

Lipidomics of milk samples from animals experimentally infected with *Staphylococcus warneri*

Jéssica Lobo Albuquerque Caldeira ¹, Richard Costa Polveiro ¹, Guilherme Filipe Costa Caldeira ¹, Arlene Bispo dos Santos Nossol ², Hebréia Oliveira Almeida Souza ², Maria Aparecida Scatamburlo Moreira ^{1*}

¹ Laboratório de Doenças Bacterianas (LDBAC), Setor de Medicina Veterinária Preventiva e Saúde Pública, Departamento de Veterinária, Universidade Federal de Viçosa, Minas Gerais, Brasil.

² Laboratório de Nanobiotecnologia Prof. Dr. Luiz Ricardo Goulart Filho, Instituto de Genética e Bioquímica, Universidade Federal de Uberlândia, Minas Gerais, Brasil.

* Corresponding author. E-mail: masm@ufv.br

Mastitis, an inflammation of the mammary gland, poses a significant threat to dairy herds, resulting in substantial losses. Among the primary causative agents of subclinical mastitis in dairy goats, *Staphylococcus* coagulase-negative bacteria, including *S. warneri*, are prominent. This study aimed to investigate the lipid profile of milk from goats experimentally infected with *S. warneri*, employing an omics approach to comprehend the changes occurring during infection. Milk samples were collected from eight Alpine Brown goats, including two uninfected and six intramammary-infected in the right udder with *S. warneri*. Samples from the left udder were also analyzed for potential differences. Analyses were conducted using Agilent Technologies' gas chromatography-mass spectrometry system (model 7890B GC System/5977B GC/MSD) with a DB-5HT capillary chromatographic column. The Scan monitoring technique was employed for GC/MS analysis. During the infection period, approximately 700 different lipids were identified in milk samples. Among these, when considering a frequency exceeding 50% in both infected and uninfected udder samples, 36 lipids were identified. Among these, 29 were common between the udders, while seven exhibited differences. Categorizing these lipids into the general compound categories, it was observed that in the infected (right) udder, Alkanes (10), Cyclical Siloxanes (7), Fatty Acids and Fatty Acid Esters (3), Alkenes (3), Alcohols (3), Complex Formula Compounds (2), Iodinated Alkanes (2), Sulfurous Acid Esters (2), Ethers (1), Silanes (1), Phthalate Esters (1), and Esters (1) were predominant. In the uninfected (left) udder, Alkanes (9), Cyclical Siloxanes (7), Alkenes (4), Fatty Acids and Fatty Acid Esters (3), Alcohols (3), Esters (3), Complex Formula Compounds (2), Iodinated Alkanes (2), Ethers (1), Silanes, and Silane Esters (1), and Cyclodextrin (1) were prevalent. This study marks the initial steps toward understanding the lipid profile of milk in *S. warneri*-infected animals. While lipid homogeneity was observed regardless of udder infection status, identified differences should not be disregarded. We emphasize that more specific classifications and robust statistical analyses are ongoing. Understanding these changes may contribute to the development of prevention and management strategies for mastitis in dairy goat herds, potentially benefiting milk production and animal health.

Key words: Caprine; Mastitis; Omics.

Lipidômica de amostras de leite de animais infectados experimentalmente com *Staphylococcus warneri*

A mastite, inflamação da glândula mamária, é prejudicial para rebanhos leiteiros. *Staphylococcus* coagulase negativo, como *S. warneri*, são principais causadores em caprinos. Este estudo analisou o perfil lipídico do leite de caprinos infectados por *S. warneri*. Foram usadas amostras de oito caprinos, sendo dois não infectados e seis infectados. Utilizando cromatografia gasosa e espectrometria de massas, identificaram-se 36 lipídios comuns em ambos os tetos e sete diferentes. Alcanos, siloxanos, ácidos graxos e ésteres foram predominantes em ambos os tetos. Este estudo destaca a importância de compreender as mudanças nos lipídios durante a mastite e seu potencial para melhorar a prevenção e manejo da doença em caprinos leiteiros.

Palavras-chave: Caprinos; Mastite; Ômica.

Acknowledge: The authors also acknowledge financial support from the FAPEMIG, CAPES and CNPq.