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VIRAL DNA DIVERSITY IN ANTIBIOTIC-FREE CHICKEN SLAUGHTERHOUSE

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Considering the great demand for organic and antibiotic-free products, it is essential to evaluate the microbial ecology present in the production environment, especially at the slaughterhouse. The viral diversity in chicken meat production environments is still poorly studied, particularly in antibiotic-free production. It has been demonstrated that phages play an important role in the transfer of antibiotic resistance genes through conjugation mechanisms. Therefore, exploring the viral diversity can help predict potential problems for public health even in an antibiotic-free environment. The present study aimed to investigate the viral diversity in a Brazilian antibiotic-free chicken slaughterhouse environment. Five pooled samples were collected froma dirty area, a clean area and the final product. The dirty area (n=1) consisted of a pooled sampled including swabs from equipment surfaces in contact with the carcass and personnels hands for a total area of 1,200 cm^2. The clean area (n=1) was a pool sample consisting of samples from the surfaces of smooth and modular conveyor belts, facilities and food handlers\' gloves for a total area of 1,200 cm^2. The final products (n=3) were composed each of pools of 10 carcasses sampled by rinsing the carcass in 200 mL of 0.85% sterile saline solution. Total DNA from the samples was extracted using the MagicPure® Stool and Soil Genomic Kit (Transgen Biotech, Beijing, China) and library sequencing was performed using NextSeq (Illumina). Raw data were evaluated with FASTQC and Trimmomatic. The assembly was performed using SPAdes and CAT_pack for taxonomic evaluation and read classification. The data were expressed in relative abundance concerning the number of reads classified as viruses. Approximately 1,570 high-quality reads were classified, with 18.82% attributed to eukaryotic viruses and 85.17% to bacteriophages. The phyla commonly found in the evaluated samples were Artverviricota, Uroviricota, and Nucleocytoviricota. Notably, the phyla Peploviricota, Preplasmiviricota, Cossaviricota, and Nucleocytoviricota were present only in surface samples. Regarding bacteriophages, the most prevalent class was Caudoviricetes (41.9%), and the order Crassvirales. These results demonstrate the viral community diversity in antibiotic-free chicken slaughterhouse environments, highlighting the importance of understanding the presence of viruses in these environments due to their

ability to modulate the microbial community and influence interspecies genetic material transfer, which is highly relevant in the context of public health.

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