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Standardizing Genomic Surveillance Methods for Enhanced Food Safety

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Background

Whole-genome sequencing (WGS) is essential for modern food safety and public health surveillance, enabling high-resolution detection and outbreak investigation of foodborne pathogens. The FDA GenomeTrakr Network relies on WGS for global comparisons, requiring well-characterized reference materials to ensure accuracy and reproducibility. The GenomeTrakr Validation Strain Set (GTVSS; ATCC® MP-44™) is a curated panel of 32 diverse bacterial isolates with defined validation roles, providing a standardized tool for end-to-end benchmarking of WGS workflows.

ATCC® will provide quantitative genomic DNA for each strain to ensure consistent input for assay development, validation, and performance comparisons.

Key features of the GTVSS

- 32 diverse foodborne and environmental isolates
- Defined roles: SNPs, AMR, plasmids, virulence, diversity
- End-to-end workflow validation
- Cross-laboratory benchmarking
- Available as cultures and quantified DNA with public genomes

Learn more about the GenomeTrakr Validation Strain Set

Methods

The GTVSS was developed by the FDA GenomeTrakr Program by selecting well-characterized isolates from food, environmental, and clinical sources. Strains were chosen to represent major pathogens and genomic diversity (e.g., genome size, GC content, plasmids, AMR, and virulence factors).

Each strain was assigned a specific validation role (e.g., SNP analysis, AMR detection, plasmid identification, and taxonomic diversity) to ensure coverage of critical WGS performance metrics. Selection was informed by GenomeTrakr proficiency testing approaches designed to assess reproducibility and analytical consistency across laboratories[1]. High-quality reference genomes have been generated and made publicly available. Corresponding live strains and quantitative genomic DNA ($\geq 1 \times 10^5$ copies/µL) for some strains are also provided by ATCC to support standardized benchmarking. ATCC® is working to make quantitative genomic DNA available for all strains by the end of July 2026.

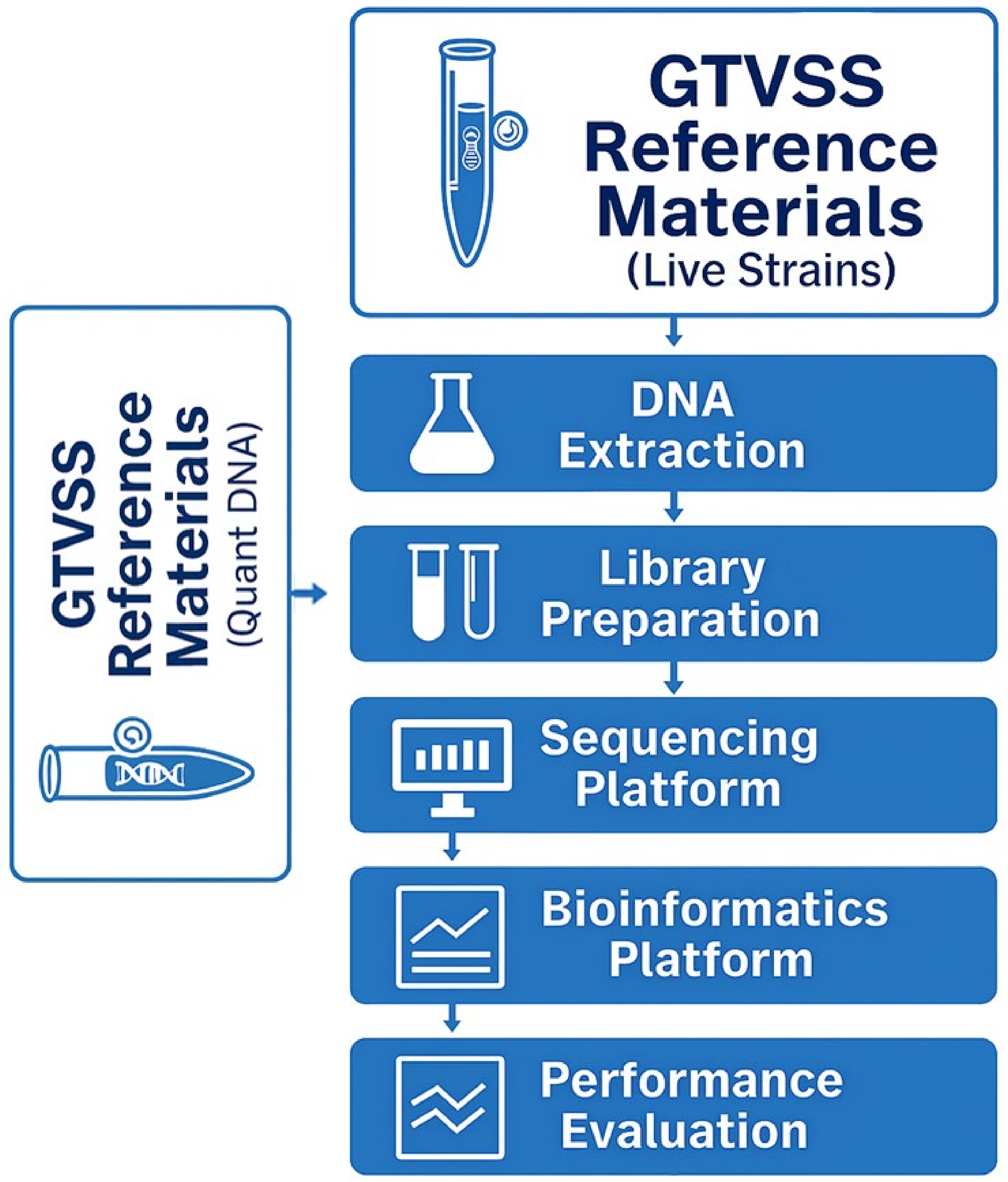
References

1. Timme RE, et al. GenomeTrakr proficiency testing for foodborne pathogen surveillance: an exercise from 2015. Microb Genom 4(7): e000185, 2018.

Results

Table 1: GenomeTrakr Validation Strain Set (GTVSS) – ATCC® item IDs for the live strains and gDNA with associated isolation source and purpose

ATCC® Id for live strains	ATCC® Id for gDNA	Species	Source of isolate	Purpose of inclusion
BAA-3422-NGS-PACK™	BAA-3422DQ™	*Bacillus cereus*	Mac and cheese	Taxonomic diversity
BAA-3417-NGS-PACK™	BAA-3417DQ™	*Campylobacter coli*	Chicken breast	Low GC
BAA-3418-NGS-PACK™	BAA-3418DQ™	*Campylobacter jejuni*	Chicken breast	Low GC
BAA-3428-NGS-PACK™	BAA-3428DQ™	*Citrobacter braakii*	Cilantro	Common contaminant
BAA-3421-NGS-PACK™	BAA-3421DQ™	*Cronobacter sakazakii*	Unknown	Taxonomic diversity
BAA-3429-NGS-PACK™	BAA-3429DQ™	*Enterobacter cancerogenus*	Cilantro	Common contaminant
BAA-3420-NGS-PACK™	BAA-3420DQ™	*Escherichia coli*	All-purpose wheat flour	Toxin detection
BAA-3423-NGS-PACK™	BAA-3423DQ™	*Escherichia coli*	Unknown	Toxin detection
BAA-3427-NGS-PACK™	BAA-3427DQ™	*Klebsiella pneumoniae*	Spice mixture	Common contaminant
BAA-3426-NGS-PACK™	BAA-3426DQ™	*Klebsiella variicola*	Spice mixture	Common contaminant
BAA-3419-NGS-PACK™	BAA-3419DQ™	*Listeria innocua*	Minced meat	Taxonomic diversity
BAA-3406-NGS-PACK™	BAA-3406DQ™	*Listeria monocytogenes*	Organic baby spinach	SNP recovery
BAA-3409-NGS-PACK™	BAA-3409DQ™	*Listeria monocytogenes*	Green chili ingredient	Well-characterized strain
BAA-3411-NGS-PACK™	BAA-3411DQ™	*Listeria monocytogenes*	Peach	SNP recovery
BAA-3412-NGS-PACK™	BAA-3412DQ™	*Listeria monocytogenes*	Peach	SNP recovery
BAA-3413-NGS-PACK™	BAA-3413DQ™	*Listeria monocytogenes*	Peach	SNP recovery
BAA-3414-NGS-PACK™	BAA-3414DQ™	*Listeria monocytogenes*	Peach	SNP recovery
BAA-3424-NGS-PACK™	BAA-3424DQ™	*Pseudomonas aeruginosa*	Arugula	Common contaminant, High GC
BAA-3425-NGS-PACK™	BAA-3425DQ™	*Pseudomonas fluorescens*	Arugula	Common contaminant, High GC
BAA-3430-NGS-PACK™	BAA-3430DQ™	*Salmonella enterica* subsp. *diarizonae*	Frilled lizard	Taxonomic diversity
BAA-3401-NGS-PACK™	BAA-3401DQ™	*S. enterica* subsp. *Enterica*	Frozen raw shrimp	SNP recovery
BAA-3403-NGS-PACK™	BAA-3403DQ™	*S. enterica* subsp. *enterica*	Human	SNP recovery
BAA-3404-NGS-PACK™	BAA-3404DQ™	*S. enterica* subsp. *enterica*	Human	SNP recovery
BAA-3405-NGS-PACK™	BAA-3405DQ™	*S. enterica* subsp. *enterica*	Human	SNP recovery
BAA-3410-NGS-PACK™	BAA-3410DQ™	*S. enterica* subsp. *enterica*	Unknown	Taxonomic diversity
BAA-3402-NGS-PACK™	BAA-3402DQ™	*S. enterica* subsp. *enterica*	Stool	Plasmid detection
BAA-3415-NGS-PACK™	BAA-3415DQ™	*Shigella dysenteriae*	Human	AMR
BAA-3416-NGS-PACK™	BAA-3416DQ™	*Shigella sonnei*	Human	Plasmid detection
BAA-3407-NGS-PACK™	BAA-3407DQ™	*Staphylococcus aureus*	Bakery whipped topping	AMR, toxin detection, low GC
BAA-3408-NGS-PACK™	BAA-3408DQ™	*Staphylococcus aureus*	Bakery environment	Toxin detection, extreme GC
BAA-3431-NGS-PACK™	BAA-3431DQ™	*Vibrio parahaemolyticus*	Human	Taxonomic diversity
BAA-3432-NGS-PACK™	BAA-3432DQ™	*Vibrio parahaemolyticus*	Human	Taxonomic diversity


GTVSS Reference Materials (Live Strains)

GTVSS Reference Materials (Quant DNA)

DNA Extraction

Library Preparation

Sequencing Platform

Bioinformatics Platform

Performance Evaluation

Figure 1: GTVSS-driven workflow for comprehensive WGS validation and benchmarking in food safety.

Conclusions

The GenomeTrakr Validation Strain Set (GTVSS) provides a standardized reference panel for validating and benchmarking whole-genome sequencing workflows in food safety.

- A standardized 32-strain panel enables robust validation of WGS workflows
- Diverse strains with defined roles and quantitative DNA support consistent performance assessment
- The approach improves reproducibility and cross-laboratory comparability
- It enables rigorous validation of WGS methods, increasing confidence in sequence data quality for regulatory and public health decision-making.

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