Suitable Approach for Quality Assurance in the Identification of the Micro-organisms Including Bacteria, Viruses and Fungi

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BACKGROUND

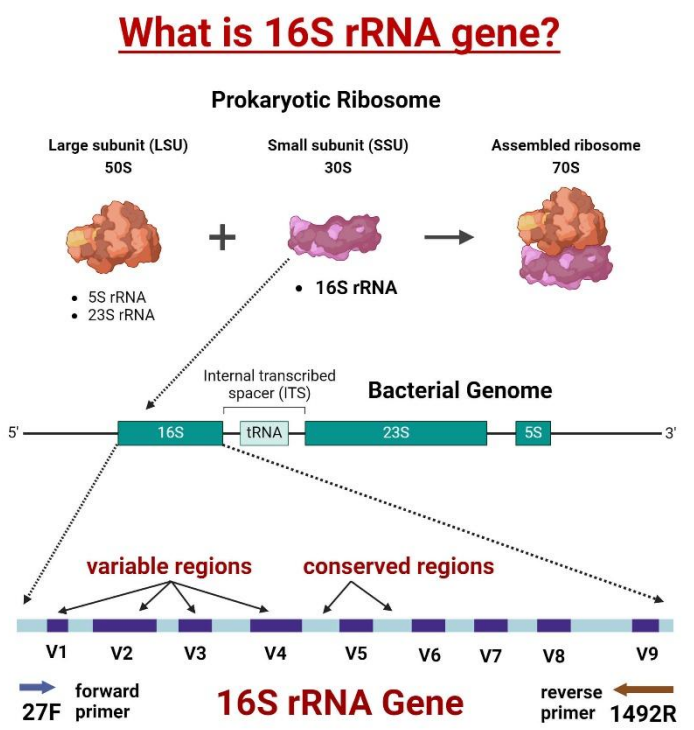
Reliable identification of microorganisms is a cornerstone in the accurate diagnosis, effective treatment, and prevention of infectious diseases in clinical settings. Nevertheless, the genetic diversity of pathogens—including bacteria, viruses, and fungi—together with the inherent limitations of conventional diagnostic methods, highlights the urgent need for standardized and efficient quality assurance strategies.

AIMS OF THE STUDY

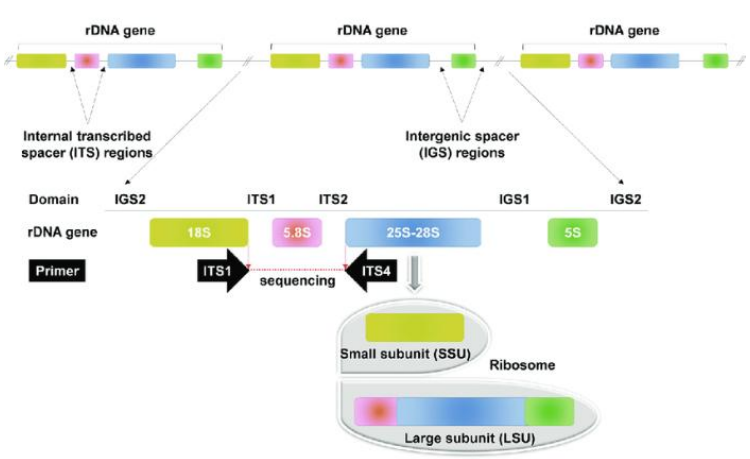
To ensure diagnostic reliability, these strategies must offer both high analytical accuracy and practical applicability within the operational capacity of medical laboratories.

MATERIALS AND METHODS

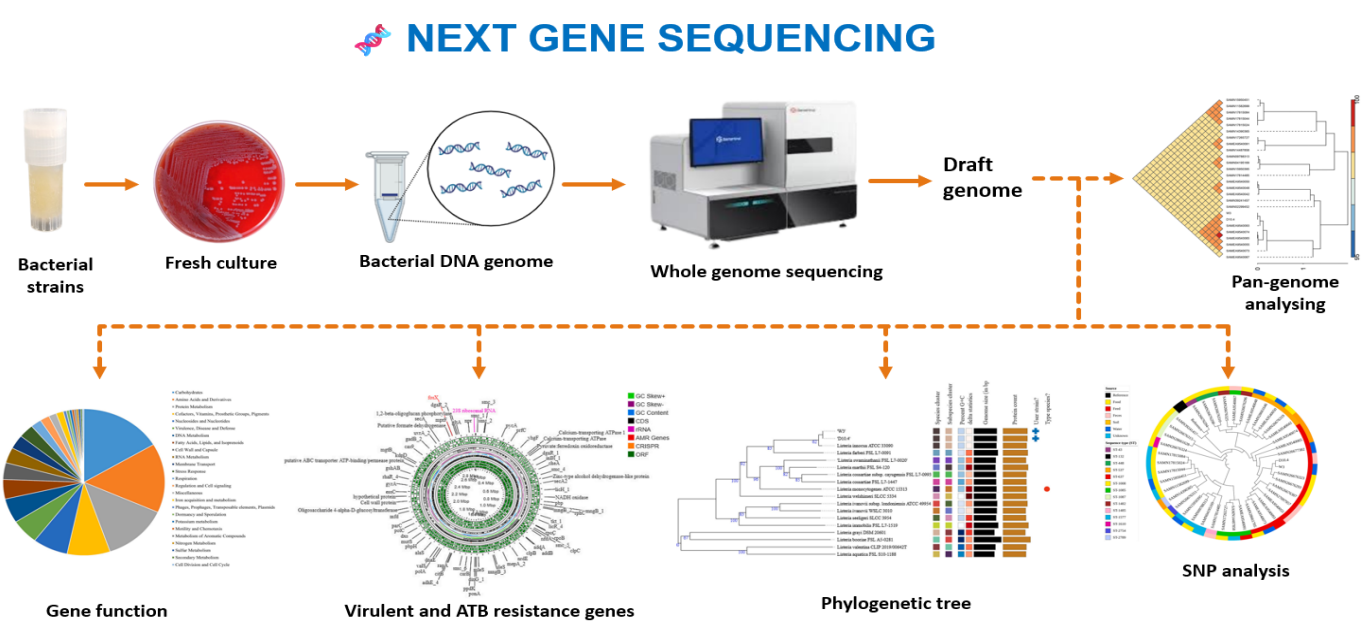
Among the most effective and widely implemented methods is Sanger sequencing, which targets highly conserved genomic regions such as the 16S rRNA gene for bacteria, ITS regions for fungi, and specific coding regions (e.g. E or RdRp) for RNA viruses. In more complex diagnostic scenarios—such as polymicrobial infections, undetermined etiologies, or discordant results between culture and molecular testing—advanced approaches like whole genome sequencing (WGS) and metagenomic sequencing serve as invaluable tools for validation and cross-verification.



Picture 1: The whole genome sequence of 16S rRNA gene can be amplified by PCR using the 27F and 1492R as the primers



Picture 2: Sanger sequencing of the full-length ITS region is a reliable tool for clinical fungal identification, especially for: The need for rapid and accurate identification for early treatment



Picture 3: The next-generation sequencing techniques offer broader genetic insights but demand substantial investment, advanced computational infrastructure, and expert interpretation—thus making them more suitable for specialized or reference laboratories

RESULTS

Sanger sequencing provides a well-standardized, cost-effective workflow that enables laboratories to directly compare microbial sequences with established international databases (e.g., NCBI, UNITE, GISAID). This not only ensures accurate confirmation of results but also aids in identifying technical errors or misclassifications due to limited internal reference libraries. By contrast, next-generation sequencing techniques offer broader genetic insights but demand substantial investment, advanced computational infrastructure, and expert interpretation—thus making them more suitable for specialized or reference laboratories

KEY WORDS

HPV genotypes, E6/E7 mRNA; Reverse transcriptase multiplex real-time PCR (RT MLP-rPCR).

DISCUSSIONS AND CONCLUSION

The integration of both traditional and next-generation sequencing techniques, supported by rigorous internal and external quality control systems, significantly enhances the reliability, reproducibility, and international compatibility of microbial diagnostic outcomes. Ultimately, this comprehensive approach contributes to more timely, targeted patient care and strengthens the overall effectiveness of infectious disease management.

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