

Investigating the Genomic Variations of Carbapenem-Resistant Enterobacteriaceae

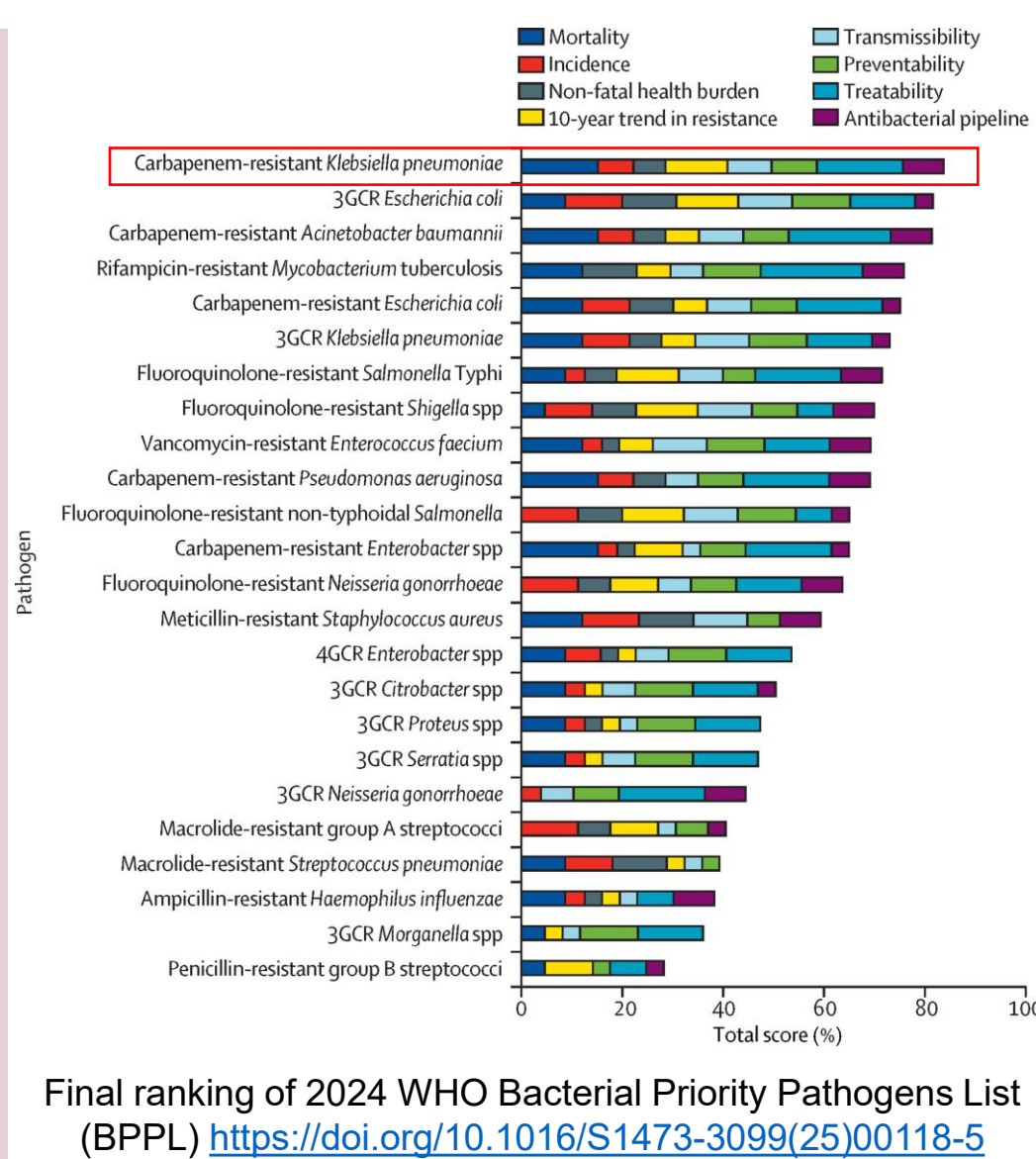
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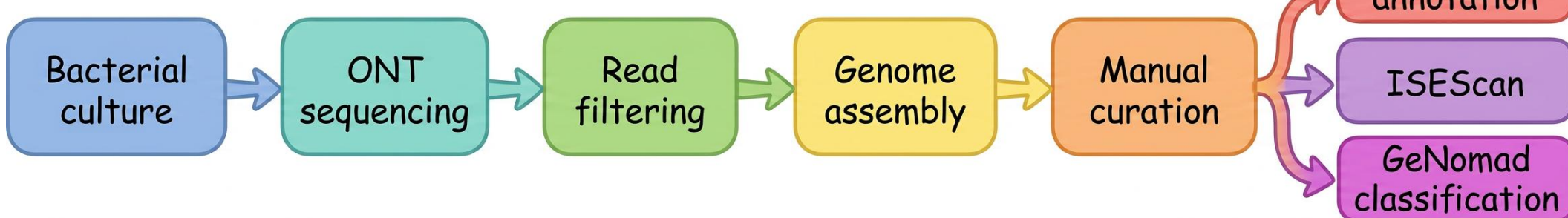
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1. Introduction

Carbapenem-Resistant Enterobacteriaceae (CRE) are a group of Gram-negative bacteria that have acquired resistance to carbapenems, which are often considered “last-resort” β -lactam antibiotics for severe bacterial infections. Common CRE species include *Klebsiella pneumoniae*, *Escherichia coli*, and *Enterobacter* spp. Among CRE, carbapenem-resistant *Klebsiella pneumoniae* (CR-KP) is one of the most clinically and epidemiologically significant drug-resistant pathogens in modern healthcare.



2. Methods



Of the 68 CR-KP isolates collected, 54 have fully resolved genomes after curation.



Manual curation was performed based on the visualized assembly paths of Flye.

3. Results and Discussion

3.1 CR-KP isolates from food and environment

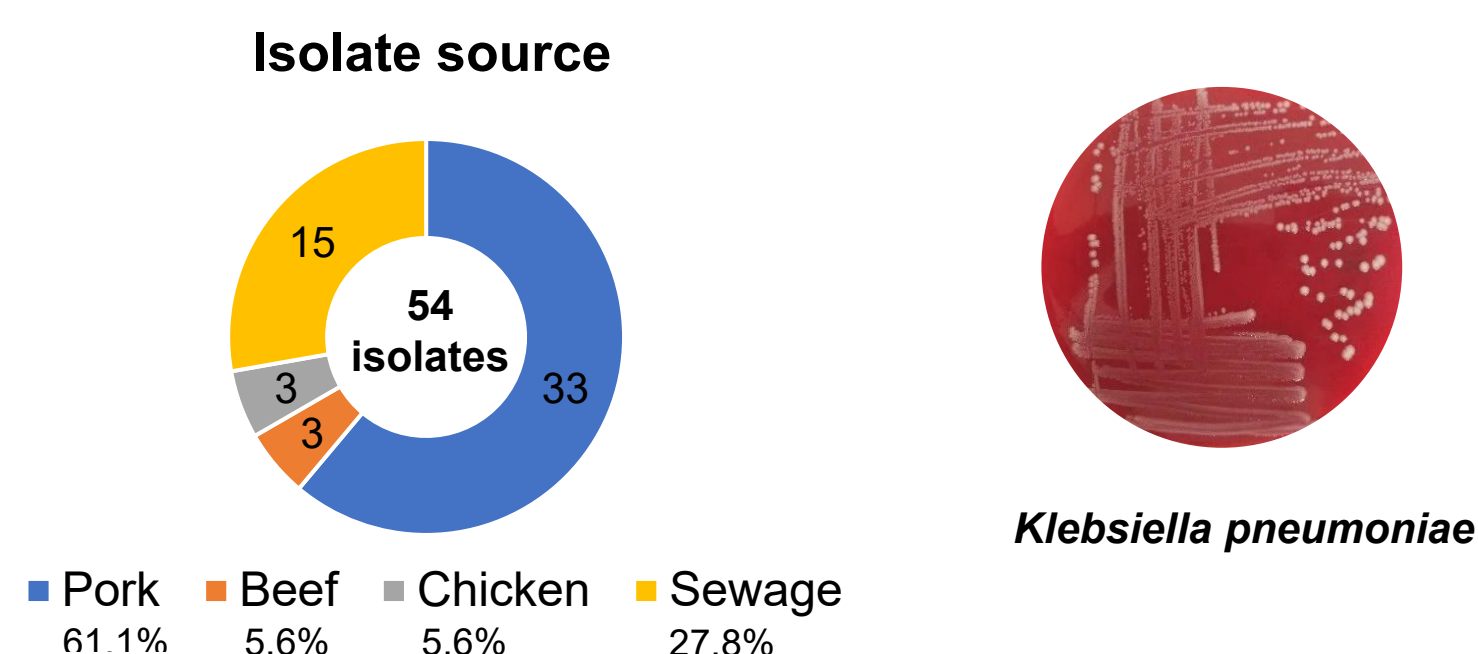


Figure 1. Collection sources of the CR-KP isolates.

Following *de novo* assembly and manual curation, 54 CR-KP isolates with fully-resolved genomes were subjected to comparative genomic analysis.

3.2 Phylogenetic analysis of CR-KP isolates

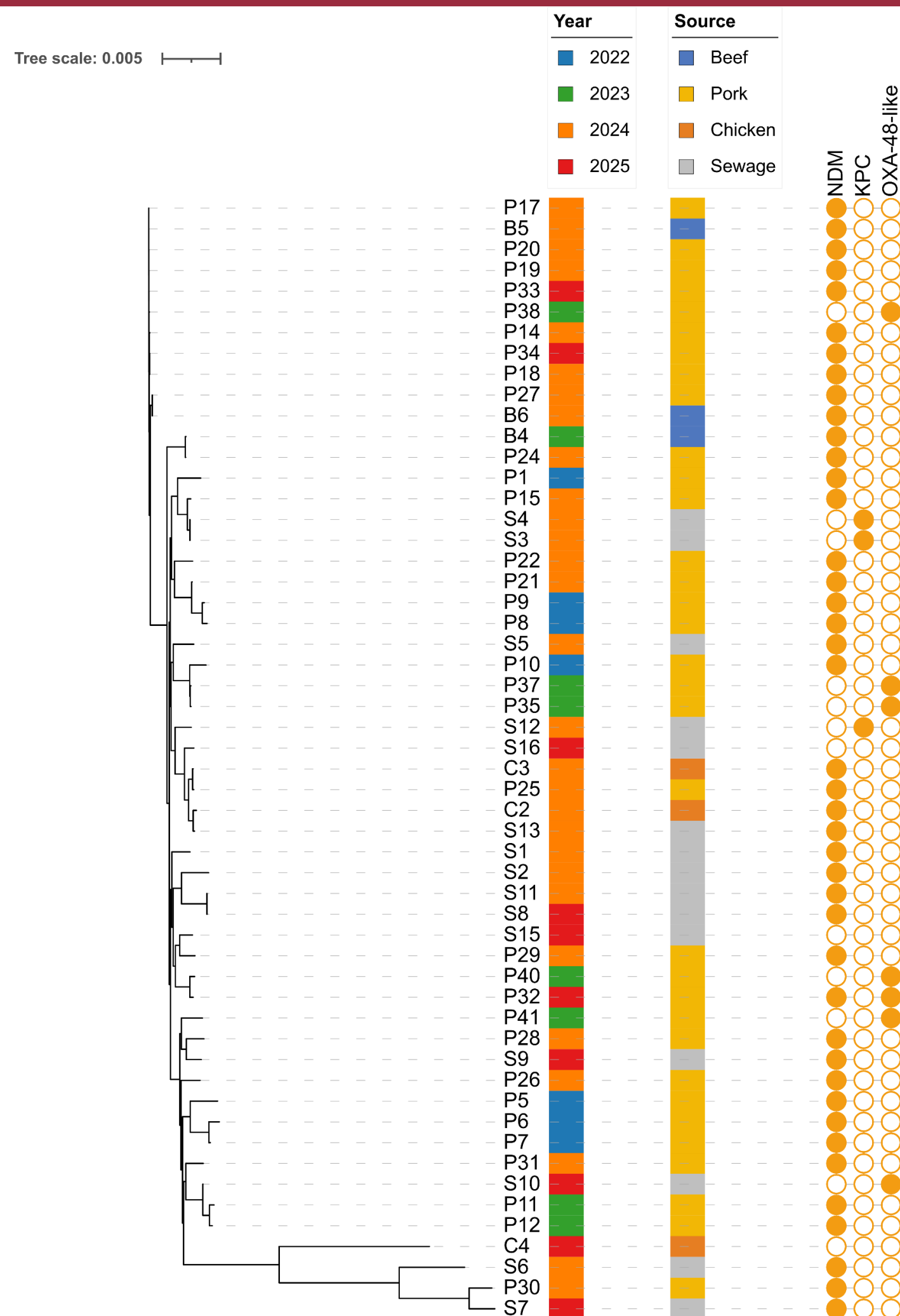


Figure 2. Phylogenetic tree of the 54 CR-KP isolates.

The phylogenetic tree was constructed by OrthoFinder (STAG algorithm). Among the 54 isolates, NDM-type carbapenemases were predominant (41/54), accounting for the majority of strains. KPC-2 was detected in three sewage isolates, whereas OXA-48-like enzymes were identified in 6 isolates. Notably, three isolates lacked detectable carbapenemase genes.

3.3 Overall statistics of the genome assemblies

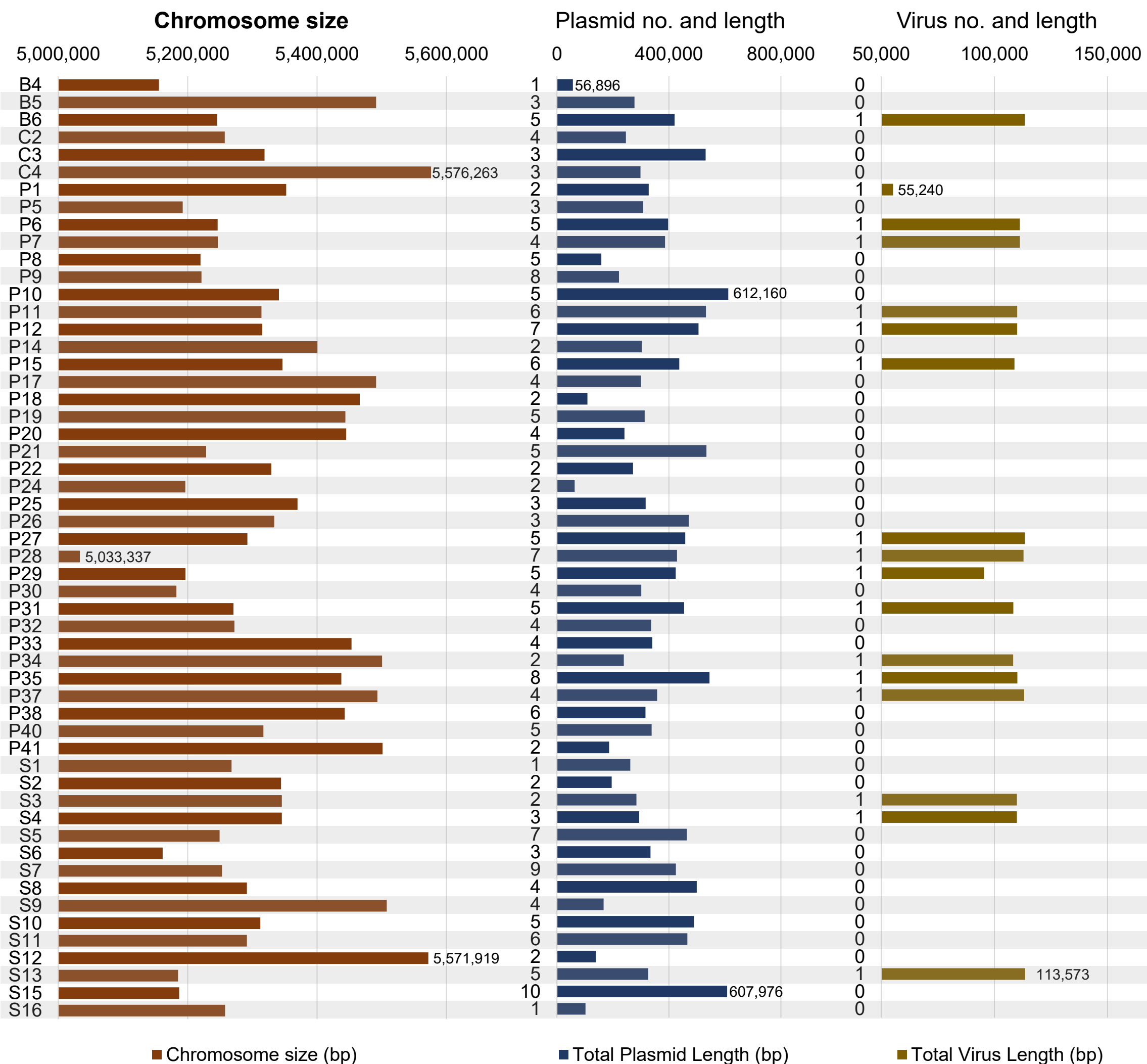


Figure 3. Chromosomes, plasmids, and viruses (bacteriophages) of the CR-KP isolates.

Among the fully resolved genomes of the 54 CRKP isolates, the circular chromosomes ranged in size from 5,033,337 to 5,576,263 bp. The number of plasmids per isolate ranged from 1 to 10, with plasmid sizes spanning 56,896 to 612,160 bp. Sixteen isolates each harbored one assembled bacteriophage, with phage genome sizes ranging from 55,240 to 113,573 bp.

3.4 Summary of IS elements in the chromosomes

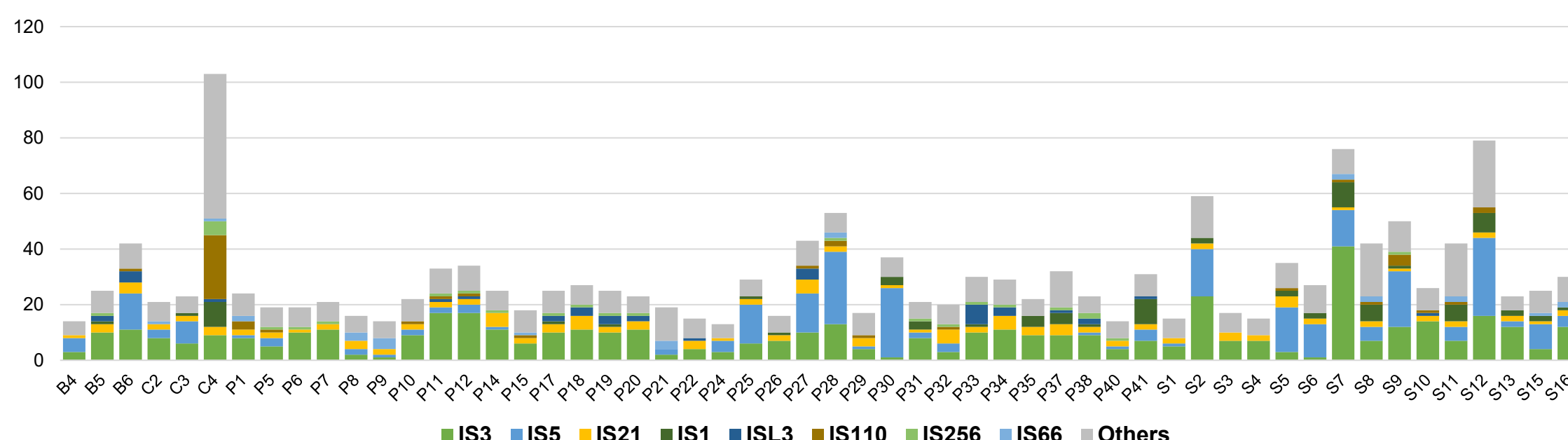


Figure 4. Distribution of IS element families in the chromosomes.

Among the IS families detected, the IS3 family was the most abundant and widely distributed, with a maximum of 41 copies observed in the sewage isolate S7.