Designer Genes C - Designer Genes - BirdSO C 2021 Invitational - 03-07-2021

The test is **open internet**.
Section 1 [Mainly MCQ] is worth 82 points. Section 2 [Mainly Short Answer] is 118 points.

Partial credit will be awarded if work is shown in the short answer section.

Tiebreakers are, in order: Questions 101, 115, 85, 1, 90, 66, and 24

Section 1

Part 1: Molecular Genetics, Heredity, and Biotechnology [19 points total]

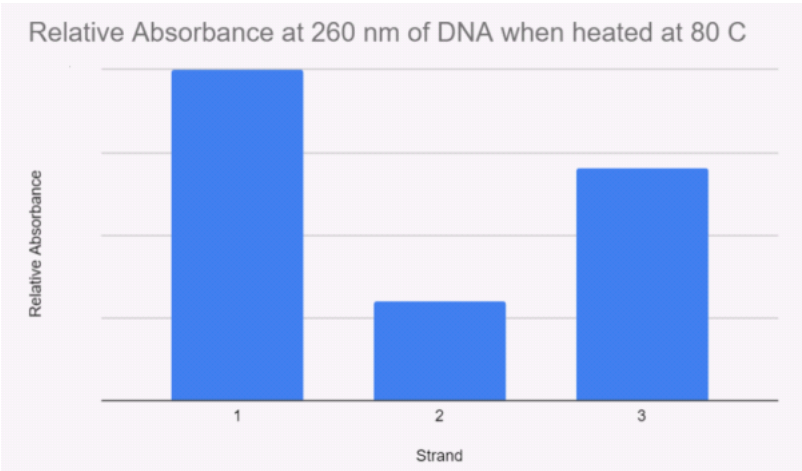
1. (3.00 pts)
Oh no! Future Dr. Sehej has mislabeled his DNA sequence samples and now does not know which strand is which. Luckily you are there, armed with your epic biochemistry knowledge. In order to help, you notice that he has performed an experiment where he heated up each of the DNA strands and tested their relative absorbance at 260 nm. He knows that the DNA sequences (labeled a to c) each correspond to exactly one of the unknown strands (labeled 1 to 3) of the graph shown below. Please let Future Dr. Sehej know which sequence to unknown strand pairing is most likely. The blanks correspond to unknown strands 1, 2 and 3 from left to right. Type a single lowercase letter 'a', 'b' or 'c' in each blank corresponding to the pairing you think is accurate.

Strands:

a. 5' GATTAGTTTA 3'
   3' CTAATCAAAT 5'

b. 5' AGCTGATGCT 3'
   3' TCGACTACGA 5'

c. 5' GCGATGCCGT 3'
   3' CGCTACGGCA 5'



a | c | b

2. (2.00 pts)

A magical genie has come along and decided to test your skills in ribosome-ology. He first obtains cytoplasmic ribosomes from E. Coli and humans in a 2 : 1 ratio (i.e. 2 E. Coli ribosomes for every 1 human ribosome) and disassembles them into their component rRNA strands. Then he pulls out a single strand of rRNA. You notice that it has a sedimentation rate of < 6 S. Given this, what is the probability that the rRNA has come from a prokaryote?

Expected Answer: 0.5

3. (3.00 pts)
You are breeding a new species of exotic plants which you know have the remarkable property that each offspring has a 70% chance of being blue and a 30% chance of being red, pairwise independent of all other offspring. You know that a total of two offspring will be produced in this breeding process.

What is the probability that

a. Both offspring are red?

b. Both offspring are blue given that the first offspring is blue?

c. Both offspring are blue given that one of them is blue?

Expected Answer: a. 0.09 b. 0.7 c. 0.53846

4. (4.00 pts)
Fill in the blanks regarding bacterial DNA replication. List one answer per line.

Replication begins at the _____ (a). Here, proteins bind to the DnaA box and open the DNA at an AT-rich region to allow _____ (b) to bind, which then begins unwinding the DNA. The resulting upstream positive supercoiling is alleviated via the action of _____ (c). Once the replisome has been formed, DNA Polymerase III synthesizes DNA, while _____ (d) creates short RNA primers to facilitate DNA Polymerase III binding to the lagging strand. Then, primers are removed by the action of various exonucleases, and these gaps are filled in by _____ (e). After this, _____ (f) are formed by DNA Ligase. Replication in bacteria often results in strands ending intertwined, if this occurs, it is resolved by _____ (g) in a process known as _____ (h).

Expected Answer: a. Origin of Replication b. DNA Helicase c. DNA Gyrase d. Primase e. DNA Polymerase I f. Phosphodiester bonds g. Topoisomerase II or IV (also accept DNA Gyrase) h. Decatenation 0.5 each

5. (1.00 pts)
You observe a population of wild pigeons and notice that 91% of them are born with a cool hat on their heads. The remaining 9% are born without a cool hat on their heads :(. Assuming that having a cool hat is dominant, to not having a cool hat, and that the population is in Hardy Weinberg equilibrium, answer the following questions.

a. What percentage of the gene pool consists of the cool hat allele?

b. What percentage of the gene pool consists of the no cool hat allele?

Expected Answer: a. 0.7 b. 0.3

6. (2.00 pts)
You found a gene in a starfish with 12 exons (and 11 introns). Assuming that all splicing combinations lead to valid proteins, how many different proteins can be created from this one gene?

Expected Answer: 2^10 or 1024

7. (2.00 pts)
You discovered a population of large brained fish and are wondering about why their population is seemingly decreasing. Upon inspection of their DNA, you notice something strange the fish are tetraploid! You also notice that they have a gene X which controls brain size. Each recessive 'x' allele corresponds to a brain with a 0.5 cm smaller radius than the expected 4 cm, while the dominant 'X' corresponds to no brain size reduction.

Assuming the fish population is in Hardy Weinberg equilibrium, use the allele frequencies below to answer the following questions.

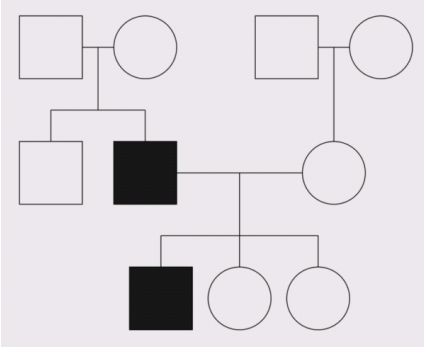
X = 0.55
x = 0.45

a. What percentage of the fish have brains with 4 cm radius?
b. What percentage of the fish have brains with 3 cm radius?

Expected Answer: a. ~9.15% b. ~36.8%

8. (1.00 pts)
List all of the following inheritance types which are possible for the pedigree shown below.

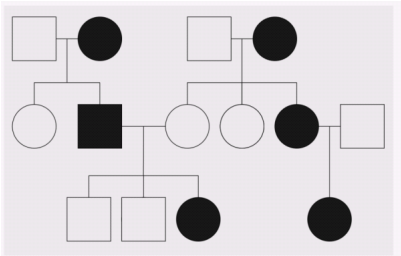
Autosomal Recessive
Autosomal Dominant
X-linked Recessive
X-linked Dominant
Mitochondrial



(Mark **ALL** correct answers)

- [x] A) Autosomal Recessive
- [ ] B) Autosomal Dominant
- [x] C) X-linked Recessive
- [ ] D) X-linked Dominant
- [ ] E) Mitochondrial

9. (1.00 pts) Identify all of the following inheritance types which are possible for the pedigree shown below.



(Mark **ALL** correct answers)

- [x] A) Autosomal Recessive
- [x] B) Autosomal Dominant
- [ ] C) X-linked Recessive
- [x] D) X-linked Dominant
- [ ] E) Mitochondrial

Part 2: Mrs. Cheney and the Heartbreakers [19.5 points total]

Mrs. Cheney's husband's heart problem is complicated.

Based on concepts from Anatomy & Physiology, they deduced the heart condition to be one of the following diseases:

1) Familial Dilated Cardiomyopathy (DCM)

2) Arrhythmogenic right ventricular cardiomyopathy (ARVC)

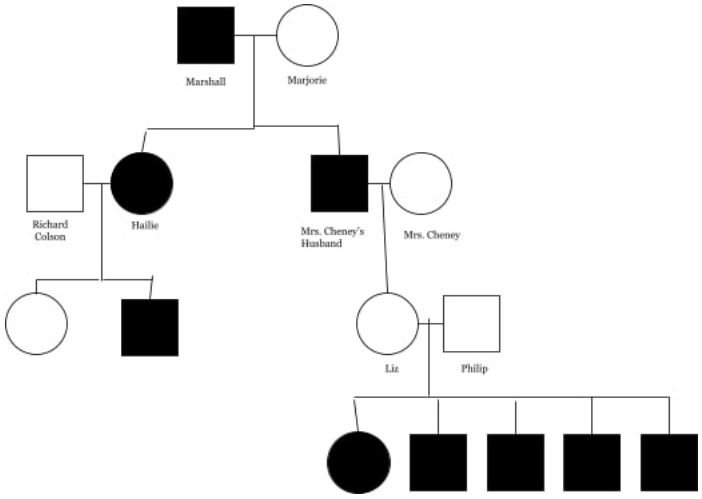
3) Short QT Syndrome (SQTS)

4) Marfan syndrome

Now they consult a geneticist to help figure out which disease Mrs. Cheney's husband has.

DCM is caused by a mutation that can either be autosomal dominant or autosomal recessive depending on the specific gene that is mutated.

Here is Mrs. Cheney's husband's pedigree:



In addition to the Cheney pedigree, it is common knowledge that the Richard Colson and Mrs. Cheney family trees have no history of DCM. On the other hand, Philip does. DCM has 100% penetrance for both mutation types.

Assume a blackened shape indicates the presence of some type of familial DCM.

There are three possible alleles in the pedigree:

D- the dominant mutation that results in a distinct type of DCM.
R- the recessive mutation that results in a distinct type of DCM (only when both alleles are present)
wt- the normal allele that does not contribute to DCM.

10. (1.00 pts) What is the genotype of Marshall?

- A) R R
- B) D wt
- C) D R
- D) R wt

11. (1.00 pts) Geneticists need to know which type of DCM Mrs. Cheney's husband has, as recessive DCM is more severe. What type of DCM does Mrs. Cheney's husband have?

- A) Dominant
- B) Recessive
- C) Both
- D) Not enough information to reasonably tell

12. (1.00 pts)
Mrs. Cheney is worried that her future offspring will have DCM. She plans to have two more children. What is the probability that at least one of those children will have some form of familial DCM?

- A) 0%
- B) 25%
- C) 50%
- D) 75%
- E) 100%

13. (1.50 pts) All five of Liz and Philip's children have DCM. What was the probability that all five would have the disease? (as a reduced fraction)

Expected Answer: 1/1024

Geneticists look at the pedigree and question whether the heart condition is familial DCM altogether. The geneticists use the same pedigree but hypothesize the condition is ARVC, an autosomal dominant condition with a 50% penetrance. Assume only Marshall and his pedigree have a history of ARVC.

14. (1.00 pts) If the pedigree is of ARVC, then which member of the pedigree must have a genotype that may result in ARVC?

- (●) A) Liz
- ( ) B) Richard Colson
- ( ) C) The children of Richard Colson
- ( ) D) Marjorie

15. (1.00 pts) If the daughter of Liz and Philip mated with one of her brothers, what is the probability their child will have AVTC?

- ( ) A) 0
- (●) B) $\frac{3}{8}$
- ( ) C) $\frac{1}{2}$
- ( ) D) $\frac{3}{4}$

16. (1.00 pts) How many individuals in the pedigree have an uncertain genotype based on just the information provided?

- ( ) A) 1
- (●) B) 2
- ( ) C) 4
- ( ) D) 7

17. (1.00 pts) Name one of the individuals that have an uncertain genotype (from the question above)

Expected Answer: Marshall, Marjorie

Marshall

To determine whether the disease is DCM or ARVC, the doctors do the following crosses:

- Richard Colson x Liz

- Liz's son x Liz's daughter

18. (0.00 pts) Which of the following conclusions is most accurate?

- A) If zero children are produced in total, DCM is the most likely condition
- B) If one child is produced, ARVC is the most likely condition
- C) If zero or two children are produced in total, it is unclear if the condition is DCM or ARVC
- D) If one or two children are produced in total, it is unclear if the condition is DCM or ARVC

19. (1.00 pts) Which of the following crosses would definitively indicate which disease is responsible for Mrs. Cheney's husband's heart problem, regardless of the result?

- A) Marshall x Liz's daughter
- B) Richard Colson x Liz
- C) Richard Colson's daughter x Philip
- D) None of the above

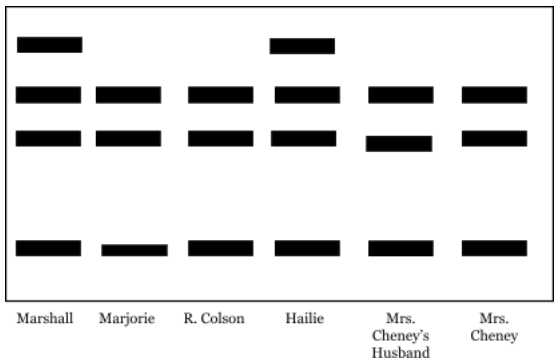
20. (2.00 pts) Under the principle of parsimony, is DCM or ARVC more likely?

- A) DCM
- B) ARVC
- C) Both are equally likely
- D) Both are equally unlikely

The confusion of all these pedigrees and crosses makes you leave genetic counseling to become a molecular geneticist.

You move onto Short QS syndrome, and learn that 60% of all patients with Short QS syndrome have "mutations in the genes KCNQ1 (11p15.5), KCNH2 (7q36.1), and KCNJ2 (17q24.3), encoding cardiac ionic potassium channels, and the gene encoding the calcium channel, CACNA2D1 (7q21.11)" (Orpha.net)

You observe KCNJ2. From your knowledge of this specific gene, you know that if either allele deviates from KCNJ2 wild type, then Short QS syndrome will happen.



21. (1.00 pts) Based on the electrophoresis above, does Mrs. Cheney's husband has Short QS syndrome?

- A) Yes
- B) No

C) All of the above

D) Not enough information

22. (2.00 pts)
What information does this electrophoresis reveal about the pedigree that one cannot deduce only from the pedigree, assuming that the pedigree depicts Short QS syndrome?

A) Hailie is heterozygous dominant for the heart disorder in question

B) Marshall is homozygous dominant for the heart disorder in question

C) The children of Liz and Philip must be homozygous dominant

D) All of the above

23. (0.00 pts)
Assuming the pedigree is of Short QS syndrome and given the electrophoresis, what is the approximate probability that Richard Colson and Hailie's next child will have four bands in their electrophoresis of KCNJ2?

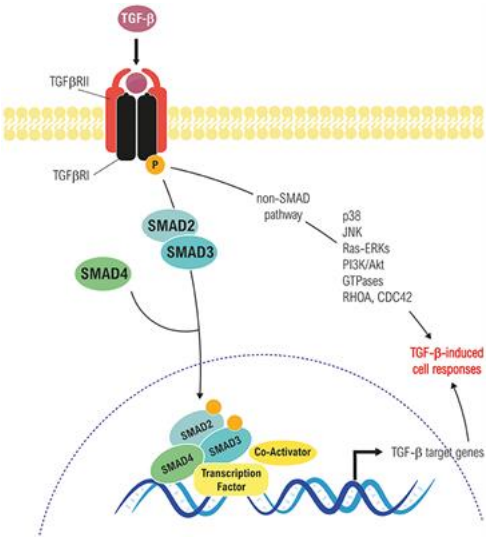
A) 0

B) $\frac{1}{4}$

C) $\frac{2}{3}$

D) $\frac{3}{4}$

Finally, time to test for Marfan's Syndrome. You get sick of genes, and now you want to test the presence of the actual protein products. Marfan's syndrome is the result of a high extracellular concentration of TGF-B.



24. (1.00 pts) A wild type individual (without Marfan's syndrome) would have:

A) Less transcription of TGF-B target genes

B) More binding between SMAD genes

C) There will be more GTPase activity

D) All of the above

25. (2.00 pts) Based on the diagram above, if the individual with Marfan's syndrome also had a missing co-activator, what would most likely be the result?

A) Transcription of TGF-B target genes would increase
B) SMAD genes would not be transcribed
C) TGF-B induced responses would decrease
D) Some TGF-B-induced responses might continue

Part 3: let your partner do this one [3 points total]

There is a population of 200 humans isolated from the rest of the world. They have alleles A and B that express codominance. 43 have A, 44 have B, and 113 have AB.

26. (1.00 pts) What is the allele frequency of B?

Expected Answer: .5025

27. (2.00 pts) In Hardy-Weinberg equilibrium, what would the expected frequency of AB be? (rounded to the nearest hundredth)

Expected Answer: 0.50

Part 4: use brain thx! [4 points total]

28. (1.00 pts) Order the following molecules in chronological order in which they are involved with microRNA biogenesis:

I: Drosha and DGCR8

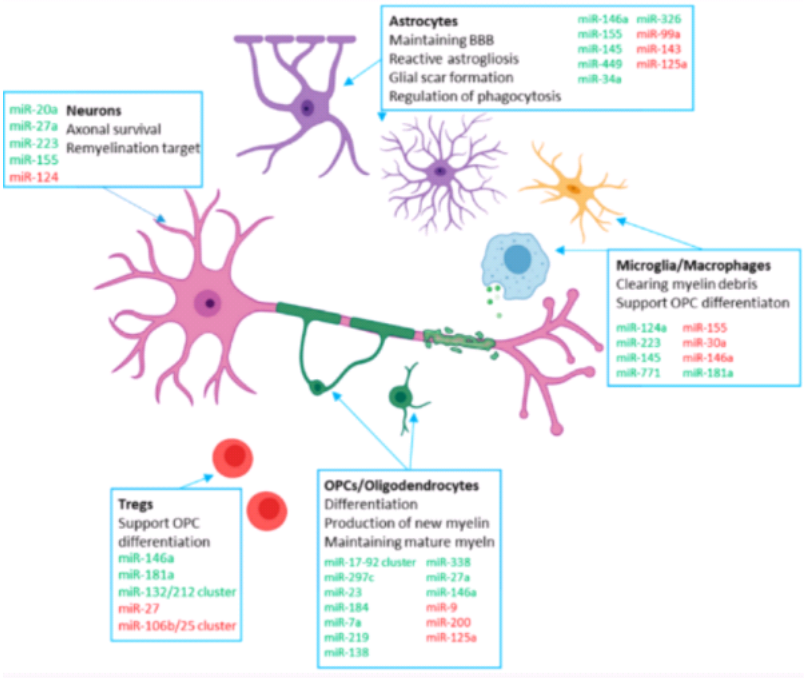
II: Exportin 5

III: RNA Polymerase II

IV: Dicer

A) III, IV, I, II
B) II, III, I, IV
C) III, I, II, IV
D) II, I, IV, III

When dicer is removed from mice, normal remyelination does not occur in mice.



Red indicates the miRNA inhibits remyelination. Green indicates miRNA that promotes remyelination. There are two important parts of remyelination: creation of the myelin and phagocytosis of the old tissue. OPCs are precursors to mature oligodendrocytes.

29. (1.00 pts) Removing dicer from which cell will most significantly hinder myelination?

- A) Neuron
- B) Astrocyte
- C) Oligodendrocyte
- D) Treg

30. (0.00 pts) Order I-IV that matches the appropriate microRNA to the correct function in the respective order: miR-23, miR-124, mir-34a, and miR-223.

I: Expressed in a cell that is not microglia to prevent microglia from inhibiting phagocytosis

II: Internally inhibits neuron from remyelination

III: Phagocytosis of old myelin tissue

IV: Maintains new myelin tissue through inhibiting lamin B

- A) IV, II, I, III
- B) IV, I, III, II
- C) III, I, IV, II
- D) II, III, I, IV

31. (1.00 pts)
OPCs are The exact mechanism of miRNAs on promoting remyelination is uncertain. When a patient with multiple sclerosis was given mature oligodendrocytes that lacked related green-colored miRNAs (indicated by the diagram), remyelination improved. From this scenario, we can conclude that miRNAs in OPCs have a similar function as:

- A) Tregs
- B) Oligodendrocytes

C) Astrocytes

D) Neuron

Part 5: 6th grade-level Designer Genes [9 points total]

POV: You walk into an invitational with a low quality designer genes test.

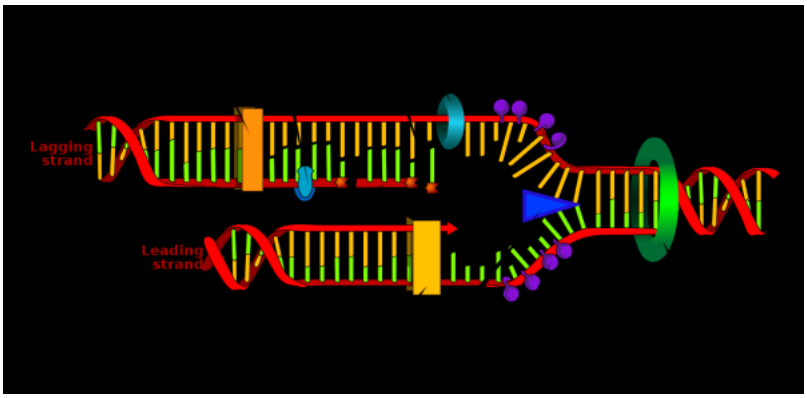
32. (1.00 pts) What year was Dolly cloned from an adult somatic cell?

A) 1823

B) 1904

C) 1994

D) 1996



33. (1.00 pts) Being as specific as possible, which type of cell is this a diagram of?

A) Prokaryotic

B) Eukaryotic

C) Plant cell

D) Animal cell

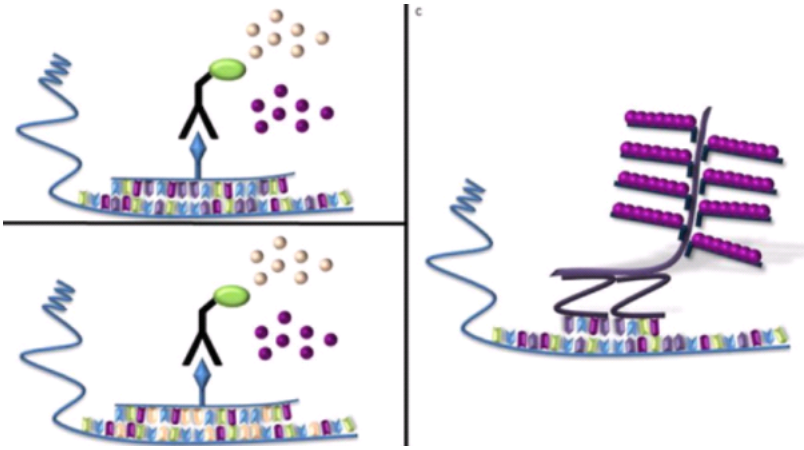
34. (1.00 pts) A cell is stripped away from all RNA polymerases. Will the cell have any immediate negative impacts on DNA replication and why?

A) Yes, because a type of RNA polymerase is a necessary enzyme for DNA replication as depicted in the diagram above

B) Yes, because a type of RNA polymerase is a necessary enzyme for DNA replication, although not depicted in the diagram above

C) No, because RNA polymerase is only relevant after pre-mRNA is transcribed

D) No, because RNA polymerase is only relevant after mRNA is transcribed



35. (1.00 pts) In situ hybridization is pictured above. What is one reason in situ hybridization is effective on viruses?

- (●) A) Some viruses are single-stranded, allowing probing to occur easily
- ( ) B) Some viruses are double-stranded, allowing complementation to happen naturally
- ( ) C) Some viruses are transcribed by RNA-dependent RNA polymerase, allowing it to be error prone, increasing diversity for probing
- ( ) D) Some viruses are transcribed by DNA-dependent RNA polymerase that prevent errors to shift results

36. (1.00 pts) Which of the following is a “con” of using FISH demonstrated in the image above?

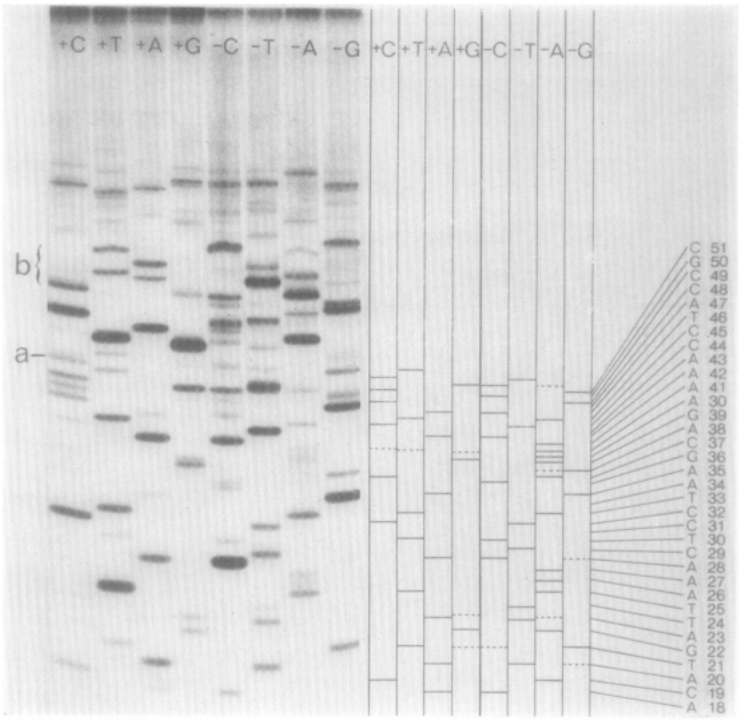
- ( ) A) Low detection rates lead to inefficiencies
- ( ) B) Can only detect presence of cells in cells that are cultured synthetically
- ( ) C) Does not provide localized information of a specific molecule, but rather simply the general “presence” of a molecule
- (●) D) A researcher must know the specific DNA sequence of the target sequence

37. (1.00 pts) Which of the following is a synthetic inducer of the lac operon?

- (●) A) Isopropyl beta d thiogalactopyranoside
- ( ) B) Lactose
- ( ) C) Allolactose
- ( ) D) All of the above

38. (1.00 pts) Which of the following most accurately describes the function of aminoacyl tRNA synthetase?

- ( ) A) Enzyme that catalyzes translation through forming peptide bonds between adjacent amino acids
- ( ) B) Enzyme that ensures amino acids are in the right chiral conformation when attached to the polypeptide
- (●) C) Enzyme that charges an appropriate tRNA through matching an appropriate amino acid with tRNA
- ( ) D) All of the above



39. (1.00 pts) Which type of DNA sequencing is depicted in the image above?

- (●) A) Sanger sequencing
- ( ) B) Next gen sequencing
- ( ) C) NexEdge sequencing
- ( ) D) Illumina sequencing

40. (1.00 pts) Which researchers discovered the semi-conservative nature of DNA?

- ( ) A) Hershey-Chase
- ( ) B) Watson-Crick
- (●) C) Messelson-Stahl
- ( ) D) Franklin-Hawkins

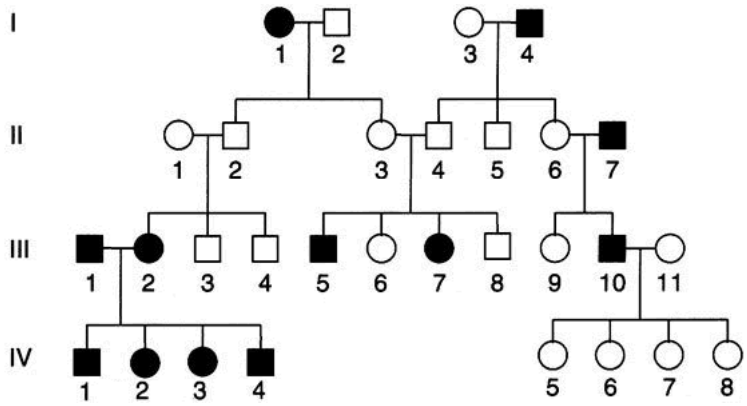
Part 6: Questions to do with a significant other [15.5 points total]

41. (2.00 pts)
After taking an ancestry test and binging “The Album”, little B found that he was “⅓ korean”. little B looked at his family tree, and found that he only has four levels of ancestors: parents, grandparents, great grandparents, and great great grandparents (little B was born around the beginning of humanity). What combination of his ancestors can be korean to get him closest to being ⅓ korean?

- ( ) A) The paternal parent is half korean and the maternal parent is quarter korean
- (●) B) The maternal parent is half korean and one great great grandparent from the paternal side is korean
- ( ) C) The great great grandparent and parent from the same lineage is korean
- ( ) D) A great great grandparent and parent from different lineages are korean

42. (2.00 pts) Which of the following reasons accurately describe why rRNA is used in phylogenetic analysis?

- (●) A) rRNA is highly conserved yet contains slight polymorphic sequences, and thus can allow for analysis between species that may have diverged many years prior
- ( ) B) rRNA contains virtually no polymorphisms, allowing it to be a reliable reference to construct cladograms that lack synapomorphies
- ( ) C) There is high diversity of rRNA among different kingdoms, allowing for one to differentiate between species of the same genera
- ( ) D) rRNA is scarce in human cells, preventing overflow of differing genetic data given a specific sample



43. (0.00 pts)
Assuming that heterozygotes have a 25% chance of getting kidney stones in a kidney and homozygous recessive individuals have a 75% chance of getting it in one kidney but a 50% chance of getting it in both kidneys, what is the probability that 5 people will have kidney stones in at least one of their kidneys in generation II (Assume each kidney has an equal, bu independent chance of getting a kidney stone)?

Expected Answer:

44. (1.00 pts) When performing immunofluorescence, why does a secondary antibody typically originate from a different host species?

- ( ) A) Lack of diversity in the same host prevents new motifs from being probed
- (●) B) An organism is unable to produce antibodies against its own antibodies
- ( ) C) Humans are unable to produce antibodies by “demand” and thus must use a different species
- ( ) D) All of the above

There are two genetic disorders in the U.S. population (the inheritance and prevalence are made up):

Scoliosis: an autosomal dominant condition.

Kyphosis: an autosomal recessive condition.

The prevalence of scoliosis in the U.S. is 4%.

The prevalence of kyphosis is 4% as well. Assume hardy weinberg conditions.

Mr. Red and Mrs. Blue are two “loving” siblings that regularly have children through incest. Mr. Red has scoliosis while Mrs. Blue does not. Only one parent of the couple has scoliosis.

Mr. Anhinga and Mrs. Mallard are also two “loving” siblings that have children through incest. Mrs. Mallard has kyphosis and Mr. Anhinga does not. Neither of their parents had kyphosis.

45. (1.00 pts) What is the genotype of Mr. Anhinga and Mrs. Mallard's mother? (K = dominant, k = recessive)

- (●) A) Kk
- ( ) B) kk
- ( ) C) KK
- ( ) D) Cannot be determined with given information

46. (2.00 pts) What is the probability of Mr. Anhinga and Mrs. Mallard's child having kyphosis?

Expected Answer: 1/3

47. (2.50 pts)
Mr. Red would like to mate, but he is afraid his child will have scoliosis. He finds a suitable mate, Mrs. Stork to impregnate. What is the difference in probability between the offspring of Mrs. Stork and Mr. Red child having scoliosis and Mrs. Blue and Mr. Red's child? Mrs. Stork's phenotype is unknown as of now!

Expected Answer: 1.37% difference or 2.74% (51.37% vs 50%)

48. (2.00 pts)
Mr. Anhinga is also interested in Mrs. Stork and wonders how much more likely his child with Mrs. Mallard will have kyphosis is compared to his potential child with Mrs. Stork. What should we tell him?

Expected Answer: it will be 5x as likely, 26.67% difference (33.33% vs. 6.67%)

49. (1.00 pts) From your answers to the two questions above, which type of inheritance pattern of a disease is most susceptible to becoming worsened through incest?

- ( ) A) Autosomal dominant
- (●) B) Autosomal recessive

Part 7: Gold Dust NayNay [12 points total]

50. (1.00 pts) Which properties are shared by RNA and DNA Polymerases?

- A) 5' triphosphate terminus
- B) 5' → 3' repair synthesis
- C) Semi-conservative replication
- D) 5' → 3' polymerization

51. (1.00 pts) Which of the following RNA molecules is not made by polymerase I, II, or III?

- A) tRNA
- B) RNA primer
- C) snRNA
- D) rRNA

52. (1.00 pts)
Tom is an E. Coli bacterium that has a mutation in CAP. Tom is in a colony of bacteria and Dr. Drew would like to pinpoint which one is Tom! Drew plates glycerol, X-gal, and a synthetic inducer of the lac operon. How can Drew identify which is Tom, assuming the rest of the colony is a wild type?

- A) Blue, for without CAP, lac operon is constantly expressed
- B) White, for without CAP, there is no transcription of the lac operon
- C) Blue, because cAMP is abundant in the presence of glycerol
- D) The bacteria will not grow in this minimal medium

53. (1.00 pts) microRNA-mediated binding of the RISC regulates which of the following:

- A) Ribosomal activity
- B) Accessibility to gene promoter
- C) mRNA degradation
- D) Protein degradation

54. (2.00 pts)
Mr. American Bittern is examining three gene sequences that influence transcription rates of a downstream gene. Which gene is the enhancer and silencer, respectively?

	WT	Gene 1 Knocked Out	Gene 2 Knocked Out	Gene 3 Knocked Out
Relative level of mRNA	1	.5	2.1	1

Expected Answer: Gene 1, Gene 2

55. (1.00 pts) Mr. Hawk has a mutation in a transcription factor that binds to an enhancer upstream of TNFR1. Which of the following best describes the resulting effect?

- A) Immune cells are unable to recognize infected cells
- B) Tumor Necrosis Factor will not be produced
- C) Apoptosis cannot occur in normal cellular tissues
- D) All of the above

56. (1.00 pts)
Mr. Kinglet is infected by only the genome of a specific type of virus (without any viral proteins). Which of the following types of viruses would successfully infect Kinglet?

- A) Negative-sense, ssRNA viruses
- B) Positive-sense, ssRNA viruses
- C) Negative-sense, dsRNA viruses
- D) None of the above

57. (1.00 pts)
A protein called MATH54 in a strain of SARS-CoV-2 is discovered to block the synthesis of pre mRNA in human cells, preventing the formation of proteins involved in immune responses. Which of the following molecules does MATH54 most likely suppress?

- A) RNA Polymerase II
- B) Reverse Transcriptase
- C) RNA-dependent RNA polymerase
- D) Cas9

58. (1.00 pts) Why are centromeres not separated during anaphase I of meiosis but arms are?

- A) Prevent crossing over in Meiosis I
- B) Disassembly of synaptonemal complex during Meiosis I
- C) Allow homologous chromosomes to separate after crossing over
- D) Prevent separation of non-sister chromatids

59. (1.00 pts) Mrs. Cardinal is triploid. Why is she infertile?

- A) Crossing over between three homologs prevents separation
- B) Homologous chromosomes cannot pair properly, so most gametes are aneuploid
- C) Nondisjunction of sister chromatids results in an extra copy of every chromosome
- D) Nondisjunction of homologous chromosomes results in genetic variation that is mutated, such as trisomy 21

60. (1.00 pts) mRNA viruses are all the craze these days with the kids!

Why might an mRNA vaccine be better than a protein-based vaccine?

- A) mRNA directly provides the actual genetic information necessary to trigger the immune response
- B) Proteins do not provide enough diversity to recognize and discriminate from native proteins
- C) mRNA is easier to produce and inject to the body as opposed to manufacturing viral proteins or weakened viruses
- D) mRNA is delivered unencapsulated, while proteins have different polarities that need to be controlled for

Section 2

Written by Fishy, Greygrey, and Kaela

Part 1: Caterpie Crossing [13 points total]

The table below shows the results of Fishy's Caterpie breeding attempt involving two Caterpies. The traits follow a dominant/recessive pattern of inheritance.

Phenotype	Number of Offspring
Green body, pink bow, yellow rings	423
Gold body, red bow, light yellow rings	430
Gold body, pink bow, light yellow rings	3
Green body, red bow, yellow rings	6
Gold body, pink bow, yellow rings	38
Green body, red bow, light yellow rings	36
Gold body, red bow, yellow rings	31
Green body, pink bow, light yellow rings	33

61. (2.00 pts) What are the parental phenotypes?

Expected Answer: 1. Green body, pink bow, yellow rings 2. Gold body, red bow, light yellow rings

62. (3.00 pts) Determine the distances between the locus for the genes coding each phenotype.

Expected Answer: 8.3mu between body color and bow color (3+6+38+36)/1000 * 100 = 8.3 7.3mu between ring color and bow color (3+6+31+33)/1000 * 100 = 7.3 15.6mu betweer body color and ring color 7.3+8.3 = 15.6

63. (2.00 pts) What is the expected number of DCOs in this cross? Round your answer to the nearest three decimal places.

Expected Answer: 0.083 * 0.073 * 1000 = 6.059

64. (3.00 pts) What is the coefficient of coincidence? Round your answer to the nearest three decimal places.

Expected Answer: 0.009/0.006059 = 1.485

65. (3.00 pts) What is the coefficient of interference? Round your answer to the nearest three decimal places.

Expected Answer: 1-1.485 = -0.485

66. (3.00 pts) What does your value for the coefficient of interference mean in the context of this problem?

Expected Answer: There are more DCOs than expected (1). A single crossover event increases the likelihood of a second crossover event. (1)

Part 2: Fishy's Wishiwashis [12 points total]

The table below shows the results of Fishy crossing two wishiwashis, one with genotype ABCD and the other abcd, resulting in 1002 offspring.

Genotype	Number of Offspring
A B C D	69
a b c d	258
A b c d	139
a B C D	42
A B c d	169
a B C d	38
a b C D	47
A B C d	49
a b c D	41
a B c d	80
A b c D	21
A b C D	16
A B c D	14
a b C d	9
A b C d	7
a B c D	3

67. (2.00 pts) Determine the map distance between genes A and B.

Expected Answer: 346/1002 * 100 = 34.5

68. (2.00 pts) Determine the map distance between genes A and C.

Expected Answer: 479/1002 *100 = 47.8

69. (2.00 pts) Determine the map distance between genes A and D.

Expected Answer: 497/1002 *100 = 49.6

70. (2.00 pts) Determine the map distance between genes B and C.

Expected Answer: 345/1002 * 100=34.4

71. (2.00 pts) Determine the map distance between genes B and D.

Expected Answer: 461/1002 * 100= 46.0

72. (2.00 pts) Determine the map distance between the genes C and D.

Expected Answer: 182/1002 * 100= 18.2

Part 3: Fishy's Valentine's Day [9 points total]

Budding plant geneticist Fishy Krishy seeks to understand the inheritance pattern for a certain flower that he wants to give to his girlfriend on their anniversary. On his expeditions, he only finds white-colored flowers and red-colored flowers. However, when he crossed a white flower and a red flower, the F1 offspring exhibited flower colors on a spectrum of intensity from white to red in varying shades of pink. He finds that in the F1 generation, only 2 of his 527 flowers are either red or white.

73. (1.00 pts) What form of inheritance is this?

Expected Answer: Polygenic inheritance

74. (2.00 pts) How many genes control the expression of the trait?

Expected Answer: 4

75. (2.00 pts) How many different phenotypic variations are there?

Expected Answer: 9

76. (3.00 pts) What fraction of Fishy's F1 flowers should exhibit the most common phenotypic variation?

Expected Answer: 3/8

77. (2.00 pts) These mathematical calculations are based on a single, simple. but a very important assumption. What is it?

Expected Answer: These traits are unaffected by environmental factors

Part 4: h E R e D i t Y [25 points total]

Oftentimes, when confronted with multifactorial traits, geneticists such as Fishy Krishy wish to determine the heritability of a trait.

78. (3.00 pts) Define heritability. What does a low or high heritability mean?

Expected Answer: Heritability is the proportion of total phenotypic variation (1) in a population due to genetic variation (1) in a specific environment. High heritability suggests a trait mostly influenced by genetic factors (0.5) whereas low heritability is a trait that is mostly influenced by environmental factors (0.5)

79. (3.00 pts) In a mathematical calculation of heritability, there are normally three primary components. Name them.

Expected Answer: Genotypic variance (1) Environmental variance (1) Genotype-by-environment interaction variance (1)

80. (2.00 pts)
In order to better understand heritability, geneticists often decompose heritability into different subcategories. One of these is Broad-Sense Heritability, which measures the contribution of genotypic variation on phenotypic variation. Given that Broad-Sense Heritability values for a trait range from 0 to 1, derive an expression to estimate a value for Broad-Sense Heritability.

Expected Answer: H^2 = VG/VP (Genotypic variation/Phenotypic variation)

81. (3.00 pts) However, for geneticists working in breeding programs, Broad-Sense Heritability is limited in its usefulness. Why is this so?

Expected Answer: Broad-Sense heritability doesn't specify the type of inheritance for a phenotypic trait (i.e, could be mendelian, quantitative, epistatic, etc.) (2). As a result, breeder may not be able to properly select for beneficial traits (1).

82. (4.00 pts)
In response to this problem, Narrow-Sense heritability, which measures the proportion of phenotypic variance due to additive genotypic variance (quantitative traits), is often the measurement of choice for breeders. However, in order to compute this, it is necessary to partition genotypic variance into three separate categories. If additive genotypic variance is one of these three, what are the other two?

Expected Answer: Dominance variance (Phenotypic expression in heterozygotes not precisely intermediate between two homozygotes) (2) Interactive variance (Deviation due to epistatic behavior between multiple loci) (2)

83. (2.00 pts)
Clearly, heritability is an important factor for breeders to consider. How might the heritability of a trait influence the ability of breeders to properly do their job? In other words, what is the significance of heritability on the effectiveness of artificial selection?

Expected Answer: Heritability is what determines the effectiveness of artificial selection (1). If phenotypic traits are not highly heritable by genetics, they cannot be artificially selected for (1).

84. (6.00 pts)
Although this estimate of Narrow-Sense heritability is ideal in theory, in practice it is much harder to measure. As a result, a separate measure is often used. In this method, Narrow-Sense heritability is defined as R/S, where R represents the selection response and S the selection differential. Classically, the computation of R and S requires only three measurements: Mean population score (M), Parent score (M1), and Offspring score (M2). Given that R = M2 - M and S = M1 - M, define the measurement of R and S.

Expected Answer: R is the difference between quantitative traits between offspring and a general population (e.g. how much is gained by mating for artificial selection) (3) S is the difference between quantitative traits between parents and a general population (e.g. how much there is to be gained by mating for artificial selection) (3)

85. (4.00 pts)
Now, consider the following situation regarding the fruit size of a berry bush where the mean population berry size is approximately 5 cm. As a breeder, you want to increase the berry size of the smallest berry-producing bushes. You select a group of berry bushes that produce a mean berry size of only 2 cm. After interbreeding these small-berry-producing bushes with other bushes, the new bushes produce berries with an average size of 3 cm. Compute a value of Narrow-Sense heritability for this berry bush. What does this mean in terms of artificial selection?

Expected Answer: h^2 = (3-5)/(2-5) = 0.67 (2) This means that the selection potential for berry size is relatively high (2)

Part 5: Fishy's Discord pfp [19 points total]

Fishy discovers a population of Espeons. Espeons have an incompletely dominant gene coding for fur length, where *FF* produces a not floofy, *Ff* produces a semi-floofy, and *ff* produces an extremely floofy phenotype.

86. (3.00 pts) For every 10 not floofy individuals that survive, 6 semi-floofy and 2 extremely floofy individuals survive. What are the relative fitness values for each phenotype?

Expected Answer: Not floofy = 1.0 (highest survival is assigned 1.0) Semi-floofy = 6/10 = 0.6 Extremely floofy = 2/10 = 0.2

87. (3.00 pts)
Assuming that the first generation (P) of 1,000 Espeons followed Hardy-Weinberg equilibrium with allele frequencies of 0.5 for both the *F* and *f* alleles, how many individuals expressed each phenotype in the first generation?

Expected Answer: 250 not floofy 500 semi-floofy 250 extremely floofy

88. (3.00 pts)
In the following generation, the Hardy-Weinberg equilibrium is modified by taking into account relative fitness values. Using the fitness values in the first part of this section, what are the genotype frequencies for the F1 generation?

Expected Answer: 0.5^2 * 1 = 0.25. 0.25/0.6 = 0.417 not floofy 0.5 * 0.5 * 2 * 0.6 * 1000 = 0.3. 0.3/0.6 = 0.5 semi-floofy 0.5^2 * 0.2 * 1000 = 0.05. 0.05/0.6 = 0.083 extremely floofy

89. (2.00 pts) The mean fitness of the population is the sum of the modified genotype frequencies. What is this value for the F1 generation?

Expected Answer: 0.6 = 0.25 + 0.3 + 0.05

90. (3.00 pts)
Is the value for the mean fitness of the population expected to change in the F2 generation assuming the same relative fitness values apply? If it does change, does this value increase or decrease? Explain using words. Do not calculate the mean fitness value for the F2 generation.

Expected Answer: Mean fitness value is expected to increase (1) because the population overall has more not floofy Espeon's (1) and the not floofy Espeons are the most fit for the environment (1)

91. (0.00 pts)
Is the value for the mean fitness of the population expected to change in the F2 generation assuming the same relative fitness values apply? If it does change, does this value increase or decrease? Explain using words. Do not calculate the mean fitness for the F2 population.

Expected Answer: Mean fitness value is expected to increase (1) because the population overall has more not floofy Espeon's (1) and the not floofy Espeons are the fittest for their environment (1) If someone actually calculates the mean fitness of the F2 population, just give 3 points. Thrown out cause duplicate

92. (1.00 pts) What type of natural selection does this scenario fall under?

Expected Answer: Directional selection

93. (1.00 pts) If given the relative fitness values of 0.3 for the *FF* phenotype, 0.2 for the *ff* phenotype, and 1.0 for the *Ff* phenotype, what type of natural selection would this be?

Expected Answer: Stabilizing selection

Part 6: Filo-jihn-ehtyks [8 points total]

Trait diversity is a result of variation in gene expression within and between species. Gene regulatory networks combine the elements of TFs, enhances, promoters, etc. Mutational events altering these elements can be regarded as either cis- or trans-acting.

94. (1.00 pts) Explain the difference between cis- and trans-acting.

Expected Answer: Cis-acting alter gene expression of a gene located on the same chromosome and typically close to the affected gene [+0.5]. Trans-acting affects gene expressior by diffusible molecules located anywhere within the genome [+0.5].

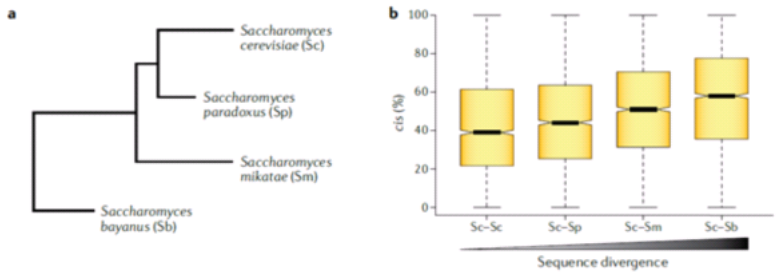
95. (1.00 pts) Which of the following are possible reasons to explain why one gene shows more variation in expression than another?

- A) Under less selective pressure
- B) A greater fraction of new mutations alter the expression
- C) Both A and B

96. (2.00 pts)
When studying different expression systems, it's important to first determine if it is based on cis-regulatory or trans-regulatory systems. There are two methods to understand the effects of each. One method is allele-specific expression. The other is by using statistical associations between gene expression and variation to identify possible eQTLs. With these methods, it is determined that trans-regulatory contributes more to gene expression than cis-regulatory. Why is this so?

Expected Answer: There is a larger mutational target size for trans-regulatory [+1]. Trans elements, on average, are able to affect the expression of more genes than cis [+1].

97. (1.00 pts)
The following is a phylogenetic tree (figure a) of 4 yeast species with different branch lengths showing relative divergence. Figure b shows the contribution of cis-regulatory difference between pairs of species shown in Figure a.



Describe the relative trend in cis-regulatory variation and divergence.

Expected Answer: Increasing contributions of cis-regulatory variation to expression differences with increasing divergence time.

98. (2.00 pts)
eQTLs contribute to genetic variance greatly as well. Variation is typically polygenic with multiple variants contributing to variability in many genes. eQTL mapping experiments with more than one generation of recombination for breakage of linked sites will be followed by something called bulk segregant analysis of those individuals with extreme phenotypes. What is bulk segregant analysis?

Expected Answer: A technique used to associate genetic markers with trait variation by contrasting allele frequencies between two groups of individuals defined by differences in trait values.

99. (1.00 pts) Mechanisms behind cis-regulatory variation can become incredibly complex. Mutations in cis-regulatory regions with the largest impact are in which region?

- (●) A) Core promoter
- ( ) B) Enhancer
- ( ) C) Silencer
- ( ) D) A and B only
- ( ) E) B and C only
- ( ) F) A and C only

Part 7: Fishy is poggers [8 points total]

Fishy is studying chromosome-inactivation in the mammal *Fake* species ((consisting of both males and females)). In F species, the 26th chromosome is inactivated in a process similar to X-inactivation. All F species individuals will inactivate either of their 26th chromosomes. All cells in an *F* species individual share the same inactivated 26th chromosome. They find that the probability of the inactivation of an allele in the gene *pog* is determined by that allele's frequency in the population. The probabilities of inactivation for any two alleles *A* and *B* are a/(a+b) and b/(a+b), respectively, where a and b are the frequencies of *A* and *B*. A population of 100 *F* species in Hardy-Weinberg equilibrium has only the dominant allele *i* and the recessive allele *d* for *pog*.

100. (4.00 pts) If 16 individuals are *dd*, how many individuals in the population are expected to have an inactivated chromosome with the *i* allele?

Expected Answer: d = .4 i = .6 (.6^2 + 2*.6 times .4 times (.6)/(.4+.6)) *100= 64.8 [+4] Explanation ii -> Xi will be inactivated id -> (i)/(d+i) that Xi will be inactivated dd -> Xd will be inactivated

101. (4.00 pts)
In a population of 200 individuals at Hardy-Weinberg Equilibrium, *pog* has alleles *i*, *d*, and *k*. 32 individuals are *ii*, 64 individuals are *id*, and 32 individuals are *ik*. How many individuals are expected to have an inactivated chromosome with the *k* allele?

Expected Answer: i = .4, d = .4, k = .2 (.2^2 +.2*.4 *(.2/.6) * 2 * 2)*200 = ~29.3

Part 8: Bob the Builder [7 points total]

BER utilizes DNA glycosylases. It is the primary repair mechanism for base lesions that are of small size.

102. (1.00 pts) Which of the following are primarily repaired through BER? Select ALL that apply.

(Mark **ALL** correct answers)
- [x] A) Deamination
- [x] B) Methylation
- [x] C) Misincorporation
- [ ] D) Long bp deletion
- [x] E) Oxidation

There are 11 glycosylases in humans which are segregated into 4 groups: UDGs, HhH, MPG, and one other.

103. (1.00 pts) UNG2 is a specific type of uracil DNA glycosylase and is located in the nucleus. Which of the following is true of UNG2? Select ALL that apply.

(Mark **ALL** correct answers)
- [ ] A) Mainly responsible for U:G base pair mismatch
- [x] B) Turnover is regulated by Cdks
- [x] C) Associates with replication complexes

104. (2.00 pts)
Somatic hypermutation and class switch recombination also utilize UNG2. Given the fact that cytidine deaminase (AID) is involved in these two processes, what is the functional role of UNG2 in these processes?

Expected Answer: Removes uracil generated by cytidine deaminases

105. (1.00 pts) TDG is another enzyme but has a function in removing the thymine in G:T bp mismatches. G:T mismatches are derived spontaneously from 5-mC deamination.

- (●) True
- ( ) False

10% of the global population have the TDG Gly199Ser variation. The function of Gly199 is to block retrograde flipping of the abasic site that would bring the site back into the DNA helix.

106. (1.00 pts) Why is the mutation into a serine more harmful?

Expected Answer: Serine strengthens the TDG interactions with the abasic site thus leading to possible DSBs, etc.

Part 9: Arginylasparaginylalanine < Aspartylasparaginylalanine [8 points total]

RNAs are much less stable than DNAs.

107. (1.00 pts) The half-lives of RNAs differ based on what kind of RNA it is. Which of the following is likely to have a longer half-live in a prokaryotic cell?

- ( ) A) mRNA
- (●) B) tRNA

108. (1.00 pts) RNAs with short half-lives are hard to analyze through Northern Blots. Which of the following can be used instead?

- (●) A) RT-PCR
- ( ) B) Normal PCR
- ( ) C) Southern Blot
- ( ) D) Eastern Blot

109. (2.00 pts)
Post-transcriptional processing occurs at the 3' and 5' ends of RNA. Primer extension can be used to map the 5' end. The first step in doing this is to create a suitable primer. Which of the following is true about this primer? Select ALL that apply.

(Mark **ALL** correct answers)

- [x] A) Hybridize 50-100 nts downstream of expected 5' end
- [x] B) 18 - 25 nts long
- [ ] C) No more than 50% GC content

☐ D) First nucleotide as G

110. (2.00 pts) Even though making a primer longer would technically increase its specificity, why do we typically limit the size of the primer?

Expected Answer: There is no significant advantage of making it larger than length of 20ish nts

111. (2.00 pts)
After primer extension occurs, reverse transcriptase is added to elongate. The cDNAs are then purified using a phenol/chloroform solution. The concentration of the cDNAs is increased by sodium acetate/ethanol precipitation. What is the function of the phenol/chloroform solution? What is the logic behind sodium acetate/ethanol precipitation?

Expected Answer: Precipitation of DNA is improved by increasing ionic strength, usually by adding sodium acetate. (1) DNA is not soluble in alcohol and will form insoluble aggregates in the form of pellets. (1) Chloroform allows proper separation of the organic phase and aqueous phase which keeps DNA protected into the aqueous phase. (1) | 3 possible but 2 max points

Part 10: H3K27me3 [9 points total]

In the developing study of disease inheritance, something that has been noted is the differing inheritance of disease without any changes in the genetic material. Geneticists called this the epigenome, which consists of all the epigenetic modifications of an individual. One of the most classical examples of epigenetic modifications is DNA methylation.

112. (2.00 pts) What is the role of DNA methylation and where does it most likely occur?

Expected Answer: (1) DNA methylation occurs in CpG islands (1). DNA methylation decreases the rate of transcription of a specific gene (1).

113. (2.00 pts) What is the difference between de novo methylation and maintenance methylation?

Expected Answer: De novo methylation occurs spontaneously (1) whereas maintenance methylation methylates the strand complementary to an inherited strand of DNA with CpG methylation. (1)

114. (1.00 pts)
The inheritance of methylation patterns can result in diseases. For example, different methylation patterns in sperm and egg cells result in different concentrations of protein products upon fertilization. In this pattern of inheritance, disease-alleles are passed on by a parent basis. What is this called?

Expected Answer: Genomic imprinting

115. (6.00 pts)

Epigenetic modifications can also occur by paramutations, where one allele induces a heritable change in the expression of the other without changing the DNA sequence. For maize the gene *b1* codes for a transcription factor that regulates the expression of anthocyanin. The dominant allele, *B-I*, is typically expressed at high levels, conferring a purple color to corn husks and stalks. A separate allele, *B'*, is expressed at a much lower level, leading to green-colored husks and stalks. However, the *B'* allele is paramutagenic: it can convert a *B-I* allele into a *B'* allele. Fishy performs a genetics experiment on maize plants. In his P generation, he crossed *B-I B-I* maize with a *B' B'* maize to produce a *B-I B'* F1 generation. The paramutation conversion rate of this gene is 14% and the reversion rate is 23%. What percent of the F1 generation is purple? Assume that conversion and reversion events occu at fertilization and reversion occurs after conversion.

Expected Answer: 94.3% 1 - { [1- (77/100)^2] * .14}

Congratulations, you've completed the 2021 BirdSO Designer Genes C test! Best of luck in your other events! We hope you enjoyed taking this test today!

~ Section 2 Authors: Greycen (Stevenson '22) & Kayla (Clark '22) & Krish (Carmel '22)