

EXAM II

Correct answers and explanations are shown in **RED**.

1. In a species of wild *Phlox* flower, a single gene locus codes for flower petal pigment. One allele of this gene codes for red pigment, and a different allele codes for blue pigment. A plant that is homozygous for the red allele produces red flowers. A plant that is homozygous for the blue pigment produces blue flowers, and a heterozygous plant produces purple flowers. Which of the following is true?
 - a. the two alleles in question exhibit incomplete dominance
 - b. the two alleles in question exhibit codominance**
 - c. purple flowers must be considered the "wild type" phenotype
 - d. a plant with purple flowers exhibits heterozygote advantage
 - e. more than one of the above is true

(Codominance means that two different products, both functional, are being produced. Incomplete dominance would mean that only half the amount of a functional product is produced by one allele, and a non-functional product is being produced by the other.)

Note that this plant has ONE gene with two alleles, but BOTH alleles produce a functional product--either a red pigment or a blue pigment. If this had been a case of incomplete dominance, then the plant might have deposited less red (or blue) pigment in its petals because one of the enzymes in the pigment pathway was faulty, resulting in only half the amount of pigment.

If you didn't recall (from fifth grade) that blue + red = purple, then you might have had trouble with this problem.)

2. If you had two purple-flowering *Phlox* (from the previous question) and you bred them together and got 10 seeds, what is the probability that 4 of the seeds will produce a blue-flowering plant, and 6 will produce a purple-flowering? (Hint: equations are on the last page!)
 - a. 0.02
 - b. .013**
 - c. 0.05
 - c. .0.63
 - d. 0.5

For this question, you needed to apply the Binomial Theorem, since you are dealing with two alternate events (purple flowers or blue flowers), each of which has its own probability. A Punnett Square of the cross in question shows the expected phenotypes in the offspring cohort:

	R	R'
R	RR	RR'
R'	RR'	R'R'

The offspring genotypes (indicated in red) show an expected ratio of 25% red, 50% purple and 25% blue flowers from this monohybrid cross.

Your total number of trials is 10 (one possible outcome for each seed), and you want to know what the PROBABILITY is that of your 10 seeds, 4 will be blue and 6 will be red. All you need to do now is plug into the Binomial Equation, like so:

$$[10! / 4! \times 6!] \times (.25)^4 \times (.50)^6$$

The answer is 0.013, or 1.3% chance. In prose, this means that 1.3% of every 10-seed sample should yield 4 blue-flowering and 6 purple-flowering plants.

3. In a cat with a sex chromosome karyotype of XXXXY, how many Barr Bodies would you expect to find in each somatic cell?
 - a. one
 - b. two
 - c. three**
 - d. four
 - e. none
4. The cat of the previous question has a condition known as
 - a. Turner Syndrome
 - c. Klinefelter Syndrome**
 - e. extra nipples
 - b. Down Syndrome
 - d. Cri-du-Chat Syndrome
5. Human stature is controlled by about seven different genes at separate loci. This trait is
 - a. codominant
 - c. polygenic**
 - e. complementary
 - b. epistatic
 - d. heterokaryotic
6. You have a stallion who expresses a dominant allele for coat color (bay) and the dominant allele for mane texture (straight). However, there are recessive alleles for each of these loci coding for black coat color and wavy mane. You don't know the genotype of your stallion, but would like to find out. To do so, you should breed him with which of the following?
 - a. a true-breeding bay mare with straight mane
 - b. a true-breeding black mare with wavy mane**
 - e. a frisky goat
 - d. an albino mare with straight mane
 - c. a mare heterozygous for both traits

(This is a simple test cross.)
7. The primary sex ratio (males: females) in the U.S. is 1.08. The secondary sex ratio is 1.06. Which of the following is the most plausible explanation for the reduction in number of males between conception and birth?
 - a. insufficient sample size
 - b. hemizyosity of males results in expression of deleterious lethal alleles on the X c'some**
 - c. males are more likely to express deleterious alleles on the autosomal chromosomes
 - d. Any given X chromosome in a female is less likely to carry a deleterious allele than an X chromosome in a male.
 - e. males prefer to stay with mom
8. Because a female has two X chromosomes and a male has only one, a female produces twice the amount of product encoded on the X chromosome as a male.
 - a. true
 - b. false**
 - c. which explains a lot, actually
9. A trait such as male pattern baldness, which exhibits opposite dominance/recessiveness in males and females is known as a(n) _____ trait.
 - a. holandric
 - c. sex-limited
 - e. sex-linked
 - b. pseudoautosomal
 - d. sex-influenced**

Use the following information to answer #10 - 13.

In unicorns, the direction of horn spiral (I'm really reaching here...) is determined, not by the genotype of the unicorn itself, but by the direction of the mitotic spindle's tilt in the ovum made by its *mother*. A female unicorn carrying the dominant allele (H) will manufacture ova with the mitotic spindle tilting to the left, and causing babies developed from her fertilized ova to have a left-spiraling horn. A unicorn carrying only the recessive allele (h) will manufacture ova with the mitotic spindle tilting to the right, and causing all her babies to have right-spiraling horns.

10. The direction of unicorn horn spiraling is determined by
 - a. simple Mendelian genetic interactions
 - d. maternal inheritance
 - b. mitochondrial inheritance
 - e. epigenesis
 - c. maternal effect**
11. A right-spiral female unicorn with the genotype Hh mates with a left-spiral male with genotype Hh. What is the likelihood that her first baby's horn will spiral to the right?
 - a. 0%**
 - b. 25%
 - c. 50%
 - d. 75%
 - e. 100%

(In a phenotypic trait determined by maternal effect, it is the GENOTYPE of the mother which determines the PHENOTYPE of the offspring's maternal effect trait. Because the

mother unicorn was Hh, all her ova will have mitotic spindles tilting to the left, and all her babies will have horns spiraling to the left (dominant allele). You don't need to do any probability calculations for this one.)

12. After a few seasons, the unicorn pair in the previous question have produced babies of both sexes and with all possible genotypes, HH, Hh and hh. In which direction will the horns of babies produced by this pair spiral?
a. right **b. left** c. both right & left d. not enough information given
13. Another unicorn pair, this time an hh male and an Hh female, mate to produce a female offspring with a left-spiraling horn. When this little filly has a baby of her own, however, its horn spirals to the left. What is her genotype?
a. HH b. Hh **c. hh** d. need more information
14. Which of the following is true of both mitochondria and chloroplasts?
a. Their DNA is circular
b. Their genetic code is always exactly the same as the "universal" code proposed by Crick
c. They can function completely without using any gene products of nucDNA
d. The genes they encode have no effect on the phenotype of the organism.
e. All of the above are true of mitochondria and chloroplasts.
15. A number of mammals have been successfully cloned, their "creators" claiming that they are completely genetically identical to the animal that donated the nucleus from which the clone was grown. Why is this not absolutely true?
a. A cloned organism's DNA replication enzymes are manufactured in the cytoplasm.
b. A cloned monkey's chloroplasts produce enough sugar to make it sweeter than the donor.
c. Mitochondria are (maternally) inherited from the animal who donated the ovum, and this animal is not the same one who donated the cloned nucleus.
d. Mutation of nucDNA usually occurs during to the cloning process
e. Unlike the animal who donated their nucleus, cloned organisms are immortal
16. The process by which genetically distinct mitochondria or chloroplasts in a single cell gradually duplicate and move into separate daughter cells over several mitotic divisions (so that eventually each daughter cell has only one genetic strain of mitochondria or chloroplast) is known as
a. Independent Assortment **d. Cytoplasmic Segregation and Recombination**
b. Principle of Segregation e. The Plastid Polka
c. Entropy
17. A woman who has the genetic disorder PKU cannot safely have children, as the toxic breakdown products of phenylalanine in her system can damage the central nervous system of her unborn child. There is absolutely no way to prevent this nervous system damage.
a. true **b. false** c. maybe, but I'm not telling

(When a PKU woman finds she is pregnant, she can stop eating foods rich in phenylalanine, which will prevent the formation of toxic waste products that could harm her unborn fetus.)

Use the following information to answer #18 - 23

A species of Amazonian Poison Dart Frog has three color morphs in its wild populations. Some frogs are solid black, some are solid red, and others are mottled with patches of both black and red. In doing a population study on these frogs, you capture 10,000 of them, sex them, record their color pattern and release them. Of the 10,000 frogs you captured, 5000 were male and 5000 were female (how convenient!). Of the male frogs, 3500 were solid black, and 1500 were solid red. Of the females, 2500 were solid black, and 1500 were solid red, and 1000 were mottled red/black.

18. When you first began studying these frogs, you hypothesized that skin color was due to an autosomal gene locus segregating three alleles, and that the allele coding for black skin (R) was

(Your null hypothesis should have stated: "There will be no significant difference between the observed ratios of the four expected phenotypic classes and those predicted by Mendel's Law." And there wasn't. Your P level must be 0.05 or lower for you to reject your null hypothesis.)

23. If your new idea is correct, and skin color in these frogs is X-linked, then the red/black color in the females is probably due to
- heterozygote advantage
 - codominance
 - incomplete dominance
 - hybrid vigor
 - mosaic expression**
24. A population of beetles you're studying in the Pacific Northwest has elytra (wing covers) that come in several different colors, including iridescent green, iridescent blue and black. If you record the relative color of the beetles in your population, the color data you are collecting would be considered
- discrete numerical data
 - parametric data
 - attribute data**
 - continuous numerical data
 - more than one of the above

(Note that attribute data are non-parametric. Answer "b" is incorrect. Also note that if you were collecting data on the proportion of green versus blue/black beetles in each sample area, these data, reported as integers, would be considered discrete numerical data defined by an attribute (in this case, elytra color).)

Use the following information to answer questions #25 - 31.

You are breeding butterflies, and are interested in determining the relationship of three different traits your particular species expresses. Wild type butterflies have a black body (wh^+), blue eyes (r^+), and silver wings (gld^+). But each of these genes also segregates a mutant allele. Butterflies who are mutant at all three loci have a white body (wh), red eyes (r) and gold wings (gld). You have no idea at the outset whether the three loci are on the same chromosome, or different chromosomes.

You do, however, have a true-breeding colony of wild type butterflies, and another true-breeding colony of white-bodied, red-eyed, gold-winged butterflies. You take a male wild type butterfly, breed it with a female mutant at all three loci, and get a clutch of 100 eggs, all of which hatch out and metamorphose into butterflies that express the wild type for all three traits.

Note that when I write the genotypes below, I am not necessarily indicating that the gene loci are either linked on a single chromosome OR that they exist in that order on a single chromosome.

25. The genotype of your 100 new butterflies is _____. To most effectively study the linkage arrangement of the three loci above, you should breed one of your 100 new individuals with a butterfly whose genotype is _____.

- $wh^+wh^+ r^+r^+ gld^+gld^+$ and $wh^+wh^+ r^+r^+ gld^+gld^+$
- $whwh rr gldgld$ and $wh^+wh r^+r gld^+gld$
- $wh^+wh r^+r gld^+gld$ and $wh^+wh r^+r gld^+gld$
- $wh^+wh^+ r^+r^+ gld^+gld^+$ and $whwh rr gldgld$
- $wh^+wh r^+r gld^+gld$ and $whwh rr gldgld$**

(All your offspring will be trihybrids, since the parents were $wh^+wh^+ r^+r^+ gld^+gld^+$ and $whwh rr gldgld$. The most effective way to study the linkage arrangements among these loci is with a test cross, breeding your trihybrids with a fully mutant individual.)

26. If the three loci are **completely unlinked** (yes, you have to know what that means, and I'm not going to tell you) then which of the following is closest to what you would expect to find in a cohort of 10,000 offspring from a test cross?
- 10,000 completely wild type
 - 5000 wild type, 5000 white/red/gold
 - 1250 wild type, 1250 white/red/gold, 1250 white, 1250 red/gold, 1250 red, 1250 white/gold, 12.5% gold, 12.5% red/white,**
 - 3333 wild type, 3333 fully mutant, 3333 white
 - 5625 wild type : 1875 white : 1875 red/gold : 625 white/red/gold

(If the loci are on separate chromosomes (which is what "completely unlinked" means), then you should get 1/8 of each phenotypic class from a test cross.)

You decided to breed a butterfly with the genotype wh^+wh r^+r gld^+gld to a butterfly with genotype $whwh$ rr $gldgld$, and successfully raised 10,000 little caterpillars into lovely little butterflies that batted around their jars for a day or so, sipping nectar, and then died. But before they went to that big Butterfly Garden in the sky, you counted up the following numbers in each of the following phenotypic classes:

PHENOTYPE	# OF INDIVIDUALS	Crossover
wild type	3900	non-recombinant
red	200	r & gld crossover
white/red	40	r & gld and gld & wh crossover
white/gold	300	r & gld crossover
red/gold	800	gld & wh crossover
gold	60	r & gld and gld & wh crossover
white	900	gld & wh crossover
white/red/gold	3800	non-recombinant
Total	10,000	

(Reciprocal classes are coded in the same color; double crossover class shown in green.)

Using your Super Cerebrum Skills, you quickly did a statistical test in your head and determined that the likelihood of these phenotypic classes occurring in the ratios shown above is significantly different from that predicted by chance alone. You surmise (correctly) that the three loci are located on the same chromosome. But how close together are they? And in what order! Ah, that's what we're here to determine, isn't it?

27. Which gene is the inside marker?
- body color (*wh*)
 - eye color (*r*)
 - wing color (*gld*)
 - need more information to determine
 - all of the loci are in the middle

(This is determined by looking at the reciprocal class with the lowest number of individuals: white/red versus gold. The inside marker is the trait which appears by itself; the other two traits remain in the same combination as they were in the parental organisms. Doing this first makes it a heck of a lot easier to figure out where crossovers ha

28. What is the measured map distance (in Centimorgans) between the *wh* and *gld* loci?
- 6.0
 - 18.0
 - 22.0
 - 24.0
 - need inside marker to determine
29. What is the actual map distance (in Centimorgans) between the *wh* and *r* loci?
- 6.0
 - 18.0
 - 22.0
 - 24.0
 - need inside marker to determine

To figure these out, you must add up totals for:

Crossover between *r* & *gld*: $[200 + 300] + [60 + 40] = 600/10000 = 6$ Centimorgans

Crossover between *wh* & *gld*: $[800 + 900] + [60 + 40] = 1800/10000 = 18$ Centimorgans

Crossover between *wh* & *r*: $[200 + 300] + [800 + 900] = 2200/10000 = 22$ Centimorgans

Measured map distance is that calculated by adding crossovers between *wh* & *r* only. The actual map distance is the total of *r* & *gld* crossovers PLUS *wh* & *gld* crossovers, since the intervening *gld* locus allows you to see crossovers that you wouldn't have seen if you hadn't considered this third trait.)

Measured map distance = 22 Centimorgans (*wh* & *r* crossovers)

That would be $1800 + 600 = 2400/10000 = 24$ Centimorgans

30. Judging from the number of crossovers you actually observed between your two outside loci, how many of the 10,000 flies would you EXPECT to have inherited a double crossover? (Hint: use the map distances you just calculated as probabilities of any given crossover!)
- a. 100 **b. 108** c. 120 d. 180 e. 220
31. From the expected number of double crossovers you calculated in #28, calculate the Coefficient of Coincidence. Judging from the c.c. you calculated, a crossover between the *wh* and *gld* loci _____ the chance of another crossover occurring between the *r* and *gld* loci.
- a. increases **b. decreases** c. does not affect

Do this by calculating the probability of a crossover in each region on either side of the inside marker that you actually saw. Because you want to know what the combined probability of a crossover in both regions is, you use the Product Rule, and multiply the two probabilities together. Therefore, if:

There was a 6% (0.06) crossover rate between *r* & *gld*.
and

There was an 18% (0.18) crossover rate between *wh* & *gld*.
then...

$0.6 \times 0.18 = 0.108 \times 10000$ butterflies = 108. This means that you *expected* 108 crossovers. However, you got only 100 in your cohort of 10000, which is fewer than you expected. The coefficient of coincidence (o/e) = $100/108 = 0.93$.

If the c.c. is less than one, we have positive interference: one crossover decreases the likelihood of the next. In our example, we saw only 93 percent of the crossovers we expected to have seen if the two crossovers did not affect each other.

32. The mutation responsible for the genetic disorder Sickle Cell Anemia affects the phenotypic expression of many traits besides the morphology and physiology of the red blood cells. This phenomenon is known as
- a. polygenic trait c. epigenesis e. heterozygote advantage
b. epistasis **d. pleiotropy**
33. The scientific team who observed the cytogenetic markers of corn, and first made the connection between crossing over and exchange of genetic material between homologous chromosomes was
- a. Sturtevant and Morgan **c. Creighton and McClintock** e. The Osmond Brothers
b. Watson and Crick d. Washburn and Eicher
34. In which of the following organisms might a somatic mutation be passed to future generations?
- a. Rhesus monkey **c. Sequoia tree** e. more than one
b. *Drosophila* d. Pepper moth of the above

(All of the above except the tree are animals, and animals do not pass somatic mutations to their offspring—only germline mutations. If a mutation occurs in a meristem cell in a plant, however, it can be passed on even though the meristem cell is—at least at first—somatic.)

35. An identifying structure visible upon microscopic study of a chromosome is called a
- Giemsa band
 - gene marker
 - tetrad marker
 - knockout marker
 - cytological marker**
36. Which of the following is TRUE of mtDNA, but NOT TRUE of nucDNA in mammals
- it can code for enzymes involved in the electron transport chain
 - both strands (sense *and* antisense) of the DNA are transcribed at any given locus
 - it is transcribed by an RNA polymerase encoded by genes in the nucleus
 - it is inherited, *either completely or in part*, from the maternal parent
 - All of the above are true of BOTH mtDNA and nucDNA**
37. A deleterious mutation in an essential gene will most often
- encode improved version of the protein coded by the gene
 - force an extragenic suppressor mutation
 - be inherited as a dominant allele
 - confer hybrid vigor
 - be lethal**
38. All members of a (hypothetical) population of snakes have a gene that encodes a certain orange pigment. However, due to the effects of nearby genes (epistatic genes, modifiers, etc.) which interact with this gene, some snakes in the population do not express the orange pigment at all (they're white). The population of snakes shows variable
- expressivity
 - penetrance**
 - transcription
 - gene markers
 - interaction
39. In another population of this snake having the same gene coding for pigment production, the amount of pigment made varies among individuals of the population due to interacting genes and environmental effects. There is a range of color morphs in this population from dark orange to various shades of pale orange to almost white. This population shows variable
- longevity
 - chromosomes
 - penetrance
 - expressivity**
 - emotion
40. In an individual organism, short-term change (via gene expression) in response to environmental factors is known as
- epigenesis
 - adaptation**
 - microevolution
 - macroevolution
 - more than one of the above
41. A particular triplet code in an enzyme gene encodes tyrosine. However, a tragic mutation has resulted in the UAC triplet changing to UAA (stop). This type of change is called a
- missense mutation
 - nonsense mutation**
 - antisense mutation
 - frameshift mutation
 - silent mutation
42. Happily for the cell in the previous question, (and strangely!), another mutation has occurred at a completely different gene! This one has altered the anticodon on a tyrosine-carrying tRNA to recognize and bind to UAA instead of UAC. The type of mutation that has resulted in the mutant tRNA is called a(n)
- intragenic suppressor
 - physiological suppressor
 - missense suppressor
 - nonsense suppressor**
 - SOS response
43. Repair enzymes which operate to correct mispairings during DNA replication are able to distinguish between template strand and newly manufactured strand because
- the new strand runs antiparallel to the template strand
 - adenines are methylated on the template strand, but not on the newly made strand**
 - the template strand has thymine dimers which serve as recognition points
 - intercalating agents in the DNA backbone act as coenzymes for repair enzymes
 - newly laid down bases are initially deaminated before replication is finished.

a. 1 b. 2 c. 3 **d. 4** e. not enough information given
(Chromosome "4" is the one formed by the crossover that links the chromatids drawn second from the top and at the very bottom of the diagram on the RIGHT SIDE.)

With the tip of your pencil, start tracing from the chromatid marked "2" in the diagram. When you get to the crossover point, note that this is a vertical crossover, and that you should cross to the opposite side and continue moving your pencil to the right. This will take you around the loop and back to the centromere on the very bottom of the diagram. This is now a dicentric chromosome, and neither part of it can participate in crossing over more than once!

Now trace with your pencil, from right to left, beginning at the chromatid marked "4". When you come to the crossover point, continue moving your pencil to the right (do not double back! This is a *vertical* crossover!). You will end up with an acentric chromosome!

Answer "b" cannot be correct in any case. The chromatid marked "d" is acentric, and chromatid 2 will end up being either dicentric (vertical crossover) or monocentric (horizontal crossover).

The correct answer is "d.")

50. In the individual showing the meiotic synapsis pattern above, what percentage of the gametes produced by meiosis are viable?

a. 0% b. 25% c. 33% **d. 50%** e. 100%

(This inversion heterozygote is semisterile.)

Okay, I promised. Here are some equations you might want to use.

$$\text{Sum Rule} = (a/n) + (a/n) + (a/n) \dots$$

$$\text{Product Rule} = (a/n) \times (a/n) \times (a/n) \dots$$

$$\text{Binomial Theorem} = [n!/s!t!] (p)^s (q)^t$$

$$\text{Coefficient of Coincidence} = \text{observed crossovers/expected crossovers}$$

$$\text{Chi Square} = \sum [(O-E)^2/E]_n \text{ with } df = n - 1$$

Table 5-2
Critical Values of the χ^2 Distribution

df \ p	0.995	0.975	0.9	0.5	0.1	0.05	0.025	0.01	0.005	df
1	.000	.000	0.016	0.455	2.706	3.841	5.024	6.635	7.879	1
2	0.010	0.051	0.211	1.386	4.605	5.991	7.378	9.210	10.597	2
3	0.072	0.216	0.584	2.366	6.251	7.815	9.348	11.345	12.838	3
4	0.207	0.484	1.064	3.357	7.779	9.488	11.143	13.277	14.860	4
5	0.412	0.831	1.610	4.351	9.236	11.070	12.832	15.086	16.750	5
6	0.676	1.237	2.204	5.348	10.645	12.592	14.449	16.812	18.548	6
7	0.989	1.690	2.833	6.346	12.017	14.067	16.013	18.475	20.278	7
8	1.344	2.180	3.490	7.344	13.362	15.507	17.535	20.090	21.955	8
9	1.735	2.700	4.168	8.343	14.684	16.919	19.023	21.666	23.589	9
10	2.156	3.247	4.865	9.342	15.987	18.307	20.483	23.209	25.188	10
11	2.603	3.816	5.578	10.341	17.275	19.675	21.920	24.725	26.757	11
12	3.074	4.404	6.304	11.340	18.549	21.026	23.337	26.217	28.300	12
13	3.565	5.009	7.042	12.340	19.812	22.362	24.736	27.688	29.819	13
14	4.075	5.629	7.790	13.339	21.064	23.685	26.119	29.141	31.319	14
15	4.601	6.262	8.547	14.339	22.307	24.996	27.488	30.578	32.801	15

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