COMPLEX PATTERNS OF INHERITANCE
- All or nearly all traits are influenced by many genes
- Mendel studied true-breeding strains that differed with regard to only one gene
- Gene interaction – a single trait is controlled by 2 or more genes, each of which has 2 or more alleles
Epistasis

- Alleles of one gene mask the expression of the alleles of another gene.
- Often arise because 2 or more different proteins involved in a single cellular function.
Types of traits

- Discrete or discontinuous
  - Clearly defined phenotypic variants
  - Purple or white flowers, red or white eyes

- Continuous or quantitative
  - Majority of traits
  - Show continuous variation over a range of phenotypes
  - Height, skin color, number of apples on a tree
  - Polygenic- several or many genes contribute to the outcome
  - Environment also plays a role
Bateson and Punnett’s Crosses of Sweet Peas Showed That Genes Do Not Always Assort Independently

- Independent assortment applies to genes on different chromosomes.
- What happens when alleles of different genes are on the same chromosome?
- Linkage - when 2 genes are close on the same chromosomes, they tend to be transmitted as a unit
- Linked genes do not follow the law of independent assortment
Bateson and Punnet crossed sweet peas for flower color and pollen shape.

Unexpected results in $F_2$

- Offspring showed 4 phenotypes but not the 9:3:3:1 ratio expected.
- Offspring had much higher rates of parental phenotypes.
- Hypothesis of independent assortment rejected.
**HYPOTHESIS** The alleles of different genes assort independently of each other.

**STARTING MATERIALS** True-breeding sweet pea strains that differ with regard to flower color and pollen shape.

<table>
<thead>
<tr>
<th>Step</th>
<th>Description</th>
<th>Experimental level</th>
<th>Conceptual level</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Cross a plant with purple flowers and long pollen to a plant with red flowers and round pollen.</td>
<td><img src="purple1.png" alt="Purple flowers, long pollen" /> × <img src="red2.png" alt="Red flowers, round pollen" /></td>
<td>$PPLL \times ppLl$</td>
</tr>
<tr>
<td>2</td>
<td>Observe the phenotypes of the $F_1$ offspring.</td>
<td><img src="purple1.png" alt="Purple flowers, long pollen" /></td>
<td>$PpLl$</td>
</tr>
<tr>
<td>3</td>
<td>Allow the $F_1$ offspring to self-fertilize.</td>
<td><img src="purple1.png" alt="Purple flowers, long pollen" /> × <img src="purple1.png" alt="Purple flowers, long pollen" /></td>
<td>Meiosis $PL$ and $pl$ gametes — more frequent $Pf$ and $pL$ gametes — less frequent</td>
</tr>
<tr>
<td>4</td>
<td>Observe the phenotypes of the $F_2$ offspring.</td>
<td><img src="purple1.png" alt="Purple flowers, long pollen" /> : <img src="purple2.png" alt="Purple flowers, round pollen" /> : <img src="red1.png" alt="Red flowers, long pollen" /> : <img src="red2.png" alt="Red flowers, round pollen" /></td>
<td>Fertilization $F_2$ offspring having phenotypes of purple flowers, long pollen or red flowers, round pollen occurred more frequently than expected from Mendel’s law of independent assortment.</td>
</tr>
</tbody>
</table>

**THE DATA**

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Purple flowers, long pollen</td>
<td>15.6</td>
</tr>
<tr>
<td>Purple flowers, round pollen</td>
<td>1.0</td>
</tr>
<tr>
<td>Red flowers, long pollen</td>
<td>1.4</td>
</tr>
<tr>
<td>Red flowers, round pollen</td>
<td>4.5</td>
</tr>
</tbody>
</table>
### THE DATA

<table>
<thead>
<tr>
<th>Phenotypes of F2 offspring</th>
<th>Observed number</th>
<th>Observed ratio</th>
<th>Expected number</th>
<th>Expected ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>Purple flowers, long pollen</td>
<td>290</td>
<td>15.0</td>
<td>240</td>
<td>9</td>
</tr>
<tr>
<td>Purple flowers, round pollen</td>
<td>19</td>
<td>1.0</td>
<td>80</td>
<td>3</td>
</tr>
<tr>
<td>Red flowers, long pollen</td>
<td>27</td>
<td>1.4</td>
<td>80</td>
<td>3</td>
</tr>
<tr>
<td>Red flowers, round pollen</td>
<td>85</td>
<td>4.5</td>
<td>27</td>
<td>1</td>
</tr>
</tbody>
</table>
Morgan found the same results in fruit flies

- Proposed the following:

1. When different genes are located on the same chromosome, the traits that are determined by those genes are most likely to be inherited together.

2. Due to crossing over during meiosis, homologous chromosomes can exchange pieces of chromosomes and create new combinations of alleles.
Morgan found the same results in fruit flies

3. The likelihood of crossing over depends on the distance between two genes.

- Crossovers between homologous chromosomes are much more likely to occur between two genes that are farther apart in the chromosome compared to two genes that are closer together.
Expected that all F₁ had gray bodies and straight wings- dominant traits

Mated with fly homozygous recessive for both traits (testcross) to produce F₂

Nonrecombinants or parental types – offspring's traits have not changed from parental generations

Recombinants or nonparental types – different combination of traits from parental generation
Recombinants are the result of crossing over
Recombination Frequencies Provide a Method for Mapping Genes Along Chromosomes

- Genetic linkage mapping or gene mapping or chromosome mapping
  - Used to determine linear order of genes that are linked to each other along the same chromosome

- Chart produced called a genetic linkage map

- Estimate relative distance between linked genes based on the likelihood that a crossover will occur between them
Recombination Frequencies Provide a Method for Mapping Genes Along Chromosomes

- Conduct a testcross
  - Map distance between 2 linked genes is the number of recombinant offspring divided by the total number of offspring times 100
  - One map unit is a 1% recombination frequency
<table>
<thead>
<tr>
<th>Map units</th>
<th>Mutant phenotype</th>
<th>Wild-type phenotype</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.0</td>
<td>Aristless, <em>al</em></td>
<td>Long aristae</td>
</tr>
<tr>
<td>13.0</td>
<td>Dumpy wings, <em>dp</em></td>
<td>Long wings</td>
</tr>
<tr>
<td>48.5</td>
<td>Black body, <em>b</em></td>
<td>Gray body</td>
</tr>
<tr>
<td>54.5</td>
<td>Purple eyes, <em>pr</em></td>
<td>Red eyes</td>
</tr>
<tr>
<td>67.0</td>
<td>Vestigial wings, <em>vg</em></td>
<td>Long wings</td>
</tr>
<tr>
<td>75.5</td>
<td>Curved wings, <em>c</em></td>
<td>Straight wings</td>
</tr>
<tr>
<td>104.5</td>
<td>Brown eyes, <em>bw</em></td>
<td>Red eyes</td>
</tr>
</tbody>
</table>
Extranuclear inheritance

- Some genes are not found on the chromosomes in the cell nucleus
- Mitochondria and chloroplasts contain their own genomes
  - Organelle genomes
  - Smaller than nuclear genome but important to phenotypes
Chloroplast genome

- Leaf pigment in four-o’clock plant does not obey Mendel’s law of segregation
- Pigmentation of offspring depended solely on pigmentation of maternal plant
  - Maternal inheritance
- Leaf pigmentation based on genetically different types of chloroplasts
- Chloroplasts of four-o’clocks inherited only through cytoplasm of the egg
Cross 1

All white offspring

Reciprocal cross of cross 1

All green offspring
Cross 2

♀ × ♂

Green, white, or variegated offspring

♀ × ♂

Reciprocal cross of cross 2

♀ × ♂

All green offspring
Normal proplastid will produce chloroplasts with a normal amount of green pigment.

Mutant proplastid will produce chloroplasts with very little pigment.

(a) Egg cell from a maternal parent with green leaves
(b) Egg cell from a maternal parent with white leaves
(c) Possible egg cells from a maternal parent with variegated leaves
In most species of plants, the egg cell provides most of the zygote’s cytoplasm, while the much smaller male gamete often provides little more than a nucleus.

- Chloroplasts are most often inherited via the egg.
- Most common transmission pattern in seed-bearing plants.

Biparental inheritance
- Both the pollen and the egg contribute chloroplasts to the offspring.

Paternal inheritance
- Only the pollen contributes these organelles.
- Most types of pine trees show paternal inheritance of chloroplasts.
Mitochondrial genomes

- Maternal inheritance is the most common pattern of mitochondrial transmission in eukaryotic species
  - Some species do exhibit biparental or paternal inheritance
- 37 genes in most mammalian mitochondrial genomes
- Mutations in human mitochondrial genes can cause a variety of rare diseases
<table>
<thead>
<tr>
<th>Disease</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leber’s hereditary optic neuropathy</td>
<td>Caused by a mutation in one of several mitochondrial genes that encode electron-transport proteins. The main symptom is loss of vision.</td>
</tr>
<tr>
<td>Neurogenic muscle weakness</td>
<td>Caused by a mutation in a mitochondrial gene that encodes a subunit of mitochondrial ATP synthase, which is required for ATP synthesis. Symptoms involve abnormalities in the nervous system that affect the muscles and eyes.</td>
</tr>
<tr>
<td>Mitochondrial encephalomyopathy, lactic acidosis, and strokelike episodes</td>
<td>Mutations in mitochondrial genes that encode tRNAs for leucine and lysine. Symptoms include strokelike episodes, secretion of lactic acid into the bloodstream, seizures, migraine headaches, and lack of coordination.</td>
</tr>
<tr>
<td>Maternal myopathy and cardiomyopathy</td>
<td>A mutation in a mitochondrial gene that encodes a tRNA for leucine. The primary symptoms involve muscle abnormalities, most notably in the heart.</td>
</tr>
<tr>
<td>Myoclonic epilepsy and ragged-red muscle fibers</td>
<td>A mutation in a mitochondrial gene that encodes a tRNA for lysine. Symptoms include epilepsy, dementia, blindness, deafness, and heart and kidney malfunctions.</td>
</tr>
</tbody>
</table>
Epigenetic inheritance

- Modification of a gene or chromosome during egg formation, sperm formation, or early stages of embryo growth alters gene expression in a way that is fixed during an individual’s lifetime.

- Permanently affect the phenotype of the individual, but they are not permanent over the course of many generations and they do not change the actual DNA sequence.
  - X inactivation
  - Genomic imprinting
X inactivation

- One X chromosome in the somatic cells of female mammals is inactivated

- 2 lines of evidence
  - Barr bodies are found in female but not male cat cells
  - Calico cat coat color pattern
Calico cat coat color pattern

- Calico pattern is explained by the permanent inactivation of one X chromosome in each cell that forms a patch of the cat’s skin
- X-linked gene for coat color
  - orange allele, $X^O$ and a black allele, $X^B$.
  - Heterozygous female cat will be calico
- At an early stage of embryonic development, one of the two X chromosomes is randomly inactivated in each of the cat’s somatic cells, including those that will give rise to the hair-producing skin cells
- A female that is heterozygous will have one or the other X inactivated in different groups of cells resulting in patches of black and orange fur
(a) Calico cat

1. In the early embryo, all X chromosomes are initially active.

2. In each embryonic cell, random inactivation occurs for one of the X chromosomes, which becomes a Barr body.

3. As development proceeds, the pattern of X inactivation is maintained during cell division.

(b) Process of X inactivation

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