

TITLE: MICROBIAL ANALYSIS OF BACTERIA AND QUALITY OF WATER OF PIG FARMS IN MATO GROSSO, BRAZIL

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ABSTRACT:

The growing global demand for pig products due to population growth, increased global trade, and improvements in production have intensified the participation of pig farming in environmental impacts, particularly those related to the quality and availability of water. High quality drinking water is an important component for the health of pigs, and data about quality of is scant in literature in Brazil. The aim of this work was to evaluate the diversity of bacteria, physical-chemical and genes of antimicrobial resistance of water in pig farms in Mato Grosso State, Brazil. Water sample from eight farms were collected during 2014-2015. After extraction, DNA was amplified with multiplex oligonucleotides barcode encoding the 16S rDNA region (V4-V5). Samples were sequenced using the Ion Torrent Genome Machine. Physicochemical parameters analyzed were turbidity, color, pH, dissolved oxygen (DO), biological oxygen demand (BOD), total alkalinity (TA), total hardness (TH), suspended solids (SS), total nitrogen (TN), nitrate (N), and phosphorus (P). Six different antimicrobial resistance genes (ARGs) were test by polymerase chain reaction. The biodiversity water farms varied between 221 and 371 OTUs. Diversity profile analysis showed *Phylum Proteobacteria* (64%), *Bacteroidetes* (12.6%) and *Firmicutes* (10.3%) more abundant and at family level *Comamonadaceae* (23.1%) and *Oxalobacteraceae* (22%). 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. Physicochemical analysis was within acceptable values. Water in pig farm had acceptable physiochemical quality but are source of ARGs and variable profile bacterial community.

Keywords: Microbiome, water, pig ARG

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