colinear-ity

37. Please describe three features of metazoan Hox genes that make them unique from all other types of genes. Please fully explain and define your response. (3 marks)

The Hox genes ~~Bracken~~ are special because of its 3 unique features (Hox genes are transcription factors) which ~~allows~~ allows/are: colinearity (developmental (spatial), temporal, quantative)

These colinearity's of the Hox genes allows it to first:

1. developmental (spatial) ~~colinearity~~: allows the gene to be expressed in the order it is on the chromosome, each section measuring/labeling of what is developed during the ~~embryonic~~ embryonic stages of development. (Each section of the gene codes for leg, head, arm, body ect....)

2. The second ~~the~~ feature is: temporal colinearity which states the Hox genes are expressed at specific times to ~~co~~ coordinate the development of the ~~gene~~ organism.

3. The 3rd feature is: quantative ~~colinear~~ colinearity which states how much of the gene is expressed; meaning multiple genes can be expressed (producing proteins) simultaneously but in different concentrations.

3

**Part B: Short Answer Questions - Please answer in the space provided (worth 15 marks)**

31. What conclusion would have been made by Pasteur if both the broth in the straight-necked flask and the broth in the swan-necked flask were filled with cells? (1 mark)

Cells cannot be spontaneously created. Cells come from pre-existing cells, conforms to the cell theory.

32. Scientifically, there is no such thing as "higher" or "lower" organisms. Justify this statement. (1 mark)

There is no such thing as a "higher" or "lower" organism because, organisms can evolve into more complex species, but these species can lose "complex" traits with time. Each species has its own unique traits adapted to its environment. In addition no organism is ~~fully~~ "higher"/"lower", ~~do~~ because of vegistal traits. ~~There~~ There is no ~~hie~~ hierchy (chain of ~~wait~~ being) stating how developed an organism is.

33. What can be deduced about mating if a population is not in Hardy-Weinberg equilibrium? (1 mark)

If the population is not in Hardy-Wein-berg equilibrium then the expected genotypic frequency would not match the observed genotypic frequency.

nonrandom mating.

34. Please list and explain two possible evolutionary consequences of gene duplication. (2 points)

Consequence 1 and explanation:

Genome duplication can lead to specialtion, via autopolypodialtion or ~~allo~~ allopolypodialtion. Ex when species/organisms self-fertilize or when 2 species fertize (Hydrialtion); their genome's can be duplicated due to errors in mitosis/meiosis which eventually leads to specialtion

Consequence 2 and explanation:

- ~~Hox genes, body plans~~
- Another possible consequence could be the duplication of "Hox genes" which may have led to the hypothesis "new genes, new body", stating the "new" genes could have gave organisms new body plans (specialtion).

Also genome duplicalion (eg. the fern) ~~can~~ produced 2n gametes instead of n → produced tetraploid could have made species reproductively/genetically isolated from eachother (example: 4n & 2n gametes produce triploid which is usually non-viable)

*Continued on next page...*

24. Imagine a recent study explored phylogenetic relationships among anolis lizards on Florida and Cuba. The results of this study indicated that the different "ecotypes" on Cuba (that is the "Trunk/crown", "Twig", "Crown", and "Trunk/ground") each had a very close relative (a sister species) present on Florida, such that the same suites of ecotypes occupying the exact same ecological niches were present in both regions. What does this tell us about adaptive radiations on Florida and Cuba?
    (a) An adaptive radiation must have occurred on Florida and also on Cuba
    (b) An adaptive radiation occurred on Florida but not Cuba
    (c) An adaptive radiation occurred on Cuba but not Florida
    (d) An adaptive radiation did not occur on Florida or on Cuba
    (e) An adaptive radiation could have occurred on Florida or on Cuba, but probably not both

25. Consider a large population in which individuals began to inbreed by reproducing with full siblings for 100 generations. If, after this period, these progeny from the 100th generation were to then reproduce with random individuals from that generation (instead of with a full sibling), what frequency of heterozygous genotype do you expect in the 101th generation progeny? Please provide an estimate for a bi-allelic locus in which the starting allele frequencies in generation 1 were $p$ and $q$ respectively, and assume that the alleles at this locus had no effect on fitness of the individuals.
    (a) less than $2pq$
    (b) $2pq$
    (c) greater than $2pq$

26. If we assume that humans and chimpanzees diverged from a common ancestor about 6 million years ago, what percentage is this period of time relative to (1) the time that has elapse since the Cambrian Explosion and (2) the time that has elapsed since our planet was formed.
    (a) about 1.1% and 0.1% respectively
    (b) about 0.1% and 0.01% respectively
    (c) about 1.1% and 0.001% respectively
    (d) about 1.1% and 0.00001% respectively

$= \frac{6}{542} = \frac{6}{4600}$ 542 4.6

6 000 000

4 600 000 000

27. The time of divergence between New World Monkeys, which occur in Central and South America, and Old World Monkeys, which occur in Africa and Asia, is younger than the age of the barrier that separates them (which is the Atlantic Ocean). What does this tell us about the mechanism of diversification of these groups.
    (a) These groups are an example of sympatric speciation due to disruptive selection
    (b) These groups are an example of allopatric speciation due to vicariance
    (c) These groups are an example of allopatric speciation due to dispersal
    (d) These groups are an example of sympatric speciation due to allopolyploidy

28. Which of the following types of natural selection does not increase genetic diversity as quantified by Simpsons index of diversity?
    (a) Disruptive selection
    (b) Negative frequency dependent selection
    (c) Stabilizing selection
    (d) B and C

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12. Imagine a gene that controls coloration of moths that has two alleles, $A_1$ and $A_2$. Assume the $A_2$ allele is completely dominant and caused dark coloration, such that $A_2A_2$ genotypes and also $A_1A_2$ genotypes were dark. Assume that allele frequencies of these alleles are initially 0.1 and 0.9 respectively for $A_1$ and $A_2$ and that genotypes match Hardy Weinberg expectations. If natural selection is extremely harsh, and all of the light colored moths are eaten before the next generation, which of the following are true?
    (a) The $A_1$ allele would be lost from the population
    (b) The $A_2A_2$ genotype exhibits homozygote advantage.
    (c) Natural selection has increased genetic diversity in this example
    (d) Genetic drift could act in this population founder bottleneck

    0.1 $A_1$ 0.9 $A_2$

13. Consider another gene that has two alleles, $A_1$ and $A_2$. Which of the following is true?
    (a) the frequency of the $A_1$ allele is equal to the square root of the frequency of the homozygous $A_1A_1$ genotype plus half the frequency of the heterozygous $A_1A_2$ genotype.
    (b) the sum of the frequencies of the homozygous genotypes cannot be 1.
    (c) the sum of the square roots of each homozygous genotype frequency must be 1
    (d) All of the above
    (e) None of the above.

    B $A_1 = A_1^2 + \frac{1}{2}(A_1A_2)$

14. In class and in the text, an example was discussed about research exploring heterozygote advantage at the HLA loci. Which of the following could explain the observation of significant heterozygote excess at the HLA-A locus in the population of Havasupai people?
    (a) People with heterozygous genotypes at the HLA-A reproduce more than people with homozygous genotypes at this locus.
    (b) Havasupai people with homozygous genotypes at the HLA-A prefer to mate with people that are not Havasupai
    (c) Homozygosity at the HLA-A locus provides a fitness advantage through immue system effects.
    (d) A and B

15. Consider two populations that both have three alleles at a gene with initial allele frequencies of 0.25, 0.45, and 0.35 respectively. Population 1 has 10,222 individuals and Population 2 has 25, 512 individuals. After two generations, which population is the most likely to have only 1 allele?
    (a) This is impossible for both populations
    (b) Population 1
    (c) Population 2
    (d) Both populations will have only 1 allele
    (e) Impossible to predict this likelihood.

    $A_1$ 0.25 $A_1^2$ = 0.0625 2555.5 6378
    $A_2$ = 0.45 = 0.2025 4599.9 11480.4
    $A_3$ = $0.35^2$ = 0.1225 3577.7 ① 8929.2 ②

16. If founder effects generally lead to lower diversity, why do some populations of humans have an atypically high incidence of disease?
    (a) Diversity is lower overall in these populations but, by chance, they happened to have a higher than typical frequency of disease causing alleles.
    (b) Diversity is higher overall in these populations because they have gene flow with another population that carries the disease causing allele
    (c) These populations have been subject to negative frequency dependent selection, which increased the frequency of the disease-causing allele.
    (d) These populations have been subject to diversifying selection, which increased allelic diversity at the locus causing the disease.

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**PART A: Multiple Choice (worth 30 marks)**

Select the option which best answers the question. There is no penalty for guessing. Each question is worth 1 mark.

1. Which of the following criteria define different populations?
   (a) groups of individuals in the same place that have different allele frequencies
   (b) groups of individuals in different places that have different allele frequencies
   (c) groups of individuals in different places that have the same allele frequencies
   (d) All of the above
   (e) A and B only

2. Which of the following is not a potential evolutionary consequence of gene flow?
   (a) Reinforcement
   (b) the homogenization of allele frequencies across two populations
   (c) increased homozygosity of deleterious recessive alleles
   (d) Speciation of hybrid individuals

3. Which of the following is a cause of inbreeding?
   (a) increased deleterious recessives
   (b) decreased frequency of advantageous heterozygous genotypes
   (c) "endogamy" – marriage within a small group
   (d) A or B

4. Which of the following phenomena does not produce relationships that are readily described by a bifurcating (splitting) phylogeny?
   (a) speciation
   (b) autopolyploidization
   (c) sexual reproduction
   (d) mitosis

5. What key features must be in place for natural selection to operate
   (a) a species must have variation in some phenotype
   (b) all phenotypic variation of a species must influence individual fitness
   (c) some phenotypic variation must be heritable
   (d) all of the above
   (e) A and C only

6. Which factor does not impose limits on artificial selection, for example how much milk we can ever get a cow to produce after selective breeding?
   (a) how much genetic variation there exists for that phenotype
   (b) the previous history of that species with respect to adaptive radiation
   (c) The impact of environmental factors on the phenotype
   (d) Other fitness impacts of selecting for extreme phenotype
   (e) the rate of mutation at genes that influence that phenotype

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