

STRONG ANTIMICROBIAL RESISTANCE IN THE ENVIRONMENT NEAR PIG FARMS IN BRAZIL: HAVE WE REACHED OUR RESILIENCE CAPACITY?

Carolina Deuttner Neumann Barroso^{1*}, José Rodolfo Panim Ciocca², Daniel Moreira Pinto Cruz², Paola Moretti Rueda², Marcelo Beltrão Molento¹

¹Universidade Federal do Paraná, Curitiba, PR, Brazil; ²World Animal Protection, São Paulo, SP, Brazil.

*Contact details – carolina.deuttner@gmail.com; molento@ufpr.br of corresponding author, who will also present the abstract on June 23rd

1. INTRODUCTION AND OBJECTIVE

The concern over the use of antibiotics have intensified over the last decade worldwide. The state of Paraná produces 270 million tons of pig meat/year, mostly by intensive farming. Pig production has been highlighted as one of the highest users of antibiotics, including of human use. Moreover, resistance to antibiotics is inherently associated with the overuse of these drugs, suffocating our resilience capacity. As animals do not metabolize about 70% of the antibiotics, many of these substances can pass into animal waste, reaching the environment, favoring the spread of multiple-resistant bacteria. A One Health approach based upon linking animal farming and environmental health, seems reasonable to reduce the problem by advocating the elimination of their inappropriate use. This project aimed to determine the presence of antimicrobial genes that would be related to resistant bacteria collected from water from rivers close to intensive pig farms in Paraná, Brazil.

2. METHODS AND RESULTS

Pig farms were selected from the West and Center-East regions of the state of Paraná. Both regions are characterized by large intensive farm units, supplying products to the meat industry. Water samples (n=11) were collected from rivers in areas upstream and downstream near pig farms by trained personnel from the Federal University of Paraná (UFPR), and the World Animal Protection (WAP) in September 2021. The collecting sites were 300 to 1000 m from the units. The EpiCollect program was used to determine the geographic coordinates

of appropriate sites. In the laboratory, the samples were prepared for microbiological cultivation and for metagenomics and microbiome analysis. The broths used were Baird Parker, Xylose Lysine Deoxycholate, Bismuth sulfite, Chromogenic broth for the isolation and differentiation of methicillin-resistant *Staphylococcus aureus* (MRSA), and Chromogenic broth for detection and differentiation between *Escherichia coli* and coliforms. For genome sequencing, the DNA was extracted from the samples using the Wizard Magnetic DNA kit and metagenomic libraries were built using the Illumina DNA prep kit. The libraries were analyzed to quantify and verify the size of the fragments. The material was also sequenced on the MiSeq platform (Illumina, USA). The resistance genes present in the metagenome were identified through database comparisons and were analyzed the presence of genes that could be resistant to tetracyclines, macrolides and aminoglycosides, most used in swine production. Water samples showed an abundance of *Pseudomonas* ssp. but remarkably only in the downstream samples had the presence of resistance genes against β -lactam antibiotics (class B and C).

2. CONCLUSIONS AND IMPLICATIONS

The data surrounding pig farms both upstream and downstream suggest the existence of a selection pressure from antibiotic use in the whereabouts of industrial farming. Therefore, we must replace intensive pig farming to a more sustainable system with controlled use of antimicrobials and a strict biosecurity protocol. This would reduce the negative input from the intensive system, which would depend less on the suppressive use of antibiotics, improving safety and the welfare of the animals.