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Genomic and proteomics approach of *Acinetobacter baumannii* MDR 107M, isolated from a hospital in Bogotá-Colombia

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Acinetobacter baumannii has become an opportunistic pathogen difficult for clinical treatment, because it has acquired resistance to diverse antibiotics. The presence of virulence factors in this microorganism has contributed to the rise of nosocomial infections. This research was focused on two aspects: first, identification of genes encoding factors associated with virulence in the genome of the multidrug-resistant strain *A. baumannii* 107m. Second, the study of Outer Membrane Proteins (OMPs) associated with virulence of this bacterium. DNA were isolated, high-throughput sequencing by Illumina (HiSeq2000) and 454 Roche; genome assembly with mapping tools such as BWA and BOWTIE, and de novo assembly with Velvet and Newbler. Annotation was performed using NCBI Prokaryotic Genome Automatic Annotation Pipeline and also manual verification was done. In order to assess the expression of some genes coding for OMPs that might be involved in virulence, we proceeded to the isolation of OMPs and their analysis by 2D electrophoresis. We selected five spots with differential expression compared to that of *A. baumannii* ATCC 19606, which were identified by mass spectrometry. Proteomic results allowed the identification of OMPs associated with iron receptors, a protein associated with cell apoptosis and proteins involved in defence. The genomic data led to the identification of 103 genes involved in adherence, biosynthesis of siderophores and invasion. Genomic and proteomic results of this study, suggest that the multidrug-resistant *A. baumannii* 107m has genes involved in pathogenesis compared to *A. baumannii* ATCC 19606, however, more experimental studies are required to verify the *A. baumannii* 107m pathogenicity.

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