American Society for Clinical Pathology (ASCP) Technologist in Cytogenetics certification (ASCP CG) Practice Test (Sample)

Study Guide

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Questions

1. What methodology is used to confirm the deletion of the ARSA region in a patient?

A. Cytogenetic microdissection

B. Fluorescence in situ hybridization (FISH)

C. Polymerase chain reaction (PCR)

D. Chromosomal banding techniques

2. In fluorescent microscopy, the exciter and barrier filters used depend on what factor?

A. Type of microscope used

B. Wavelength of light used

C. Stain, as the wavelength for emission can vary

D. Type of sample being analyzed

3. Which characteristic is essential for a chromosome to be included in the modal number?

A. Presence of staining

B. Presence of a centromere

C. Length of the chromosome

D. Region of the genome

4. Which type of probe is preferred for metaphase analysis?

A. FISH probe

B. SKY probe

C. CGH probe

D. BAC probe

5. What is a characteristic feature of constitutive heterochromatin?

A. It is transcriptionally active

B. It often contains repetitive sequences

C. It is usually found near the telomeres only

D. It is easily visible with all staining techniques

6. What is the primary purpose of using Trypsin-EDTA in cell culture?

A. To fix cells for staining

B. To encourage cell growth

C. To detach cells from a culture surface

D. To enhance DNA replication

7. What is the maximum number of color combinations that can be obtained from 5 fluorochromes?

A. 16

B. 31

C. 25

D. 20

8. Which AML type is characterized by no associated chromosomal changes?

A. AML M3

B. AML M2

C. AML M1

D. AML M0

9. Colagenase, pronase, and trypsin are classified as what type of enzymes?

A. Oxidative enzymes

B. Hydrolases

C. Proteolytic enzymes

D. Ligases

10. What is a common feature of AML subtypes M0 and M1 in terms of differentiation?

A. Both display high levels of cell differentiation

B. Both types are associated with a lack of differentiation

C. Both types have chromosomal changes

D. Both types exhibit unique genetic markers

Answers

1. B
2. C
3. B
4. B
5. B
6. C
7. B
8. D
9. C
10. B

Explanations

1. What methodology is used to confirm the deletion of the ARSA region in a patient?

A. Cytogenetic microdissection

B. Fluorescence in situ hybridization (FISH)

C. Polymerase chain reaction (PCR)

D. Chromosomal banding techniques

Fluorescence in situ hybridization (FISH) is a powerful technique used to confirm deletions at specific chromosomal regions, such as the ARSA region. FISH employs fluorescent probes that bind to particular regions of chromosomes, allowing for visualization of chromosomal abnormalities directly in interphase or metaphase cells. This method is particularly effective for demonstrating deletions, as it can show the presence or absence of signals from the fluorescent probes that correspond to the target area on the chromosome. When confirming a deletion, FISH can compare the intensity of signals in the patient's cells with those in control cells. If the ARSA region is deleted in the patient's genome, a significant reduction or complete absence of the fluorescent signal for that specific probe will be observed, indicating that the region is missing. This capability makes FISH not only a confirmatory tool but also a routine methodology in clinical cytogenetics for evaluating genetic material. Other methodologies have different applications and limitations. Cytogenetic microdissection is primarily used to isolate and study specific chromosomal regions but is less effective for routine diagnosis and confirmation of deletions. Polymerase chain reaction (PCR), while sensitive for detecting genetic material, does not provide direct visualization of chromosomal structure and is better suited for

2. In fluorescent microscopy, the exciter and barrier filters used depend on what factor?

A. Type of microscope used

B. Wavelength of light used

C. Stain, as the wavelength for emission can vary

D. Type of sample being analyzed

In fluorescent microscopy, the exciter and barrier filters are crucial components that ensure the correct wavelengths of light are used to excite the fluorophores in a sample and to filter the emitted light before it reaches the detector. The choice of filters is predominantly influenced by the specific fluorophore being used in the staining process since each fluorophore has unique excitation and emission wavelengths. When a sample is stained with a particular fluorophore, it will emit light at a specific wavelength when excited by a particular wavelength of light. Therefore, the exciter filter must be suited to allow the light that excites this specific fluorophore to pass through. Simultaneously, the barrier filter needs to allow the emitted light to pass while blocking any excitation light and any other wavelengths that are not associated with the fluorophore's emission spectrum. This reliance on the characteristics of the stain for selecting the appropriate wavelengths for filtering makes it clear that the choice of exciter and barrier filters specifically depends on the stain and its associated emission wavelengths, making this the correct answer.

3. Which characteristic is essential for a chromosome to be included in the modal number?

A. Presence of staining

B. Presence of a centromere

C. Length of the chromosome

D. Region of the genome

The presence of a centromere is essential for a chromosome to be included in the modal number. The centromere is a key structural feature of chromosomes that plays a crucial role during cell division by ensuring proper segregation of chromosomes into daughter cells. Chromosomes are defined by their centromeres, as they determine the formation of sister chromatids and the overall shape of the chromosome. In cytogenetic studies, the modal number refers to the most frequently observed number of chromosomes in a given set or sample. For a chromosome to be counted toward this number, it must be recognizable as a distinct chromosome, which is facilitated by the presence of a centromere. Without a centromere, a structure may not be adequately identified or classified as a chromosome within the modal analysis. While staining, chromosome length, and regions of the genome provide valuable information regarding the characterization and identification of chromosomes, they are not definitive criteria for establishing whether a structure qualifies as a chromosome in the context of determining the modal number. Thus, the presence of a centromere is the critical characteristic that distinguishes chromosomes and enables them to be included in the modal assessment.

4. Which type of probe is preferred for metaphase analysis?

A. FISH probe

B. SKY probe

C. CGH probe

D. BAC probe

For metaphase analysis, the preferred type of probe is the SKY probe. SKY, or spectral karyotyping, utilizes a combination of fluorescently labeled probes that allow for the simultaneous visualization of all chromosomes in different colors during metaphase. This technique enhances the ability to detect chromosomal abnormalities, such as translocations, deletions, or duplications, with a high degree of accuracy. In metaphase, chromosomes are condensed and clearly separated, making it an optimal stage for analysis. The spectral capabilities of SKY provide clear and distinguishable signals from each chromosome, allowing for comprehensive karyotyping. This is particularly beneficial in complex cases where traditional methods might struggle to resolve intricate abnormalities. Other types of probes, while valuable for specific applications, do not offer the same broad advantages in a metaphase context. FISH probes are often used for specific target regions rather than for whole chromosome analysis. CGH probes focus on copy number variations across the genome but typically require more detailed analysis rather than immediate visualization of the chromosomal structure. BAC probes can be helpful but are generally less effective in providing the comprehensive overview needed for metabolism during metaphase compared to SKY. In summary, the effectiveness of SKY probes in facilitating detailed and distinct visual assessment of all chromosomes during metaphase

5. What is a characteristic feature of constitutive heterochromatin?

A. It is transcriptionally active

B. It often contains repetitive sequences

C. It is usually found near the telomeres only

D. It is easily visible with all staining techniques

Constitutive heterochromatin is defined by its characteristic features, with one of the most significant being that it often contains repetitive sequences. This type of heterochromatin is largely made up of DNA sequences that are repeated multiple times within the genome, such as satellite DNA and certain transposable elements. These repetitive sequences contribute to the structural integrity of chromosomes and play a role in the regulation of gene expression and chromosome stability. While transcriptional activity is typically associated with euchromatin, constitutive heterochromatin is generally transcriptionally inactive. Additionally, the statement about constitutive heterochromatin being found only near telomeres is overly restrictive, as it can also be located around centromeres and other chromosomal regions. Furthermore, constitutive heterochromatin is not easily visible with all staining techniques, as visibility varies depending on the specific method used and is typically identifiable with specialized techniques that highlight its dense packing. Thus, the option referencing the presence of repetitive sequences accurately captures a defining characteristic of constitutive heterochromatin.

6. What is the primary purpose of using Trypsin-EDTA in cell culture?

A. To fix cells for staining

B. To encourage cell growth

C. To detach cells from a culture surface

D. To enhance DNA replication

The primary purpose of using Trypsin-EDTA in cell culture is to detach cells from a culture surface. Trypsin is a proteolytic enzyme that breaks down proteins, facilitating the dissociation of adherent cells from the substrate they are cultured on. When cells need to be passaged or analyzed, Trypsin-EDTA is applied, allowing for the separation of the cells without causing damage to their structure or function. In this context, the use of EDTA serves to chelate calcium ions, which helps to disrupt cell adhesion more effectively. This combination is essential in maintaining the viability of the cells during the detachment process. By employing Trypsin-EDTA, researchers can ensure that the cells remain healthy and suitable for further experimentation or culture conditions. The other choices involve processes that are not associated with the specific function of Trypsin-EDTA. For instance, using it for cell fixation or staining contradicts its role, as fixation typically involves a different set of chemicals that preserve cell morphology rather than detaching cells. Encouraging cell growth is related to the culture medium and conditions rather than the detachment process, while enhancing DNA replication pertains to cellular processes that are independent of the detachment method employed.

7. What is the maximum number of color combinations that can be obtained from 5 fluorochromes?

A. 16

B. 31

C. 25

D. 20

To determine the maximum number of color combinations that can be obtained from 5 fluorochromes, consider that each fluorochrome can either be present or absent in a combination. This binary choice results in combinations where any number from 0 to all 5 fluorochromes can be used. Mathematically, this can be illustrated as follows: - For each fluorochrome, there are 2 possibilities: it can be included in the combination or it can be excluded. - Therefore, for 5 fluorochromes, the total combinations can be calculated using the formula for combinations which states that the number of combinations is equal to \(2^n \), where \(n \) represents the number of items (in this case, fluorochromes). Calculating this gives: \(2^5 = 32 \) However, one of those combinations includes the scenario where no fluorochromes are used at all (the empty combination), which doesn't provide useful information in terms of color combinations. Thus, you subtract that one combination from the total, leading to: 32 (total combinations) - 1 (empty combination) = 31 This indicates that with 5 fluorochromes, you can achieve a maximum of 31 different

8. Which AML type is characterized by no associated chromosomal changes?

A. AML M3

B. AML M2

C. AML M1

D. AML M0

AML M0, or acute myeloid leukemia with minimal differentiation, is indeed characterized by the absence of prominent chromosomal abnormalities typically associated with other subtypes of acute myeloid leukemia. This subtype is defined by a lack of myeloid maturation and often presents a more challenging diagnostic scenario due to the minimal differentiation of the leukemic cells. In the context of acute myeloid leukemias, many subtypes exhibit specific chromosomal changes, which can be crucial for diagnosis, prognosis, and treatment decision-making. For example, AML M3 (promyelocytic leukemia) is frequently associated with the translocation t(15;17), which results in the fusion of the promyelocytic leukemia (PML) gene and the retinoic acid receptor alpha (RARA) gene. Similarly, AML M2 (acute myeloblastic leukemia with maturation) often involves chromosomal abnormalities such as t(8;21), and AML M1 is associated with isolated abnormalities like 5q- or inv(16). In contrast, AML M0 is typically diagnosed based on the presence of blast cells that lack myeloid maturation and do not exhibit the defining chromosomal translocations or abnormalities associated with the other subtypes.

9. Colagenase, pronase, and trypsin are classified as what type of enzymes?

A. Oxidative enzymes

B. Hydrolases

C. Proteolytic enzymes

D. Ligases

The correct classification for collagenase, pronase, and trypsin is that they are proteolytic enzymes. Proteolytic enzymes, also known as proteases, are responsible for the breakdown of proteins into smaller peptides or amino acids by catalyzing the hydrolysis of peptide bonds. Collagenase specifically targets collagen, a major protein found in connective tissues, breaking it down for various biological processes. Pronase is a broad-spectrum protease that can digest a variety of proteins, while trypsin is a serine protease that primarily acts on the peptide bonds formed by the amino acids lysine and arginine. Understanding this classification is important in fields such as cytogenetics and molecular biology, as these enzymes are often used to prepare samples or facilitate processes like cell culture or tissue digestion. The other enzyme categories mentioned, such as oxidative enzymes, hydrolases, and ligases, do not accurately describe the primary function of collagenase, pronase, and trypsin. Hydrolases encompass a broader category, which includes proteases, but the more specific term for these particular enzymes is proteolytic. Ligases, on the other hand, are enzymes that join two molecules together, which is distinctly different from the function

10. What is a common feature of AML subtypes M0 and M1 in terms of differentiation?

A. Both display high levels of cell differentiation

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C. Both types have chromosomal changes

D. Both types exhibit unique genetic markers

The correct answer emphasizes the commonality of a lack of differentiation in acute myeloid leukemia (AML) subtypes M0 and M1. In these subtypes, leukemic cells typically exhibit minimal to no signs of myeloid differentiation. In M0, there is an absence of identifiable differentiation and an increase in blast cells that are morphologically undifferentiated. This subtype is characterized by a predominance of primitive myeloid cells that lack specific lineage markers. M1, while showing some myeloid features, predominantly consists of blasts that are only mildly differentiated, indicating early stages of myeloid cell development. It is characterized by a higher percentage of immature blasts in the bone marrow but still doesn't demonstrate full myeloid maturation. Subtypes M0 and M1 are particularly notable for their aggressive nature, often leading to rapid disease progression without effective differentiation of the cells. Therefore, the shared characteristic of being associated with a lack of differentiation underlines the distinction of these AML subtypes within the broader classification of acute leukemias. While other answers may imply features related to differentiation or genetic markers, they do not accurately represent the unified characteristic of both M0 and M1, reinforcing the importance of recognizing the lack of