

Antibiotic resistance

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Surgical [antibiotic prophylaxis](#) refers to the [administration](#) of [antibiotics](#) before a [surgical procedure](#) to prevent the development of [surgical site infections](#) (SSIs). The [goal](#) of prophylactic antibiotics is to reduce the risk of [bacterial contamination](#) during [surgery](#) and to prevent [postoperative infections](#). However, it is important to use antibiotics judiciously to minimize the development of [antibiotic resistance](#).

Single-center retrospective observational studies

There has been an upward [trend](#) in [Carbapenem-resistant *Klebsiella pneumoniae*](#) infections in [China](#). This epidemiological trend needs to be examined to enable better disease control. Chen et al. sought to analyze the [genomic](#) characteristics, including the prevalent sequence type (ST), [resistance](#), [virulence](#), and evolutionary relationship, of *K. pneumoniae* strains isolated from patients with different types of [infections](#) in northern China to provide theoretical support for the effective [prevention](#) and control of the evolution and [transmission](#) of *K. pneumoniae*.

The STs were analyzed using multi-locus sequence typing (MLST). Drug susceptibility tests were used to examine the resistance of these STs to various [antibiotics](#). A phylogenetic tree of these isolates was constructed using the National Center for Biotechnology Information genome as the reference. [Antibiotic resistance](#) genes were identified by comparing the genomic sequences against those in the Comprehensive Antibiotic Resistance Database. Virulence genes were identified using the Virulence Factor database, while the pathogenicity of the isolates was predicted using PathogenFinder.

In total, 38 clinical isolates of *K. pneumoniae* were identified and sequenced by high-throughput sequencing. Multidrug-resistant ST11 and hypervirulent ST23 were found to be the prevalent *K. pneumoniae* strains. The distribution of the ST11 strains was strongly correlated with stays in the neurosurgery department (chi square test, $P=0.02$), while the ST23 strains were more frequently isolated from patients with liver abscesses and gallbladder infections. The ST23 strains were

significantly more pathogenic than the other STs (Wilcox test, $P < 0.001$). The resistance analysis showed that the *rmtB* genes were significantly correlated with amikacin resistance ($P < 2.2 \times 10^{-16}$, $R^2 = 1$). The ST11 strains were also found to co-harbor the KPC-2, *rmtB*, and TEM-1 genes. To the best of our knowledge, this is the first study to report on the dissemination of such multidrug-resistant *K. pneumoniae* ST11 strains in Tianjin.

The carbapenem-resistant *K. pneumoniae* (CRKP) ST11 may become highly virulent *K. pneumoniae* (CR-hvKP) due to the acquisition of virulence plasmids. Attention should be paid to the evolutionary pressure of a caused by the overuse of antibiotics, which may trigger the further development of multidrug-resistant *K. pneumoniae* infections ¹⁾.

This study provides a valuable contribution to understanding carbapenem-resistant *K. pneumoniae* infections, particularly the roles of ST11 and ST23 strains in northern China. Despite its limitations, the genomic analysis highlights critical issues regarding antibiotic resistance, virulence, and the potential evolution of CR-hvKP. Future research incorporating larger sample sizes, clinical data, and experimental validation will further solidify these findings and support effective prevention and control strategies.

¹⁾

Chen W, Cai Z, Liu S, Sotgiu G, Martin-Loeches I, Cao Y. A single-center retrospective study of the molecular epidemiological characteristics of different *Klebsiella pneumoniae* infections in northern China. *J Thorac Dis.* 2024 Nov 30;16(11):7739-7750. doi: 10.21037/jtd-24-1148. Epub 2024 Nov 29. PMID: 39678907; PMCID: PMC11635258.

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