

VIRAL DNA DIVERSITY IN ANTIBIOTIC-FREE CHICKEN SLAUGHTERHOUSE

Emanoelli Aparecida Rodrigues dos Santos¹, Patrícia Regina Lopes Melo¹, Evelyn Cristine Silva^{1,2}, Leonardo Ereno Tadielo³, Gabriella Rodrigues Cazolda¹, Gean Carlo Azinari¹, Karina Pires Gutierrez², Bruna Lindolfo da Silva², Wanderson Sirley Reis Teixeira¹, Carlo Spanu⁴, João Pessoa Araújo Junior², Fábio Sossai Possebon^{1,2}, Juliano Gonçalves Pereira¹

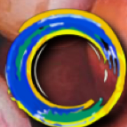
¹. SÃO PAULO STATE UNIVERSITY (UNESP), SCHOOL OF VETERINARY MEDICINE AND ANIMAL SCIENCE, BOTUCATU / SÃO PAULO, BRASIL

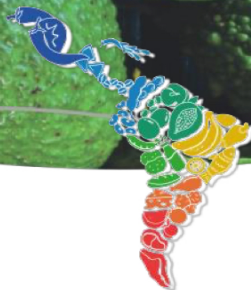
². SÃO PAULO STATE UNIVERSITY (UNESP), INSTITUTE FOR BIOTECHNOLOGY, BOTUCATU / SÃO PAULO, BRASIL

³. DEPARTAMENTO DE PRODUÇÃO ANIMAL E ALIMENTOS, UNIVERSIDADE DO ESTADOS DE SANTA CATARINA (UDESC), LAGES / SANTA CATARINA, BRASIL

⁴. DIPARTIMENTO DI MEDICINA VETERINARIA, UNIVERSITÀ DEGLI STUDI DI SASSARI (VIA VIENNA, 2 07100 SASSARI, ITALY), SASSARI, ITÁLIA

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 from a dirty area, a clean area and the final product. The dirty area (n=1) consisted of a pooled sample including swabs from equipment surfaces in contact with the carcass and personnel's hands for a total area of 1,200 cm². 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 cm². 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 Pevloviricota, 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



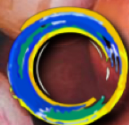


IAFP Latino 2024

Simpósio Latinoamericano
em Segurança dos Alimentos
Santos - SP - Brasil
11 a 14 Nov, 2024

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

Agradecimentos: The authors would like to thank FAPESP for funding this study (Process 22/03062-6; 23/01185-6 and 23/01195-1) and CAPES, Brazil (Code 001 and CAPES PRINT Project, 88881310254/2018-01).



BRAFP



International Association for
Food Protection