

TITLE: CHARACTERIZATION OF THE LUNG VIROME IN NURSERY PIG

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**ABSTRACT:**

The microbiota of piglets is of particular interest, as it may affect the susceptibility to infections and interfere with growth performance. To date, no characterization of the respiratory microbiota of piglets in the initial periods of life has been performed. Lungs tissues from six piglets with clinical signs suggestive of respiratory disease were collected in different farms. DNA and RNA extractions were carried out and submitted to high performance sequencing. The reads obtained were filtered through the Trimmomatic program, reassembled using Spades software 3.10.1 and analyzed with the of the Kraken bioinformatics tool. The total number of reads sequenced in the pool was 312,958. Reads were compared to the database of viral sequences at the protein level using K-mer to lowest common ancestor mapping. On average, 10% of the reads showed similarity to viral sequences deposited in the database GenBank. Most of them displaying similarity with genomes of members of the families *Anelloviridae* and *Parvoviridae*. The most often identified viral genomes were Torque Teno Sus virus (TTSuV) and Porcine Parvovirus (PPV), respectively. Besides, among the viral contigs, 71% presented similarity with sequences of eukaryotic virus genomes and 29% with prokaryotic viral genomes. Whereas TTSuV seems to be a non pathogenic virus often detected in pigs at varying ages, PPV is notoriously recognized as cause of reproductive problems in sows, particularly fetal mummification. The detection of PPV genomes in lungs tissues of piglets with respiratory problem requires further investigation. The lungs have been shown to be colonized by a number of viruses, many of which have not yet been described in this organ. More complete analyzes are necessary to understand the impact of these viral infections in the lungs affected by respiratory infections.

**Keywords:** bioinformatics analysis, high performance sequencing, porcine respiratory disease complex, viruses.

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