

Application of Single Cell Microbial Function Analysis Technology in the Study of Drug-resistant Bacterial Heterogeneity

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Abstract: Currently, single-cell sequencing technology can accurately detect and analyze the biological functions of individual cells, which has been widely applied in microbiome research. Moreover, microbial diversity is a crucial aspect of microbiology. Different microbial communities exhibit unique physiological functions and varying adaptability to environmental changes, which are closely linked to their biological functions. Therefore, using single-cell sequencing technology to study the diversity of drug-resistant bacteria can reveal the mechanisms of interaction among microorganisms from multiple perspectives and provide new insights into this diversity.

Keywords: single cell microorganism; biological function; analytical technology; drug-resistant bacteria; heterogeneity

1. Introduction

In recent years, as the misuse of antibiotics has become increasingly severe, drug-resistant bacteria have become a major concern in clinical settings. Drug-resistant bacteria are microorganisms that have developed resistance to current treatment regimens, and their diversity is one of the reasons why antibiotics cannot fully cure diseases. Therefore, it is crucial to conduct in-depth research on drug-resistant bacteria, explore their development mechanisms, and develop targeted treatment strategies. Traditional methods, such as routine culture and animal models, often focus on describing the macroscopic physiological characteristics of bacteria. These methods have limitations when studying bacterial species, making it difficult to reveal the relationship between bacterial biological functions, physiological characteristics, and sensitivity to antimicrobial drugs. In recent years, single-cell sequencing technology has provided new research approaches and insights into the biological functions and drug resistance of drug-resistant bacteria.

2. Overview of single-cell microbial functional analysis technology

2.1 Introduction to single cell technology

Single-cell analysis is a crucial method for studying cellular heterogeneity at the single-cell level. Currently, single-cell technology is primarily used in the metabolic profiling of microorganisms, effectively addressing the challenges of sample collection and gene annotation in microbial community diversity analysis, including bacteria, fungi, and archaea. The heterogeneity of single-cell microbial communities, encompassing different functional groups, metabolic pathways, tissue types, and cell types, can rapidly and accurately reflect the overall dynamic changes in microbial populations. However, the physiological, growth, and metabolic heterogeneity of single-cell microbial communities limit the study of their structure and function. Therefore, it is particularly important to conduct in-depth research on these functions, especially the information of key functional genes[1].

2.2 Overview of microbial function analysis technology

In recent years, with the continuous advancement of single-cell sequencing technology, researchers have been able to delve into biological functions at the single-cell level. Currently, single-cell sequencing technology is primarily categorized into three types: the first type involves high-throughput sequencing techniques, such as the Sanger method and amplification methods; the second type includes traditional methods, such as nucleic acid extraction, gene amplification, and library construction; the third type is metagenomics methods, such as metagenomic sequencing. As high-throughput sequencing technology continues to evolve, single-cell sequencing has become a crucial tool in microbial research. Compared to traditional methods, single-cell sequencing allows for direct data analysis and functional annotation at the single-cell level, making the data processing process simpler and faster, which aids in a deeper understanding of the mechanisms of microbial life activities[2].

2.3 Development status of single cell microbial function analysis technology

Single-cell functional analysis technology has evolved from metagenomics to the current single-cell functional analysis techniques, which have been widely applied in microbiome research. Currently, single-cell sequencing technology has become a key tool in microbiome studies. However, due to the heterogeneity among microbial cells and the complexity of biological activities within individual cells, using single-cell sequencing technology for microbial function research still faces several challenges. By analyzing the metabolic products of individual cells, single-cell sequencing technology can determine their biological functions, enabling accurate detection and analysis of biological activities within individual cells. Additionally, it involves the analysis of antibiotic resistance in bacteria.

3. Overview of drug-resistant bacteria

Drug resistance refers to the reduced sensitivity of bacteria to antibiotics. The primary causes include: (1) genetic mutations; (2) the use of chemically synthesized antibiotics; (3) antibiotic selection pressure. Due to the severe side effects of antibiotics in treating bacterial infections, their use is gradually being restricted. Various drugs are associated with bacterial resistance, including cephalosporins, aminoglycosides, macrolides, and quinolones. Different types of bacteria exhibit varying degrees of resistance to the same antibiotic. Over time, bacteria adapt to different drug effects by altering their structure and metabolic processes, resulting in varying degrees of resistance. Additionally, there are differences among resistant bacterial strains, which are reflected in their genes, metabolic functions, and virulence [3].

3.1 Concept of heterogeneity

Heterogeneity refers to the spatial and temporal distribution differences among biological individuals or populations, typically manifested as genetic differences between species and the adaptive responses of individuals or populations to environmental factors during evolution. Heterogeneity is primarily categorized into two types: spatial heterogeneity and temporal heterogeneity. Spatial heterogeneity involves the distribution differences of microbial individuals or populations across different geographical regions, while temporal heterogeneity refers to the evolutionary rate of microbial populations over time, which can lead to population numbers increasing in a short period, decreasing in density, or even disappearing. The drug resistance heterogeneity in bacteria is mainly reflected in changes in genome structure, gene expression levels, metabolic products, and virulence genes [4].

3.2 Significance of research on heterogeneity of drug-resistant bacteria

The study of the heterogeneity of drug-resistant bacteria is an important part of the study of drug resistance mechanism, which provides a scientific basis for the rational use of antibacterial drugs in clinical treatment. In-depth study of the heterogeneity of drug-resistant bacteria will provide theoretical guidance for the accurate diagnosis, treatment and prevention of drug-resistant bacteria.

4. Application of single-cell microbial function analysis technology in the study of heterogeneity of drug-resistant bacteria

Single-cell microbial functional analysis technology, based on single-cell sequencing, can analyze the composition, diversity, abundance, and function of different microbial communities. This method aids in understanding the interactions between these communities and reveals the functional mechanisms within microbial populations. Compared to traditional methods, this technology is characterized by high throughput, low cost, and ease of operation, making it particularly suitable for studying the heterogeneity of drug-resistant bacteria. In this study, single-cell microbial functional analysis technology was used to analyze two strains of drug-resistant bacteria, focusing on several key aspects: (1) the characteristics of microbial community composition; (2) the differences in diversity and abundance within microbial communities; (3) the distribution of functional genes within microbial communities. The study included whole-genome sequencing of both strains of drug-resistant bacteria, as well as comparative analyses using single-cell metagenomic sequencing data and multiple databases[5].

5. Conclusion

Currently, single-cell sequencing technology has been widely applied in microbiome research, offering advantages such as ease of operation, rapid analysis, and low cost. However, this technology is primarily used for bacterial studies, and it still faces numerous challenges in studying the heterogeneity of drug-resistant bacteria, particularly in accurately identifying and analyzing the biological functions within individual cells.

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