Week 5
Genetics: BIO-2306

The concepts this resource covers are the topics typically covered during this week of the semester. If you do not see the topics your particular section of class is learning this week, please take a look at other weekly resources listed on our website for additional topics throughout the semester.

We also invite you to look at the group tutoring chart on our website to see if this course has a group tutoring session offered this semester.

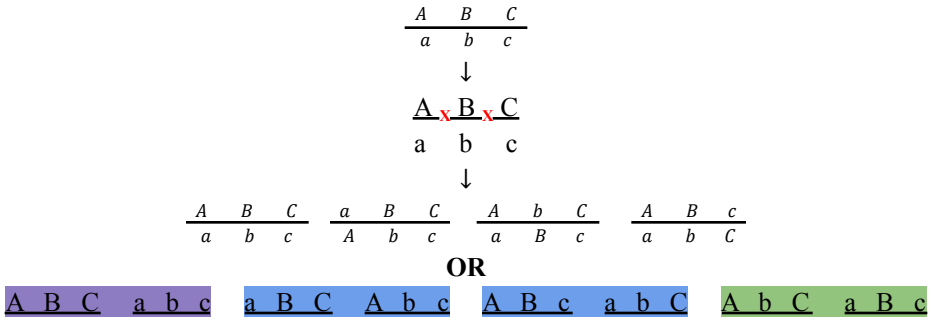
If you have any questions about these study guides, group tutoring sessions, private 30 minute tutoring appointments, the Baylor Tutoring YouTube channel or any tutoring services we offer, please visit our website www.baylor.edu/tutoring or call our drop in center during open business hours. M-Th 9am-8pm on class days 254-710-4135.

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



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

Genotype (not including the constant A C Dc)	**Number**
A+ C+ Dc+	342
A C Dc	323
A+ C+ Dc	12
A C Dc+	13
A+ C Dc+	79
A C+ Dc	81
A C+ Dc+	76
A+ C Dc	74

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

A+ C+ Dc+ A+ C+ Dc

A C Dc A C Dc+

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

Genotype (not including the constant A C Dc)	**Number**
A+ Dc+ C+	342
A Dc C	323
A+ Dc+ | C	79
A Dc | C+	81
A | Dc+ C+	76
A+ | Dc C	74
A+ | Dc | C+	12
A | Dc+ | C	13

4. Calculate the recombination frequency (f_R) for each crossover
   - **a.** **A - Dc** for single and double crossovers
     - *i.* $f_R = \frac{76+74+12+13}{1000} \text{x } 100\% = 17.5\%$
   - **b.** **C - Dc** for single and double crossovers
     - i. $f_R = \frac{79+81+12+13}{1000} \text{x } 100\% = 18.5\%$
5. Calculate **coefficient of coincidence** and **interference**

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

$$cc = \frac{observed\ DCO}{expected\ DCO} = \frac{DCO}{(A-dc) * (C=Dc) * total\ progeny} = \frac{12+13}{0.185 * 0.175 * 1000} = 0.772$$

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

*larger values of **I** means greater interference between crossovers*

I = 1.0 - cc = 0.228

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, $\mathbf{V_P = (V_D + V_A + V_I) + V_E + V_{GE}}$ *

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**) → $R = h^2 \times S$

Selection Differential: the difference between the selected populations' mean and that of the total population for the characteristic

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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)

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

*Delections 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

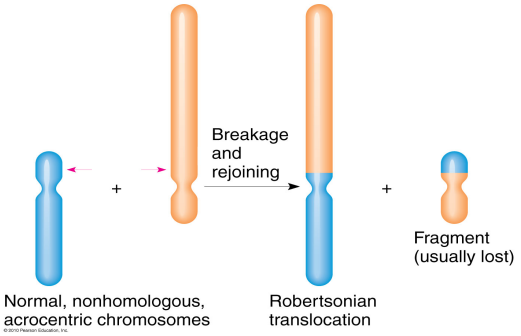
Note: may cause homologs to knot/tear in anaphase

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



Above: Robertsonian Translocation

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

Allopolyploid: 2 sets from different species → Infetile F_1 hybrid undergoes asexual reproduction, producing fertile F_2

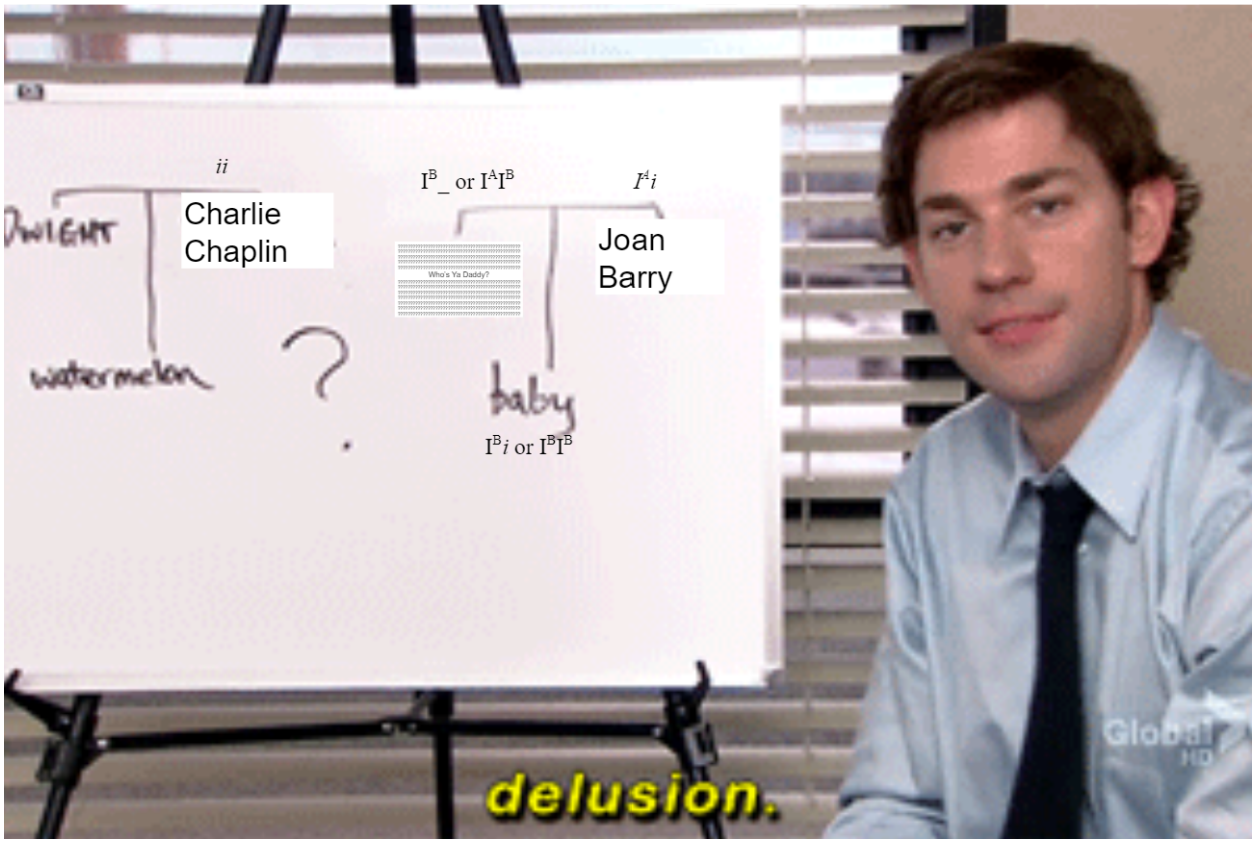
*Generally, *even* polyploids are more fertile than *odd* polyploids

Concept Check: *(Answers found on last page)*

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. Va: 0.2
        ii. Vd: 0.4
        iii. Vi: 0.1
        iv. Ve: 0.1
        v. Vge: 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, AabbCcddEeFF, 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 ≥ 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! Thanks for checking out these weekly resources! Don't forget to check out our website for group tutoring times, video tutorials and lots of other resources: www.baylor.edu/tutoring!
Answers to check your learning questions are below!

Answers:

1. **False**
2. (parts)
   - **a. R = 0.24 cm**
     - i. S = 1.2
       1. Vp = 1
       2. $h^2 = 0.2$
       3. $R = h^2 \times S$
       4. R = 0.24 cm
   - **b. 15.04 cm**
3. **C**
4. **D**
5. **B**
6. **C**