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) 0.5 0.25 0.1 0.05 0.01
- Selection Intensity (I) 0.8 1.27 1.76 2.06 2.67
- Standardized Selection Point (Z) 0 0.67 1.28 1.65 2.33

1. (15) Short Answer. Answer each of the following questions in the space provided. You will be counted off for explanations that are not succinct.

a) Give an example of an allopolyploid and an autopolyploid. Describe the differences between them with respect to origin and fertility.

   **Allopolyploid:** wheat, cotton...
   **Autopolyploid:** banana, apples...

   Allopolyploids are fertile and derived from two different species (usually through an autopolyplication event). Autopolyploids are infertile and are derived from manipulating or crossing within the same species (or closely related species).

b) What is a Founder Population? Give an example of a founder population in humans.

   A small population broken off from a large population and now colonizing a new place. Examples include the Amish in the US or the colonizers of Pitcairn Island.

c) Briefly describe why the following statement is false concerning heritability. Heritability estimates measure the degree to which a trait is determined by genes.

   **It measures how much genetic variability there is in the population compared to environmental variability.**
2. (5) Consider deletions of portions of a chromosome. In class, we discussed several ways that deletions are created. Describe one way a deletion can be formed and circle whether it will be a terminal or interstitial deletion.

Terminal: Ionizing radiation can break the DNA. Or stress breaks it.
Interstitial: Unequal recombination, Looping + Breaking

3. (15) We are interested in whether or not a certain gene (with alleles, T and t) in a population has Hardy-Weinberg proportions.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Observed</th>
<th>Expected</th>
<th>Chi-Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>TT</td>
<td>540</td>
<td>547.52</td>
<td>0.2959</td>
</tr>
<tr>
<td>Tt</td>
<td>278</td>
<td>302.97</td>
<td>2.0605</td>
</tr>
<tr>
<td>tt</td>
<td>56</td>
<td>43.50</td>
<td>3.5874</td>
</tr>
<tr>
<td>Total</td>
<td>874</td>
<td>873.99</td>
<td>5.9439</td>
</tr>
</tbody>
</table>

a) The allele frequencies are: T .7769 and t .2231
b) Complete the table.
c) Give the statistical conclusion for this experiment.
   Reject the hypothesis
   df = 1

d) Statement your conclusion from this experiment (the genetic conclusion). Be careful with your wording.
   There is enough evidence to conclude this population does not have Hardy proportions for this gene.

4. (15) The Genetics Department is interested in increasing the wing beat frequency (beats per sec) of Drosophila melanogaster (fruit fly). From preliminary studies, we know the mean wing beat frequency for our (unusual) strain as 15bps, with a standard deviation of 1.2bps. Heritability in the narrow sense is 65%. For our experiment, we will keep the highest 10% of the flies. Give Units for your answers.

a) 17.112 bps Give the mean of the flies that are kept.
   \( M = 15 \text{ bps} \)
   \( \sigma = 1.2 \text{ bps} \)
   \( h^2 = 0.65 \)
   \( I = 1.76 \)
   \( z = 1.28 \)

b) 2.112 bps Give the Selection Differential.
   \( I = 0 \)

c) 16.378 bps Give the mean of the offspring for the next generation.
   \( M + I \cdot h^2 \)
4. (12) An individual is heterozygous for an inversion as diagrammed below:

<table>
<thead>
<tr>
<th>Normal Chromosome</th>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
<th>G</th>
</tr>
</thead>
<tbody>
<tr>
<td>Inverted Chromosome</td>
<td>A</td>
<td>B</td>
<td>E</td>
<td>D</td>
<td>C</td>
<td>F</td>
<td>G</td>
</tr>
</tbody>
</table>

a) This inversion is **paracentric**
b) Give the **four** chromatids that result when there is crossing over between C and D.

- ABCDEFG
- ABCDEBA
- ABEOCFG
- GFEDCFG

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

\[ 0.1849\ AA + 0.4902\ Aa + 0.3249\ aa \]

a) Give the allelic frequencies.

\[ \begin{align*}
A &= 0.43 \\
\bar{a} &= 0.57
\end{align*} \]

b) This population is undergoing migration from a large population with Genotypic Frequencies \(0.16\ AA + 0.48\ Aa + 0.36a\). The migration rate is 0.30. Calculate the allele frequency for A after one generation.

\[ \begin{align*}
A &= 0.421 \\
n & = 0.3 \\
(1 - n)(\bar{q}^3) & = (1 - 0.3)(0.49)^3 \\
\bar{p} & = 0.43
\end{align*} \]

c) Consider the original population in a). Assume that AA has a fitness of 1.0, Aa has a fitness of 1.1 and aa has a fitness of 0.2. Compute the allele frequency of A for the next generation.

\[ \begin{align*}
A &= 0.5760 \\
A &= 0.1849 \times 1.1 + 0.5760 \times 0.5760 + 0.3249 \times 0.3249 \\
&= 0.7393 + 0.1849 \times 0.5760 + 0.3249 \times 0.3249 \\
&= 0.7393 + 0.1849 \times 0.7891 + 0.3249 \times 0.7891 \\
&= 0.7393 + 0.1849 \times 0.7891 + 0.3249 \times 0.7891 \\
&= 0.5760 + 0.2343 + 0.5833 + 0.0823
\end{align*} \]

You may need to use some of these equations:

\[ p^2W_{AA} + 2pqW_{Aa} + q^2W_{aa} \]
\[ p^2 + Fpq \]
\[ (1 - m)p + mP \]
\[ (1 - \mu)p + \nu(1 - p) \]
\[ q^2 + Fpq \]
6. (8) Over the summer, your instructor visited the Raptor Center in Española, NM. They are studying the Tuoyoni Swift. They have determined three traits that are located on the same chromosome, Beak Shape, Pin Feather Color, and Claw Color. The linkage map is given below. The coefficient of coincidence was determined to be 0.75. In an experiment with these birds, a true breeding strain of swifts with Straight Beaks, Black Pin Feathers, and Yellow Claws is crossed with a true breeding strain with Curved Beaks, Gray Pin Feathers, and Brown Claws. The F₁ is testcrossed. Give the expected frequency of the given types among the test cross offspring.

<table>
<thead>
<tr>
<th>Beak Shape</th>
<th>Pin Feather Color</th>
<th>Claw Color</th>
</tr>
</thead>
<tbody>
<tr>
<td>Straight</td>
<td>Yellow</td>
<td>Dominant</td>
</tr>
<tr>
<td>Curved</td>
<td>Gray</td>
<td>Recessive</td>
</tr>
<tr>
<td></td>
<td>Black</td>
<td></td>
</tr>
</tbody>
</table>

10 8

a) Straight Beaks and Black Pin Feathers
\[ \frac{1}{2}(1 - 10) = 0.95 \]

\[ F₁: \begin{array}{ccc}
\text{Straight} & \text{Black} & \text{Yellow} \\
\text{Curved} & \text{Gray} & \text{Brown} \\
0.10 & 0.08 & 0.08 \\
\end{array} \]

\[ c = 0.75 \]

\[ DCO = (1)(0.08)(0.75) = 0.06 \]

b) Curved Beaks with Yellow Claws
\[ \frac{1}{2}[1 - 0.006 + 0.08 - 0.006] \]
\[ = 0.084 \]

7. (4) We are interested in several characteristics on a species of salamander. In particular, we are interested in Speed, Tail Length, and Skin Shading. We know these traits are on the same chromosome, and are interested in estimating the genetic map. For our experiment, we cross two pure breeding lines, then take a testcross (the usual experiment). The results are summarized below.

<table>
<thead>
<tr>
<th>Speed</th>
<th>Tail Length</th>
<th>Skin Shading</th>
<th>Number Observed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fast</td>
<td>Short</td>
<td>Dark</td>
<td>2,330</td>
</tr>
<tr>
<td>Fast</td>
<td>Short</td>
<td>Light</td>
<td>6</td>
</tr>
<tr>
<td>Fast</td>
<td>Long</td>
<td>Dark</td>
<td>135</td>
</tr>
<tr>
<td>Fast</td>
<td>Long</td>
<td>Light</td>
<td>52</td>
</tr>
<tr>
<td>Slow</td>
<td>Short</td>
<td>Dark</td>
<td>150</td>
</tr>
<tr>
<td>Slow</td>
<td>Short</td>
<td>Light</td>
<td>206</td>
</tr>
<tr>
<td>Slow</td>
<td>Long</td>
<td>Dark</td>
<td>4</td>
</tr>
<tr>
<td>Slow</td>
<td>Long</td>
<td>Light</td>
<td>2,129</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td>5,012</td>
</tr>
</tbody>
</table>

The order of the loci on the chromosome is:

i) Speed Length Skin

ii) Length Skin Speed

iii) Skin Speed Length
8. (7) These are several statements about population genetics.
   1. Can change genotypic frequencies
   2. Consequence of the Founder Effect.
   3. Leads to the loss of one allele in the long run.

   For each population genetic term, circle the number for ALL statements that are true for that type. Each statement can be used more than one time.

   a) Mutation
      - 1
      - 2
      - 3 Possible, but not likely
   b) Migration
      - 1
      - 2
      - 3
   c) Selection
      - 1
      - 2
      - 3
   d) Random Drift
      - 1
      - 2
      - 3
   e) Inbreeding
      - 1
      - 2
      - 3

9. (7) 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.

   A) Aneuploidy
   B) Euploidy
   C) Inversion
   D) Translocation
   E) Deletion
   F) Duplication

   A   Klinefelter Syndrome is an example.
   E   Cri-du-Chat is an example.
   C   Effect is seen among offspring only if there is recombination.
   F   A way for evolution to get new genes.
   D   Thus mutation causes pairing of nonhomologous chromosomes during Meiosis.
   E   Caused by ionizing radiation.
   A   Rate of mutation increases with increasing maternal age. (B is also possible)