Occurrence of hypervirulent K2 serotype *Klebsiella pneumoniae* ST2398, clonal complex 65, in the context of an invasive liver abscess syndrome

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**Introduction and Purpose**

We further analyzed a *Klebsiella pneumoniae* (KP) isolate from a 61-year old male patient with invasive liver abscess syndrome and endophthalmitis without travel history to Asia, but reported a recent journey to Brazil.

**Methods**

The isolate was sequenced on a MiSeq sequencer (Illumina, San Diego, CA, USA) aiming at a coverage of at least 60-fold. Quality trimming of reads was performed with CLC Genomics Workbench 9.0.1 (Qiagen, Hilden, Germany) using a minimum Phred (Q) score of 28. De novo assembly was performed using CLC Genomics Workbench 7.0.4 (Qiagen) with optimal word sizes based on the maximum N50 value. For the assembled genome, the coverage (mean depth) was 85, the number of contigs was also 85, the N50 was 164 351, the maximum contig length was 368 426 nt and the total genome size was 5 459 317 nt. The multilocus sequence typing (MLST) sequence type (ST) was extracted from the assembled genome using Seqsphere+ version 3.0 (Ridom, Muenster, Germany) and appeared to be a new ST that was subsequently submitted to the MLST database (http://bigdb.web.pasteur.fr/klebsiella/klebsiella.html). A clonal complex analysis was performed by eBURST (http://eBURST.mlst.net/). Genes relating to virulence were detected using the mapping unit of CLC Genomics Workbench to map reads and/or by blasting assembled genomes to a pseudomolecule generated by concatenating a set of *K. pneumoniae* genes. Finally, the genetic similarity of our isolate with other K. pneumoniae strains [Struve et al., Mbio 2015] was determined by a gene-by-gene comparison using Seqsphere+ version 3.5.0 (Fig. 1).

**Figure 1** Consensus tree for 68 samples including our strain KP FR 2016 [Holt et al., PNAS 2015]. Tree is based on 2358 columns, pairwise ignoring missing values. Distance is based on columns from KP sensu lato cgMLST scheme provided by Seqsphere+.

**Discussion**

Biofiling of different KP clones revealed several clusters, of which our isolate belonged to clonal complex 65. A recent analysis conducted by Holt et al., PNAS 2015 showed that ST23 and ST65 strains are dominant among hypervirulent KP strains. Our isolate is very close to ST65 and was assigned to ST2398. In Europe several cases have also been described, with many cases in France. Our case illustrates worldwide occurrence of hypervirulent strains. Adequate infection control and antimicrobial stewardship measures must be in place to contain further spread.

**Study accession number**

Generated raw reads were submitted to the European Nucleotide Archive (ENA) of the European Bioinformatics Institute (EBI) under the study accession number PRJEB19331

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