

Hypervirulent *Klebsiella pneumoniae* in a tertiary hospital of Copenhagen

Karen Leth Nielsen¹, Frederik Boëtius Hertz¹, Kristian Schønning¹, Susanne Häussler^{1,2}

1. Department of Clinical Microbiology, Copenhagen University hospital – Rigshospitalet, Copenhagen, Demark
2. Twincore, Center for Experimental and Clinical Infection Research, a joint venture of the Helmholtz Centre for Infection Research and the Hannover Medical School

BACKGROUND AND AIM

Hypervirulent *Klebsiella pneumoniae* (HvKp) have been reported worldwide and may cause invasive community-acquired infections in previously healthy patients. These can be multidrug-resistant but are often even susceptible to commonly used antibiotics. Therefore they often remain undetected, thus, increasing the potential to disseminate.

- The aims of this study were
- (1) to identify how often hypervirulent isolates occur in a tertiary hospital in Denmark
 - (2) to characterize the isolates with respect to resistance genes
 - (3) to determine whether we have observed clonal transmission within the hospital.

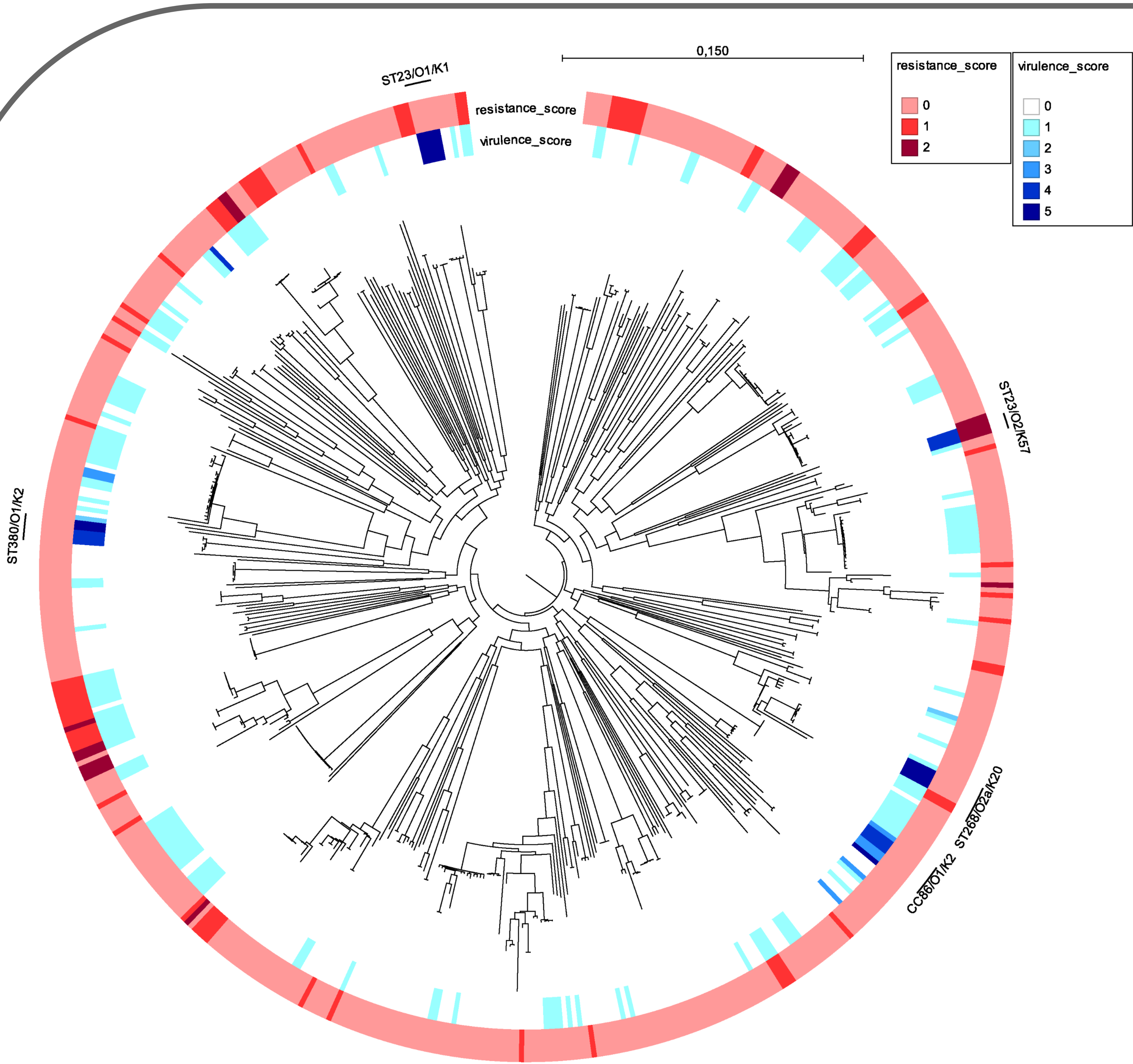


Figure 1: Phylogenetic tree of clinical *K. pneumoniae* isolates illustrated with virulence score and resistance score, respectively.

RESULTS

- Out of 684 *Klebsiella pneumoniae* isolates, 25 (3.7%) HvKp were identified from 18 patients (Table 1):
 - 8 isolates with a virulence score of 5,
 - 10 isolates with a virulence score of 4.
 - 653 isolates were not hypervirulent and exhibited a virulence score of 0-3.
- The 30-day mortality for the hypervirulent isolates was 5/18 (28%).
- Two patients carried multidrug-resistant HvKp, whereas the remaining isolates had a resistance score of 0.
- We identified transmission between patients carrying multidrug-resistant isolates but found no signs of clonal transmission for the remaining hypervirulent isolates.

Table 1: Hypervirulent isolates classified as virulence score 4 + 5 along with the ST-type, resistance score, capsule type and *bla* resistance gene (apart from *bla*_{SHV})

Virulence score	n	MLSTs	Resistance score	Capsule type	<i>Bla</i> *
5	8	ST380 (2)	0	K2	
		ST268 (2)	0	K20	
		ST23 (2)	0	K1	
		ST2039 (2)	0	K2	
4	10	ST86 (3)	0	K2	
		ST5 (1)	0	K39	
		ST380 (2)	0	K2	
		ST373 (1)	0	K2	
		ST23 (2)	2	K57	<i>bla</i> _{CTX-M} , <i>bla</i> _{NDM}
		ST113 (1)	0	K35	

CONCLUSION

- We identified that HvKp occur in our patients and identified transmission of a multidrug-resistant HvKp.
- The mortality was high.
- The majority of HvKp had no acquired resistance, and hence, were only identified by systematic whole-genome sequencing.

METHODS

- K. pneumoniae* isolates from Copenhagen University Hospital – Rigshospitalet since 2019 regardless of the source of infection
- Whole-genome sequencing (Illumina), assembly with Spades, annotated genomes using Prokka
- Kleborate + Kaptive on 684 isolates to identify capsule types, MLST types, resistance genes and virulence genes including a virulence score (with a score of 4 and 5 indicating hypervirulence).
- Possible transmission events were identified with Parsnp/1.5.0, RAxML/8.2.11, HarvestTools/1.3 and snpdist/0.7.0 within each ST-type.