

TITLE: BACTERIOPHAGE PROFILE IDENTIFIED IN SERA OF SWINE AFFECTED WITH POST-WEANING MULTISYSTEMIC WASTING SYNDROME

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ABSTRACT

Bacteriophages are viruses that infect bacteria and represent the most abundant organisms on Earth. They can integrate into the bacterial chromosome, not only conferring genetic variability to the bacteria but also serving as a vehicle to transfer the bacterial genes horizontally. Occasionally they encode and disseminate virulence factors in bacterial populations. The phages are responsible for gene disruption and genomic rearrangements, which can prevent or provoke the lytic infection of the bacteria. Thus, phages can influence the bacterial composition of a given microbiota and play an important role in bacterial adaptation and evolution. This study aimed to analyze the profile of phage population present in sera from pigs, presenting clinical signs characteristic of post-weaning multisystemic wasting syndrome, a disease of great economic importance in pig rearing systems worldwide. Sixteen swine serum samples were submitted to DNA extraction and enrichment and afterwards, they were sequenced by high throughput sequencing and analyzed by the metagenomic approach. A total of 37,649 viral sequences obtained, 9,368 (24,8%) presented similarity with bacteriophages. The family *Microviridae* was detected with 9,265 (98,8%) reads. *Chlamydia*, *Bdellovibrio* and *Spiroplasma* phages were identified as the main species within this family. Sequences of members of family *Siphoviridae* (38/0.4%) showed similarity of *Lactococcus*, *Bacillus*, *Enterococcus*, *Lactobacillus*, *Bacteroides* and *Listeria* phages. Within the *Myoviridae* family (36/0.38%) were recovered sequences similar to *Burkholderia* phage. In the family *Podoviridae* (29/0.3%) the sequences detected showed similarity to the phage of *Burkholderia*, *Pseudomonas*, *Shigella*, *Enterobacteria* and *Pseudomonas*. The phages identified in this sequencing are causative of infections in bacteria that are described as being responsible for diseases in animals. Therefore, the population of these bacteria is being regulated by the type of infection caused by these phages, which may be helping in the maintenance or lysis of these microorganisms. Thus, the phage population in these pigs may be indirectly affecting the health of these animals. Little is known about the interference of these phages on these bacteria, however the results provides a reference for future studies comparing the profile of bacteriophages in healthy swine.

Keywords: Phages, swine, metagenome, high-throughput sequencing

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