
Research article

Genomic epidemiology of multidrug-resistant *Klebsiella pneumoniae* reveals lineage-specific resistance patterns with limited virulence determinants

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Supplementary

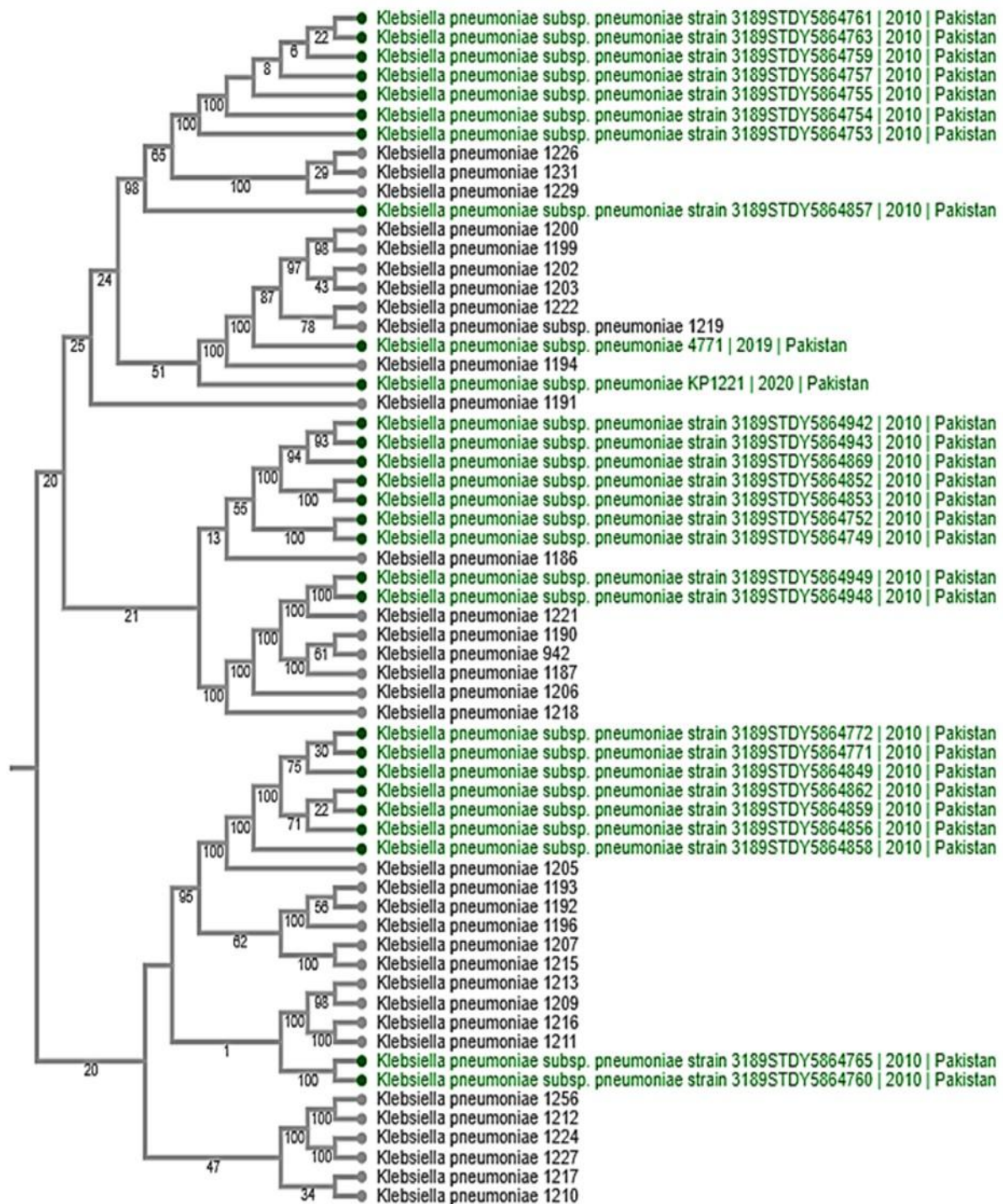


Figure S1. Maximum likelihood phylogenetic tree of *K. pneumoniae* isolates. Our study genomes are labeled in black, while publicly available Pakistan genomes retrieved from BV-BRC collected between 2010 and 2020 are labeled in green.

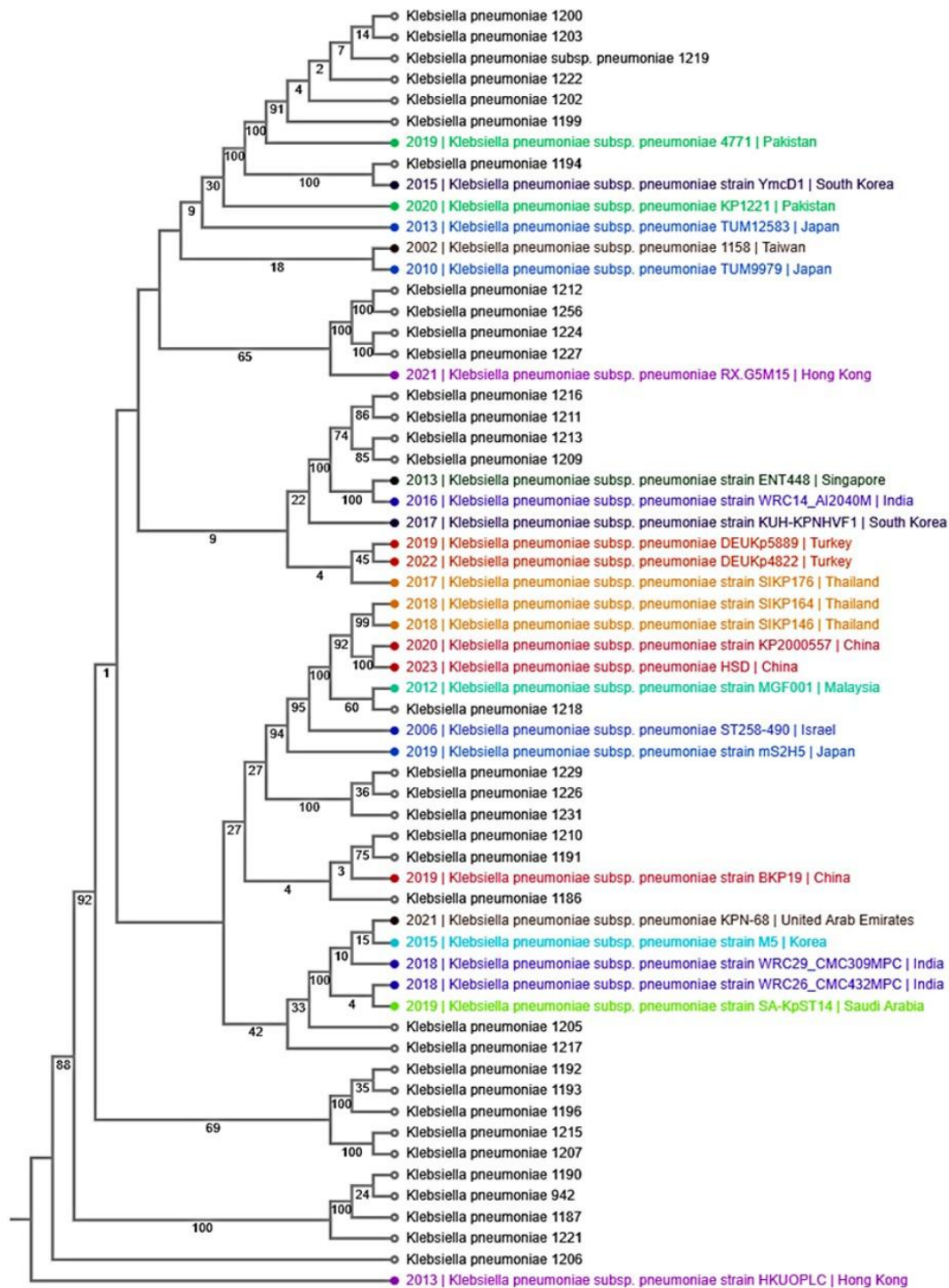


Figure S2. The phylogenomics tree shows the evolutionary relationship of our study *K. pneumoniae* genomes with global isolates. Our study genomes are shown in black, and publicly available global genomes retrieved from the BV-BRC are color-coded according to geographic origin.



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