Hello everybody, I hope you survived your first genetics exam! We all may be at slightly different paces for this next unit, but I will make sure that all necessary chapters are being covered! If you ever can’t find material for the section you are covering, check the **keywords** associated with the week’s resource.

Remember: the Tutoring Center offers free individual and group tutoring for this Genetics. Our Group Tutoring sessions will be Thursdays from 5:15-6:15 PM at the Sid Rich basement, room 75! You can reserve a spot at [https://baylor.edu/tutoring](https://baylor.edu/tutoring). I hope to see you there!

**Keywords:** Testcross, Linked Genes, Heritability, Chromosome

### Topic of the Week: Three Point Testcrosses (7.3)

**Three-Point Testcross:** a single testcross used to show a double crossover

**Why:** use a gene in between 2 loci of crossovers

\[
\begin{array}{ccc}
A & B & C \\
\downarrow & & \\
\Lambda x & B & x & C \\
a & b & c
\end{array}
\]

\[
\begin{array}{cccccccc}
A & B & C & a & B & C & A & b & c \\
\downarrow & & & a & b & c & a & B & c & a & B & c & a & b & c
\end{array}
\]

**Gametes:** ^nonrecombinant^ ^single crossover^ ^double crossover^

**How:** follow the following steps to solve the position of genes and

**Ex.** In a three point testcross of genes A, C and Dc, a true breeding recessive male is crossed with a heterozygous female. The resulting cross yields 1000 offspring:

1. Write out genotypes or phenotypes of offspring and categorize them by crossover (on noncrossover) pairs
   a. The **double crossover** (DCO) will be the smallest number of progeny
   b. The **non-recombinant** group will be the largest number of progeny
2. Locate find the middle gene by comparing the DCO with the nonrecombinant

<table>
<thead>
<tr>
<th>Genotype (not including the constant ( \Lambda _ _ _ Dc ))</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>( A^+ _ _ _ Dc^+ )</td>
<td>342</td>
</tr>
<tr>
<td>( A _ _ _ Dc )</td>
<td>323</td>
</tr>
</tbody>
</table>

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Where: the middle gene is the place where the DCO is different than the non-recombinant

<table>
<thead>
<tr>
<th>Genotype (not including the constant A C De)</th>
<th>Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>A+ De+ C+</td>
<td>342</td>
</tr>
<tr>
<td>A De C</td>
<td>323</td>
</tr>
<tr>
<td>A+ De+ C</td>
<td>79</td>
</tr>
<tr>
<td>A De C+</td>
<td>81</td>
</tr>
<tr>
<td>A+ De+ C+</td>
<td>76</td>
</tr>
<tr>
<td>A+ De C</td>
<td>74</td>
</tr>
<tr>
<td>A+ De+ C+</td>
<td>12</td>
</tr>
<tr>
<td>A De+ C</td>
<td>13</td>
</tr>
</tbody>
</table>

3. Rewrite the genotypes in proper order (ie with Dc+ in the middle)

4. Calculate the recombination frequency ($f_R$) for each crossover
   a. A - De for single and double crossovers
      i. $f_R = \frac{76+74+12+13}{1000} \times 100\% = 17.5\%$
   b. C - De for single and double crossovers
      i. $f_R = \frac{79+81+12+13}{1000} \times 100\% = 18.5\%$

5. Calculate coefficient of coincidence and interference

Coefficient of Coincidence: the frequency of DCO’s relative to total crossovers

$$ cc = \frac{\text{observed DCO}}{\text{expected DCO}} = \frac{12+13}{0.185 + 0.175 + 1000} = 0.772 $$

Interference: the presence of one crossover event tends to inhibit the occurrence of another

*larger values of I means greater interference between crossovers*

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**Highlight #1: Heritability and Selection (24.3-4)**

**Heritability:** the proportion of *phenotypic variance* which can be explained by *genetic variance*

**Phenotypic Variance** ($V_p$): $V_p = V_G + V_E + V_{GE}$

- **Genetic variance** ($V_G$): $V_G = V_D + V_A + V_I$
  - **Dominant Genetic Variance** ($V_D$): variance due to the dominant allele
  - **Additive Genetic Variance** ($V_A$): variance due to additive alleles
  - **Additive Allele:** when the number of alleles at a given locus is proportional to the magnitude of a quantitative characteristic
- **Gene Interaction Variance** ($V_I$): variance from interactions among genes
- **Environmental variance** ($V_E$): variance in organisms’ environment
- **Gene-environment interaction** ($V_{GE}$): the role on the environment on genes in phenotype determination

*thus, $V_p = (V_D + V_A + V_I) + V_E + V_{GE}$*

**Broad-Sense Heritability** ($H^2$): $H^2 = \frac{V_G}{V_p}$

**Narrow-Sense Heritability** ($h^2$): $h^2 = \frac{V_A}{V_p}$

**Artificial Selection:** man-made selection for specific characteristics

- **Response to Selection:** the extent of selected character change in a generation ($R$) $\rightarrow R = h^2 \times S$
  - **Selection Differential:** the difference between the selected populations’ mean and that of the total population for the characteristic

**Highlight #2: Chromosomal Mutations (8.2-4)**

**Chromosomal Mutation:** changes that vary the number and/or structure of chromosomes within an individual

- **Rearrangements:** changes in the overall structure of individual chromosomes
  - **Unequal Crossing Over:** misalignment of chromosomes in *prophase 1* causes a deletion and insertion
  - **Duplication:** mutation where part of the chromosome is copied (in tandem, displaced, in reverse or segmentally displaced)
    *changes *gene dosage*
  - **Deletion:** loss of a chromosome section (often causing intact segment to loop out at prophase)
  - **Pseudodominance:** when a deletion removes a wild type allele at a locus, where recessive allele is unmasked (ie. it appears to be dominant)

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Ben Fitch

**Haploinsufficient Genes:** one copy of a gene is not enough to give a wild-type phenotype

*Deletions may reveal abnormal phenotypes at this locus

**Inversion:** chromosome segment is turned 180°

Paracentric: does not incorporate centromere → **nonviable** recombinants
Pericentric: does incorporate centromere → **nonviable** recombinants

*Note:* may cause homologs to knot/tear in anaphase

**Translocation:** movement of genetic material between **non-homologs**

Non-reciprocal: unequal exchange of chromosomal segments
Reciprocal: equal exchange

Robertsonian Translocation:
reciprocal translocation between two acrocentric chromosomes (exchange of long (q) and short (p) arms) where the smaller chromosome is functionally deleted

**Aneuploidy:** change in the number of individual chromosomes (Robertsonian Translocations or Nondisjunction)

**Nullisomy** (2n-2): loss of two non-homologous chromosomes

**Monosomy** (2n-1): loss of one individual chromosome

**Trisomy** (2n+1): gain of one individual chromosome

**Trisomy 21 (Down Syndrome):** developmental and physical delays

Primary: caused by nondisjunction in **Anaphase II** (2n+1 = 47)

Familial: caused by a robertsonian translocation between chromosomes 14 and 21 (2n = 46)

https://www.youtube.com/watch?v=eruPJS_guNE

**Tetrasomy** (2n+2): gain of two non-homologous chromosomes

**Polyploidy:** change in the number of sets of chromosomes (ex. 3n, 4n, 5n, 7n, etc.)

Autopolyploid: 2 sets come from the same species → Infertile

Allopolyplloid: 2 sets from different species → Infetile F1 hybrid undergoes asexual reproduction, producing fertile F2

*Generally, even polyploids are more fertile than odd polyploids

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**Week 5 Concept Check:**

1. T/F an individual three point testcross has an interference of 0.6, meaning that one crossover tends to encourage an additional crossover at another locus

2. A herd of bulls is selected for horn length. The average size of a bull horn is 14.8 cm.
a. If a group of bulls with 16 centimeter horns are selected, what is the response to selection?
   i. $V_a: 0.2$
   ii. $V_d: 0.4$
   iii. $V_i: 0.1$
   iv. $V_e: 0.1$
   v. $V_{ge}: 0.2$

b. What is the new length of horn in the herd?

3. In G1, an individual had homologous chromosomes (1) ABCD*EFGHI and (2) ABCD*EFGHI. In Anaphase 2, these chromosomes are (1) ABCD*EFGHIGHI and (2) ABCD*EF. What likely happened (select the best answer)
   a. An inversion
   b. Aneuploidy
   c. Unequal crossing over
   d. A deletion

4. In G1, an individual had non-homologous chromosomes (1) ABCD*EFGHI and (2) RSTU*VWXYZ. What type of exchange occurred if these chromosome are (1) D*EFGHI and (2) ABCRSTU*VWXYZ in Telophase 1?
   a. Robertsonian translocation
   b. Inversion
   c. Reciprocal translocation
   d. Non-reciprocal translocation

5. What type of chromosomal mutation is shown? AABCD*GHE → AAG*DCBHE
   a. Paracentric inversion
   b. Pericentric inversion
   c. Haploinsufficiency
   d. Reverse translocation

6. Length in a species of blind sharks is determined at 6 loci by additive alleles. A shark, aabbccddeeFF, is 1.8m long and another, AabbCeddEeFF, is 2.3m. How long would a shark aaBbCCddEeFF be?
   a. 2.8 m
   b. 2.9 m
   c. 2.4 m
   d. 2.3 m
THINGS YOU MAY STRUGGLE WITH:

1. In a testcross evaluating recombination frequency, the recombinant progeny will be those which exist in the smallest numbers.
2. If the recombination frequency between two genes is $\geq 50\%$, the two are treated as two separate linkage groups, or on separate chromosomes, because they assort independently.
3. Heritability is a measure on a population scale, and is thus limited because it cannot be applied to individuals. Additionally, it does not measure the degree to which traits are genetically determined.
4. Translocation is not crossing over because it involves exchange between non-homologs.
5. Polyploidy means that at least one parent must have had nondisjunction of all chromosomes

CONGRATS: You made it to the end of the resource! Again, group tutoring will be every Thursday from 5:15-6:30 PM. You can reserve a spot at https://baylor.edu/tutoring. I hope to see you there!

Answers:
1. False
2. (parts)
   a. $R = 0.24\, \text{cm}$
      i. $S = 1.2$
         1. $V_p = 1$
         2. $h^2 = 0.2$
         3. $R = h^2 \times S$
         4. $R = 0.24\, \text{cm}$
   b. 15.04 cm
3. C
4. D
5. B
6. C

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