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IDENTIFICATION OF MICROBIAL DIVERSITY ON CUTTING ROOM SURFACES AFTER PRE-OPERATIONAL CLEANING IN A POULTRY SLAUGHTERHOUSE

Luiz Gustavo Bach[1], Gabriela Zarpelon Anhalt Braga[1], Márcia Cristina Bedutti[1], Layza Mylena Pardinho Dias[2], Camila Lampugnani[1], Jhennifer Arruda Schmiedt[1], Pamela Suelen Piacentini Picolli[1], Leonardo Ereno Tadielo[3], Emanoelli Aparecida Rodrigues dos Santos[3], Evelyn Cristine da Silva[3], Fábio Sossai Possebon[3], Vinicius Cunha Barcellos[1], Luciano dos Santos Bersot[1]

[1.] Universidade Federal do Paraná, Programa de Pós-Graduação em Ciência Animal, Palotina / Paraná, Brasil
[2.] Universidade Federal do Paraná, Programa de Residência em Medicina Veterinária, Palotina / Brazil, Brasil
[3.] Universidade Estadual Paulista, Faculdade de Medicina Veterinária e Zootecnia, Botucatu, São Paulo, Brasil

During slaughter and processing, chicken meat has contact with equipment and utensils and can become constant sources of microbial contamination, both from spoilage and pathogenic microbial groups. The microorganisms that contaminate the processing environment need to be eliminated every day by the SSOP because they can form biofilms increasing the chance of contamination of the products. Thus, the aim of our study was to evaluate the diversity of viable microbial genera on meat processing surfaces in the cutting room of a poultry slaughterhouse after the pre-operational cleaning process. Over a period of 10 weeks, we collected samples from five different polypropylene, stainless steel, and polyurethane surfaces immediately after performing the SSOP procedure. The samples were collected through swabs in an area of 400cm² per collection point. The collection points were distributed throughout the cutting room of the chicken's cut room in a slaughterhouse, and all of them maintained direct contact with the raw materials. After collection, the swabs were stored in Falcon tubes containing 0.1% peptone saline solution and polysorbate 80 until the beginning of the analysis. The tubes containing the swabs were subjected to vortex orbital agitation and 0.1µl was cultured by the spread plate technique in Petri dishes containing PCA agar, with incubation at 36±1°C/24±2h. From the surface growth, 3mL of sterile saline solution was added to the cultures, which were removed from the agar by scraping and homogenization with the aid of a sterile pipette tip. After this step, the liquid was transferred to 5mL Eppendorf tubes and frozen at -20°C. Of the 50 samples collected, 23 obtained plate multiplication in sufficient amounts of DNA to be subjected to sequencing of the V3-V4 regions of the 16S rRNA gene where we evaluated the alpha and beta diversities. The sequencing analysis resulted in a total of 28 genera for all points in the cutting room, manly *Staphylococcus* (13.4%), *Acinetobacter* (9.1%), *Pseudomonas* (8.7%), *Serratia* (5.3%) and *Aeromonas* (4.4%). When we evaluated separately, we identified six main genera, being *Staphylococcus* (33.9%), *Acinetobacter* (20.6%) and *Chryseobacterium* (13.3%) on a polypropylene conveyor belt, on a second of the same material we identified nine genera, mainly *Staphylococcus* (16.7%), *Acinetobacter* (13.7%) and *Sphingomonas* (10.5%) and on the third polypropylene conveyor belt a total of 12 genera were observed, with emphasis on *Bacillus* (25%), *Acinetobacter* (15%) and *Serratia* (6.4%). On the

stainless-steel surface, *Streptomyces* (33.3%), *Massilia* (7.3%) and *Aeromonas* (6.8%) were the main among the 18 genera identified. On polyurethane conveyor belt, of the 18 genera present, *Pseudomonas* (16.3%), *Staphylococcus* (15.3%) and *Serratia* (13.6%) were the most frequent. No statistically significant differences ($p>0.05$) of alpha and beta diversity were identified between the different materials and types of surfaces. We conclude that there is a high persistence of several genera of viable microorganisms on surfaces in the broiler processing industry and may be related to tolerance to sanitizers and the ability to form biofilms on abiotic surfaces. The detection of viable bacteria on the clean surfaces of the cutting room after the SSOP is an important piece of information that must be considered by the quality and food safety management teams of the industries.

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