



Whole-Genome Sequencing Reveals Genetic Diversity among *Staphylococcus aureus* Isolates from Texas Dairy Farms

Poster

Ecología microbiana y Microbioma

Maria Camila Duarte V ¹, Jennifer Miller ², Christopher Grim ², Zhao Chen ³, Angela Perdomo ¹, Alexandra Calle ¹.

(1) Texas Tech University, School of Veterinary Medicine, School of Veterinary Medicine, 7671 Evans Drive, Amarillo, United States.

(2) Food and Drug Administration, United States.

(3) Joint Institute for Food Safety and Applied Nutrition, United States.

mariadua@ttu.edu

Introduction:

Staphylococcus aureus remains a leading cause of mastitis in dairy cattle, contributing to economic losses due to reduced milk yield and quality. Understanding the genomic diversity of *S. aureus* circulating in dairy environments is critical for improving control strategies and exploring potential connections to isolates recovered from food and humans.

Purpose:

This study aimed to evaluate the genomic relatedness and diversity among *S. aureus* isolates collected from a Texas dairy farm to identify genetically distinct strains for downstream phenotypic and metabolic investigations.

Methods:

From July 2022 to August 2023, 282 samples were collected from milk, feed, feces, udders, and environmental sources. Presumptive *Staphylococcus* colonies were first identified using the MALDI-TOF system and further confirmed by whole-genome sequencing (WGS) on the Illumina NextSeq 2000 platform. Genome assemblies were

classified using GTDB-Tk R207_v2, and single-nucleotide polymorphism (SNP) distances were calculated to assess genetic relatedness. Based on FDA guidance, genomes differing by <21 SNPs were considered closely related (same strain), while genomes differing by ≥ 21 SNPs represented unique strains.

Results:

MALDI-TOF confirmed 109 *S. aureus* isolates, while WGS analysis identified 150 *S. aureus* genomes, demonstrating higher discriminatory power of genomic sequencing. SNP-based comparison revealed 11 genetically distinct *S. aureus* strains, whereas several isolates were identified as duplicates or near-identical lineages (<21 SNPs). The distinct genotypes originated from multiple sample types, including milk, feed, and environmental swabs, suggesting persistent reservoirs within the dairy ecosystem. These 11 core genotypes will be prioritized for subsequent metabolic and phenotypic studies to assess strain-level functional diversity.

Significance:

This study provides one of the most comprehensive WGS-based characterizations of *S. aureus* from a Texas dairy farm, integrating species identification and genomic diversity data. The results establish a foundation for connecting genomic variability with metabolic behavior, supporting targeted surveillance and control strategies in dairy production systems.

Palabras Clave

(1) *Staphylococcus aureus*, (2) Genetic diversity, (3) Dairy farms, (4) Whole-genome sequencing, (5) Microbial Ecology.

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