

Carbapenemase genes and plasmids in hypervirulent *Klebsiella pneumoniae* isolates from hospitalized patients in Germany

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Introduction

Klebsiella pneumoniae (*Kp*), an opportunistic bacterium in animals and humans and common cause of nosocomial infections, has evolved into a novel pathotype known as hypervirulent (hv) *Kp*. Hv*Kp* strains are associated with severe infections, and the distinct virulence and resistance traits are often located on plasmids. Recently, convergence plasmids carrying both antibiotic resistance and virulence-associated genes have been reported in many countries worldwide [1]. This study investigated the presence of resistance- and virulence-associated genes in *Kp* isolates from German patients including comprehensive plasmid analyses.

Materials & Methods

Whole genome sequencing (short and in part long-read sequencing) was performed. Bioinformatics tools (Kleborate, MOBsuite, AMRfinder) were applied to identify *Kp* multi-locus sequence types (ST), capsule types, plasmid types, resistance and virulence genes. Whole genome alignment aided phylogenetic studies of similar plasmid types available in public databases and already described as virulence, resistance or convergence plasmids.

Results

Genome analysis identified various virulence genes in 38 isolates that were classified as hv*Kp* (virulence score ≥ 3) [1]. 69% of the isolates belonged to ST23, ST395, ST147 and ST101. The dominant capsule types were KL107, K1 and K2. Carbapenemases NDM-1/-5 and OXA-48/-244 were detected in 15 and 14 hv*Kp* isolates, respectively. MOBsuite analyses revealed a high diversity of plasmid types. One major resistance plasmid type carrying only *bla*_{OXA-48-like} genes was found in 13 isolates (6 different ST). The typical hv associated plasmid type with virulence genes *iuc* and *iro* was found in 15 isolates (mainly sequence type ST23). The most frequent plasmid type was detected in 20 isolates (8 different ST) and carried virulence genes (*rmpA/A2*, *iuc*); but in 13 isolates these plasmids also harboured *bla*_{NDM} carbapenemase genes (convergence/hybrid plasmids).

Summary

This study showed the presence of typical hv*Kp* strains of ST23 with and without additional resistance plasmids in Germany. A remarkable number of isolates of known global epidemic lineages (ST147, ST395, ST101) carried convergence plasmids contributing to the increased pathogenic potential and the high antibiotic resistance burden of these strains. Our findings shed light on the intricate interplay between resistance and virulence traits that has to be investigated in future studies.

[1] Wahl *et al.* IJMM 2024