MIST: A Microbial Identification and Source Tracking System For Next-Generation Sequencing Data

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The professional Committee of Microbiology of the National Pharmacopoeia Commission organized the drafting of the Technical Guidelines for Microbial Whole Genome Sequencing (WGS), aiming to standardize the method process and technical indicators of microbial WGS and ensure the accuracy of identification. Based on the guidelines, we developed MIST, an integrated microbial identification system, designed to meet the needs of microbial identification and contamination investigation in food and drug quality control.

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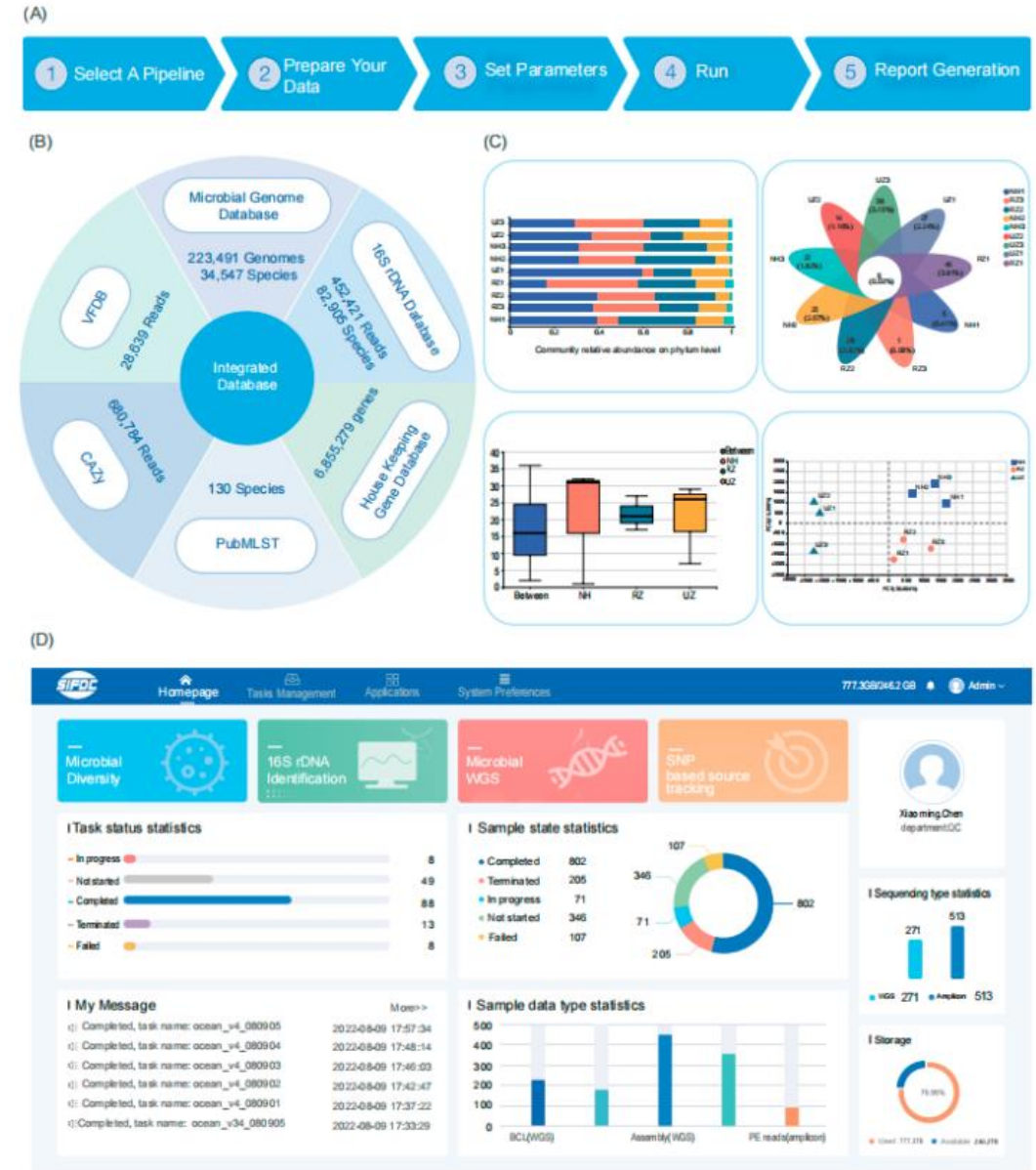
Summary

Whole genome sequencing, amplicon and metagenomic sequencing are increasingly used in research to produce complicated environmental sequence datasets, which paved the way for a cultivation-independent genetic content assessment and exploitation of the entire communities of organisms. Therefore, it is urgent to develop WGS and amplicon-based microbial species identification pipelines in the field of food safety and drug control. Here we provide a system to analyze the WGS, amplicon sequences for microbial identification, MLST typing and SNP source tracking. In our system, one important potential use of the WGS microbial identification pipeline is to identify contaminated sequences or metagenome samples. Simultaneously, it has great value in speeding up the pathogen detection in clinical laboratory, while the existing identification and taxonomy methods may be unreliable with contaminated samples.

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