

# **Mendel's Laws**

## **Haldane's Mapping Formula**

Math 186 / Math 283

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# Gregor Mendel (1822-1884)

- In 1857-1865, he grew 28000 pea plants and recorded 7 *traits* (also called *characters*) for each plant:

| Trait                  | Phenotype       |                  |
|------------------------|-----------------|------------------|
|                        | <i>Dominant</i> | <i>Recessive</i> |
| <i>Seed shape</i>      | round (R)       | wrinkled (r)     |
| <i>Seed color</i>      | yellow (Y)      | green (y)        |
| <i>Pod shape</i>       | inflated (I)    | constricted (i)  |
| <i>Pod color</i>       | green (G)       | yellow (g)       |
| <i>Flower color</i>    | purple (P)      | white (p)        |
| <i>Flower position</i> | axial (A)       | terminal (a)     |
| <i>Height</i>          | tall (T)        | short (t)        |



- He kept track of traits in parents and offspring through many generations over all the years of experiments.

## Mendel's model of inheritance (using modern terminology)

- Each trait is determined by a *gene*.
- Each gene comes in 2 possible versions, called *alleles*.
- Each individual has two of each gene.  
(Cells are *diploid*.)

## Example for height and pea shape

| Trait      | Phenotype       |                  |
|------------|-----------------|------------------|
|            | <i>Dominant</i> | <i>Recessive</i> |
| Seed shape | round (R)       | wrinkled (r)     |
| Height     | tall (T)        | short (t)        |

- An individual may have *genotype* TTRr.
- Two copies of each gene: height TT, shape Rr.
- TT results in a tall plant.
- Rr: when both alleles are present, the *dominant* one wins, so the seed shape is round.
- *Genotype* TTRr gives *phenotype* tall and round.

# Terminology

- *Dominant*: If genotype is TT or Tt, plant is tall.  
*Recessive*: If genotype is tt, plant is short.  
The dominant allele is uppercase and the recessive allele is lowercase.
- *Homozygous*: both alleles same (TT or tt).  
*Heterozygous*: mixed alleles (Tt).
- TT: homozygous dominant  
tt: homozygous recessive  
Tt: heterozygous dominant

# Mendel's First Law

## Law of Segregation

- Half the *gametes* (eggs/sperm) an individual produces have one copy of the gene and half have the other copy.  
(Gametes are *haploid* – just one copy of each gene.)
  - **An individual with Rr:** half their gametes have R and the other half have r.
  - **An individual with RR:** half their gametes have the “first” R and half have the “second” R.  
You can't tell them apart, so they are all R.

# Mendel's First Law

## Law of Segregation

- Individuals inherit one allele of each gene from each parent (one via the sperm, one via the egg).
- **Example:**  
If egg has genotype TR and sperm has genotype Tr, the offspring has genotype TTRr.

## Mendel's Second Law

### Law of Independent Assortment

- Different genes are inherited independently.
- **Example for two traits at a time:**
  - *Female genotype: TtRr*  
*Egg genotypes: TR, Tr, tR, tr*  
each in  $\frac{1}{4}$  of the egg cells.
  - *Male genotype: TTRr*  
*Sperm genotypes: TR, Tr*  
each in  $\frac{1}{2}$  of the sperm cells.



# Cross $TTRr \times TtRr$

## Punnett Square

- Table showing how genotypes in parents → genotypes in offspring.

|        |                 | Male            |                 |
|--------|-----------------|-----------------|-----------------|
|        |                 | <b>TR (1/2)</b> | <b>Tr (1/2)</b> |
| Female | <b>TR (1/4)</b> | TTRR (1/8)      | TTRr (1/8)      |
|        | <b>Tr (1/4)</b> | TTRr (1/8)      | TTrr (1/8)      |
|        | <b>tR (1/4)</b> | TtRR (1/8)      | TtRr (1/8)      |
|        | <b>tr (1/4)</b> | TtRr (1/8)      | Ttrr (1/8)      |

# Cross $TTRr \times TtRr$

## Punnett Square

- Table showing how genotypes in parents → genotypes in offspring.

|        |                 | Male            |                 |
|--------|-----------------|-----------------|-----------------|
|        |                 | <b>TR (1/2)</b> | <b>Tr (1/2)</b> |
| Female | <b>TR (1/4)</b> | TTRR (1/8)      | TTRr (1/8)      |
|        | <b>Tr (1/4)</b> | TTRr (1/8)      | TTrr (1/8)      |
|        | <b>tR (1/4)</b> | TtRR (1/8)      | TtRr (1/8)      |
|        | <b>tr (1/4)</b> | TtRr (1/8)      | Ttrr (1/8)      |

- Combine equivalent genotypes:  
 $P(\text{TTRr}) = 1/8 + 1/8 = 1/4$   
 $P(\text{TtRr}) = 1/8 + 1/8 = 1/4.$

# Cross TTRr x TtRr

## Phenotypes

| <i>Genotype</i>                                      | <i>Phenotype</i>      |
|--|-----------------------|
| TTRR (1/8)<br>TTRr (1/4)<br>TtRR (1/8)<br>TtRr (1/4) | Tall & round (3/4)    |
| TTrr (1/8)<br>Ttrr (1/8)                             | Tall & wrinkled (1/4) |

# Exceptions to Mendel's Laws

These laws are true for the genes Mendel observed, but exceptions to these laws in more experiments lead to many discoveries, including:

- Genes come in chromosomes. The law of independent assortment is only for genes on different chromosomes.
- Sex chromosomes pair XX (female mammals), XY (male mammals), breaking the 2 of each gene rule.
- Some genes have more than 2 alleles.  
Some traits are determined by combinations of multiple genes.  
Dominant / recessive rules can be more complex.

## Multiple alleles: ABO gene

- Human ABO gene determines blood type.
- Alleles A, B, i.

| <i>Genotype</i> | <i>Phenotype</i> |
|-----------------|------------------|
| AA or Ai        | blood type A     |
| BB or Bi        | blood type B     |
| AB              | blood type AB    |
| ii              | blood type O     |

# Thomas Morgan (1866-1945)

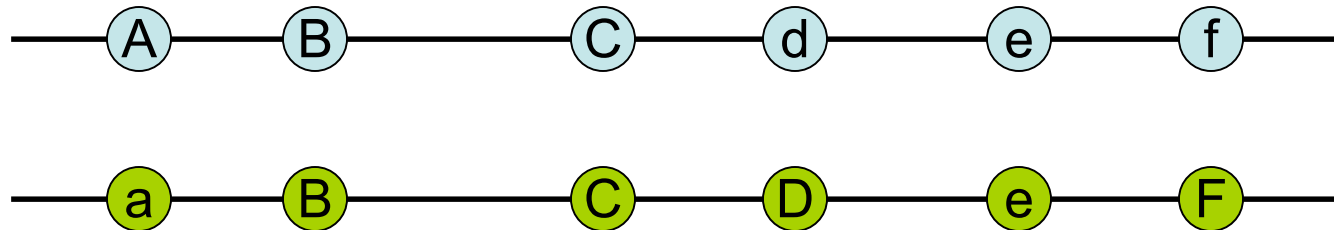
- Morgan studied *Drosophila melanogaster* (fruit flies).
- He found traits that did not combine in the predicted proportions. He called them *linked genes*.
- This lead him to discover chromosomes (1908).
- He won the Nobel Prize in Physiology or Medicine 1933 for this.  
The first U.S. born scientist to win a Nobel Prize.  
The first Nobel prize in genetics.



# Linked genes

- When gametes are formed in *meiosis*, the two copies of each chromosome may be mixed together via *crossovers*.

- **Mother's two copies of chromosome 1:**

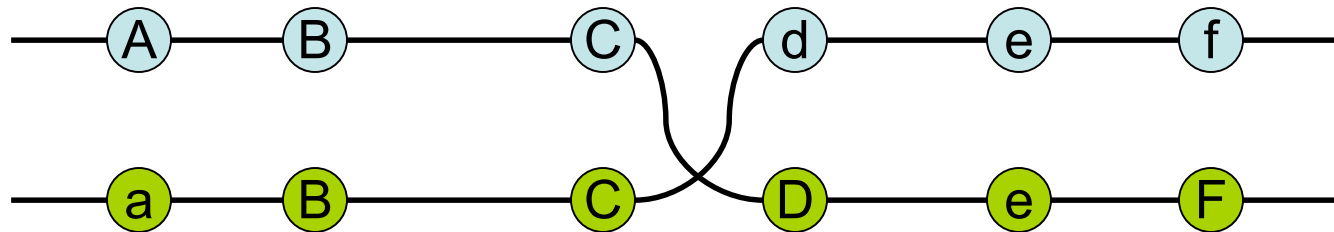


- Mother's autosomal (non-sex) cells are diploid: they have one copy of both.

# Linked genes

- When gametes are formed in *meiosis*, the two copies of each chromosome may be mixed together via *crossovers*.

- **Crossover produces two eggs:**



- Each egg has one of each chromosome. Each meiosis is different, though.



## Probabilities for linked genes

- Genes on the same chromosome do not sort independently.
- Closer genes have a higher probability of staying together. Example numbers:

| DF  | Df  | dF  | df  |
|-----|-----|-----|-----|
| .49 | .01 | .01 | .49 |

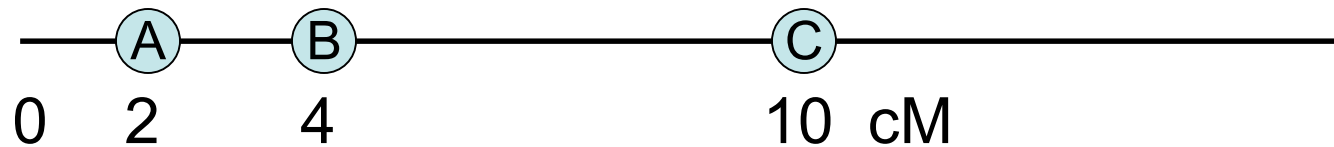
instead of all being 1/4.

- The two recombination probabilities are equal (.01) and the two nonrecombination probabilities are equal (.49).
- The *recombination rate* is  $r = .01 + .01 = .02 = 2\%$  instead of 50%.

# Mapping genes

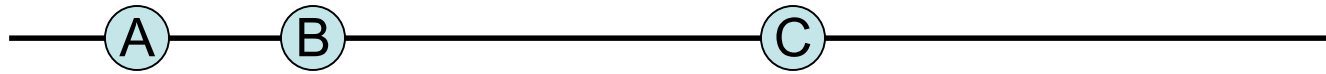
- We will make a scale along the chromosome in units called *centi-Morgans* (abbreviated cM) or *Morgans* (abbreviated M).
- The unit *Morgan* is defined so that crossovers occur at an average rate 1 per Morgan (M) or .01 per centi-Morgan (cM).
- If the recombination rate is *exactly*  $r=2\%$ , then D and F are *approximately* 2 centi-Morgans apart (2 cM) on the scale.
- We'll work out the exact formula.

# Crossover probabilities



- If there is an even number of crossovers between two sites, they wind up on the same gamete. The net effect is no recombination.
- If there is an odd number of crossovers between sites, they recombine.
- $AB$  = event “recombination between A & B”  
= “odd # of crossovers between A & B”
- $P(AB) = r_{AB}$
- Make analagous definitions for AC, BC.

# Recombination rates aren't additive



- Assume crossovers between A & B are independent of crossovers between B & C.\*
- $$P(AC) = P(AB \cap BC^c) + P(AB^c \cap BC)$$
$$= P(AB)P(BC^c) + P(AB^c)P(BC)$$
- $$r_{AC} = r_{AB}(1 - r_{BC}) + (1 - r_{AB})r_{BC}$$
$$= r_{AB} + r_{BC} - 2r_{AB}r_{BC}$$

**\*Note:** There is a phenomenon called *crossover interference*, which prevents crossovers from occurring too close to each other. There are more complicated formulas for that.

# Haldane's Mapping Function

- $r$  = recombination rate, on a scale from 0 to  $\frac{1}{2}$  .
- $d$  = distance in Morgans (1 M = 100 cM).

$$r = \frac{1}{2}(1 - e^{-2d})$$

$$d = -\frac{1}{2}\ln(1 - 2r)$$

- $r$  is often on a scale from 0% to 50%, and  $d$  is often in centi-Morgans.  
**They need to be converted to the other scales to use those formulas.**

# Haldane's Mapping Function

- **What is the distance if the recombination rate is 2%?**

- $r = 2\% = .02$

$$\begin{aligned}d &= -\frac{1}{2} \ln(1 - 2(.02)) \\ &= -\frac{1}{2} \ln(.96) = 0.02041 \text{ M}\end{aligned}$$

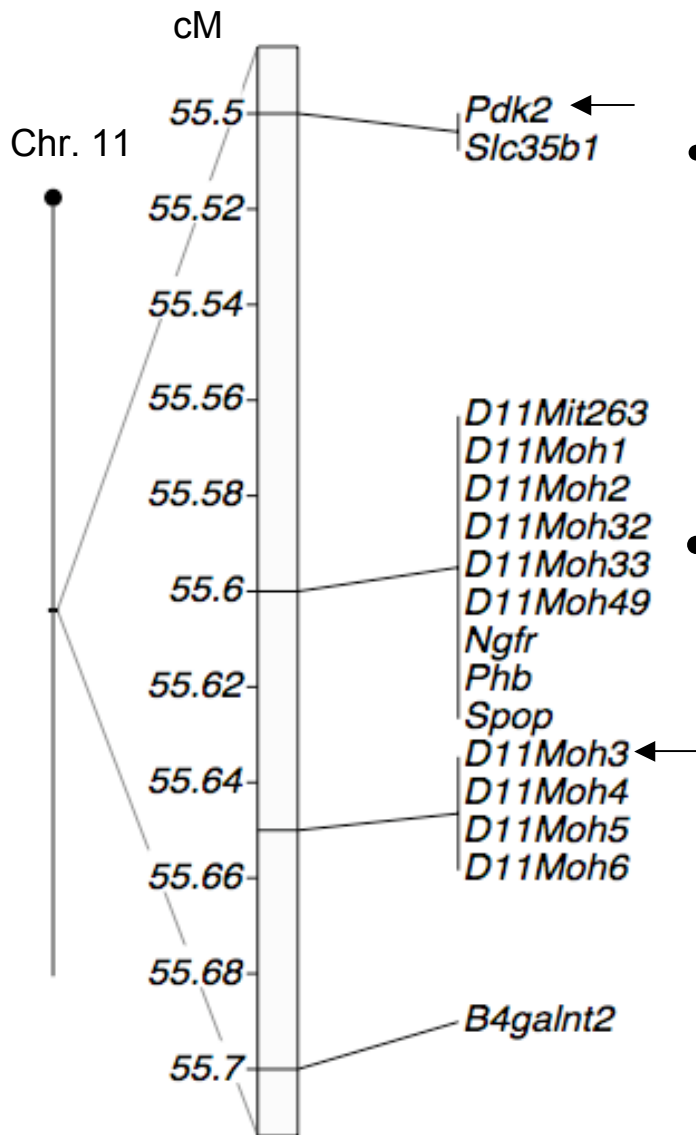
so  $d = 2.041 \text{ cM}$ .

- For small values,

$$r \text{ (0 to } \frac{1}{2} \text{ scale)} \approx d \text{ (in Morgans)}$$

$$r \text{ (% scale)} \approx d \text{ (in centi-Morgans)}$$

# Mouse linkage map



- Distance between *Pdk2* and *D11Moh3*:

$$d = 55.65 - 55.50 = 0.15 \text{ cM}$$

$$= 0.0015 \text{ M}$$

(use the absolute value)

- Recombination rate

$$r = \frac{1}{2} (1 - e^{-2(0.0015)})$$

$$= 0.001497$$

$$= 0.1497\%$$

Mouse chr. 11: 55.50-55.70 cM.

Linkage map obtained from Mouse Genome Database (MGD),  
The Jackson Laboratory, Bar Harbor, Maine. Feb. 17, 2008.

<http://www.informatics.jax.org>