Genomic and Ecological Insights into Hypervirulent Klebsiella pneumoniae Colonization and Transmission in Healthy Individuals and Liver Abscess Patients

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Objectives: Intestinal reservoirs and transmission of highly virulent *Klebsiella pneumoniae* (hvKp) remain poorly understood. Deciphering the genomic link between hvKp colonization in healthy individuals and invasive diseases, particularly liver abscesses, is crucial for enhancing clinical surveillance and risk prevention.

Methods: Whole-genome sequencing was performed on hvKp from 377 patients with liver abscess and 1,006 healthy individuals. Epidemiological characterization was performed via plasmid replicon typing, and core-genome phylogenetic analysis. Metagenomic sequencing of 129 fecal samples was used to compare gut microbiota composition between hvKp carriers and non-hvKp carriers, and to evaluate ecological interactions, including competition mediated by colibactin-producing strains.

Results: hvKp colonization occurred in 50.7% of liver abscess patients and 3.0% of healthy individuals. ST23 and ST65 were the predominant sequence types, with KL1 and KL2 as dominant K-loci. hvKp strains derived from healthy individuals exhibit close phylogenetic relationships with clinical liver abscess isolates, indicating comparable pathogenic potential. Three hvKp of healthy individual carried the conjugative *iuc3* plasmid with complete T4SS. Gut microbiota analysis revealed decreased *Escherichia coli* abundance and a high prevalence of colibactin genes (93.3%) in hvKp carriers, suggesting hvKp-mediated competitive exclusion.

Conclusion: Healthy community individuals serve as a more diverse reservoir for hvKp with identical virulence potential. The persistent colonization and dissemination of hvKp are supported by the mobility of plasmids carrying *iuc3*, colibactin-enhanced competition, and distinct microbiota ecosystems. Our study offers key genomic and ecological insights to inform risk assessment and prevention strategies against hvKp.

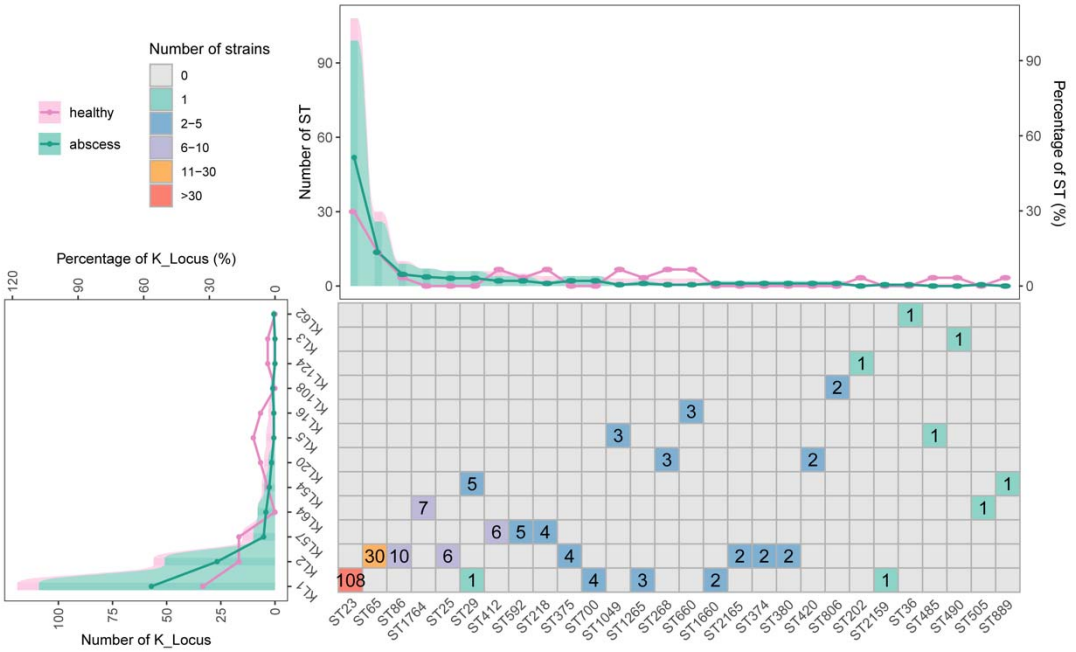

Figure 1. Distribution profiles of ST and KL of hvKp.

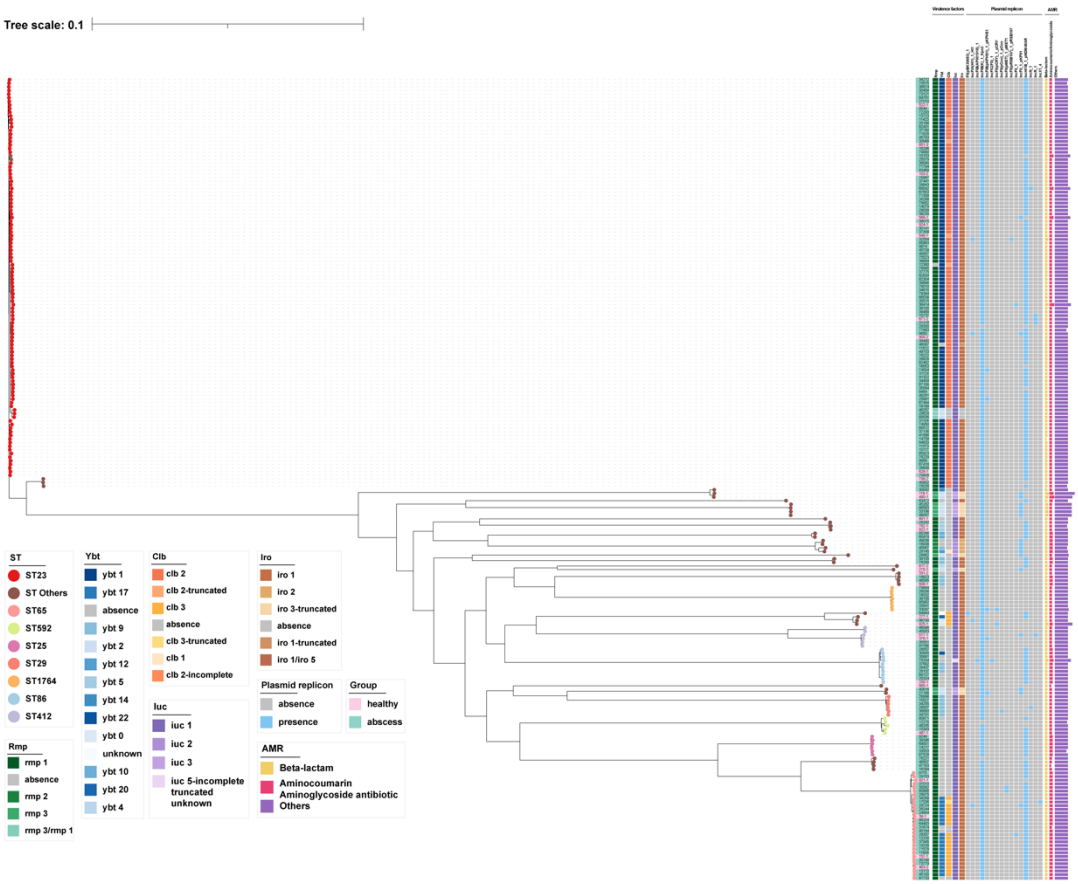

Figure 2. Population structure and phylogenetic landscape of hvKp strains.

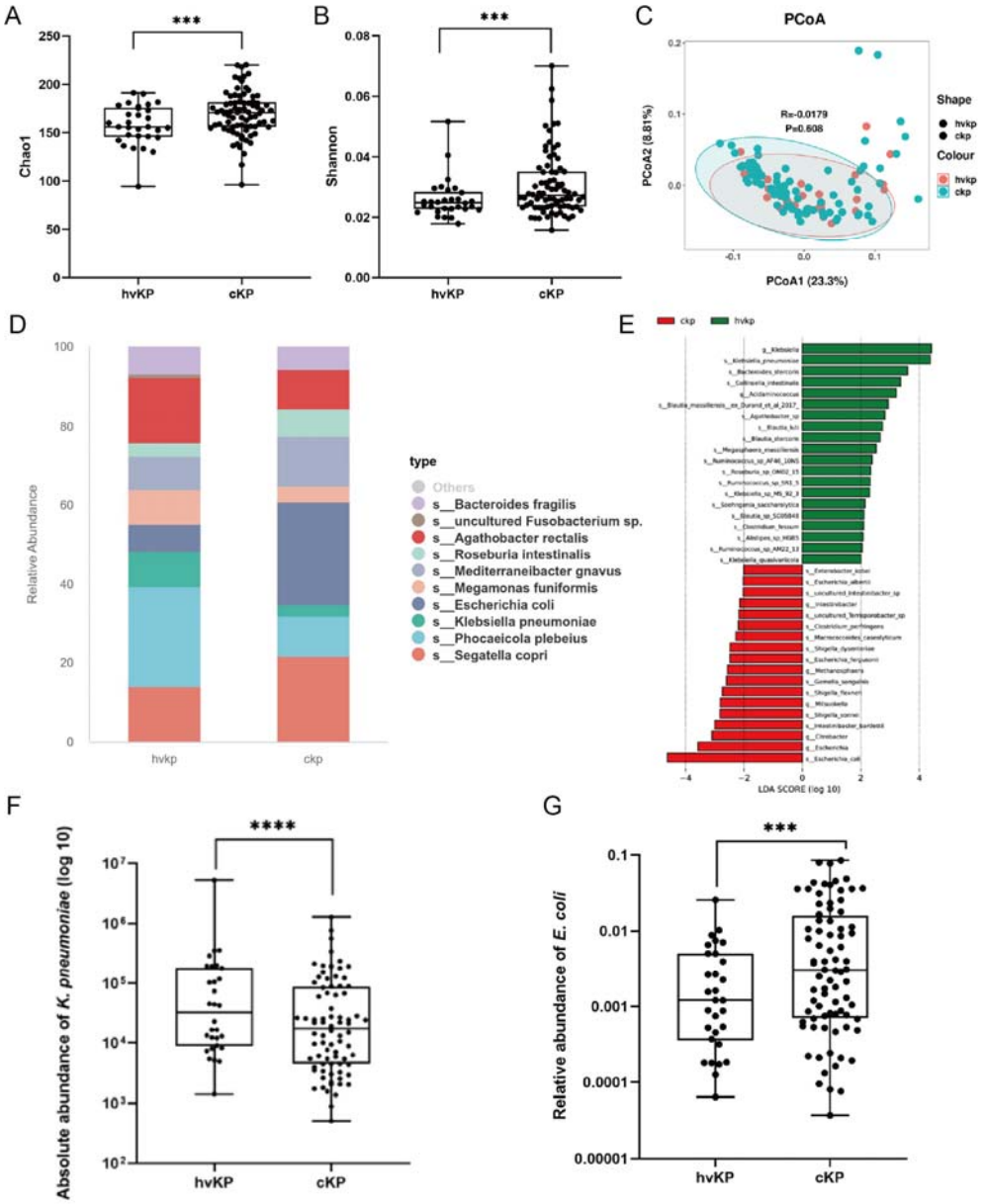

Figure 3. characteristics of microbiota diversity.