## **Asthma Exacerbations: The Genes Behind** the Scenes

Instructions for obtaining 1.2 Continuing Medical Education Credits

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## **CME Items**

- 1. Which of the following is the most common trigger of asthma exacerbations in young children?
  - a. Rhinovirus C.
  - b. Influenza virus.
  - c. Rhinovirus A.
  - d. An allergen.
- 2. Which of the following does a single-nucleotide polymorphism refer to?
  - a. An insertion or deletion of bases in the DNA sequence of an organism.
  - A variant DNA sequence in which the base of a single nucleotide has been substituted by another base.
  - c. The difference in the number of copies of alleles inherited from ancestral populations.
  - d. A type of structural variation that affects a large region of the DNA sequence.
- 3. Which of the following applies to admixture mapping analysis?
  - a. It prioritizes regions where local genetic ancestry is associated with a certain trait of interest.
  - b. It uses more stringent genome-wide significance thresholds than genome-wide association studies.
  - c. It has not been carried out for asthma exacerbations.
  - d. It usually reveals genetic variants that exhibit similar minor allele frequencies across ancestral groups.
- 4. Which are the most commonly explored human genetic variations?
  - a. Indels.
  - b. Deletions.
  - c. Copy number variations.
  - d. Single-nucleotide polymorphisms.
- 5. Which of the following applies to a genome-wide association study?
  - a. It interrogates genetic variation across the genome without requiring a previous biological hypothesis.
  - b. It interrogates genetic variation located exclusively in coding regions of the genome.
  - c. It interrogates genetic variation in a discrete region of the genome.
  - d. It interrogates the relationship between gene expression and a trait of interest.
- 6. On which of the following have most of the pharmacogenomic genome-wide approaches applied to asthma exacerbations focused on?
  - a. Long-acting β-agonists.

- b. Inhaled corticosteroids.
- c. Leukotriene receptor antagonists.
- d. Short-acting \(\beta\)-agonists.
- 7. Which of the following is true?
  - a. Gene body DNA methylation usually leads to gene repression.
  - b. Promoter DNA methylation is associated with active transcription.
  - c. Most CpGs in the human DNA methylome are located in regions of high CpG density.
  - d. Most CpGs in the human DNA methylome are hypermethylated.
- 8. Which of the following is true?
  - a. The microRNAs that predict future asthma exacerbations with an adequate AUC have been validated across multiple populations.
  - b. The microRNAs involved in asthma exacerbations participate in phosphoinositide 3-kinase/protein kinase B and mitogen-activated protein kinase signalling.
  - c. None of the microRNAs associated with asthma have previously been associated with other respiratory traits.
  - d. MicroRNAs are pretranscriptional regulators that exert their effects by binding to the 3' untranslated regions of mRNAs leading to mRNA deadenylation and subsequent degradation.
- 9. Which of the following is true?
  - a. Differentially methylated regions consider only the effect of 1 CpG per region.
  - b. Multiple histone modifications have been associated with asthma exacerbations.
  - Hypomethylation at CEACAM5 has been associated with a higher risk of asthma exacerbations.
  - d. The 3 main epigenetic mechanisms that cooperate to regulate gene expression comprise DNA methylation, histone modifications, and noncoding RNAs.
- 10. Which of the following is true?
  - a. Microorganisms can interact with their host's biological layers to modulate the risk of a disease or condition.
  - b. There are no differences between the bronchial transcriptome of frequent exacerbators and that of infrequent exacerbators.
  - c. Blood hypomethylation in asthma is largely driven by a higher eosinophil count in blood.
  - d. Multiple differentially methylated regions have been revealed for asthma exacerbations.