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

a) Explain **WHY** we expect heritability to decrease over several generations of selection.

   As you select, you are reducing the genetic variation (eliminating poor genotypes). This reduces heritability.

b) **OUTLINE** how autoreduplication can create a new species (allopolyploid).

   An allopolyploid is derived from two species who cross. The hybrid is sterile, but can undergo autoreduplication (DNA replication without division) to produce a fertile polyploid.

c) Explain **WHY** the following statement is incorrect: “Heritability tells us how much genetics determine a trait.”

   **Heritability** is only a measure of association between the variation in genotypes and the variation in phenotypes.

d) Why do experiments in phytotrons and incubators help us to select for various traits.

   The reduce VCE, thus making heritability larger. This leads to faster selection.
2. (6) We are interested in whether or not a certain gene (with two alleles, R and r) 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>RR</td>
<td>345</td>
<td>335.35</td>
<td>0.2778</td>
</tr>
<tr>
<td>Rr</td>
<td>189</td>
<td>208.3</td>
<td>1.7891</td>
</tr>
<tr>
<td>rr</td>
<td>42</td>
<td>32.35</td>
<td>2.8802</td>
</tr>
<tr>
<td>Total</td>
<td>576</td>
<td>576</td>
<td>4.9471</td>
</tr>
</tbody>
</table>

a) The allele frequencies are: R 0.7630 and r 0.2370.

b) State your conclusion from this experiment (the genetic conclusion). Be careful with your wording.

**Reject. There is sufficient evidence to conclude this gene in this population does not have Hardy-Weinberg proportions.**

3. (12) In their spare time, the TAs race cockroaches. It has become quite a competition among the various labs in the Department. The Quantitative labs have designed a breeding scheme to give them an advantage at the weekly Roach Down. They have a strain of cockroaches with an average time of 18.9 sec and a standard deviation of 1 sec. They have decided to use the fastest 50% in a mass selection scheme.

a) The following is the curve showing the race times for the original population of cockroaches. The vertical lines are the mean and the two standard deviations. Give the value for the mean and clearly label the values of the two standard deviations.

![Graph showing race times with mean and standard deviations marked.](image)

b) Show on the graph the **truncation selection point**. Shade the individuals selected as parents.

c) Compute the mean of the selected individuals. Show that on the graph.

\[
18.9 - (1.8)(1/sec) = 18.1 \text{ sec}
\]

d) The TAs have estimated \( h^2 \) as 67%. After a single generation, the offspring population will still be normally distributed. Draw that curve on the graph and label the mean. Include the value for the mean.

\[
18.9 - (1.8)(.67)(1) = 18.364\text{ sec}
\]
4. (12) An individual is heterozygous for an inversion as diagrammed below:

Normal Chromosome
A B C D E F

Inverted Chromosome
A B D C E F

a) This inversion is **Pericentric**

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

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

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

\[0.1024 \text{ AA} + 0.4352 \text{ Aa} + 0.4624 \text{ aa}\]

a) Give the allelic frequencies.

\[A = 0.32 \quad a = 0.68\]

b) This population undergoing mutation. The mutation rate from a to A is 0.0001 and from A to a is 0.0005. Calculate the allele frequency for A after one generation (DO NOT ROUND).

\[A = 0.319908 \quad \left(0.32\left(1-0.0005\right) + (0.68)(0.0001)\right)\]

c) Consider the original population in a). Assume that AA and Aa have fitness of 1.0, and aa has a fitness of 0.1. Compute the allele frequency of A for the next generation.

\[
\begin{array}{cccc}
A & 0.48096 & 1.024 & 0.7852 & 0.9624 \\
 & 1 & 1 & 1 & 1 \\
A & 1.024 & 0.7852 & 0.94624 & 0.51384 \\
 & 0.7852 & 0.94624 & 0.51384 & 0.58910 \\
 & 0.48096 & 0.79200 & 0.58910 & 0.58910 \\
\end{array}
\]

You may need to use some of these equations:

\[p^2W_{AA} + 2pqW_{Aa} + q^2W_{aa}\]

\[p^2 + Fpq\]

\[(1-m)p + m^2\]

\[(1-\mu)p + \nu(1-p)\]

\[2(1-F)pq\]

\[q^2 + Fpq\]
6. (6) The following is a list of the three processes that make up the Central Dogma of Genetics. Fill in the number of the process BEST described by each phrase. Each number is used at most once.
   1. Transcription
   2. Translation
   3. Replication

   7 The last step in the creation of proteins.
   3 Occurs only once per cell cycle.

7. (6) The following is a list of the three molecules that make up the Central Dogma of Genetics. Fill in the number of the process BEST described by each phrase. Each number is used at most once.
   1. DNA
   2. Protein
   3. RNA

   1 The longest of the three molecules.
   3 The shortest lived (in general) of the three molecules.

8. (8) These are several statements about population genetics.

   1. Associated with the Founder Effect.
   2. Can bring about large changes in allele frequencies in a short time.
   3. Can increase homozygosity without changing allelic frequencies significantly.

   For each type of chromosomal mutation, circle the number for ALL statements that are true for that type. Each attribute can be used more than one time.

   a) Mutation 1 2 3
   b) Migration 1 2 3
   c) Selection 1 2 3
   d) Random Drift 1 2 3
   e) Inbreeding 1 2 3
9. (8) These are several statements about chromosome structure mutations.

1. Can be caused by breakage and incorrect repair.
2. May have no effect on a parent and a profound effect on its offspring.
3. Involves more than one chromosome.

For each type of chromosomal mutation, circle the number for ALL statements that are true for that type. Each attribute can be used more than one time.

a) Deletion  
   - 1  
   - 2  
   - 3
b) Duplication  
   - 1  
   - 2  
   - 3
c) Paracentric Inversion  
   - 1  
   - 2  
   - 3
d) Translocation  
   - 1  
   - 2  
   - 3
e) Pericentric Inversion  
   - 1  
   - 2  
   - 3

10. (10) These are several mechanisms we studied in population genetics.

1. Mutation
2. Inbreeding
3. Assortative mating
4. Selection with a recessive lethal trait.
5. Migration into the study population from a population where the recessive allele is predominant.

The following are some mechanisms of population genetics. For each, indicate the statement that best describes the mechanism. **Each number is used once and only once!!**

- 1 Is absolutely essential for evolution to occur.
- 2 Will lead to an increase in expression of recessive lethals in the population.
- 3 Changes the genotypic frequencies, but not the allele frequencies, for some, but not all, loci.
- 4 The frequency of the dominant allele will increase.
- 5 The frequency of the dominant allele will decrease.

11. (2) Kirk relates the story that the Central Dogma is named such because it was developed at “The Central Pub.” Circle your favorite response:

   a) Cool. It’s good to see important theories developed in a drunken stupor.
   b) That one sounds pretty fishy.
   c) OK, maybe geneticist do have some humor.
   d) Kirk would say anything to get our attention.
   e) Other