The aim of this study was to test the benefits of the use of NGS technologies and a de novo assembly approach for the genome characterization of isolates from an outbreak. Six isolates from an outbreak of carbapenemase producing *Klebsiella pneumoniae* ST11 OXA-48 were sequenced with Illumina and one of them (F64) was selected to be sequenced with PacBio in order to have an internal genome reference for the outbreak.

The same ADN from the *Klebsiella* genome F64 was sequenced with PacBio and with Illumina. PacBio reads were assembled using HGAP pipeline and independently Illumina reads were assembled with SPADES. Both assemblies were compared and evaluated with QUAST.

The number of mismatches per 100,000 bp was 1.91

**Comparison of PacBio assembly with HGAP and Illumina assembly with SPAdes**

**QUAST Evaluation**

The error rate of PacBio assembly evaluated by QUAST was around 0.00191 % considering correct the Illumina sequence.

**PacBio** allows getting really high quality, closed genome to get a high quality internal reference.

**NGS** is the new gold standard in studies of transmission dynamics and strain relatedness.

**Comparative genomics** analysis allows the complete characterization of a set of isolates from an outbreak.

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