

TITLE: GENETIC VARIABILITY OF *Mycoplasma hyopneumoniae* IN SWINE LUNG SAMPLES OF THE STATE OF MINAS GERAIS, BRAZIL

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ABSTRACT:

Pig farming has significant importance to Brazilian economy. The systems of pig production face economic losses resulting from respiratory diseases, and the major respiratory disease is Enzootic Pneumonia (EP). EP is caused by the bacteria *Mycoplasma hyopneumoniae* (Mhyo) and the disease is characterized by a dry and chronic cough that affects pigs of any age, mainly in the finishing production stage. It is known that Mhyo has genomic and proteomic diversity, as well as differences in virulence among your strains. The objective of this work was to evaluate the genetic diversity of Mhyo based on seventeen genes encoding immunogenic proteins (*mhp 0443*, *mhp 0660*, *mhp 0107*, *mhp 0067*, *mhp 0487*, *mhp 0272*, *mhp 0099*, *mhp 0360*, *mhp 0580*, *mhp 418*, *mhp 0461*, *mhp 372*, *mhp 199*, p46, p97, p42 and nrd). We select two regions of the State of Minas Gerais and 148 pig lung samples from twelve farmers were collected and subjected to DNA extraction. First, the DNA were used in a PCR assay to identify Mhyo. Then, the positive samples were submitted to other PCR of seventeen genes selected and bioinformatics analysis were performed using the program BioNumerics and applying UPGMA method. We identify that 88 (59.6 %) samples were positive in PCR of Mhyo. These positive samples to Mhyo were tested to seventeen genes and they had a wide variation in the percentage of positive samples for each gene: 100 % *mhp 0660*; 98.9 % *mho 0443* and *mhp 0107*; 94.3 % *mhp 0067*, *mhp 0487* and nrd; 92 % *mhp 0461*; 90.8 % *mhp 0580*; 85.1 % *mhp 0099*; 81.6 % p42; 78.2 % p46; 67.8 % *mhp 0272* and p97; 66.7 % *mhp 373*; 59.8 % p37; 46 % *mhp418*; 35.6 % *mhp 199*. We observed variations (100 – 35.6 %) in the distribution frequency in field samples of these genes. Through bioinformatics analysis, the samples were characterized in 59 different genetic groups based on the absence or presence of the genes studied. This result demonstrated that the strain of Mhyo possesses a wild genetic variability in farms of Minas Gerais. This study showed that the genes *mhp 0060*, *mhp 0443* and *mhp 0580* should be investigated since they presented high prevalence among the lung samples

used in this study, and the circulating strain of Mhyo in Minas Gerais has a wild genetic variability.

Keywords: *Mycoplasma hyopneumoniae*; Enzootic Pneumonia; genetic variability; PCR.

Development Agency: CNPq, CAPES, FAPEMIG.