

Jorde: Medical Genetics, 5th Edition

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Chapter 1: Background and History

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Multiple Choice

1. Achondroplasia has a high mutation rate. This is most likely the result of
- Paternal age effect
 - Maternal age effect
 - Large gene size
 - Methylated CG dinucleotide
 - None of the above

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Answer: d

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Correct Feedback: This has been shown to be the cause of achondroplasia.

Incorrect Feedback: This has not been shown to be the cause of achondroplasia.

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2. The effect of mutations in the SHOX gene would best be described as
- Haploinsufficiency
 - Dominant negative
 - Autosomal recessive
 - Gain of function
 - X-linked recessive

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Answer: a

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Correct Feedback: The effect is best described as haploinsufficiency.

Incorrect Feedback: This does not explain the effects of mutations in the SHOX gene.

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3. Which of the following mechanisms is known to cause Prader-Willi syndrome?
- Chromosome duplication
 - Translocation
 - Uniparental disomy
 - Autosomal trisomy
 - Autosomal monosomy

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Answer: c

Correct Feedback: Prader Willi syndrome is effected by genomic imprinting. Thus, a uniparental disomy could cause the disease.

Incorrect Feedback: This would not cause Prader Willi syndrome.

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4. Suppose you have established that a disease gene is closely linked to a marker whose location is known. Which of the following would **not** be useful in defining the disease gene's location?

- a. Testing for unmethylated CG islands
- b. Existence of a chromosome deletion in a patient
- c. Existence of trisomy in a patient
- d. DNA sequencing
- e. Testing for cross-species conservation

Answer: c

Correct Feedback: This would not be useful in defining the disease gene's location.

Incorrect Feedback: This could help you find the disease gene's location.

5. Which of the following is **least** likely to be seen in a patient with Huntington disease?

- a. Dementia
- b. Affective disorder
- c. New mutation
- d. Delayed age of onset
- e. Loss of motor control

Answer: c

Correct Feedback: This is rarely seen in Huntington disease. It has one of the lowest known mutation rates of all human disease genes, estimated at approximately 1 per 1 million (per locus per generation).

Incorrect Feedback: This is seen with Huntington disease.

6. Which of the following is not a characteristic of osteogenesis imperfecta?

- a. Locus heterogeneity
- b. Allelic heterogeneity
- c. Pleiotropy
- d. Imprinting
- e. Dominant negative mutation effects

Answer: d

Correct Feedback: Imprinting is more common with Prader-Willi and Angelman syndromes.

Incorrect Feedback: This is a characteristic of osteogenesis imperfecta.

7. In which of the following diseases are dominant negative mutation effects seen?

- a. Huntington disease

- b. Cystic fibrosis
- c. Retinoblastoma
- d. Marfan syndrome
- e. None of the above

Answer: d

Correct Feedback: Marfan syndrome shows dominant negative effects.

Incorrect Feedback: One of the above shows dominant negative effects.

8. Which of the following is **not** true of Fragile X syndrome?
- a. It is associated with methylation
 - b. It can be diagnosed using a karyotype
 - c. It is caused by a trinucleotide repeat expansion
 - d. It displays nearly 100% penetrance
 - e. None of the above

Answer: d

Correct Feedback: Fragile X syndrome is an X-linked dominant condition with 80% penetrance in males and 30% penetrance in females.

Incorrect Feedback: This is true of Fragile X syndrome.

9. Which of the following diseases follow(s) a "2-hit model"?
- a. Osteogenesis imperfecta
 - b. Adult polycystic kidney disease
 - c. Cystic fibrosis
 - d. Retinoblastoma
 - e. B and D

Answer: e

Correct Feedback: e. Retinoblastoma and Adult polycystic kidney disease both follow a 2-hit model.

Incorrect Feedback: a. Osteogenesis imperfecta does not follow a 2-hit model. b. This is true but is not the only true answer. c. Cystic fibrosis does not follow a 2-hit model. d. This is true but is not the only true answer.

10. The recurrence risk for trisomy 13 is increased by
- a. Advanced paternal age
 - b. 13/15 translocation in one of the parents
 - c. Extensive methylation of chromosome 13
 - d. Advanced maternal age