Spring 2018

BIOL241 – Introduction to Genetics

and Molecular Biology

Final Exam (110 points)

5/1/2018

*Please use scantron sheet for Question A (1-40).*

**Name:\_\_\_\_\_\_\_\_\_\_KEY\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**Purdue ID:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

Question A: (80) Question B: (8)

Question C: (14) Question D: (8)

**Total:**

**A. Multiple-choice questions (80 points; 2 points each; please use scantron sheet)**.

**1) In 2D gel, the proteins in the cell lysates are first separated by:**

1. The mass-to-charge ratios of the proteins.
2. Acetylation of the lysines in the proteins.
3. Molecular mass of the proteins.
4. Electrical charge of the proteins.
5. Trypsin-mediated cleavage of the proteins.

**2) Regarding gene density in eukaryotic genomes, which of the following statements is accurate?**

1. In human genome, the densities of genes vary among different chromosomes.
2. In a given species, the densities of genes on different chromosomes are similar.
3. The densities of genes from different species are similar, approximately 2 kb of genomic DNA per gene.
4. The densities of genes from different species are similar, approximately 125 kb of genomic DNA per gene.
5. Different eukaryotic species contain similar fraction of repetitive DNA in their genomes.

**3) Genes related by gene duplication event in a genome are referred as:**

1. Orthologs.
2. Paralogs.
3. Contigs.
4. Homologs.
5. Analogs.

**4) When comparing the genomes of eukaryotic species, which of the following statements is correct?**

1. The amount of DNA is conserved across species.
2. The number of genes is conserved across species.
3. The number of introns per gene is conserved across species.
4. The number of identified protein domains is conserved across species.
5. The average size of introns is conserved across species.

**5) When a haploid *petite* mutant mates with haploid normal yeast, the resulting diploid zygote exhibits the normal phenotype. After sporulation (meiosis), all haploid progeny are normal. Based on this, which of the following statements is corret?**

1. This pattern describes neutral petite, and the haploid progeny are heteroplasmic.
2. This pattern describes segregational petite, and the haploid progeny are homoplasmic.
3. This pattern describes neutral petite, and the haploid progeny are homoplasmic.
4. This pattern describes suppressive petite, and the haploid progeny are homoplasmic.
5. This pattern describes suppressive petite, and the haploid progeny are heteroplasmic.

**6) A different yeast *petite* mutant is isolated. To determine the type of mutation causing this phenotype, the haploid *petite* and wild type strains are crossed. The diploid zygotes are normal, and half the haploid ascospores after sporulation are mutant. The explanation for this mutation is that**:

1. The inheritance of mitochondrial genome in yeast is strictly maternal.
2. The inheritance of mitochondrial genome in yeast is from both parents.
3. It affects mitochondrial genes, which disrupt mitochondrial function, but gives normal mitochondria proliferation advantage.
4. It affects mitochondrial genes, which disrupt mitochondrial function, but gives defective mitochondria proliferation advantage.
5. It disrupts a nuclear gene that participates in mitochondrial function.

[7 and 8 are a set]

**7) The coiling of snail shell is controlled by a single maternal-effect locus, where D (dextral) is dominant and d (sinistral) is recessive. Based on this, which of the following crosses will produce all dextral progeny?**

1. DD males crossed with dd females.
2. Dd males crossed with dd females.
3. Dd males crossed with Dd females.
4. dd males crossed with dd females.
5. None of the above.

**8) In snail shell coiling, which of the following crosses will produce a mixture of dextral and sinistral progeny in 1:1 ratio?**

1. DD males crossed with dd females.
2. Dd males crossed with dd females.
3. Dd males crossed with Dd females.
4. dd males crossed with Dd females.
5. None of the above.

**9) Regarding prions, which of the following statements is correct?**

1. The inheritance of prion diseases in human in maternal.
2. Transmission of prions is sensitive to treatment of protease.
3. Transmission of prions is sensitive to DNase treatment.
4. Mutant prion proteins cause diseases by inducing the transcription and expression of additional prion proteins.
5. Mice with cellular PrP genes deleted are sensitive to mutant prion infection.

**10) The wingless (wg) protein is secreted from a source and capable of specifying more than one cell type by forming a concentration gradient. Based on this, wg can be described as:**

1. A maternal-effect morphogen.
2. A homeotic gene and a paracrine gene.
3. A juxtacrine gene and a morphogen.
4. A paracrine gene and a morphogen.
5. An autocrine gene and an inductive signaling gene.

**11) A tissue from the leg bud during chick development is transplanted into the wing bud. Later on, the transplanted tissue forms structures of wing origin. Based on this, you can conclude that:**

1. The cells in transplanted tissue undergo mitotic recombination.
2. The cells in the transplanted tissue respond to the expression of master regulatory genes from the surrounding host cells.
3. The cells in the transplanted tissue respond to lateral inhibition from the surrounding host cells.
4. The cell fate of cells in the transplanted tissue has not been determined.
5. The cell fate of cells in the transplanted tissue has been determined.

1**2) Germ stem cells in *Drosophila* testes divide to generate two daughter cells, one of which maintains the stem cell identity and the other one loses contact with the hub structure and initiates differentiation program (loses the stem cell identity). Which of the following descriptions best characterizes the molecular event responsible for this process?**

1. Regulating translocation of transcription factors into the nucleus.
2. Activation of Ras small GTPase.
3. Lateral inhibition mediated by the Notch pathway.
4. Asymmetric cell division by exposing daughter cells to different surroundings.
5. Partitioning cytoplasmic factors in asymmetric cell division.

**13) To pinpoint the determinants for *bicoid* and *nanos*** **mRNA localization, you have generated several chimera constructs (fusions). After transgenic wild type flies expressing these constructs are established, you perform RNA in situ hybridization (to detect the localization of mRNA) on the embryos using *nanos* coding region as a probe. Which of the following constructs will yield *nanos*-positive signal at both the anterior and posterior poles?**

1. nanos 5’UTR – bicoid coding region – bicoid 3’UTR.
2. bicoid 5’UTR – bicoid coding region – nanos 3’UTR.
3. nanos 5’UTR – nanos coding region – nanos 3’UTR.
4. bicoid 5’UTR – nanos coding region – nanos 3’UTR.
5. nanos 5’ UTR – nanos coding region – bicoid 3’ UTR.

**14) Which of the following patterns best describes the expression of *giant*, a gap gene during *Drosophila* embryogenesis?**

1. Uniform throughout the entire embryo.
2. Localized to either anterior or posterior pole.
3. A broad stripe at a specific region.
4. 7 stripes.
5. 14 stripes.

**15) Which of the following patterns best describes the mutant phenotype of *fushi tarazu*, a pair-rule gene during *Drosophila* embryogenesis?**

1. The entire anterior portion is absent.
2. Several consecutive segments are absent.
3. Structures in every other segment are absent.
4. Structures in every segment are absent.
5. No segment is missing, but the identity of one segment is transformed into another.

**16) Comparing the expression of *engrailed* (a segment polarity gene) mRNA in *giant-* (*giant* is a gap gene) and *Antp-* (Antp is a homeotic gene) mutants during *Drosophila* embryogenesis, you will expect:**

1. The engrailed mRNA is localized to the anterior pole in *giant-* mutant, but localized to the posterior pole in *Antp-* mutant.
2. Stripes of engrailed mRNA missing in both *giant-* and *Antp-* mutants.
3. All stripes of engrailed mRNA present in both *giant-* and *Antp-* mutants.
4. Stripes of engrailed mRNA missing in *giant-* mutant, but all stripes of engrailed mRNA present in *Antp-* mutant.
5. All stripes of engrailed mRNA present in *giant-* mutant, but stripes of engrailed mRNA missing in *Antp-* mutant.

[Questions 17-21 deal with *C. elegans* vulva formation.]

**17) In *C. elegans* vulva formation, which of the following genes contains a serine/threonine kinase domain?**

1. Lin-3.
2. Lin-12.
3. Lin-45.
4. Let-23.
5. Let-60.

**18) During *C. elegans* vulva formation, two precursor cells are competing to become the anchor cell. The formation of anchor cell from these two precursor cells is mediated by lateral inhibition. Based on this, which of the following genes is expected to be involved in this process?**

1. Lin-3.
2. Lin-4.
3. Lin-12.
4. Lin-14.
5. Let-60.

**19) What is the phenotype when the Pn.p cells carry one copy of *let-60V12* mutation?**

1. Wild type.
2. Vulvaless.
3. Multiple vulva structures.

**20) What is the phenotype when the Pn.p cells carry one copy of *let-60V12* mutation, but are homozygous for *lin-45-*?**

1. Wild type.
2. Vulvaless.
3. Multiple vulva structures.

**21) The *C. elegans* *let-60* is a target of microRNA *let-7*. Based on this, what is the expected effect of a *let-7*loss-of-function mutation on the phenotype of Pn.p cells expressing let-60V12?**

1. It enhances (worsens) the *let-60V12* phenotype because the let-60V12 protein level is higher.
2. It suppresses the *let-60V12* phenotype because the let-60V12 protein level is lower.
3. It has no effect on let-60V12 phenotype because let-60 is epistatic to let-7.
4. It suppresses the *let-60V12* phenotype because the requirement of let-7 function is cell-autonomous.
5. It has no effect on the *let-60V12* phenotype because let-7 is epistatic to let-60.

[Questions 22-25 deal with *Drosophila* R7 formation]

**In *Drosophila*, two genes, *Sevenless (sev)* and *bride-of-sevenless (boss),* are involved in forming the R7 photoreceptor cells. The Boss proteins are expressed on the surface of R8 cells, whereas Sev receptor tyrosine kinase is expressed in the R7 precursor cells.**

**22) If the R8 cell is genotypically *boss+* and the R7 precursor cells are genotypically *boss-*, what will the phenotype be?**

1. One R7 cell.
2. No R7 cell.
3. Multiple R7 cells.

**23) If the R8 cell is genotypically *sev-* and the R7 precursor cells are genotypically *sev+* what will the phenotype be?**

1. One R7 cell.
2. No R7 cell.
3. Multiple R7 cells.

**24) The function of GTPase-activating protein (GAP) is to accelerate the rate of GTP hydrolysis of Ras small GTPase. Based on this, what is the expected phenotype of a fly homozygous for GAP-?**

1. One R7 cell.
2. No R7 cell.
3. Multiple R7 cells.

**25) What is the expected phenotype of a fly homozygous for both *sev-* and *GAP-*?**

1. One R7 cell.
2. No R7 cell.
3. Multiple R7 cells.

**26) The inheritance of hereditary retinoblastoma is autosomal dominant. This is because:**

1. Inactivating one copy of Rb is sufficient to deregulate cell proliferation.
2. Mutations in Rb that cause abnormal cell proliferation are dominant-active mutations.
3. The mutation rate at the Rb locus is unusually high.
4. Mutations in Rb that cause abnormal cell proliferation are dominant-negative mutations.
5. The chance of losing the wild type Rb in some eye cells during heterozygous individuals’ lifetime is high.

[27-31 deals with the cell cycle checkpoint discussed in class]

**27) Regarding RB and E2F functions, which of the following statements is correct?**

1. Phosphorylated RB enters the nucleus and regulates the expression of S phase genes.
2. The expression of RB proteins oscillates with cell cycle.
3. E2F functions as a transcription repressor for genes required for DNA synthesis.
4. E2F binds to RB and prevents RB from entering the nucleus.
5. The binding of RB to E2F is regulated by cyclin-dependent kinase.

**28) In this system, over-expression of cyclin is likely to:**

1. Decrease the level of active cyclin-dependent kinase.
2. Increase the presence of Rb proteins in the nucleus
3. Decrease the level of E2F proteins in the nucleus.
4. Increase the level of phosphorylated Rb.
5. Decrease the expression of p21 proteins.

**29) In this system, DNA damages can cause a G1-S arrest by:**

1. Increase p21 expression, which blocks cyclin-dependent kinase activity.
2. Increase p21 expression, which degrades Rb.
3. Increase p53 expression, which degrades E2F.
4. Increase p53 expression, which degrades p21.
5. Decrease p53 expression, which activates the expression of p21.

**30) In this system, excessive DNA damages can cause apoptosis by:**

1. Expressing PUMA, which disrupts the binding of Rb to E2F.
2. Expressing p21, which degrades Bcl2.
3. Expressing BAX, which inhibits the activity of cyclin/CDK complex.
4. Expressing PUMA, which binds to Bcl2 and releases BAX.
5. Expressing Bcl2, which binds to PUMA and releases BAX.

**31) Which of the following scenarios is likely to cause DNA replication even in the presence of DNA damage?**

1. Loss-of-function mutations in both copies of E2F.
2. Loss-of-function mutations in both copies of cyclin-dependent kinase.
3. Loss-of-function mutations in both copies of cyclin.
4. Gain-of-function mutation in one copy of Rb.
5. Loss-of-function mutations in both copies of the p53 gene.

**32) Which of the following terms best describes the process of cancer cells inducing blood vessel formation?**

1. Genomic instability.
2. Angiogenesis.
3. Epithelial-mesenchymal transition.
4. Extravasation.
5. Loss of heterozygosity.

**33) B cells are clonal, meaning that each B cell expresses only one successfully rearranged immunoglobulin (Ig). This is caused by:**

1. The exposure of immature B cells to foreign antigens.
2. Junctional diversity.
3. Hypermutation at Ig locus.
4. Allelic exclusion.
5. Alternative splicing.

**34) In mouse, the heavy chain locus contains 134 V segments, 13 D segments, 4 J segments, and 8 C segments. How many different Ig heavy chains can be generated by somatic DNA recombination alone?**

1. 55744.
2. 6968.
3. 1742.
4. 536.
5. 134.

**35) Regarding T cell receptor, which of the following statement is correct?**

1. T cell receptor recognizes antigens presented by MHC molecules.
2. T cell receptor recognizes free antigens and induces expression of cytokines.
3. T cell receptor consists of two heavy chains and two light chains.
4. T cell receptor locus does not undergo somatic gene rearrangement.
5. T cell receptor is only expressed in cytotoxic T cells, but not in T helper cells.

**36) Regarding non-synonymous substitutions, which of the following statements is correct?**

1. These are nucleotide changes that alter amino acid sequence.
2. The rates of non-synonymous substitutions are higher than those of synonymous substitutions.
3. Non-synonymous substitutions are typically found in the sequences between genes.
4. Non-Synonymous substitutions are typically found in 5’- and 3’UTRs, whereas synonymous substitutions are found in introns.
5. Non-Synonymous substitutions are typically found in 5’- and 3’UTRs, whereas synonymous substitutions are found in exons.

**37) Which of the following statements best describes allopatric speciation?**

1. Evolution of reproductive isolation by having different mating seasons.
2. Evolution of reproductive isolation by developing incompatible gametes.
3. Evolution of reproductive isolation within a population in the absence of a geographical barrier.
4. Evolution of reproductive isolation within a population in the presence of a geographical barrier.
5. Evolution of reproductive isolation by forming sterile hybrid progeny.

**38) Which of the following statements best describes over-dominance?**

1. Heterozygous individuals have fitness advantages over homozygous individuals.
2. Homozygous dominant individuals have fitness advantages over heterozygous individuals.
3. Homozygous dominant individuals have fitness advantages over homozygous recessive individuals.
4. Homozygous recessive individuals have fitness advantages over homozygous dominant individuals.
5. Homozygous recessive individuals have fitness advantages over heterozygous individuals.

[39 and 40 are a set]

**Population A consists of 100 hens that are fully isogenic and that are reared in a uniform environment. The average weight of the eggs the lay is 52 g and the variance is 3.5 g2. Population B consists of 100 genetically variable hens that produce eggs with a mean weight of 52 g and a variance of 21.0 g2. Population B is raised in an environment that is equivalent to that of Population A.**

**39) Regarding the VG and VE for both populations, which of the following statements is correct?**

1. The VG for population A is 0 g2 and the VE for population A is 21.0 g2.
2. The VG for population A is 3.5 g2 and the VE for population A is 0 g2.
3. The VG for population B is 17.5 g2 and the VE for population B is 21.0 g2.
4. The VG for population B is 21.0 g2 and the VE for population B is 3.5 g2.
5. The VG for population B is 17.5 g2 and the VE for population B is 3.5 g2.

**40) What is the broad-sense heritability in Population A?**

1. 0
2. 0.16
3. 0.067
4. 0.83
5. 0.2

**B)** A hypothetical study investigated the vitamin A content and the cholesterol content of eggs from a large population of chickens. The variances (*V*) were calculated, as shown below:

|  |  |  |
| --- | --- | --- |
| **Variance** | **Vitamin A** | **Cholesterol** |
| *VP* | 123.5 | 862.0 |
| *VE* | 96.2 | 484.6 |
| *VA* | 12.0 | 192.1 |
| *VD* | 15.3 | 185.3 |

1. Calculate the broad-sensed heritability and narrow-sensed heritability for both traits (**4 points**).

For vitamin A, H2=(12+15.3)/123.5=0.22, and h2=12/123.5=0.097

For cholesterol, H2=(192.1+185.3)/862=0.438, and h2=192.1/862=0.22

1. In the population of animals studied, which trait would respond best to selection (**1 point**)? Please briefly explain your answer (**1 point**).

The cholesterol trait will respond better to selection because its narrow-sensed heritability (h2) is higher.

1. A project is undertaken to decrease the cholesterol content of the eggs. The mean cholesterol content of a large chicken population is currently 187mg. To decrease the egg cholesterol content, chickens with a mean of 160mg cholesterol content are interbred as parents of the next generation. What mean cholesterol content can be expected in the descendants of these chickens (**2 points**)?

S=160-187=-27mg

R=(-27mg)\*(192.1/862)=-6.017mg

-6.017+187=180.98mg

**C)** A homozygous plant with 14 cm diameter flowers is crossed with a homozygous plant of the same species that has 30 cm diameter flowers. The F1 plants all have flowers 22 cm in diameter. After F1 sibling mating, an F2 generation resulted in many plants, whose floral diameter ranged in 2-cm intervals from 14 to 30 cm (14, 16, 18, 20, 22, 24, 26, 28, 30).

a) How many genes are involved in the floral diameter determination in these plants? **(2.5 points)**

Since there are 9 distinct F2 classes, 4 genes are involved.

b) If the F2 generation contains 512 plants, how many of these F2 plants are expected to have 30 cm diameter flowers? **(2.5 points)**

The 30cm diameter flower plants will carry 8 additive alleles. Hence 512\*(1/2)8\*8!/(8!0!)=2

c) If the F2 generation contains 512 plants, how many of these F2 plants are expected to have 22 cm diameter flowers? **(2.5 points)**

The 22cm diameter flower plants will carry 4 additive alleles. Hence 512\*(1/2)8\*8!/(4!4!)=140

d) If a F1 plant with 22 cm diameter flowers was mated with one of the F2 plant with 14 cm diameter flowers, what phenotypic ratios would be predicted in the progeny? **(4 points)**

Because the genotypes of the parents are AaBbCcDd (22cm) and aabbccd (14cm), this cross will yield 5 classes:

0 additive allele (14cm) = (1/2)4\*4!/(4!0!)= 1/16 or 0.0625

1 additive allele (16cm) = (1/2)4\*4!/(3!1!)= 4/16 or 0.25

2 additive alleles (18cm) (1/2)4\*4!/(2!2!)= 6/16 or 0.375

3 additive alleles (20cm) (1/2)4\*4!/(1!3!)= 4/16 or 0.25

4 additive alleles (22cm) = (1/2)4\*4!/(0!4!)= 1/16 or 0.0625

e) If a few F2 plants with 28 cm diameter flowers were selected to start a new population, what is the expected floral diameter of this new population? **(2.5 points)**

Because all the phenotypic variance is caused by additive alleles, h2 is 1. Hence the average floral diameter of the new population is 28 cm.

**D)** The narrow-sensed heritability of the number of peas per pod in a population of sugar snap peas in 0.5. The mean of the population is 6.2 peas per pod. A plant breeder selects one plant with 6.8 peas per pod and crosses with a second plant that has 8.0 peas per pod.

a) What is the selection differential of this cross **(2 points)**?

S=(6.8+8)/2-6.2=1.2 peas per pod

b) What is the expected number of peas per pod among the offspring of this cross **(2 points)**?

R=1.2\*0.5=0.6

6.2+0.6=6.8 peas per pod

c) If the additive variance of the original population is 0.7 peas per pod2, what is the phenotypic variance (**2 points**)?

As h2=VA/VP, VP=VA/h2

VP=0.7/0.5=1.4 peas per pod2

d) If the number of peas per pod has a narrow-sensed heritability of 0, what is the expected number of peas per pod among the offspring of this cross **(2 points)**?

If h2=0, then R=0, the new average will still be 6.2