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## Occurrence of hypervirulent K2 serotype *Klebsiella pneumoniae* ST2398, clonal complex 66, in the context of an invasive liver abscess syndrome

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**Background:** Apart from resistant Gram-negative strains, also so-called hypervirulent strains spread around the world and cause severe infections. Antimicrobial resistance and hypervirulence are mostly not overlapping. Hypervirulent strains typically have a hypermucoviscous phenotype and a combination of virulence genes, including *rpmA*, *magA*, *ent*, *iutA*, *ybtS*, *kfu*, *ycfM*, *KPN* and *mrkD*.

**Material/methods:** We further characterized a *Klebsiella pneumoniae* strain isolated from a liver abscess in the context of an invasive liver abscess syndrome with severe endophthalmitis. MICs for various antibiotics were obtained by broth microdilution antimicrobial susceptibility testing. Phenotypic detection of ESBL or AmpC production was determined with the combination disc test as recommended by EUCAST, using cefotaxime, ceftazidime and cefepime ± clavulanate and the ceftoxitin-cloxacillin disc test, respectively. The isolate was subjected to whole-genome sequencing (WGS) on a MiSeq instrument (Illumina, San Diego, CA, USA) for generating paired-end 250-bp reads, aiming at a coverage of at least 60-fold after using the Nextera XT kit (Illumina) for the DNA

library preparation. Subsequently, genetic data analyses were performed using CLC Genomics Workbench (Qiagen, Denmark) and BLAST Ring Image Generator.

**Results:** The isolate was susceptible to ampicillin/sulbactam (MIC 2 mg/L), piperacillin-tazobactam (MIC 1 mg/L), cephalosporins (MIC for ceftazidime, cefotaxime and cefepime 0.25 mg/L) and carbapenems (MIC for meropenem 0.5 mg/L, ertapenem 0.125 mg/L). ESBL and AmpC production could be excluded. The *rmpA*, *iutA*, *entB*, *ybtS* and *mrkD* virulence genes were found to be present in the strain. WGS data revealed high similarity of our strain with the genome of the Taiwanese clonal complex 23 strain NTUH-K2044, but had a new multi-locus sequence type. The sequence type was assigned ST2398. Subsequently, E-burst analyses revealed that our isolate belongs to the clonal complex 66.

**Conclusions:** This report underlines worldwide occurrence of hypervirulent strains and urges to focus on adequate infection control and antimicrobial stewardship measures to contain further spread.