High-risk *Klebsiella pneumoniae* shows hospital-centered genomic connectivity with divergent sublineage dissemination

Ke Wang[1,2#], Meng Wang[1,2#], Si Liu[1,2,3], Qian Wang[1,2], Chaoqun Yao[1,2,3], Haibin Li[1,2], Qi Wang[1,2], Ruobing Wang[1,2], Yuge Zhao[1,2,3], Longyang Jin[1,2], Qi Ding[1,2], Ruiqi Wang[1,2], Yanan Wang[4], Anyun Zhang[5], Rong Zhang[6], Hui Wang[1,2,3*]

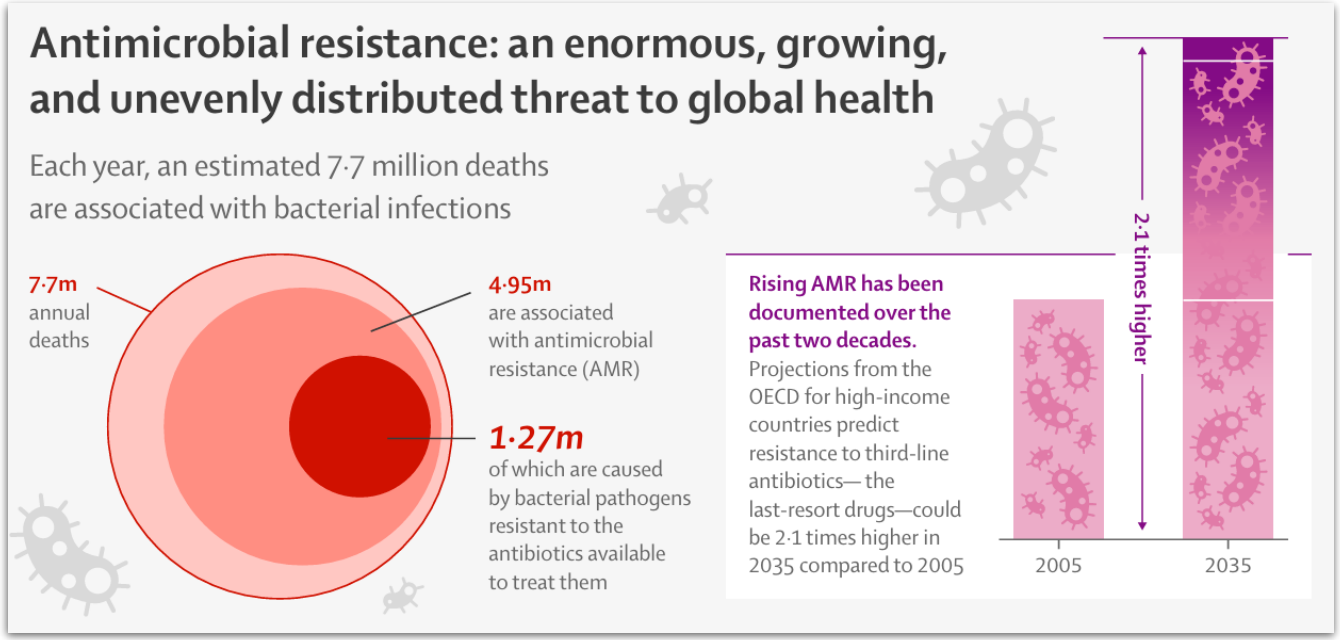
[1]Department of Clinical Laboratories, Peking University People's Hospital, Beijing, China
[2]Beijing Key Laboratory of Innovative & Transformable Warning and Intervention Technologies for Drug-Resistant Pathogens, Beijing, China
[3]Institute of Medical Technology, Peking University Health Science Center, Beijing, China
[4]International Joint Research Center of National Animal Immunology, College of Veterinary Medicine, Henan Agricultural University, Zhengzhou, China
[5]Animal Disease Prevention and Food Safety Key Laboratory of Sichuan Province, Key Laboratory of Bio-Resource and Eco-Environment of Ministry of Education, College of Life Sciences, Sichuan University, Chengdu, China
[6]Department of Clinical Laboratory, Second Affiliated Hospital of Zhejiang University, School of Medicine, Hangzhou, China

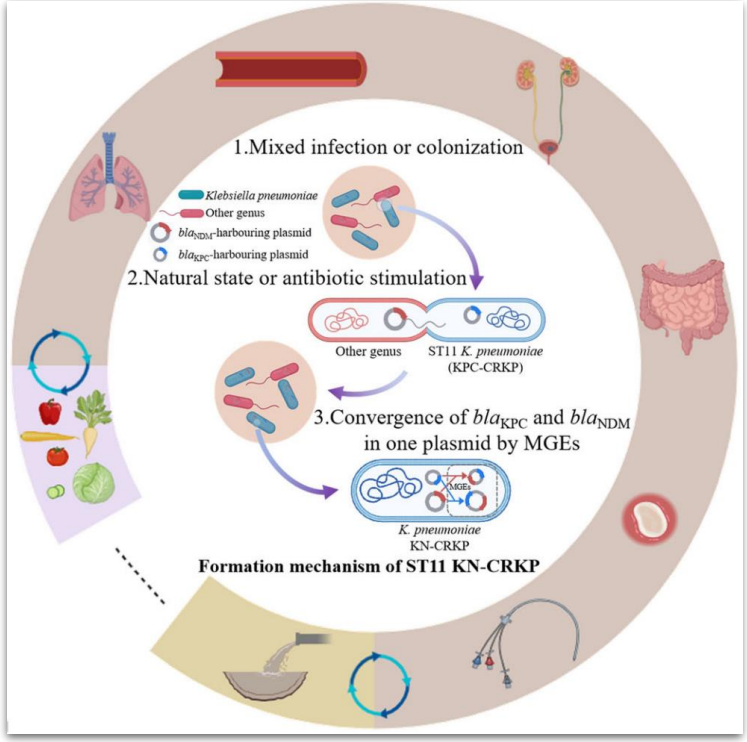


Ke Wang, Meng Wang, Si Liu, Qian Wang, Chaoqun Yao, Haibin Li, Qi Wang, et al. 2026. "High-risk *Klebsiella pneumoniae* shows hospital-centered genomic connectivity with divergent sublineage dissemination." ***iMeta*** 5: e70193.
https://doi.org/10.1002/imt2.70193

Introduction

- Antimicrobial resistance (AMR) is a major threat to global public health.
- Hospital outbreaks and rapid spread of carbapenem-resistant *Klebsiella pneumoniae* (CRKP) pose a major public health challenge.
- The emergence of strains carrying multiple carbapenemases further complicates treatment and infection prevention and control.

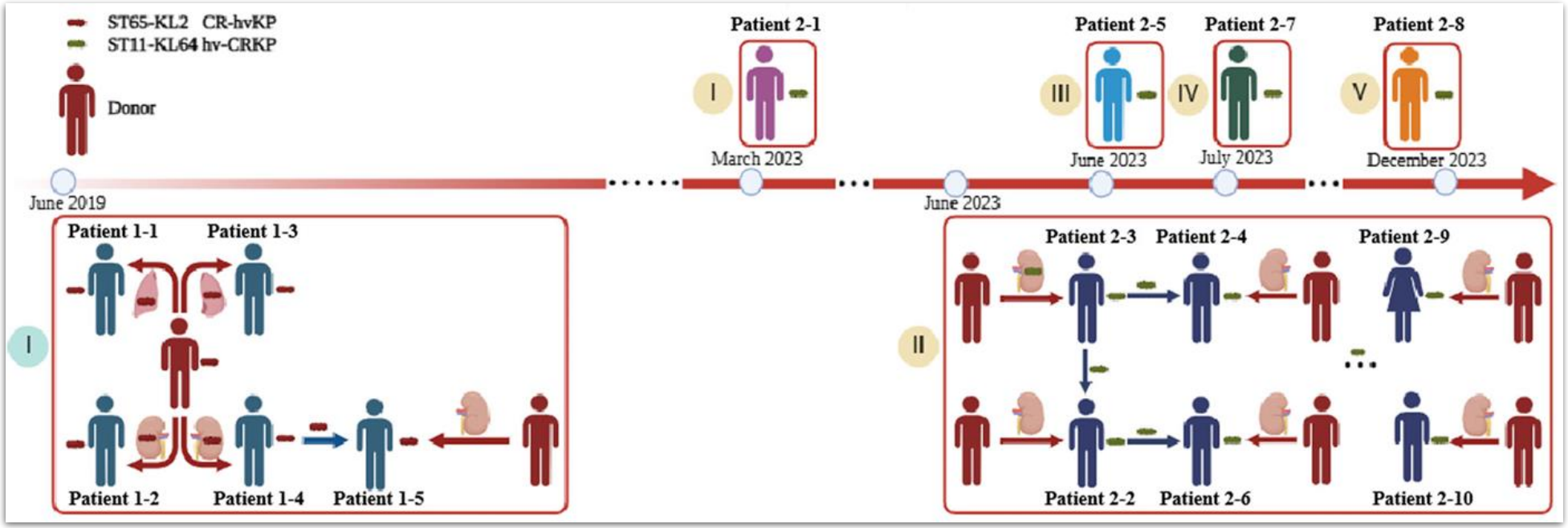




Zhang F et al. Nat Commun. 2025 Jul 1;16(1):5574

Introduction

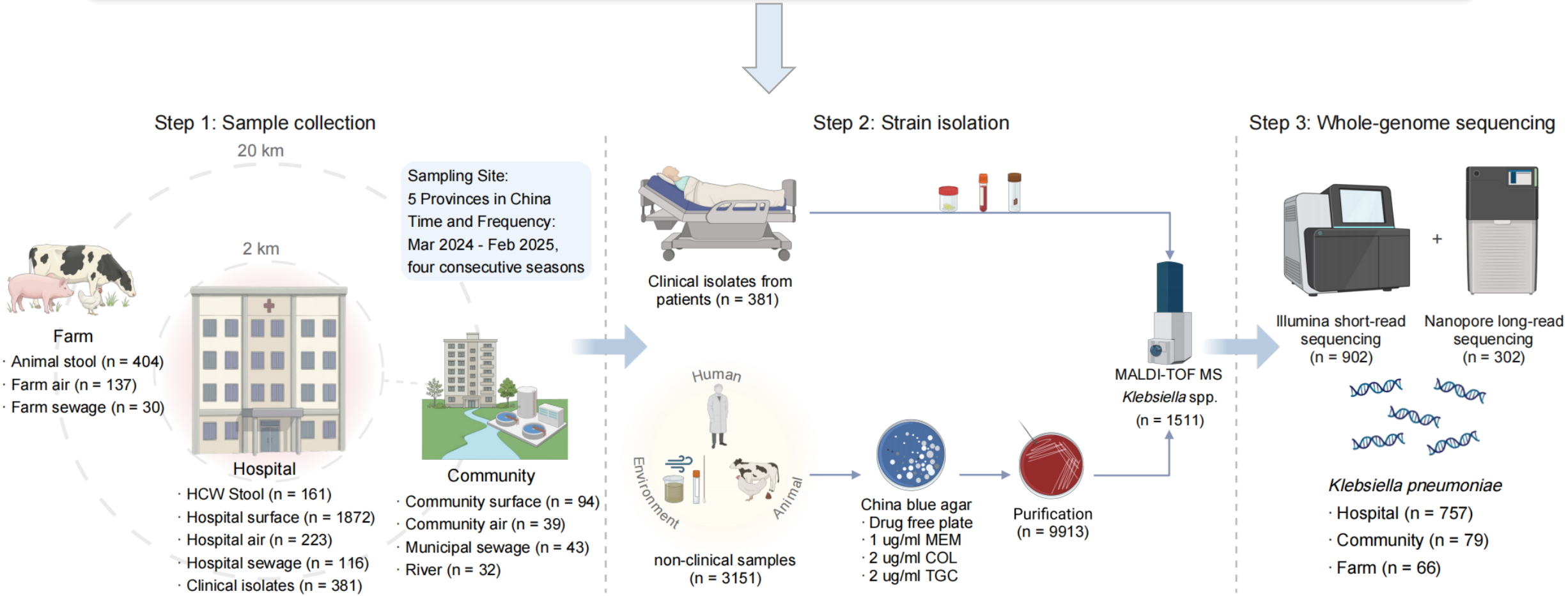
- Although *K. pneumoniae* is found across human, environment and animal niches, surveillance has focused mainly on hospital infections and outbreaks, with less attention to communities and farms.
- Fragmented and delayed surveillance focused on hospital outbreaks makes it difficult to track transmission across the One Health continuum.



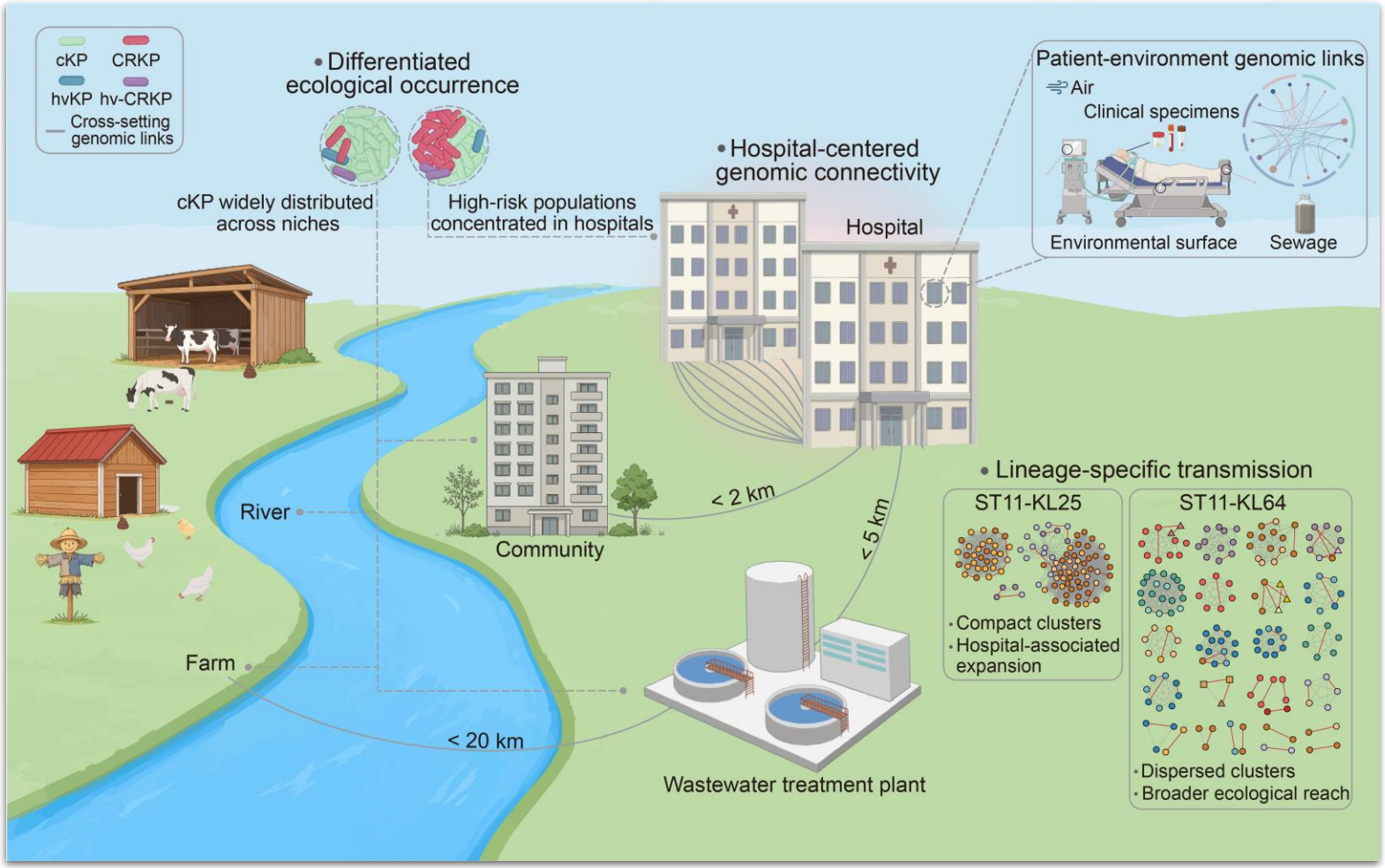
Zhang F et al. Commun Biol. 2024 Dec 2;7(1):1602

Study design

How are high-risk *K. pneumoniae* distributed and transmitted in hospitals and their surrounding environments?



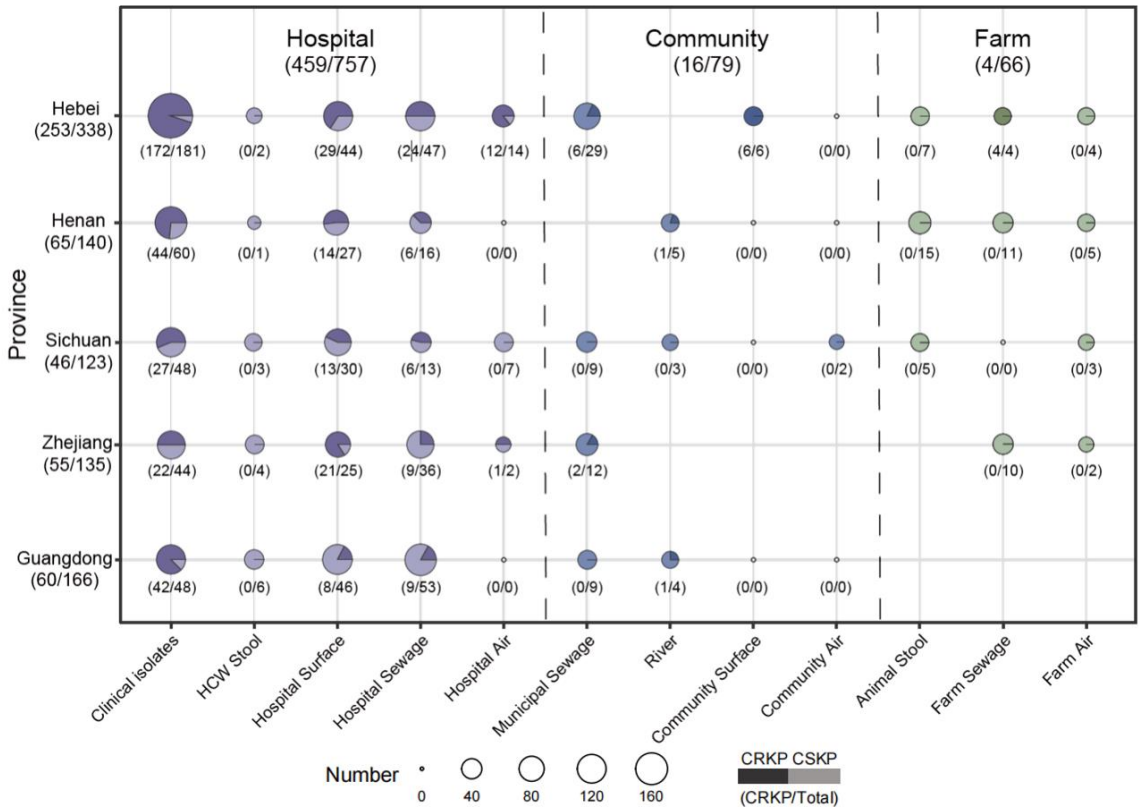
Highlights

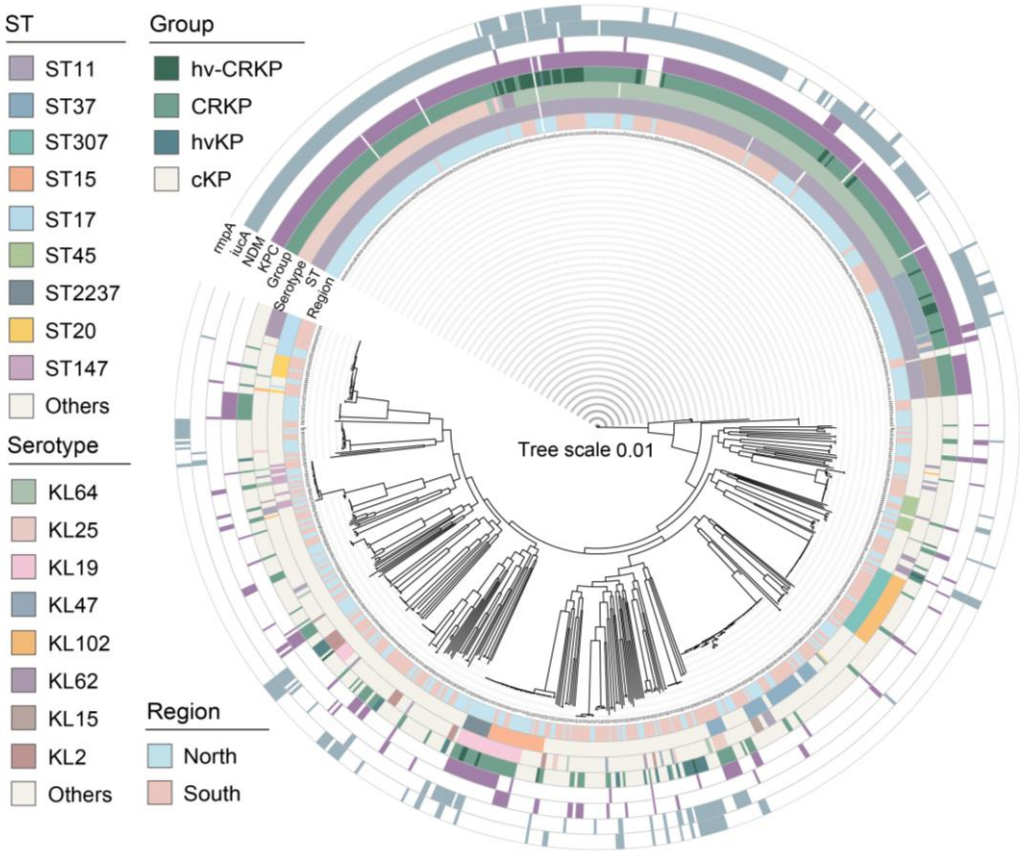


- Classical *K. pneumoniae* predominates in community and farm settings, whereas high-risk *K. pneumoniae* lineages show predominantly hospital-associated genomic links.
- Cross-setting genomic links are uncommon and often involve aquatic sources.
- ST11-KL64 showed dispersed clusters with broader ecological reach, whereas emerging ST11-KL25 showed sustained hospital-associated expansion.

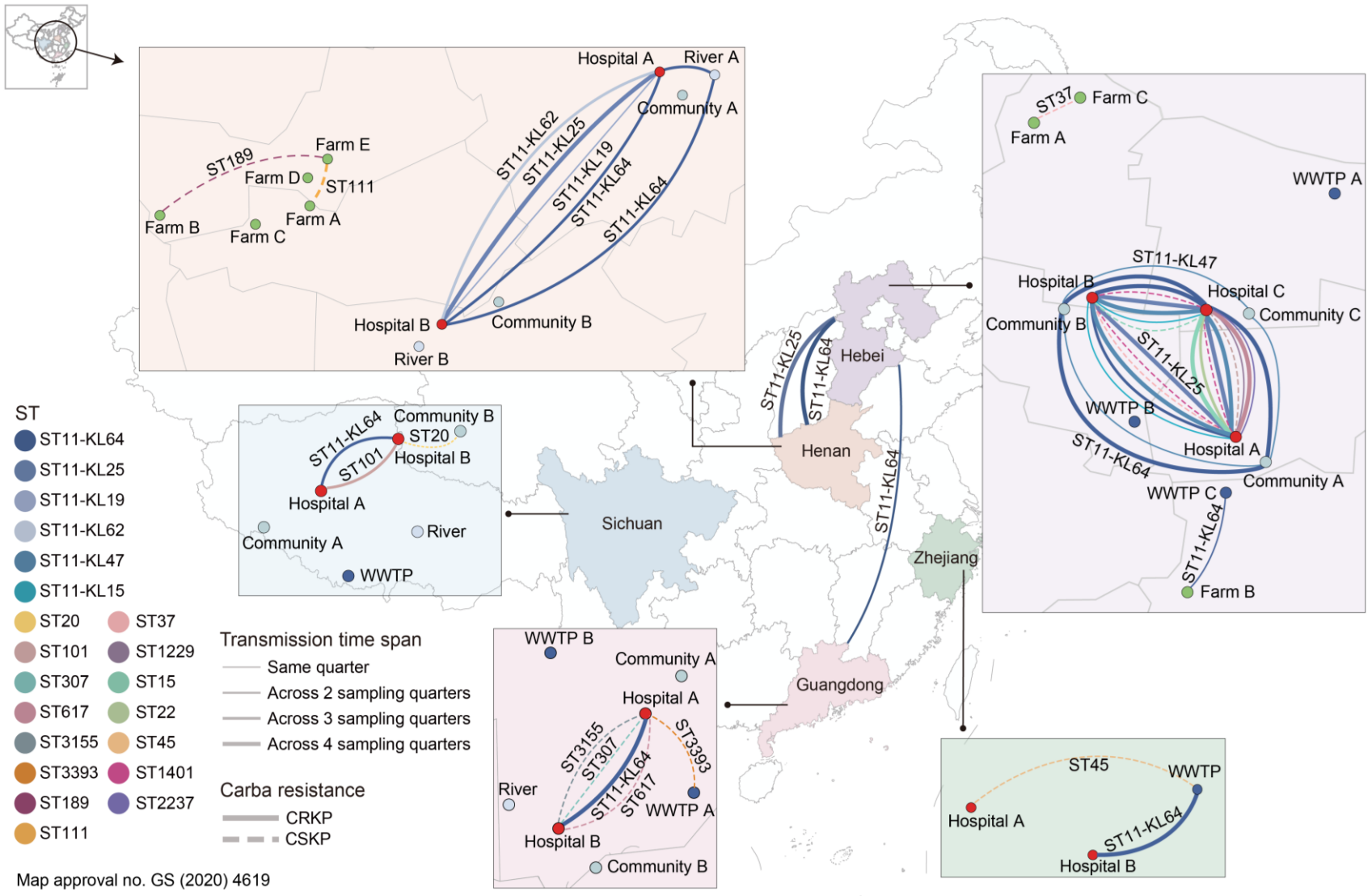
Carbapenem-resistant populations were concentrated in hospitals

- Among 902 isolates, 394 were cKP, 427 were CRKP, 29 were hvKP, and 52 were hv-CRKP.
- Hospitals accounted for 95.47% (485/508) of high-risk isolates (CRKP, hvKP, and hv-CRKP), while cKP predominated in community and farm samples.
- Diversity was driven largely by cKP (154 STs); CRKP and hv-CRKP were concentrated in ST11, whereas hvKP was mainly ST23.
- Environmental isolates showed the greatest ST diversity (154 STs).



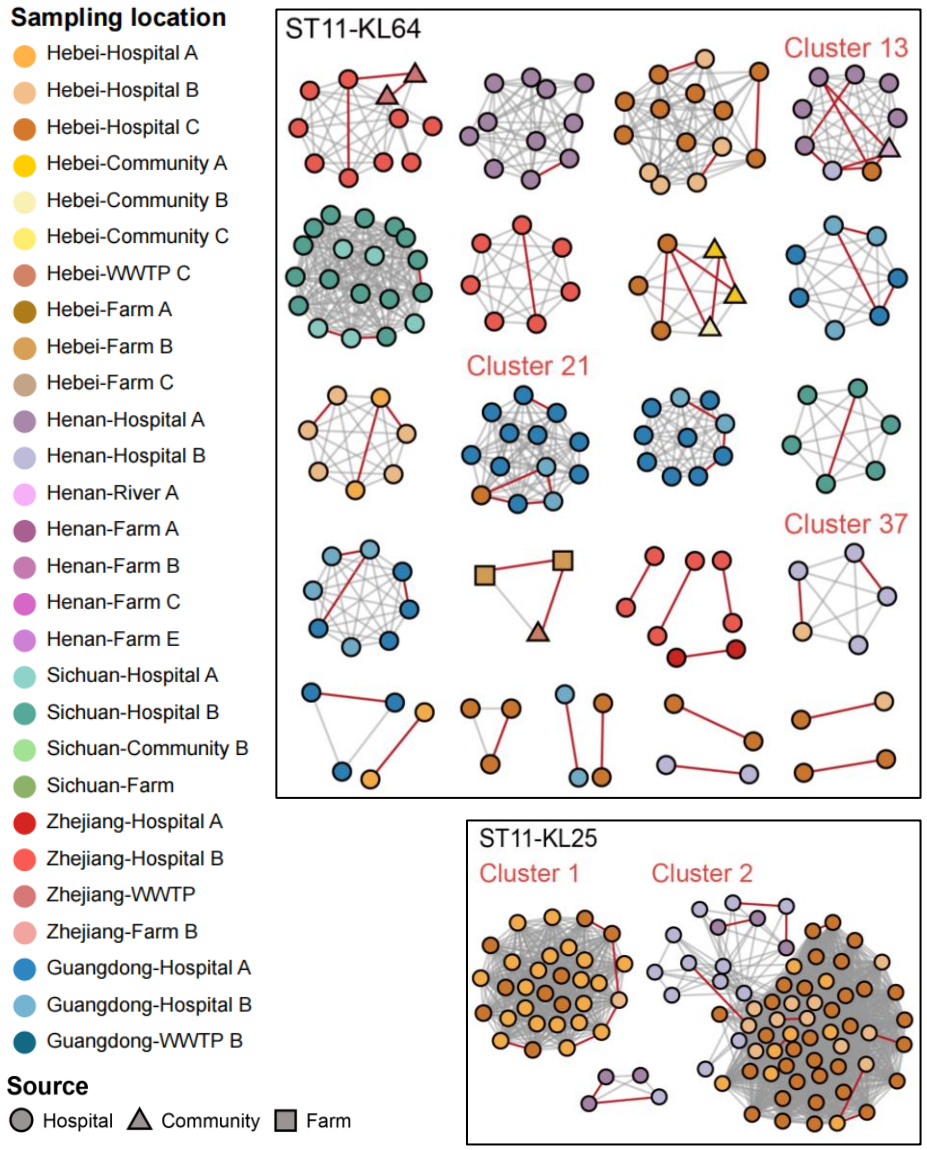


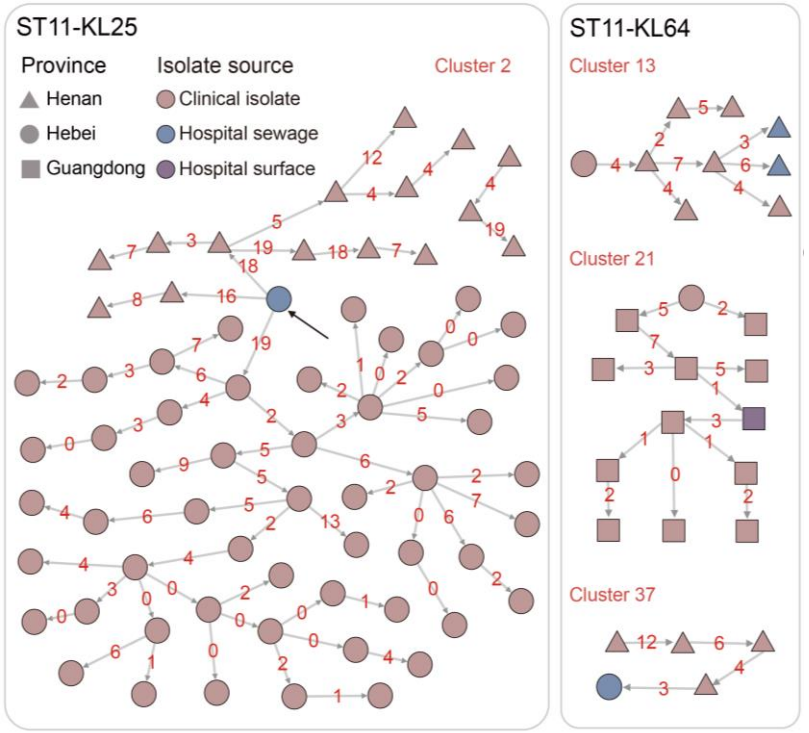
Genomic links formed a hospital-centered network



- We identified 169 putative transmission events among 902 isolates.
- Of the 169 putative events, 82.8% (140/169) occurred within or between hospitals.
- Ten events (10/169) linked different settings, but we found no evidence of a sustained transmission chain across hospitals, communities, and farms.

ST11-KL25 and ST11-KL64 showed distinct dissemination patterns





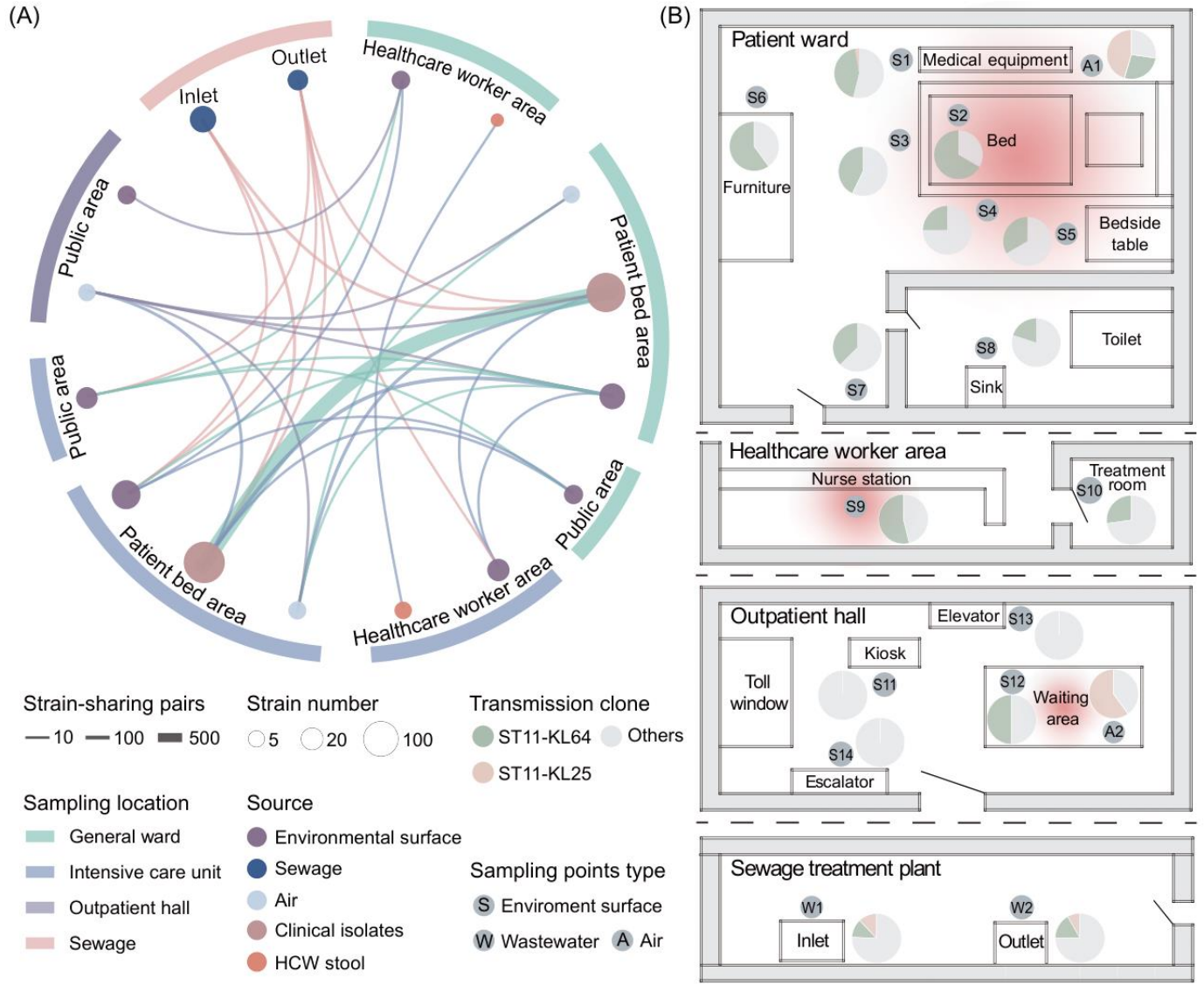
ST11-KL25

- Three closely connected clusters, accounted for 64.3% of all closely related isolate pairs.
- Related isolates were detected only in hospitals, where the lineage continued to expand.

ST11-KL64

- 28 small, geographically dispersed clusters, accounted for 21.2% of all closely related isolate pairs.
- Broader ecological reach, with related isolates also found in communities and farms.

Hospital environmental connectivity across clinical areas

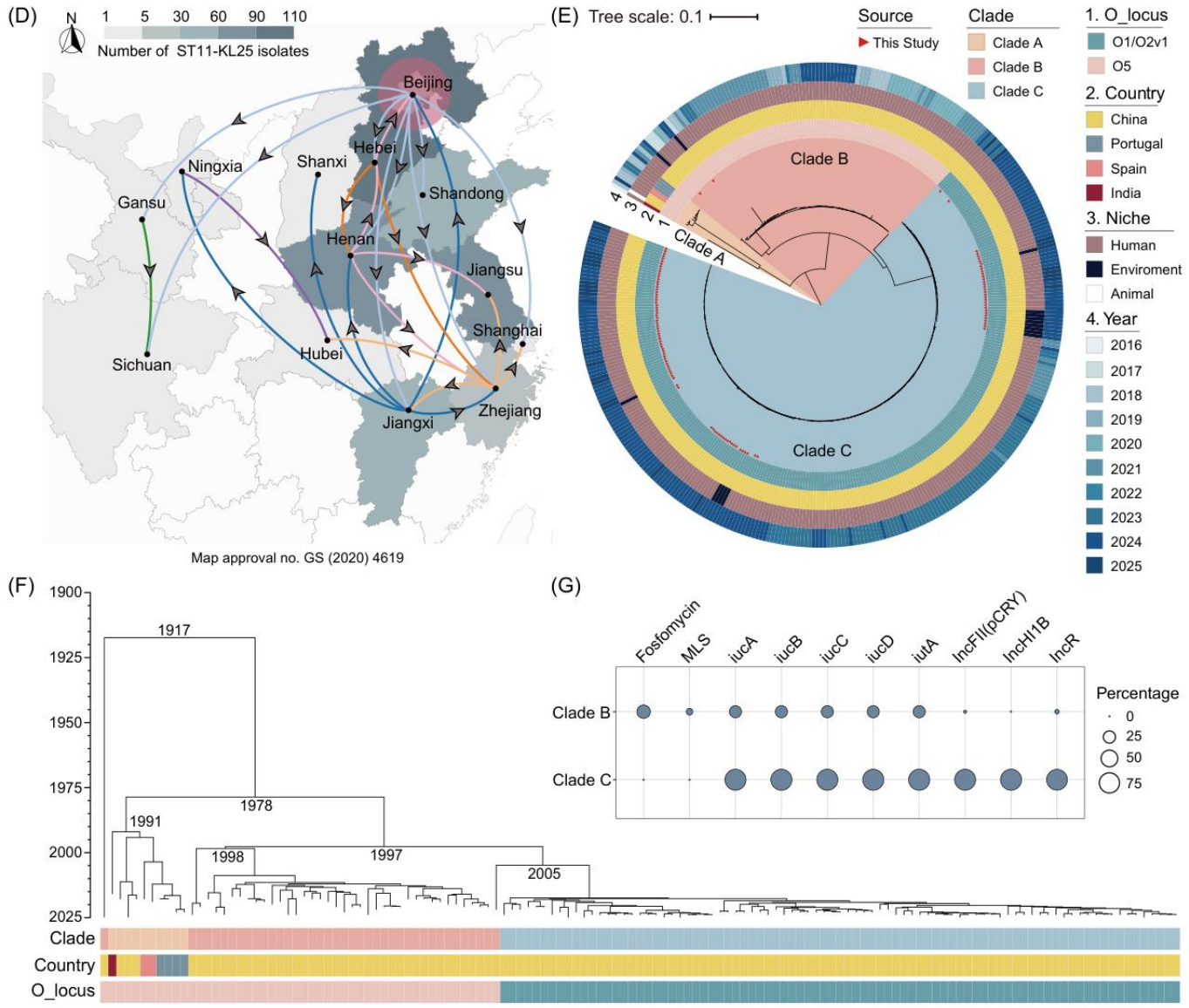


- Hospital sampling points included 14 environmental surface points, 2 air points, and 2 wastewater points.
- Closely related isolate pairs (≤ 21 SNPs) were detected across sampling points.
- Potential risk locations included patient bedside areas, nursing stations, and outpatient waiting areas.
- Potential environmental vehicles for high-risk lineages:

  ST11-KL64: surface (52.7%, 313/594);

  ST11-KL25: air (11.8%, 212/1797).

Emerging ST11-KL25 underpinned hospital-associated CRKP spread



- ST11-KL25 expanded during the surveillance period.
- The estimated time to the most recent common ancestor (tMRCA) was 1913. Phylogeographic analysis identified Beijing, China, as a major source.
- The phylogeny comprised three major clades (A, B, and C). The O antigen shifted from O5 in Clade A and B to O2v1 in Clade C.
- Compared with Clade B, Clade C had a narrower resistance profile but greater virulence potential, and carried the complete *iucABCD-iutA* virulence locus.

Summary

- Across five Chinese provinces, our One Health surveillance network found that classical *K. pneumoniae* predominated in community and farm isolates, whereas carbapenem-resistant or hypervirulent isolates were mainly from hospitals.

- Genomic links were concentrated within or between hospitals. Cross-setting links were uncommon and often involved isolates from aquatic environments.

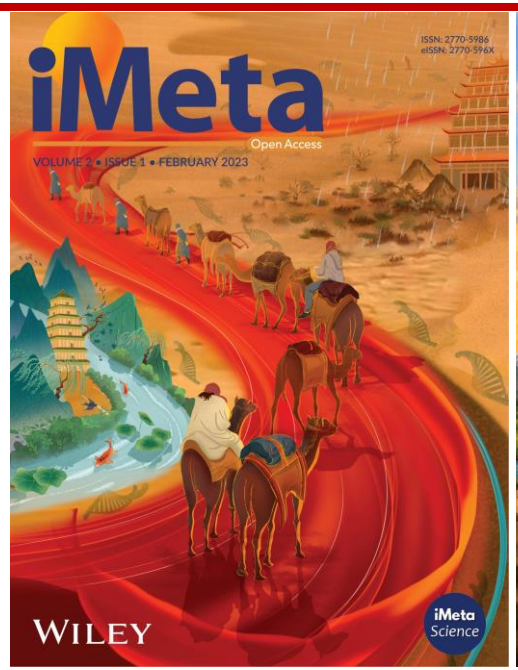
- ST11-KL64 formed multiple small, geographically dispersed clusters with broad ecological reach. ST11-KL25 formed three hospital-associated clusters, consistent with clonal expansion within hospitals.

- ST11-KL25 is an emerging CRKP lineage, characterized by the O2v1 antigen and a complete *iucABCD-iutA* locus.

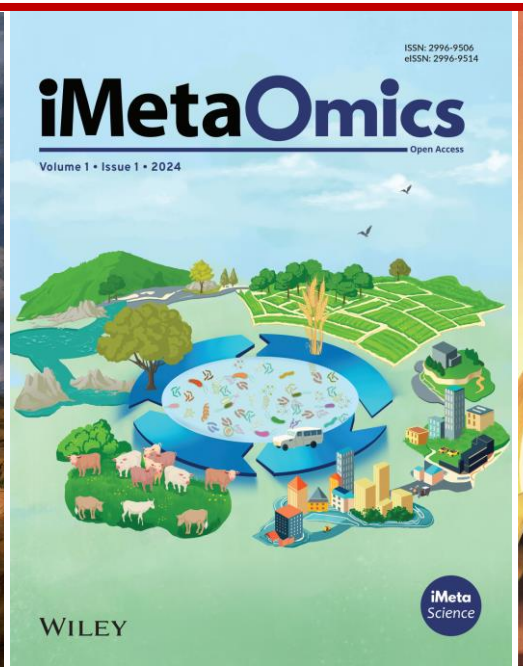
Ke Wang, Meng Wang, Si Liu, Qian Wang, Chaoqun Yao, Haibin Li, Qi Wang, et al. 2026. "High-risk *Klebsiella pneumoniae* shows hospital-centered genomic connectivity with divergent sublineage dissemination." ***iMeta*** 5: e70193. https://doi.org/10.1002/imt2.70193

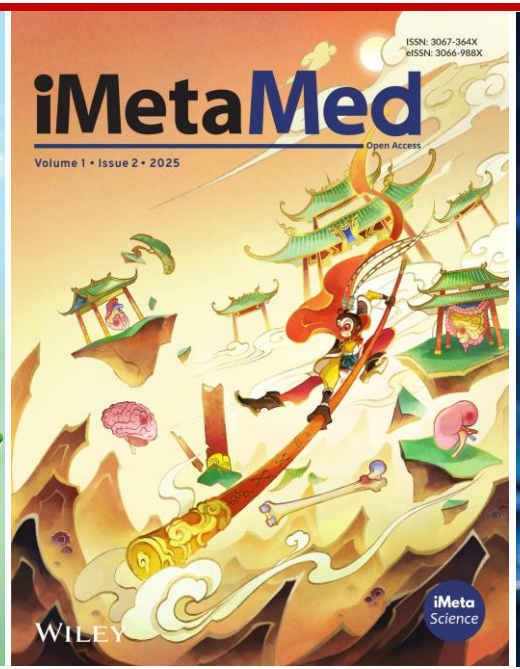
iMeta: Biology and Medicine in Info and Meta Era

WILEY











"***iMeta***" launched in 2022, impact factor (IF) **44.4**, ranking top 47/22643 in the world. It aims to publish innovative and high-quality papers with broad and diverse audiences. Its scope is similar to *Cell*, *Nature* and *Science*. Its unique features include video abstract, bilingual publication, and social media with 800,000 followers. Indexed by **SCIE/ESI**, **PubMed**, **Google Scholar** etc.

"***iMetaOmics***" launched in 2024, indexed by **ESCI**, **PubMed**, with a **target IF>15, and its scope is similar to** *Nature Communications*, *Science Advances*, *Advanced Science*, *Nucleic Acids Research*, etc.

"***iMetaMed***" launched in 2025, with a target IF>15, similar to *Med, Cell Reports Medicine, eBioMedicine, eClinicalMedicine* etc.

"***iMetaBio***" launched in 2026, with a target IF>15, similar to *Cell Reports, Cell Reports Medicine, eBioMedicine, eClinicalMedicine*

Society: http://www.imeta.science

Publisher: https://wileyonlinelibrary.com/journal/imeta

Submission: iMeta: https://wiley.atyponrex.com/journal/IMT2
iMetaOmics: https://wiley.atyponrex.com/journal/IMO2
iMetaMed: https://wiley.atyponrex.com/journal/IMM3

iMetaScience

iMetaScience

office@imeta.science
imetaomics@imeta.science

Promotion Video

Update
2026/10/19