

TITLE: DETECTION OF ANTIMICROBIAL RESISTANCE GENES AND EVALUATION OF WATER QUALITY FROM PIG FARMS

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ABSTRACT:

There is a growing global demand for pork products due to population growth. Pig farming produces large quantities of wastewater, leading to increased release of contaminated water into the environment and pollution of soil and water resources, compromising the quality of water used for human and animal consumption. Antimicrobial agents are widely used in animal production and can be a threat to human and animal health as wastewater is considered a reservoir of antimicrobial resistance genes (ARGs) that compromise the health of water resources. This study aimed to evaluate water quality and the presence of resistance genes in water samples from pig farms. The study was conducted in eight pig farms in the state of Mato Grosso, Brazil. The farms were evaluated by using a questionnaire on hygiene conditions. Approximately 0.5 L of water was used for microbiological analysis and approximately 1 L of each sample for used to DNA extraction and the detection of 16 resistance genes (sul I, sul II, ampC, blaPSE I, blaZ, ermA, ermB, ermC, tet (K), tet (M), msrA, mecA, femA, ant(4')-Ia, aac(6')-aph(2''), and aph3'-IIIa) was performed by the polymerase chain reaction (PCR). Statistical analysis was performed with the software R version 3.0.1. The percentage of ARGs and the association between the variables were calculated via microbiological examination, physicochemical examination, and the binomial regression between ARGs. In all cases, the $p \leq 0.05$ was considered significant. Areas with multidrug resistance were considered those that contained ARGs to three or more classes of antimicrobials. All evaluated samples contained genes that conferred resistance to at least three of the six studied classes of antimicrobial agents, indicating a multidrug resistance pattern in the drinking water of the animals. The genes sul I, sul II, blapse I, ermB, and blaZ were detected in all samples; genes aac(6')-aph(2''), aph3'-IIIa, and ant(4')-Ia were detected in 87.5% of the samples; whereas genes ermA, femA, and ampC were detected in 75% of the samples. There was no association between resistance genes, physicochemical examination, microbiological examination (fecal and total coliforms), and the presence of resistance genes. The water of pigs was within acceptable standards for animal consumption but contained many resistance genes, which might be due to the use of irrigation systems with wastewater from decantation ponds combined with the indiscriminate use of antibiotics.

Keywords: ARGs, farm water, coliform, multidrug resistance

Development Agency: Didn't have.