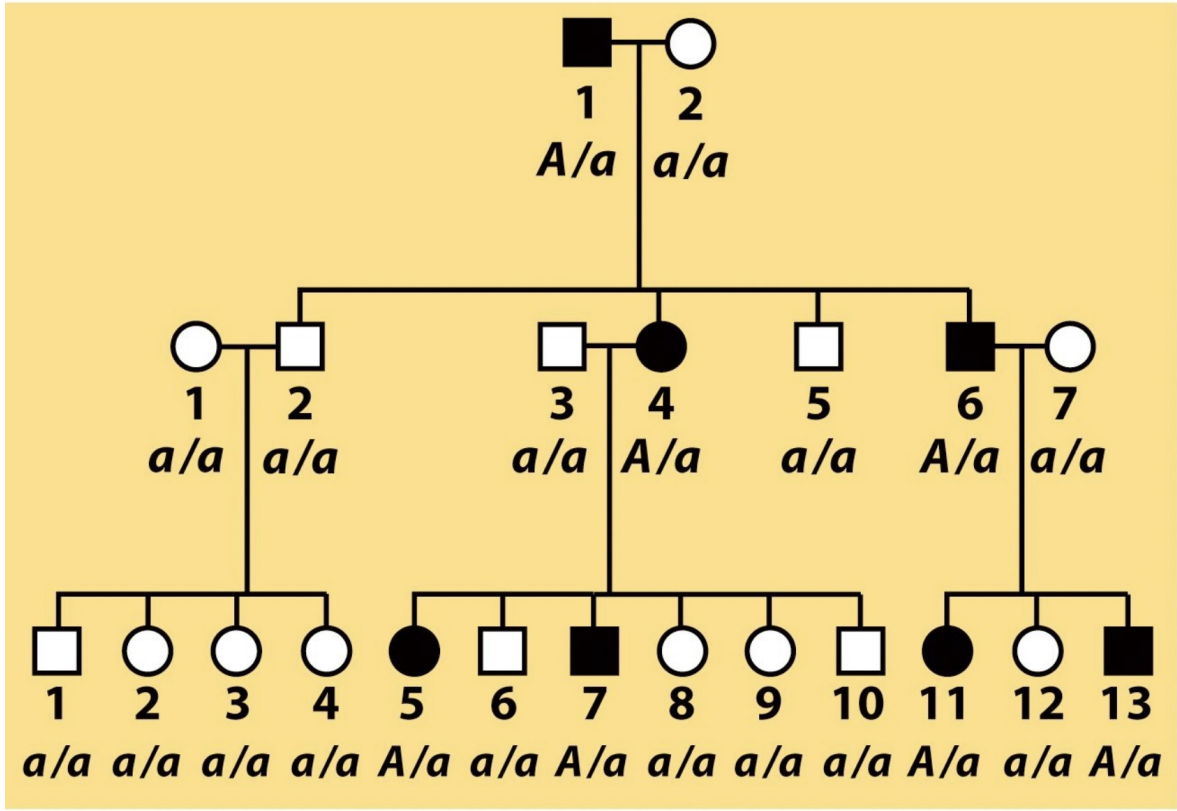


B acts to inhibit the processing of a white precursor into a green product.

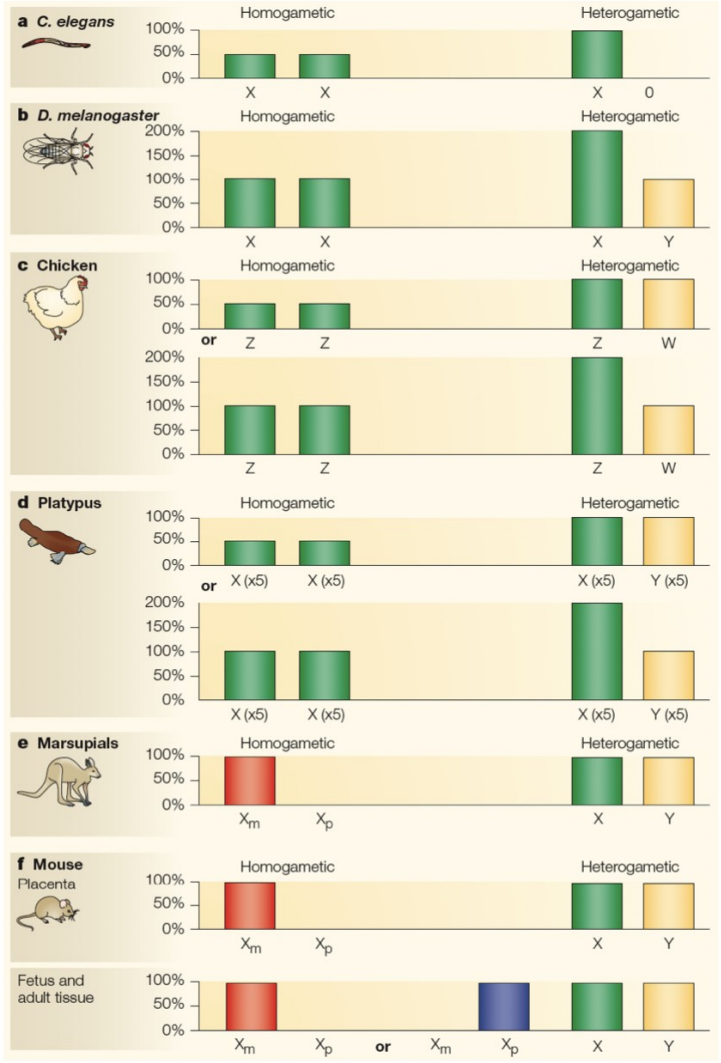
In the absence of the B gene product the A product processes the green precursor into a yellow product.

Pedigrees


Male
Female
Mating
Parents and children: 1 boy; 1 girl (in order of birth)
Dizygotic (nonidentical twins)
Monozygotic (identical twins)
Sex unspecified
Number of children of sex indicated
Affected individuals
Heterozygotes for autosomal recessive
Carrier of sex-linked recessive
Death
Abortion or stillbirth (sex unspecified)
Propositus
Method of identifying persons in a pedigree: here the propositus is child 2 in generation II, or II-2
Consanguineous marriage


1 A/a
2 a/a
1 a/a
2 a/a
3 a/a
4 A/a
5 a/a
6 A/a
7 a/a
1 a/a
2 a/a
3 a/a
4 a/a
5 A/a
6 a/a
7 A/a
8 a/a
9 a/a
10 a/a
11 A/a
12 a/a
13 A/a

Dosage compensation



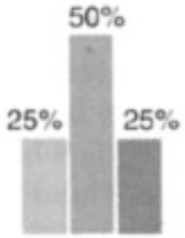
Quantitative Traits

The number of genes: n = 1

	A^1	A^0
A^1	2	1
A^0	1	0

1/4 show either extreme trait.

$$\frac{1}{4^n} = \frac{1}{4^1}$$



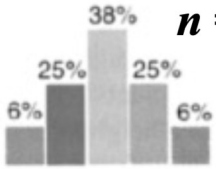
$n = 1$

The number of genes: n = 2

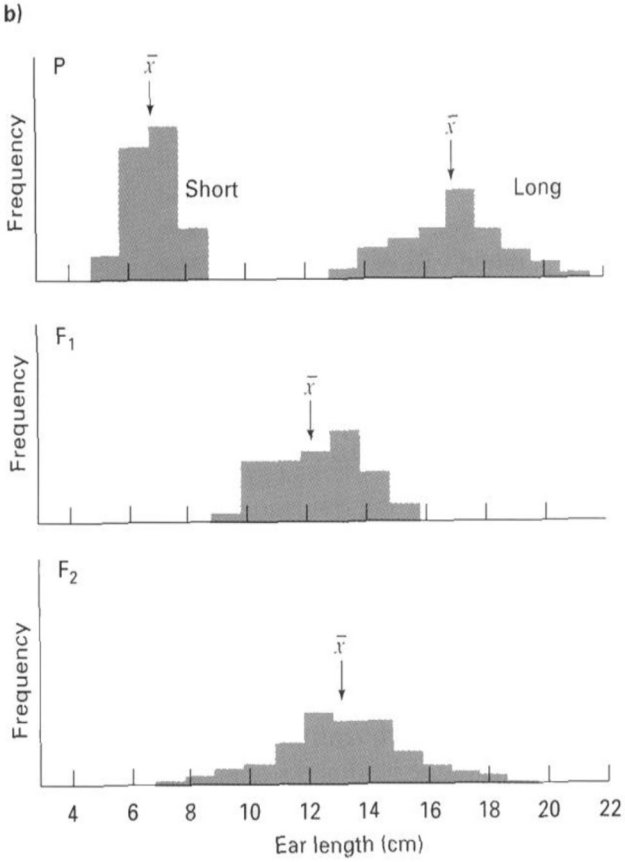
	A^1B^1	A^1B^0	A^0B^1	A^0B^0
A^1B^1	4	3	3	2
A^1B^0	3	2	2	1
A^0B^1	3	2	2	1
A^0B^0	2	1	1	0

1/16 show either Extreme trait.

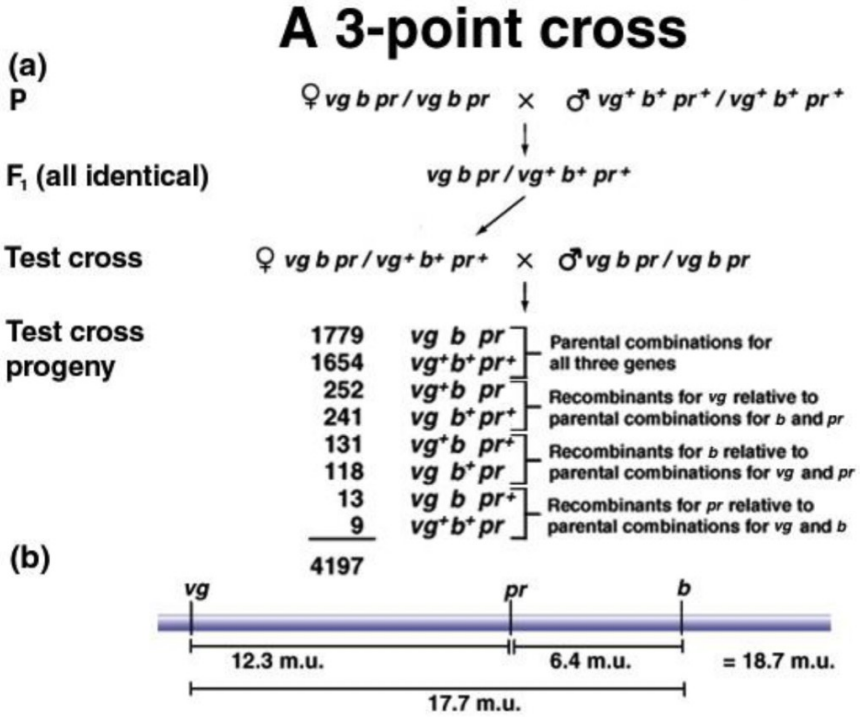
$$\frac{1}{4^n} = \frac{1}{16} = \frac{1}{4^2}$$



$n = 2$



Gene linkage and mapping



$$\frac{252 + 241 + 131 + 118}{4197} \times 100 = vg\text{-}b = 17.7 \text{ m. u.}$$

Genetic map distance (recombination frequency) = $\frac{\text{\# of recombinant gametes}}{\text{Total gametes}} \times 100$

Genetic map distance measured in centiMorgans (cM)

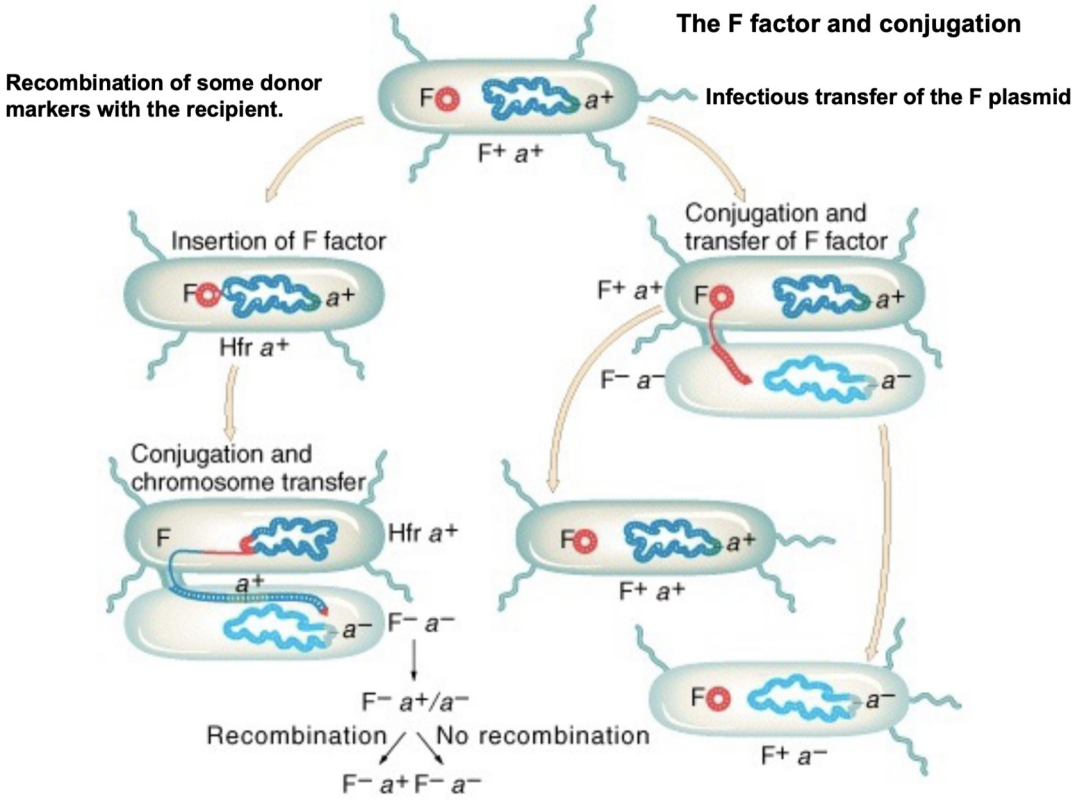
Chi-squared test

- **First determine the number of each phenotype that have been observed and how many would be expected given basic genetic theory.**
- **Then calculate the chi-square statistic using this formula.**
- **The "X" is the Greek letter chi; the "∑" is a sigma; it means to sum the following terms for all phenotypes. "obs" is the number of individuals of the given phenotype observed; "exp" is the number of that phenotype expected from the null hypothesis.**
- **Note that you must use the <u>number</u> of individuals, the counts, and NOT proportions, ratios, or frequencies.**

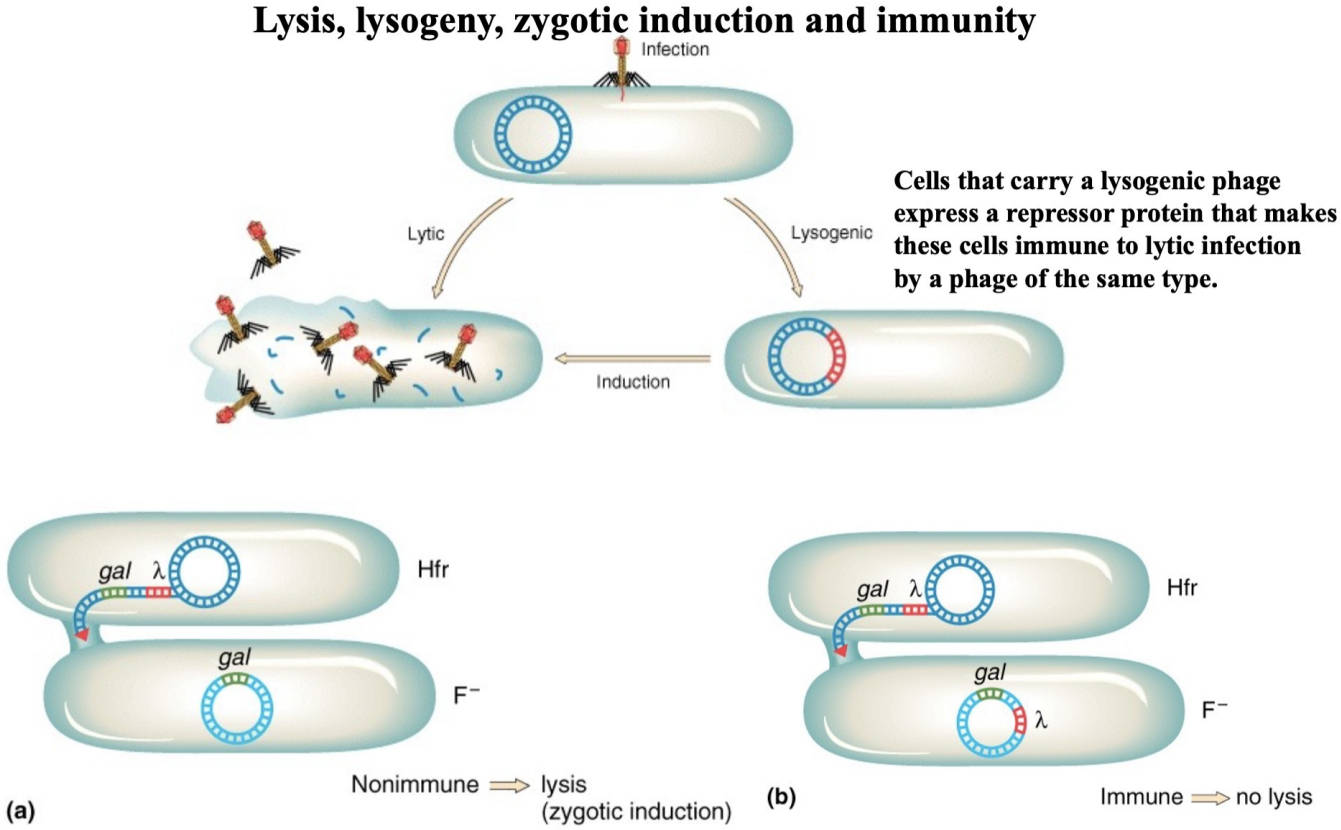
Formula

$$X^2 = \sum \frac{(obs - \exp)^2}{\exp}$$

Gene transfer

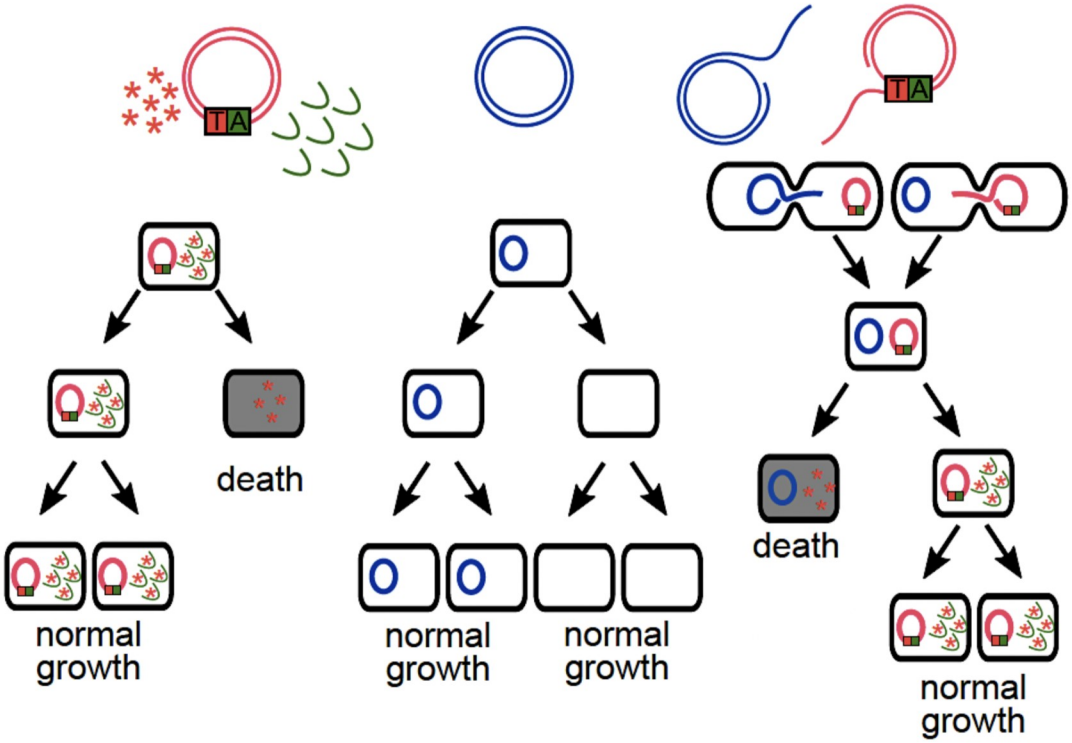


Phages

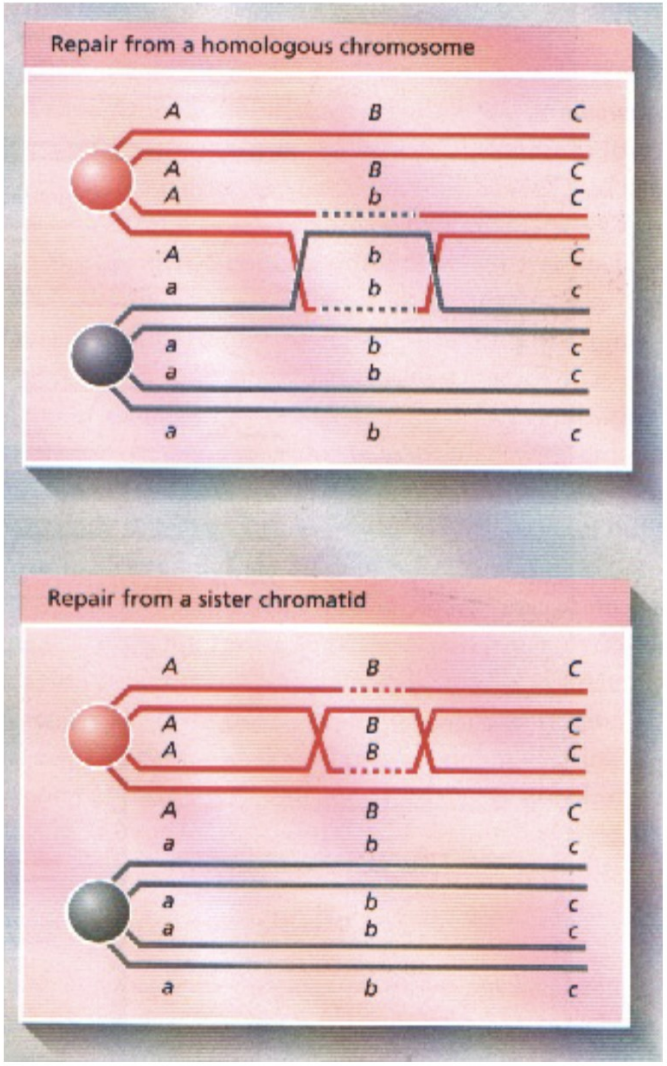

Lysis, lysogeny, zygotic induction and immunity
Infection
Lytic
Lysogenic
Induction
Cells that carry a lysogenic phage express a repressor protein that makes these cells immune to lytic infection by a phage of the same type.
gal
λ
Hfr
F⁻
(a)
Nonimmune
lysis
(zygotic induction)
(b)
Immune
no lysis

Toxin-antidote cassettes

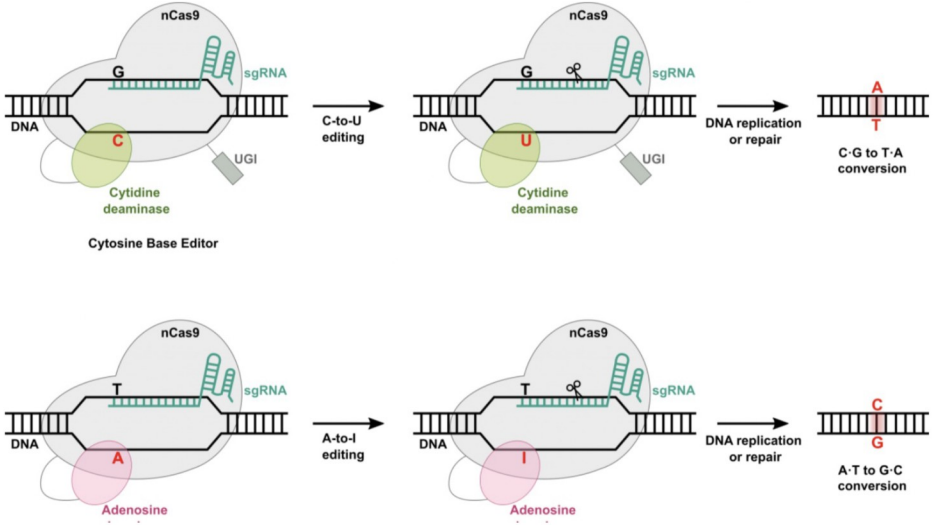
TA cassettes "encourage" their own transmission and kick plasmids of the same incompatibiity group that lack them out of the population

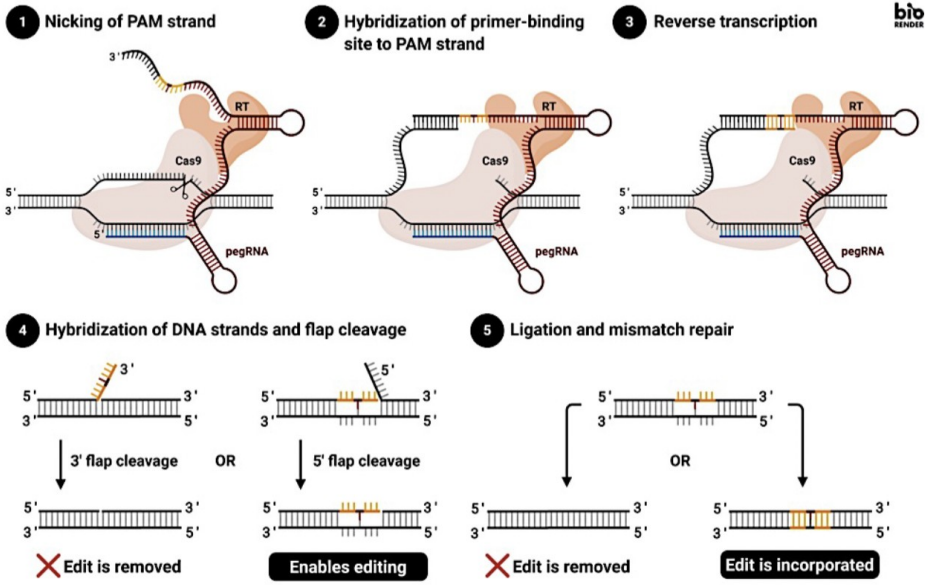


Recombination

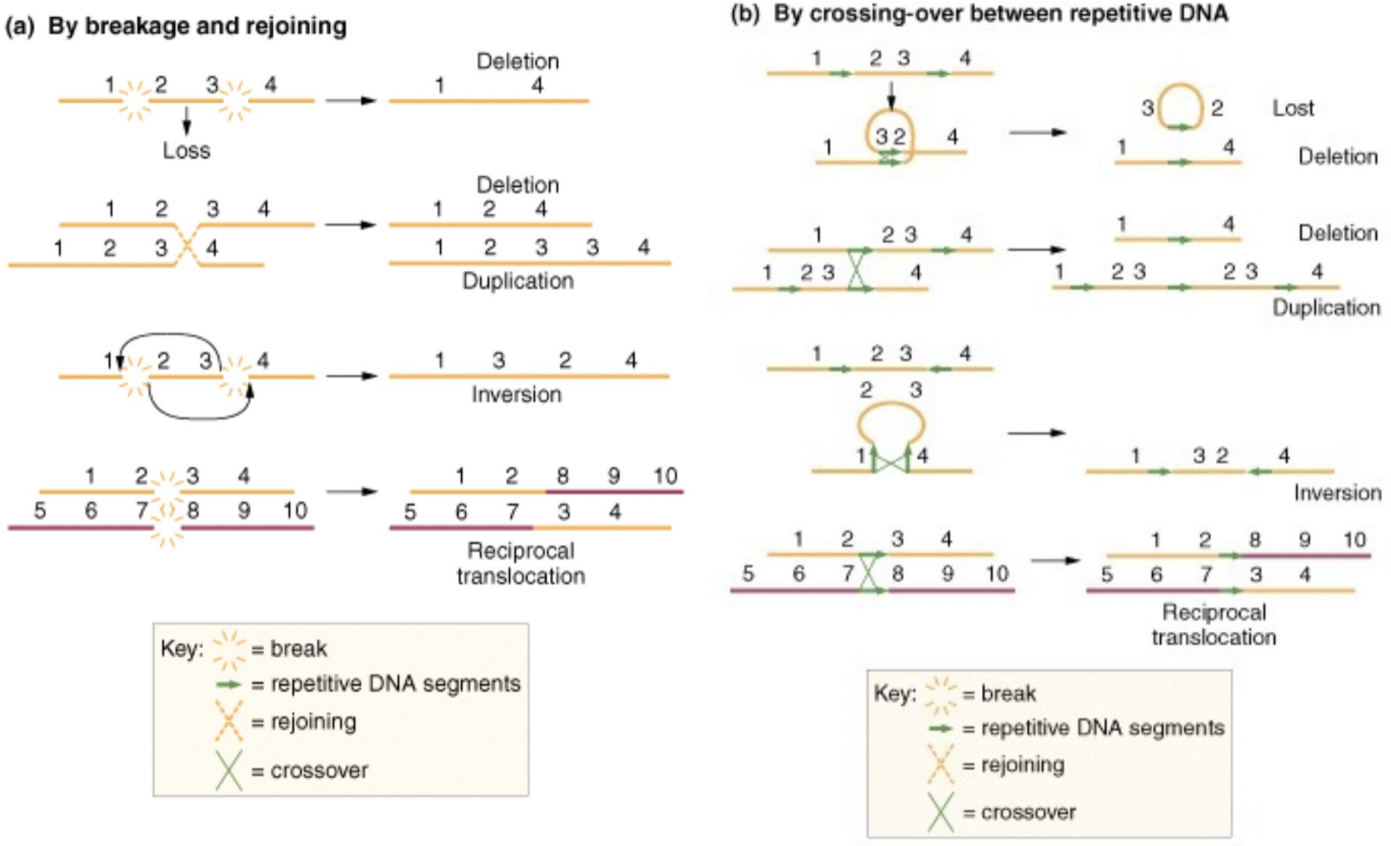


Gene editing: CRISPR

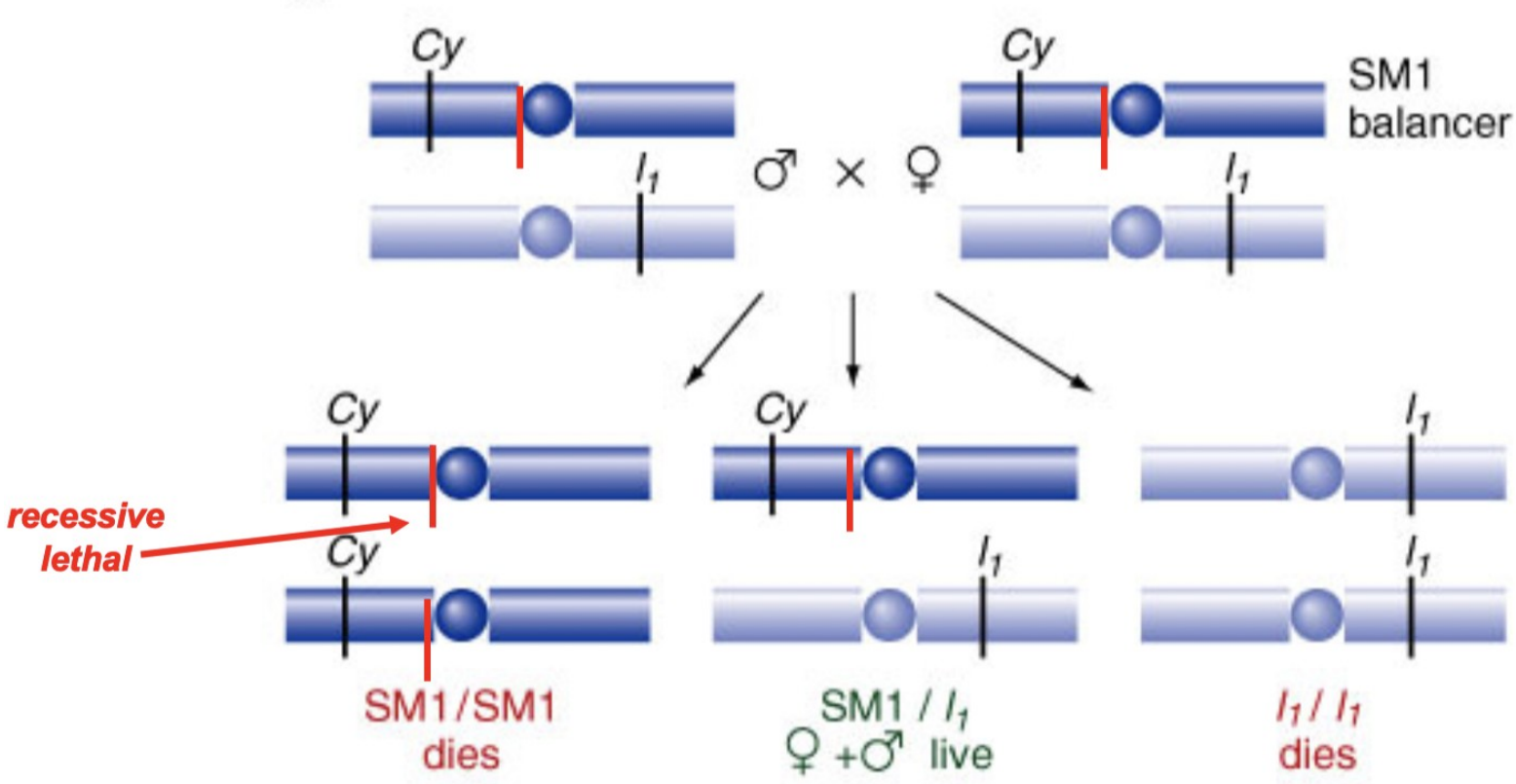




Chromosomal rearrangements

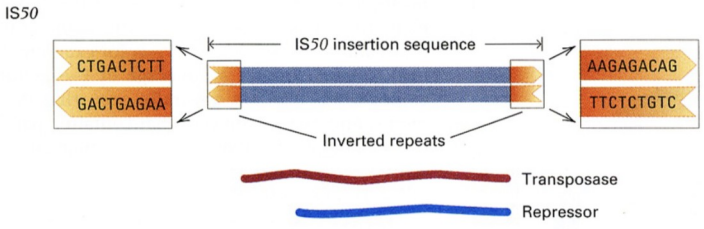


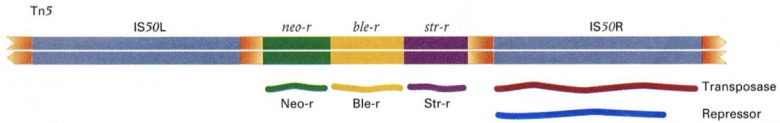
Balancer chromosomes

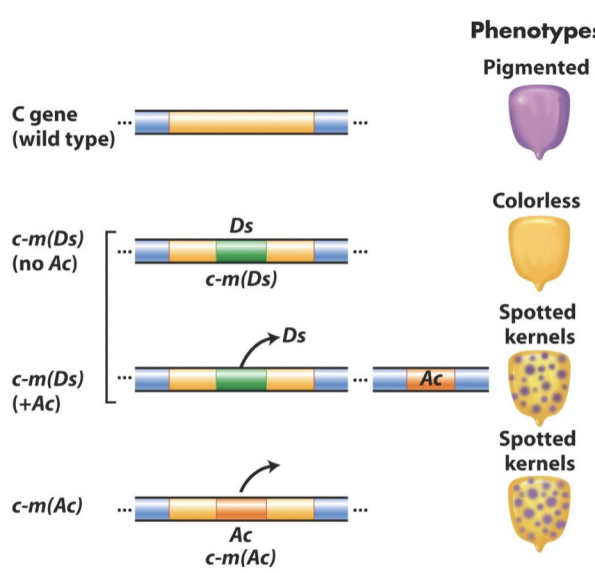


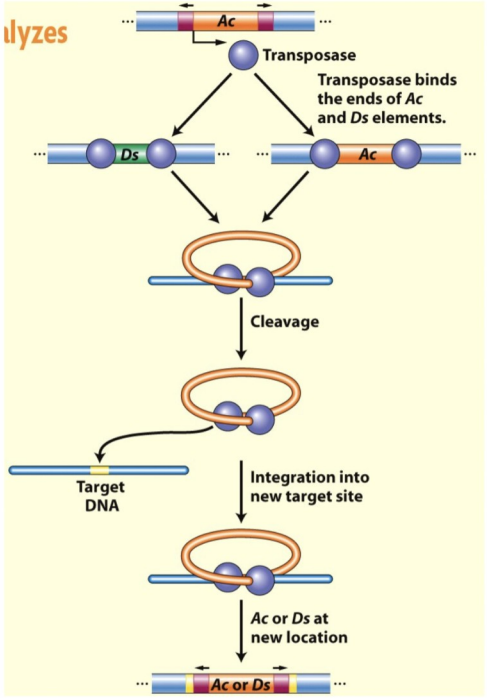
Transposons

- Recommend reviewing P elements









Transposon art. Mobile genetic elements caused these prized color patterns in morning glories.