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Complete genome sequencing reveals a melting pot of diverse Klebsiella pneumoniae pathogens in two Detroit hospitals

DETROIT MEDICAL CENTER



Hosoon Choi, PhD,[†] Chetan Jinadatha, MD, MPH,[†] Keith Kaye, MD, MPH,[†], Piyali Chatterjee PhD,[†] Yonhui Allton, MT, MHA,[†] Mark Stibich, PhD,^{5,6} Paul Kilgore MD, MPH,[†] Steve Egbert, BS,⁶ Sorabh Dhar, MD,^{5,6}

¹Central Texas Veterans Healthcare System, ²University of Michigan, ³Wayne State University/Detroit Medical Center, ⁴John D Dingell VAMC, ⁵MD Anderson Cancer Center, ⁶Xenex Disinfection Services

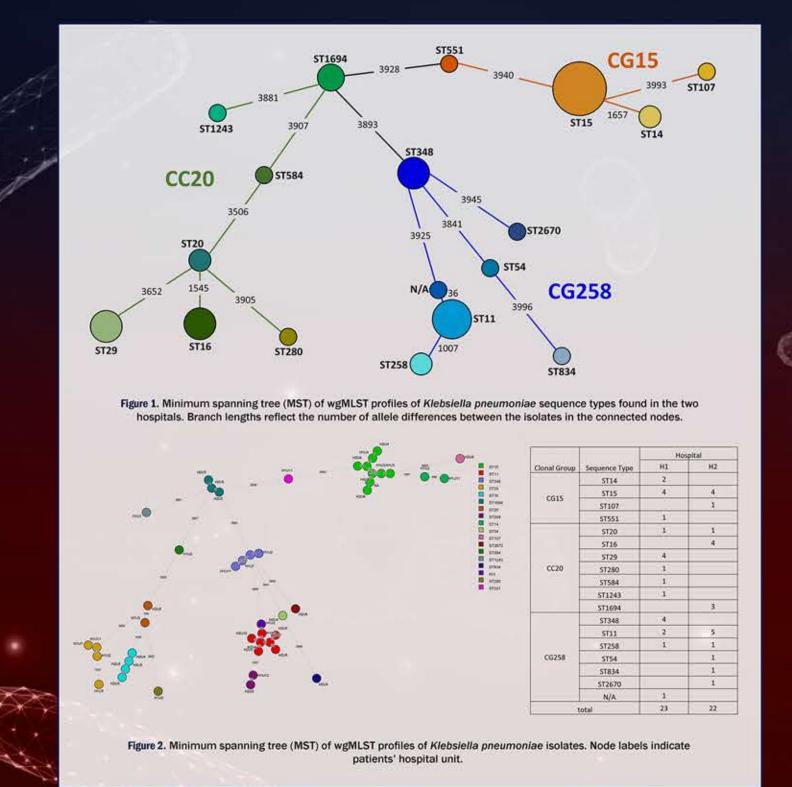
Introduction:

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- Klebsiella pneumoniae is one of the leading causes of healthcare-associated infections.
- Multidrug-resistant Klebsiella pneumoniae that produce extended-spectrum β-lactamase (ESBL) enzymes have been reported with increasing frequency and cause infection with significant morbidity and mortality.
- Whole genome sequencing analysis of Klebsiella pneumoniae clinical isolates were performed to study the transmission of Klebsiella pneumonia in hospital settings.

Methods:

- Clinical bacterial isolates from patients admitted to two disparate, geographically distinct tertiary care hospitals (H1, H2) in Detroit, Michigan, after 48 hours of admission from 2017- 2019 were collected and sequenced.
- Genomic DNA was extracted using the QIAamp DNA Micro Kit (Qiagen, Hilden, Germany). Libraries were prepared from 200 ng of DNA using the Nextera® DNA Flex Library Prep Kit (Illumina, San Diego, CA), and paired-end reads (2 × 151 bp) were generated using the Illumina NextSeq reagent kit and NextSeq instrument (Illumina, San Diego, CA).
- De Novo assembly was completed using SPAdes version 3.7.1 assembler on the Bionumerics calculation engine (Applied Maths NV, Sint-Martens-Latem, Belgium).
- wgMLST (whole genome multilocus sequence typing; assembly-free and assembly-based calls) was performed using calculation engine on the Bionumerics v7.6 platform.
- Minimum spanning tree with the isolates was constructed and arranged by their MLST Pasteur serotype and hospital/ward of the patient isolate collection.



Results:

- In total, 17 different MLST Pasteur serotypes were observed from wgMLST analysis of forty-six Klebsiella pneumoniae clinical patient isolates.
- All of the Klebsiella pneumoniae HAI isolates obtained from the two hospitals were genetically distinct.
- There were three distinct clusters on the minimum spanning tree. Out of 17 sequence types (STs), 4 were present in both hospitals.
- Though there was no predominant ST type, ST15 and ST11 were the
 most frequent isotypes (18% each). Both ST15 and ST11 were evenly
 spread across both hospitals, but the patterns were unique. While ST15
 was predominantly found in two units (H1U3 and H2U4), ST11 was
 found in multiple units. ST348 and ST29 were predominantly found in
 H1, whereas ST16 was found in H2.

Conclusions:

Our data suggests that-

- Majority of Klebsiella pneumoniae infection is sporadic and there was no evidence of hospital spread.
- The WgMLST analysis showed that the isolates were distributed across the three main distinct evolutionary origin of Klebsiella pneumoniae.
 The diversity of isolates was comparable within and between two hospitals.
- Our study showed that the global spread of various serotypes of Klebsiella pneumoniae has already reached a significant level in these two Detroit hospitals and possibly in the catchment area.

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