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 pathogenisis. 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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