DIRECTIONS: Read each question carefully at the beginning of the exam period. Ask for help if the question is unclear. The number in parentheses by each question is the points for that question. Enough space is given for each question for a complete answer. Partial credit is given for partial answers. Please fill in your name and student ID on each page now!!

You may need the following section of the Chi-square table for p=0.05.

<table>
<thead>
<tr>
<th>d.f.</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chi-Square</td>
<td>3.84</td>
<td>5.99</td>
<td>7.82</td>
<td>9.49</td>
<td>11.07</td>
<td>12.59</td>
<td>14.07</td>
<td>15.51</td>
<td>16.92</td>
<td>18.31</td>
<td>19.68</td>
</tr>
</tbody>
</table>

You may also need this table:

- Proportion Selected (p)
- Selection Intensity (I)
- Standardized Selection Point (Z)

You may also need this table:

<table>
<thead>
<tr>
<th>Proportion Selected (p)</th>
<th>0.5</th>
<th>0.25</th>
<th>0.1</th>
<th>0.05</th>
<th>0.01</th>
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</thead>
<tbody>
<tr>
<td>Selection Intensity (I)</td>
<td>0.8</td>
<td>1.27</td>
<td>1.76</td>
<td>2.06</td>
<td>2.67</td>
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<tr>
<td>Standardized Selection Point (Z)</td>
<td>0</td>
<td>0.67</td>
<td>1.28</td>
<td>1.65</td>
<td>2.33</td>
</tr>
</tbody>
</table>

1. (9) Short Answer. Answer each of the following questions in the space provided. You will be counted off for explanations that are not succinct.
   a) What is assortative mating? What effect does it have on a population undergoing assortative mating?
   - Assortative mating is mating based on similarity of phenotypes. This leads to an increase in homozygosity for genes related to the characteristic, and loci linked to them.

   b) List three effects of a Founder Population.
   1. Allele frequencies are different from the original population
   2. Strong selection
   3. Inbreeding leading to increased homozygosity
   4. Random drift leading to loss of alleles
   5. Homozygosity of deleterious traits, possibly lowering population size

   c) During interphase, consider if we have a loop in the DNA that breaks. The cell’s repair mechanism fixes the DNA. There are three ways to “fix” the break, two of which lead to mutations. What are the two mutations and how does the DNA repair give that mutation?
   1. If the loop is left out of the repair, then the loop will be deleted.
   2. If the loop is repaired, but in the wrong orientation (backwards), then the region will be inverted.

   9
2. (6) The following are some statements concerning heritability. For each, indicate whether the statement is **TRUE** or **FALSE**.

   a) **TRUE** (FALSE) Heritability for any trait will be nearly the same for all or most subpopulations for a species.

   b) **FALSE** (TRUE) Heritability for a natural population is expected to be relatively high.

   c) **TRUE** (FALSE) Heritability is a measure of how important genes are to that trait.

3. (9) Following are six of the violations of Hardy-Weinberg populations. For each set of short term and long term results, indicate which mode of evolution best exemplifies them. If more than one seems to apply, choose the one that best fits the description.

   1. Inbreeding
   2. Assortative Mating
   3. Migration
   4. Mutation
   5. Selection
   6. Small Population Size

<table>
<thead>
<tr>
<th>Short Term Results</th>
<th>Long Term Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>4: Very small change in allele frequencies</td>
<td>Can lead to difference over a very long time</td>
</tr>
<tr>
<td>2: No change in allele frequencies</td>
<td>Increases homozygosity only at some loci</td>
</tr>
<tr>
<td>5: Can be quick change in allele frequencies</td>
<td>End frequencies depend on different viability</td>
</tr>
</tbody>
</table>

4. (15) In my hometown, we bred fleas for jumping distance (yes, it was a small town). The specific species used has a mean of 22.7 cm, with a standard deviation of 0.3 cm. We decided to improve the flea stock and used a mass selection scheme with 10% selection. From others, we know that heritability in the narrow sense to be 45%. **Give Units for your answers.**

   \[ M = 22.7 \text{ cm} \]
   \[ \sigma = 0.3 \text{ cm} \]

   a) \[ 23.28 \text{ cm} \] Give the mean of the fleas that are kept. \[ M + \sigma \]

   b) \[ 0.528 \text{ cm} \] Give the Selection Differential.

   c) \[ 22.9376 \text{ cm} \] Give the mean of the offspring for the next generation.
5. (10) An individual is heterozygous for an inversion as diagrammed below:

Normal Chromosome  
A B C D E F G

Inverted Chromosome  
A B F E D C G

a) This inversion is\[\text{Pericentric}\] Paracentric
b) Give the four chromatids that result when there is crossing over between C and D.

\[\begin{align*}
A B C D & \rightarrow E F G \\
A B F E & \rightarrow D C G \\
A B F E & \rightarrow D C G \\
G F E D & \rightarrow C G
\end{align*}\]

6. (12) We are interested in four traits located on one of the chromosomes for a species of field mouse. The linkage map is given below. The researcher will take a true breeding strain of mice with \text{Long Tail, Dark Color, Plain Ears, and Wide} and cross it with a true breeding strain of mice with \text{Short Tail, Light Color, Tufted Ears, and Narrow}. The resulting F\(_1\) will be test crossed. Give the expected frequency of the given types among the test cross offspring.

<table>
<thead>
<tr>
<th>Tail Length</th>
<th>Fur Color</th>
<th>Ears</th>
<th>Width</th>
<th>Dominant \ recessive</th>
</tr>
</thead>
<tbody>
<tr>
<td>Long</td>
<td>Dark</td>
<td>Tufted</td>
<td>Wide</td>
<td>3 \quad 5 \quad 4</td>
</tr>
<tr>
<td>Short</td>
<td>Light</td>
<td>Plain</td>
<td>Narrow</td>
<td>C=0.75</td>
</tr>
</tbody>
</table>

a) 0.485 \hspace{1cm} \text{Long Tail and Dark Color}

b) 0.01925 \hspace{1cm} \text{Dark Color, Plain Ears, and Narrow}

c) 0.0435 \hspace{1cm} \text{Light Color and Wide}

\[
\text{F}_1: \quad \begin{array}{cccccc}
\text{Long} & \text{Dark} & \text{Plain} & \text{Wide} \\
\text{Short} & \text{Light} & \text{Tufted} & \text{Narrow}
\end{array} \]
7. (6) Indicate the chromosomal mutation that is described in each situation. If more than one seems to apply, chose the one that best fits the description. Chromosomal mutations can be used more than one time.

1. Aneuploidy
2. Euploidy
3. Inversion
4. Translocation
5. Deletion
6. Duplication

1
Extra copies of ONE chromosome
2
Can cause a partial trisomy among the offspring, even if there is no recombination
2
Commercial Apples are an example

8. (12) Consider a population with the following genotypic frequencies:

0.5041 BB + 0.4118 Bb + 0.0841 bb

a) Give the allele frequencies for alleles B and b.

B 0.71
b 0.29

b) Assume that the mutation rate from B to b is 2x10^{-4} and from b to B is 3x10^{-4}. Give allele frequency for B in the next generation (do not round).

Freq(B) = 0.708667

c) Use the original population (part a). Assume that bb has a fitness of W=0.2, and Bb has a fitness of W=0.6. Compute the allele frequency for B for the next generation.

Freq(B) = 0.8173
9. (16) Experiments involving the venus fly trap are centered around creating linkage maps for three traits. The following are the results of the standard testcross of an F1 population. The results of the test cross were:

<table>
<thead>
<tr>
<th>Trap</th>
<th>Color</th>
<th>Stature</th>
<th>Number Observed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hair trigger</td>
<td>Red</td>
<td>Flat</td>
<td>15</td>
</tr>
<tr>
<td>Normal</td>
<td>Pink</td>
<td>Erect</td>
<td>23</td>
</tr>
<tr>
<td>Normal</td>
<td>Red</td>
<td>Flat</td>
<td>3,118</td>
</tr>
<tr>
<td>Hair trigger</td>
<td>Pink</td>
<td>Erect</td>
<td>3,280</td>
</tr>
<tr>
<td>Hair trigger</td>
<td>Pink</td>
<td>Flat</td>
<td>551</td>
</tr>
<tr>
<td>Normal</td>
<td>Red</td>
<td>Erect</td>
<td>529</td>
</tr>
<tr>
<td>Normal</td>
<td>Pink</td>
<td>Flat</td>
<td>405</td>
</tr>
<tr>
<td>Hair trigger</td>
<td>Red</td>
<td>Erect</td>
<td>437</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td></td>
<td><strong>8,358</strong></td>
</tr>
</tbody>
</table>

a) The order of the loci on the chromosome is:
   i) Trap  Color  Stature
   ii) Color  Stature  Trap
   iii) Stature  Trap  Color

   **13.38 cM** Use the order given in a). Give the map distance between the leftmost trait and the center trait (include Units).

b) **0.6315** Regardless of the value you calculated in b), assume the recombination rates are 0.09 and 0.08. Find the coefficient of Coincidence.

c) **21**

10. (5) Circle **ALL** the mutations that are expected to have no effect on an individual with the mutation, but have a chance for a large effect on their offspring.

   a) Duplication
   b) Transposition
   c) Paracentric Inversion
   d) Pericentric Inversion
   e) Translocation