Genetics – Exam 3A – Key
MONDAY 11 DECEMBER 2006

INSTRUCTIONS

• fill out the scantron card with a #2 pencil

• PRINT your name, date and lab section in the spaces provided

• TO RECEIVE A GRADE you must print your student number, fill in corresponding bubbles in the spaces provided on the card & indicate that you have taken EXAM 3A

• read ALL questions carefully before answering any of them

• if a question has more than one correct answer, chose the one that is MOST correct

• circle answers on the exam pages BEFORE filling marking answers on the scantron

• mark only ONE answer for each question on the scantron card

• mark all answers carefully – dark and only within the bubbles for each question

• you MUST sign the sheet at the front of the room when handing in your exam to receive a grade
PART A: GENOMES, CHANGE & PROCESSES (40 points)

1. A conservative mechanism of transposition does not
   A) require transposase
   B) require terminal inverted IS sequences
   C) involve excision of the transposon from one site and insertion in a second site
   D) involve replication of a copy at one site that inserts in a second site
   E) have the potential to cause mutations in the host

2. Retrotransposons mobilize by
   A) excision
   B) transcription
   C) translocation
   D) conversion
   E) transposition

3. Bacterial insertion sequence (IS) elements
   A) are not components of larger simple transposons
   B) do not begin and end with inverted repeat sequences
   C) are not sites of elevated recombination
   D) do not encode their own transposase enzyme
   E) do not have the potential to interrupt genes

4. Eukaryotic RNA retrotransposons
   A) encode polymerase to replicate DNA for insertion elsewhere
   B) encode reverse transcriptase to make DNA from single-stranded RNA
   C) are also known as short-terminal-repeat (STR)-retrotransposons
   D) do not have the potential to interrupt genes
   E) resemble bacterial transposons

5. The defining feature of a transposon family is the
   A) enzyme that will induce transposition
   B) set of gene products they encode
   C) host gene(s) at the target sequence where they preferentially insert
   D) organism they infect
   E) laboratory researcher who was responsible for their identification
6. Mutations can be
   A) dominant
   B) random
   C) silent
   D) spontaneous
   E) all of the above

7. Mutations that can not revert include
   A) silent, neutral, missense & nonsense mutations
   B) large deletions & insertions
   C) lethal, sterile & temperature sensitive mutations
   D) frameshift mutations of 1 base pair
   E) transversions & transitions

8. A transition mutation from T = A will be
   A) A = T
   B) T = A
   C) C = G
   D) G = C
   E) any of the above

9. A mutagen that would most likely induce the transition in #8 is
   A) 5-BU
   B) EMS
   C) aflatoxin B1
   D) γ-rays
   E) A) or B)

10. Transversions can not be
    A) spontaneous events
    B) induced by alkylating agents (e.g., EMS)
    C) induced by bulky addition products (e.g., aflatoxin)
    D) induced by non-ionizing radiation (e.g., UV)
    E) generated by DNA repair (e.g., SOS)
11. Spontaneous mutation during DNA replication results when slippage occurs in the

A) daughter strand, causing insertions in the daughter strand
B) template strand, causing insertions in the daughter strand
C) daughter strand, causing insertions in the template strand
D) template strand, causing deletions in the template strand
E) daughter strand, causing deletions in the daughter strand

12. A point mutation that leads to substitution of a chemically dissimilar amino acid is called

A) exact
B) silent
C) synonymous
D) missense
E) nonsense

13. Reversion of $A = T \rightarrow G \equiv C$ transition mutations can not be

A) spontaneous
B) induced with alkylating agents
C) induced with base analogues
D) induced with intercalating agents
E) induced with UV radiation

14. $T_{on} E. coli$ colonies grown in the absence of T1 bacteriophage are then replica plated in the presence of phage. Only a few $T_{on} E. coli$ colonies grew on the new plates, but all of these were in identical positions on each of these plates. This result shows that

A) replica plating is not accurate
B) phage are mutagenic
C) intelligent design theories are needed to explain the results
D) resistance to phage was adaptive and induced by exposure
E) mutations were pre-existing in the original population

15. Mutation frequency in this population is

A) 0.563
B) 0.452
C) 0.250
D) 0.129
E) 0.125
16. Mutation rate in the population shown in #15 is... not counted, due to error below
   A) 0.563
   B) 0.452 the correct answer does not appear,
   C) 0.250 but would be 4/15 = 0.267
   D) 0.129
   E) 0.125

17. A culture of wild type *E. coli* was grown from a single cell to a density of 10^8 cells/ml. 100 separate 0.1 ml volumes from this culture were plated with T1 bacteriophage. If 17 plates developed T1 phage-resistant colonies, the mutation rate is
   A) 1.7 × 10^-8 mutations/gene/cell division
   B) 1.9 × 10^-9 mutations/gene
   C) 1.9 × 10^-8 mutations/gene/cell division
   D) 8.3 × 10^-8 mutations/cell division
   E) 1.7 × 10^-9 cell divisions/mutation/gene

18. Gene conversion
   A) is recombination without the exchange of downstream markers
   B) involves intermediate heteroduplex DNA molecules (hybrid DNA of two non-sister chromatids)
   C) occurs during crossing over in meiosis
   D) is the change of an allele sequence by error-prone DNA repair to the homologous sequence available on a non-sister chromatid
   E) all of the above

19. Error-prone DNA repair mechanisms include
   A) homologous recombination
   B) non-homologous end joining
   C) mismatch repair
   D) excision repair
   E) all of the above

20. Double-stranded DNA damage induces
   A) single strand invasion based on DNA sequence homology
   B) SOS repair
   C) error-prone repair by strand exchange with sister chromatids
   D) error-free repair by strand exchange with non-sister chromatids
   E) excision repair
21. During crossing over, Holiday junctions of heteroduplex DNA are formed with non-sister chromatids as shown below. Recombination of flanking genetic markers will result through resolution of the Holiday junction by breakage and exchange of DNA strands at

A) positions 1 and 2
B) positions 1 and 4
C) positions 2 and 3
D) positions 3 and 4
E) all positions

22. Aberrant euploidy in an organism that is normally a diploid of $2n = 6$ would be

A) AA BB C
B) AA BB CC D
C) AAA BB CC
D) AAA BBB CCC
E) AA B CCC

23. Partially homologous chromosome sets are found in

A) allopolyploids
B) euploids
C) monoploids
D) autoployploids
E) diploids

24. The probability that a triploid $3n = 42$ plant will generate a viable diploid gamete is

A) $\left(\frac{1}{2}\right)^{3n} = 2.274 \times 10^{-13}$ (or about 1 in $4.4 \times 10^{12}$)
B) $\left[\frac{1}{(3n)}\right]^3 = 1.35 \times 10^{-5}$ (or 1 in 74,088)
C) $\left(\frac{1}{2}\right)^n = 6.104 \times 10^{-5}$ (or 1 in 16,384)
D) $\left[\frac{1}{(3n)}\right]^2 = 0.001$ (or 1 in 1764)
E) $\left[\frac{1}{(3n)}\right]^{0.5} = 0.154$ (or about 1 in 6)
25. The mutant allele \( r \) is expressed as red leaves in autotetraploid poinsettia plants. The proportion of red plants expected in the progeny of the cross of \( R/r/r/r \times R/R/r/r \) is

A) \( \frac{1}{2} \)  
B) \( \frac{1}{3} \)  
C) \( \frac{1}{6} \)  
D) \( \frac{1}{12} \)  
E) \( \frac{1}{24} \)

26. Aneuploidy arises through

A) trisomy  
B) nondisjunction  
C) allopolyploidy  
D) segregation  
E) hybrid dysgenesis

27. Chromosome structure mutations do not include

A) transversions  
B) inversions  
C) duplications  
D) translocations  
E) deletions

28. Mechanisms for generating chromosome rearrangements include

A) double stranded breakage and rejoining  
B) illegitimate recombination  
C) legitimate recombination  
D) homologous recombination  
E) A) and B)

29. Single chromosome breaks can result in

A) deletions  
B) duplications  
C) inversions  
D) translocations  
E) translocations
30. Chromosome duplications are classified as
   A) tandem or reverse
   B) paracentric or pericentric
   C) terminal or interstitial
   D) adjacent or distributed
   E) adjacent or alternate

31. Illegitimate recombination involving the repeat sequences indicated by arrows below can generate a(n)
   A) deletions
   B) inversions
   C) duplications
   D) duplications & deletions
   E) duplications & inversions

32. Complementation tests with deletions & recessive point mutations resulted in the data below. Genes in brackets are not separated by deletion break points. Gene order is
   C) 5 – 2 – 7 – 8 – 6 – 3 – 9 – 1 – 4
   D) 1 – 9 – 3 – 6 – 8 – 7 – 2 – 5 – 4

33. Template strands are black & coding strands are gray. Two chromosome breaks, one between genes A & B and the other between genes C & D, give rise to an inversion in which transcription of gene B will occur
   A) on the lower strand from left → right
   B) on the lower strand from right → left
   C) on the upper strand from left → right
   D) on the upper strand from right → left
   E) on either B) & D), depending on how the sequence rejoins
34. Illegitimate recombination involving the repeat sequences indicated by arrows below can generate a(n)
   A) deletion
   B) duplication
   C) duplication & deletion
   D) inversion
   E) translocation

35. If gene order is $a \bullet c d$, recombinant meiotic products generated in a heterozygote for an inversion of genes $b \rightarrow c$, when a cross over occurs between $b \& \bullet$ are
   A) $a b \bullet c d$ and $a c \bullet b d$
   B) $a b \bullet c a$ and $d c \bullet b d$
   C) $a b \bullet c d$ and $d c \bullet b d$
   D) $a \bullet b c \bullet a$ and $d b c d$
   E) $a b c a$ and $d \bullet b c \bullet d$

36. If gene order is $a \bullet b c d$, recombinant meiotic products generated in a heterozygote for an inversion of genes $b \rightarrow c$, when a cross over occurs between $b \& c$ are
   A) $a \bullet b c d$ and $a \bullet c b d$
   B) $a \bullet b c a$ and $d \bullet c b d$
   C) $a \bullet b c d$ and $d \bullet c b d$
   D) $a \bullet b c \bullet a$ and $d b c d$
   E) $a b c a$ and $d \bullet b c \bullet d$

37. Alternate segregation in the translocation heterozygote below will likely generate
   A) $N_1 + N_2$ viable normal sequence and $T_1 + T_2$ inviable segmental aneuploid gametes
   B) $N_1 + N_2$ viable normal sequence and $T_1 + T_2$ viable translocation gametes
   C) $N_1 + T_1$ and $N_2 + T_2$ inviable segmental aneuploid gametes
   D) $N_1 + T_1$ and $N_2 + T_2$ viable translocation gametes
   E) $N_1 + T_2$ and $N_2 + T_1$ inviable segmental aneuploid gametes
38. Fine structure analyses of the rII region of T4 bacteriophage identified the smallest distance that can be separated by recombination represents adjacent

A) nucleotide pairs
B) exons
C) complementation groups (cistrons)
D) genes
E) operons

39. A high concentration pairwise infection with rII mutant T4 phage forms rare plaques on E. coli K (not due to reversion). The lysate from these rare plaques is then plated at low concentration on E. coli K and is expected to form plaques

A) always
B) rarely
C) ½ of the time
D) never
E) with an unknown probability, there is not enough information given

40. Fine structure analyses of the rII region of T4 bacteriophage suggested that genes are best defined as fundamental and indivisible units of

A) change – mutation occurs as changes in whole genes (alleles) only
B) function – complementation occurs between whole gene products only
C) movement – transposition and insertion occurs between whole genes only
D) structure – recombination occurs between whole genes only
E) all of the above

PART B: COMPREHENSIVE (20 points)

41. Properties of genetic material do not include

A) ubiquity – it is found in all life on earth
B) replication – it is copied and inherited
C) change – it mutates and gives rise to variation
D) metabolism – it provides energy (ATP) for cell functions
E) function – it encodes polypeptides and provides the blueprint for life
42. Mendelian phenotypes are associated with
   A) many genes
   B) strong environmental components
   C) discontinuous distributions
   D) measuring (rather than counting)
   E) all of the above

43. A trait is said to be “fixed” and does not return to a baseline state after relaxing artificial selection because
   A) all genes influencing the trait are heterozygous
   B) no genetic variability (G) remains in the population
   C) environmental factors (E) no longer influence the trait
   D) a physiological plateau is attained that cannot be surpassed
   E) all of the above

44. The meiotic stage illustrated below is
   A) metaphase I
   B) anaphase I
   C) prophase II
   D) metaphase II
   E) anaphase II

45. Exception(s) to Mendel’s laws include
   A) equal segregation of alleles except when odd numbers of alleles are present
   B) independent assortment of genes except when they are linked and < 50 cM apart
   C) F1 hybrid crosses progeny demonstrate the particulate nature of hereditary material except in the case of quantitative phenotypes
   D) F1 dihybrid cross progeny ratios (9:3:3:1) reflect independent functions except in the case of epistasis
   E) all of the above

46. If we make no assumptions about I1 and I2, the mode of inheritance in this pedigree can not be
   A) autosomal dominant
   B) autosomal recessive
   C) X-linked recessive
   D) X-linked dominant
   E) any of the above
47. If I1 and I2 are true breeding in #46, the probability that IV1 is an affected male is
   A) 1/6
   B) 1/9
   C) 1/12
   D) 1/18
   E) 1/24

48. If the mode of inheritance in #46 is autosomal recessive, the probability that at least 2 individuals out of 3 in generation IV would be unaffected is
   A) 0.999
   B) 0.966
   C) 0.702
   D) 0.263
   E) 0.033

   \[
   (p + q)^n = \sum_{k=0}^{n} \frac{n!}{k!(n-k)!} p^k q^{n-k}
   \]

49. If AB/AB is crossed to ab/ab, and the F1 is testcrossed, the percent of the testcross progeny that will be phenotypically AB if the two genes are 25 cM apart is
   A) 75
   B) 56.3
   C) 37.5
   D) 25
   E) 12.5

50. Auxotrophic strains of Neurospora, mutant for serine (s) and glycine (g) were crossed and the following asci were counted. The distance between the centromere and the s and g genes in #50 is... not counted, due to error below
   A) 16 cM
   B) 8 cM
   C) 4 cM
   D) 2 cM
   E) 1 cM

   \[
   \text{cM} = \left( \frac{1}{2} \frac{M^2}{\text{total}} \right) \times 100
   \]

51. The distance between the s and g genes in #50 is... not counted, due to error below
   A) 11 cM
   B) 9.75 cM
   C) 6.5 cM
   D) 3.25 cM
   E) ... forget it... the genes are unlinked!
52. Interrupted-mating crosses in *E. coli* between Hfr *leu+ his+ gly+* and F– *leu– his– gly–* show that *his+* enters the F– last. In a fine mapping study using the same two strains *his+* recombinants are selected and tested by replica plating for the presence of the *leu+ gly+* alleles with the following results. Gene order is

<table>
<thead>
<tr>
<th>Genotypes</th>
<th># Colonies</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Leu+ his+ gly+</em></td>
<td>259</td>
</tr>
<tr>
<td><em>Leu– his+ gly–</em></td>
<td>29</td>
</tr>
<tr>
<td><em>Leu– his+ gly+</em></td>
<td>11</td>
</tr>
<tr>
<td><em>Leu+ his+ gly–</em></td>
<td>1</td>
</tr>
</tbody>
</table>

53. Oddly enough, another starfish turned up off the coast of North Korea after a recent nuclear test, but this one had no arms at all. When this animal was bred with the wild-type 5-arm variety, half of the F1 had no arms, and the other half had five. Crosses among 0-arm F1 animals gave 72 0-arm and 35 5-arm F2. The new 0-arm allele is

A) recessive (a) to the wild-type 5-arm allele (A)
B) homozygous sterile and recessive (a²) to the wild-type 5-arm allele (A)
C) dominant (A) to the wild-type 5-arm allele (a)
D) homozygous lethal and dominant (A¹) to the wild-type 5-arm allele (a)
E) co-dominant (A²) with the wild type 5-arm allele (A¹)

54. True-breeding blue and yellow frogs are crossed and have all red frogs in the F1 generation. When these F1 frogs are crossed among themselves, 32 blue, 41 yellow and 87 red frogs are counted in the F2 generation. The pattern of inheritance is likely

A) recessive epistasis
B) recessive suppression
C) duplicate recessive genes
D) duplicate additive genes
E) dominant epistasis

55. You first test the simple hypothesis that the frog coloration in #54 is under the control of a single gene with co-dominant alleles, and calculate $\chi^2 =$

A) 0.258, with 0.90 > $P$ > 0.75, you do not reject the hypothesis
B) 2.238, with 0.5 > $P$ > 0.25, you do not reject the hypothesis
C) 8.307, with $P$ < 0.025, you reject the hypothesis
D) 12.326, with $P$ < 0.005, you reject the hypothesis
E) 21.775, with $P$ < 0.001, you reject the hypothesis
56. The phenylalanine (PHE) fraction of all amino acids expected from the synthesis of message codons with polynucleotide phosphorylase and ribonucleotides uracil and guanine in a 3:1 ratio is

A) 27/64 or 0.422
B) 9/32 or 0.281
C) 3/16 or 0.188
D) 9/64 or 0.141
E) 3/64 or 0.047

57. This DNA sequence encodes a two amino acid polypeptide if transcribed from

ATC TCA ATG AAT CAT GTA TAC TTA TAG CGG ATT
TAG AGT TAC TTA GTA CAT ATG AAT ATC GCC TAA

A) left \(\rightarrow\) right on the upper strand
B) right \(\rightarrow\) left on the upper strand
C) left \(\rightarrow\) right on the lower strand
D) right \(\rightarrow\) left on the lower strand
E) B) and D)

58. Consensus sequences for transcription and transcript modification are found in

A) promoters
B) introns
C) 5’enhancers
D) 3’ UTR
E) all of the above

59. In the \textit{lac} operon system, lactose will be metabolized at low levels in

A) \(I^+ P^- O^+ Z^+ Y^+ A^+\) cells when glucose is absent
B) \(I^+ P^+ O^- Z^- Y^- A^+\) cells when glucose is present
C) \(I^- P^+ O^+ Z^+ Y^+ A^-\) cells when glucose is absent
D) \(I^- P^+ O^+ Z^- Y^+ A^-\) cells when glucose is absent
E) \(I^+ P^+ O^- Z^- Y^+ A^-\) cells when glucose is present

60. Pleiotropy is

A) multiple promoter consensus sequences recognized by one RNA polymerase
B) multiple transcription factors recruited to one enhancer sequence
C) multiple mRNA transcripts generated from one gene
D) multiple phenotypes associated with one gene
E) multiple genes influencing one phenotypes