

Basic Bioscience

Final Examination Essay

Submission Deadline: within 48 hours

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Question 1 (expected answer length: 2 pages A4) (total 50 marks)

DNA sequencing technology allows us to identify bacteria species accurately. However, other classification and identification methods are still being used widely. In your own words, explain

1. Why identifying bacteria species is important? (5 marks)

Identifying bacteria species is important for several reasons. First, it allows us to better understand the evolutionary relationships and origins of different bacteria. Knowing the species provides insight into its genetic makeup, physiology, and ecological role. Second, identifying species is critical for public health purposes. It enables tracking of disease outbreaks, development of diagnostic tests, and treatment plans tailored to specific pathogens. Certain species may require different interventions or control measures. Finally, identification aids industrial and commercial applications of bacteria. Species information guides bioengineering efforts to harness bacteria for food production, bioremediation, chemical synthesis, and other uses. In summary, determining the bacterial species provides foundational knowledge about its characteristics and how it interacts with humans and the environment. Accurate identification underpins microbiology research, medicine, public health, and biotechnology.

2. What are other methods used to identify and classify bacteria? (15 marks)

In addition to DNA sequencing, other important techniques are still widely used to identify and classify bacteria species. Microscopic examination of cell morphology, size, and structural features provides clues about phylogenetic relationships and taxonomic groupings. Staining methods such as Gram staining distinguish between major bacterial cell wall types, differentiating Gram-positive and Gram-negative species. Biochemical testing assesses metabolic properties and products, enzymatic activities, and nutrient requirements that can aid identification. Culture techniques look at growth conditions, colony characteristics, and byproducts to characterize species. Analyzing cell wall components like fatty acids and quinones also facilitates classification. While DNA sequencing delivers precise species identification, these traditional microbiological methods help paint a broader picture of bacterial properties and hierarchies when used alongside genomic analysis. They remain essential tools that complement and expand on the insights from DNA sequencing.

3. How DNA sequencing is different from other methods for classification and identification of bacteria? Explain the principles. (15 marks)

DNA sequencing stands out from other methods for classifying and identifying bacteria due to its unparalleled precision and accuracy. This technique allows for a comprehensive analysis of the entire genetic code, enabling a direct comparison of species' DNA and establishing precise relationships. In contrast, alternative methods may lead to classification errors, particularly given the unique nature of bacteria. DNA sequencing not only ensures accuracy in identification but also provides insights into the inherent nature of bacteria.

The principles underlying DNA sequencing encompass chemical degradation, where the DNA strand is broken into fragments; sequencing by synthesis, involving the identification of bases during the synthesis process; sequencing by ligation, which utilizes ligases to identify specific DNA sequences; and nanopore technologies, where DNA strands pass through nanopores for analysis. These diverse approaches contribute to the method's superiority in offering a detailed and reliable understanding of bacterial species, setting it apart as a preferred tool for classification and identification.

4. What are the advantages and disadvantages of DNA sequencing and other methods? (15 marks)

DNA sequencing stands out for its remarkable accuracy and ability to provide comprehensive genetic information, allowing for precise identification of bacterial species and even specific strains. The unbiased approach of DNA sequencing, not dependent on growth conditions, is advantageous, especially for fastidious or slow-growing species. While the continuous advancements in technology have led to increased speed and reduced costs, the complexity of interpreting the vast genetic data and the requirement for specialized equipment and expertise remain notable challenges. Despite these challenges, DNA sequencing offers a powerful and evolving tool for bacterial identification, particularly in research and settings with the necessary infrastructure and expertise.

Traditional culture-based methods, including colony counting and established protocols, provide a cost-effective alternative for routine bacterial identification in many settings. These methods have been relied upon for decades, with the advantage of familiarity and existing infrastructure in laboratories. However, their limitations become apparent in terms of specificity, as they may struggle to distinguish between closely related species or strains. Additionally, the slower turnaround time associated with culturing bacteria can be a disadvantage, especially in situations requiring rapid identification for infectious disease diagnosis. Moreover, some bacterial species may be challenging to culture, limiting the effectiveness of these methods in detecting certain organisms. The choice between DNA sequencing and other methods hinges on factors such as cost, speed, and the specific

requirements of the identification task.

Question 2 (expected answer length: 2 pages A4) (50 marks)

The advent of gene editing techniques has ushered in a new era, empowering humanity to intricately manipulate the genetic fabric of living organisms. This transformative capability not only underpins groundbreaking scientific research but also holds the potential to revolutionize medical interventions and address hereditary disorders. Among the diverse array of gene editing methods, two prominent players, namely site-directed mutagenesis and CRISPR-Cas9 technology, stand out for their pivotal roles in advancing our genetic manipulation capabilities.

At the forefront of precision genetic manipulation, site-directed mutagenesis provides researchers with the tools to make nuanced alterations at the molecular level. This technique is instrumental in unraveling the intricacies of gene functions and understanding their profound impacts on living organisms. For instance, the manipulation of the BRCA1 gene, associated with an elevated risk of breast and ovarian cancers, exemplifies the potential of site-directed mutagenesis. Introducing specific mutations into this gene allows scientists to meticulously observe resultant changes in cellular behavior, thereby gaining invaluable insights into the mechanisms driving cancer development.

The CRISPR-Cas9 system has emerged as a transformative force in genetic engineering, enabling precise and efficient modification of DNA sequences. Its versatility spans various domains, showcasing its potential in diverse applications.

In the realm of medical treatments, CRISPR-Cas9 holds great promise for addressing genetic diseases by correcting or replacing faulty genes. Ongoing research explores its application in treating complex conditions such as sickle cell anemia and beta-thalassemia, where targeted editing of specific genes opens avenues for curative therapies.

Beyond the medical sphere, agriculture has witnessed the transformative impact of gene editing. Employing these techniques enhances crop characteristics, such as improved resistance to pests, diseases, or environmental stress. Notably, genetically modified crops with heightened nutritional content contribute to bolstering global food security.

The biotechnology and pharmaceutical industries leverage gene editing to optimize the production of therapeutic proteins and develop novel drugs. Precise modifications to the genetic makeup of microorganisms or cell lines are pivotal in achieving efficient production of valuable compounds, fostering innovation in medicine and biotechnology.

Moreover, CRISPR-Cas9 has become an indispensable tool for basic research, facilitating the study of specific gene functions and unraveling complex biological processes. The generation of genetically modified organisms enables scientists to delve into the intricate mechanisms of diseases, behavior, and various biological phenomena.

Amidst the transformative potential of gene editing, ethical considerations and meticulous regulation become imperative. Responsible and ethical use of these technologies is paramount to navigate the complex challenges and ethical implications associated with manipulating the fundamental building blocks of

life. Striking a balance between scientific progress and ethical integrity is crucial to ensure the sustained and responsible advancement of gene editing technologies.