DRAFT GENOME SEQUENCE OF PASTEURELLA MULTOCIDA
STRAIN 11246

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Background, Pasteurella multocida Strain 11246 serotype A is the most common bacterial agent isolated from lesions caused by pneumonia in pigs. Although this pathogen is considered a secondary opportunistic agent in enzootic pneumonia caused by Mycoplasma hyopneumoniae, there are evidences showing its involvement as a primary agent. However, little is known about its pathogenesis. In this context, to detect potential virulence associated genes, we sequenced the genome of P. multocida isolated from pneumonia lesions, in a group of specific pathogen-free animals (SPF) experimentaly exposed to this phatogen; Results, the paired-end sequences were produced by Illumina MiSeq platform (2x250 bp). Low quality reads and adapters were removed using SeqyClean V 1.2.3, in addition to that, all sequences with phred quality score < 25 and length < 180 bases were also removed. After quality control, 1,377,920 reads were assembled using the Newbler Assembler (Roche) V. 2.9. De novo assembly produced 12 Scaffolds with 2,242,954 bp in length with GC content of 40.37%. N50 of final scaffold reached 527 kb, with 638 kb being the largest scaffold and 390 kb being the largest contig. The genome contain 2,016 predicted coding regions, 4 ribosomal 16S RNA, and 51 predicted tRNAs. The sequence identified the presence of kmt gene in our samples, this gene is a specie-specific for Pasteurella multocida. The presence of two additional genes hyaD and hyaC with 99% of identity with P. multocida A:1 strain X-73 further classify this bacteria as sorotype A. Twelve virulence-associated genes of P. multocida were identified in the sequenced genome: A) outer membrane and porin proteins(oma87, psl, ompH); B) a type 4 fimbriae (ptfA); C) a filamentous hemagglutinin (pfhA); D) neuraminidases (nanB, nanH); E) iron acquisition related factors (exbBD-tonB, hgbA, hgbB), and F) superoxid dismutases (sodA, sodC). In total, out of the 2,016 predicted genes, 6 did not match when compared with genes at NCBI-NR with e-value 1e-05. It can be an indicative that those genes are excluvive of our genome until now; Conclusions, we have identified 6 unique genes in the studied genome. In addition to that, 12 genes were associated with virulence of P. multocida. Further investigationg are being conducted by our group to use those genes as a genetic marker for the pathogenicity of this bacterium. With the availability of the P. multocida sequence we will be able to conduct comparative, epidemiological and evolutionary studies.

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