High-Resolution Microbial Profiling Across Unexplored Niches Using CoSMIC

(No. T4-2368)

Principal investigator

Ziv Reich

Faculty of Biochemistry
Department of Biomolecular Sciences

Overview

Microbial profiling methods based on 16S rRNA sequencing are limited by primer bias, short-read coverage, and databases dominated by human-associated microbes. These limitations reduce phylogenetic resolution and hinder accurate species detection in underexplored environments. CoSMIC is a hybrid profiling approach that combines long-read sequencing with short-read analysis over multiple 16S regions, enabling precise, cost-effective identification of microbial communities. It overcomes traditional biases and offers robust profiling even in low-biomass or fragmented DNA samples.

Applications

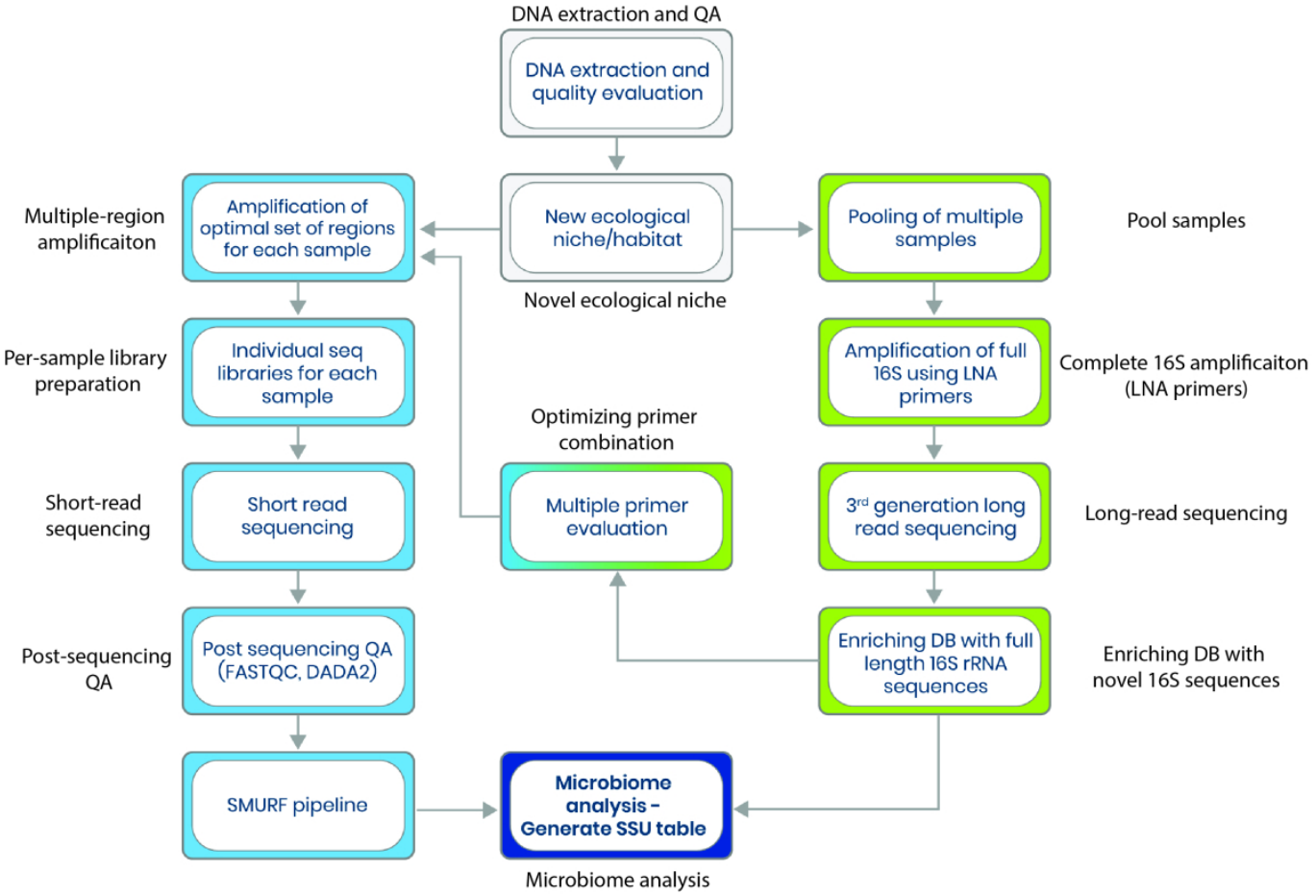
- Microbiome mapping in agricultural soils for precision farming (e.g., irrigation and pesticide optimization)
- Development of microbial inoculants to enhance seed, soil, or antimicrobial traits
- Surveillance of bacteria-prone environments (e.g., aquaculture, hospitals, food processing)
- Microbial monitoring in water treatment and quality assessment.

Differentiation

- Improved PCR-quantification fidelity
- Reduced bias by adding niche-specific full-length sequences to reference databases
- Accurate species detection via high phylogenetic resolution
- Cost-efficient, adaptable primer selection with reduced primer bias

Development Stage

Validated in diverse plant, soil, and marine sponge samples; benchmarked against metagenomics and commercial kits. CoSMIC has demonstrated superior resolution, reduced ambiguity, and high alignment accuracy in experimental settings.


DNA extraction and QA
DNA extraction and quality evaluation
New ecological niche/habitat
Novel ecological niche
Multiple-region amplificaiton
Amplification of optimal set of regions for each sample
Per-sample library preparation
Individual seq libraries for each sample
Short-read sequencing
Short read sequencing
Post-sequencing QA
Post sequencing QA (FASTQC, DADA2)
SMURF pipeline
Optimizing primer combination
Multiple primer evaluation
Pooling of multiple samples
Pool samples
Amplification of full 16S using LNA primers
Complete 16S amplificaiton (LNA primers)
3rd generation long read sequencing
Long-read sequencing
Enriching DB with full length 16S rRNA sequences
Enriching DB with novel 16S sequences
Microbiome analysis - Generate SSU table
Microbiome analysis
Lorem ipsum