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Comparative Genomic Analysis Between Pathogenic and Non-Pathogenic Strains of Pasteurella multocida #P073

Description:

Presenters: Mauricio Cantao *EMBRAPA - Swine and Poultry*, **J. X. de Oliveira Filho** *Federal University of Rio Grande do Sul*, **J. D. Kich** *Embrapa Swine and Poultry National Research Center*, **C. S. Klein** *Embrapa Swine and Poultry National Research Center*, **Ricardo Zanella** *EMBRAPA/CNPq*, **M. A. Z. Mores** *Embrapa Swine and Poultry National Research Center*, **R. Rebelatto** *Embrapa Swine and Poultry National Research Center*, **N. Mores** *Embrapa Swine and Poultry National Research Center*

P073 - Comparative Genomic Analysis Between Pathogenic and Non-Pathogenic Strains of Pasteurella multocida

Pasteurella multocida is a bacterium that causes respiratory illness in swine. Although this pathogen is considered to be a secondary opportunistic agent in enzootic pneumonia caused by *Mycoplasma hyopneumoniae*, there are evidences showing its involvement as a primary agent. The objective of our study is to detect potential virulence associated genes. To accomplish this goal, we sequenced the genome of a non-pathogenic (17078 Strain) and pathogenic (11246 Strain) *P. multocida* isolated from lung lesions in swine commercial herd, and confirmed in a group of specific pathogen-free animals. The sequencing was performed on Illumina MiSeq platform (2x250 bp) and the quality control was conducted using SeqyClean V 1.2.3 Software. All reads were assembled using MaSuRCA V. 2.0.3 Assembler. *De novo* assembly for *P. multocida* strain 11246 produced 10 Scaffolds with 2,244,069 bp, GC content of 40,4% and N50 of scaffold with 530 kb. The genome contains 2,014 ORFs, 5 ribosomal 16S RNA, and 47 tRNAs. The assembly for *P. multocida* strain 17078 produced 12 Scaffolds with 2,323,935 bp, GC content of 40,26% and N50 of scaffold with 515 kb. The genome contains 2,093 ORFs, 5 ribosomal 16S RNA, and 46 tRNAs. Twelve virulence-associated genes of *P. multocida* were identified in both sequenced genomes. An important variation was identified between groups of bacterias in the filamentous hemagglutinin (pfhA) gene. This gene plays an important role in the bacteria surface adhesion. Further investigations are being conducted by our group to verify whether others genes can be related to pathogenic strain in *P. multocida*.

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