

TITLE: EVALUATION OF CLEANING PROCESS IN A CHICKEN MEAT INDUSTRY FACILITIES BY THE IDENTIFICATION OF *Listeria monocytogenes*, *Salmonella* sp., AND MICROBIOME ANALYSIS

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ABSTRACT:

Sanitation procedures performed in food industries can interfere with the hygienic-sanitary quality of products. The objective of this study was to evaluate the operational and pre-operational cleaning process of a chicken slaughterhouse through the detection of *Listeria monocytogenes*, *Salmonella* sp. and microbiome analysis. Surface samples of equipment and utensils were collected before (n=160) and after (n=160) industrial cleaning processing to count aerobic mesophiles (ISO 4833-1), enterobacteria (ISO 21528-2), *Pseudomonas* sp. (ISO 13720), and to seek the presence of *L. monocytogenes* (ISO 11.290-1) and *Salmonella* sp. (ISO 6579). From the collected samples, 12.5% (n=40) were submitted to 16S RNA gene sequencing to assess microbial ecology. The cleaning process reduced 53% of mesophilic aerobic counts, 97% of enterobacteria, 94% of *Pseudomonas* sp. and eliminated *Salmonella* sp., however, was ineffective for *L. monocytogenes*. The presence of 133 genera was identified before processing, being *Pseudomonas* sp. (45.4%), *Acinetobacter* sp. (16.6%) and *Aeromonas* sp. (5.4%) the main ones. Of the 313 species identified, *Pseudomonas fluorescens* (22.9%), *Acinetobacter johnsonii* (13.8%), *P. putida* (6.2%) and *Aeromonas salmonicida* (3.1%) were the predominant ones. After cleaning processing, 63 genera were observed, composed by *Aneurinibacillus* sp. (19.5%), *Pseudomonas* sp. (12.8%), *Acinetobacter* sp. (11.3%), *Anoxybacillus* sp. (7.7%) and *Enterococcus* sp. (6.7%). Among the 123 species, the most identified ones were *Aneurinibacillus aneurinilyticus* (16.9%), *P. fluorescens* (7.7%), *Anoxybacillus flavithermus* (7.1%), *Enterococcus cecorum* (6.2%) and *Escherichia coli* (3.8%). Among the identified genera and species, the microorganisms were divided in three groups, one composed of microorganisms related to the processing of the products (*Aneurinibacillus* sp., *Anoxybacillus* sp. and *Enterococcus* sp.), the second identified after cleaning (*Stenotrophomonas* sp., *Magnetospirillum* sp. and *Citrobacter* sp.) and the last one by microorganisms that inhabited both steps (*Pseudomonas* sp., *Acinetobacter* sp. and *Aeromonas* sp.). The results of the study demonstrate a considerable reduction of indicator microorganisms and *Salmonella* sp. after the cleaning process, except with *L. monocytogenes*. Beside the cleaning process, some bacteria as *Pseudomonas* sp., *Acinetobacter* sp. and *Aeromonas* sp. remained on the analyzed surfaces, being tolerant and capable of originating biofilms.

Keywords: Chicken meat industry; foodborne pathogens; microbiome; sanitation; 16S RNA gene

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