

Complete de novo genome characterization of isolates from outbreaks by means of PacBio and Illumina sequencing technologies

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

	F64 SPADES Illumina	F64 HGAP PacBio
# misassemblies	3	0
# relocations	1	0
# translocations	2	0
# inversions	0	0
# misassembled contigs	3	0
Misassembled contigs length	149711	0
# local misassemblies	4	0
# mismatches	107	0
# indels	23	0
# short indels	21	0
# long indels	2	0
Indels length	132	0

QUAST EVALUATION

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

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NGS Sequencing

Characterization of a set of outbreak isolates

Comparative Genomics

Genome Assembly

Functional Annotation





- 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



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

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