



Klebsiella pneumoniae genomic epidemiology and antimicrobial resistance

One Health genomic surveillance of *K. pneumoniae*

11 September 2025

Intended Learning Objectives

Specific objectives of this session:

1. Understand why a One Health framework is important to combat AMR and its implications for public health responses
2. Learn about key findings from One Health studies of *K. pneumoniae*
3. Know about genomic methods to study *K. pneumoniae* in a One Health framework, including:
 - 3.1 SLs, AMR, and virulence gene profiling
 - 3.2 Pangenome analysis
 - 3.3 Genetic relatedness of clones
 - 3.4 Plasmid typing
 - 3.5 Genome-wide association studies

Outline

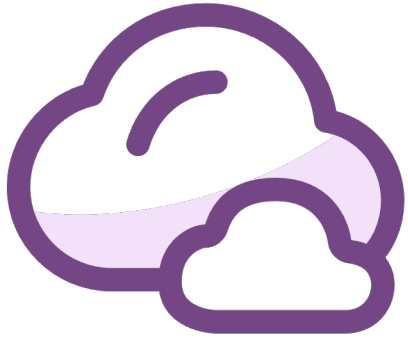
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1. One Health & why it matters for public health
2. Non-human reservoirs of *K. pneumoniae*
3. Studies of *K. pneumoniae* in a One Health context
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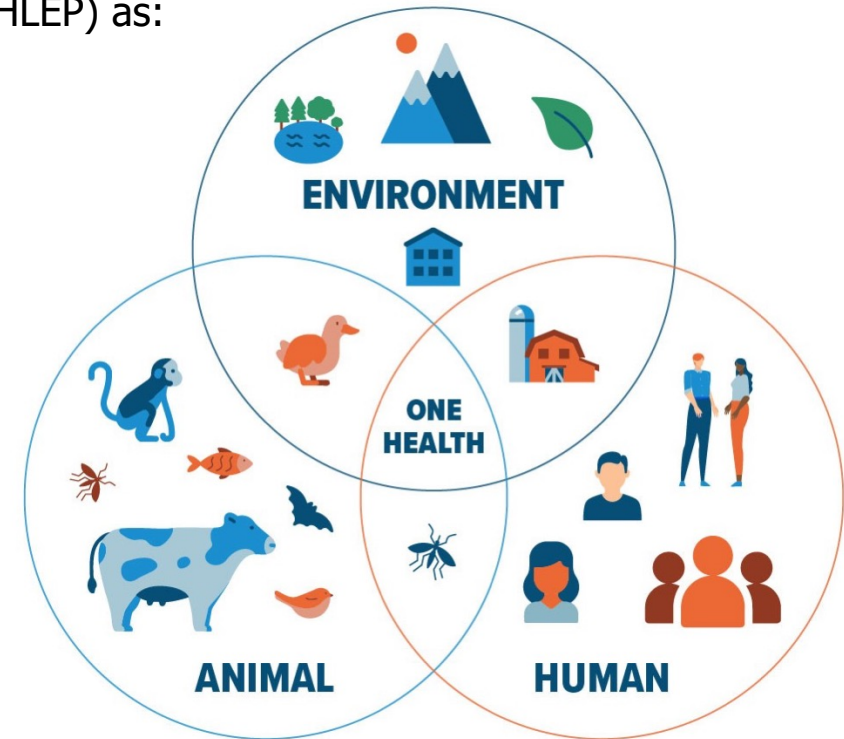
What is One Health?

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One Health has been defined by the One Health high-level expert panel (OHHLEP) as:

"One Health is an integrated, unifying approach that aims to sustainably balance and optimize the health of humans, animals, plants and ecosystems. It recognizes the health of humans, domestic and wild animals, plants and the wider environment (including ecosystems) are closely linked and interdependent.

The approach mobilizes multiple sectors, disciplines and communities at varying levels of society to work together to foster well-being and tackle threats to health and ecosystems, while addressing the collective need for clean water, energy and air, safe and nutritious food, taking action on climate change, and contributing to sustainable development."



One Health prioritised in strategies against AMR



ECDC One Health Framework

May 2024

One Health

Find out more about One Health – a key priority of the interim Australian Centre for Disease Control (CDC).

PRESS RELEASE | NOVEMBER 28, 2023

One Health Framework for Action Set to Enhance the Quality of Health Care Services Across Central Asia



Regjeringen.no

National one-health strategy against antimicrobial resistance 2024–2033

Africa CDC endorses a One Health approach

to addressing shared health threats at the human-animal-environment interface for a safer and healthier Africa

African Union
Africa CDC
Centre for Disease Control and Prevention
Safeguarding Africa's Health

One Health prioritised in strategies against AMR

ONE HEALTH JOINT PLAN OF ACTION (2022-2026)

**WORKING TOGETHER FOR
THE HEALTH OF HUMANS, ANIMALS,
PLANTS AND THE ENVIRONMENT**

Quadrupartite Joint Secretariat
on AMR



Is One Health important?



Global burden of bacterial antimicrobial resistance 1990–2021: a systematic analysis with forecasts to 2050

*GBD 2021 Antimicrobial Resistance Collaborators**

Deaths per year by 2050:

1.9M attributed to AMR

8.2M associated to AMR

Forecasting the Fallout from AMR: Averting the Health and Economic Impacts through One Health Policy and Investment

A policy brief from the EcoAMR series

Cost of AMR per year:

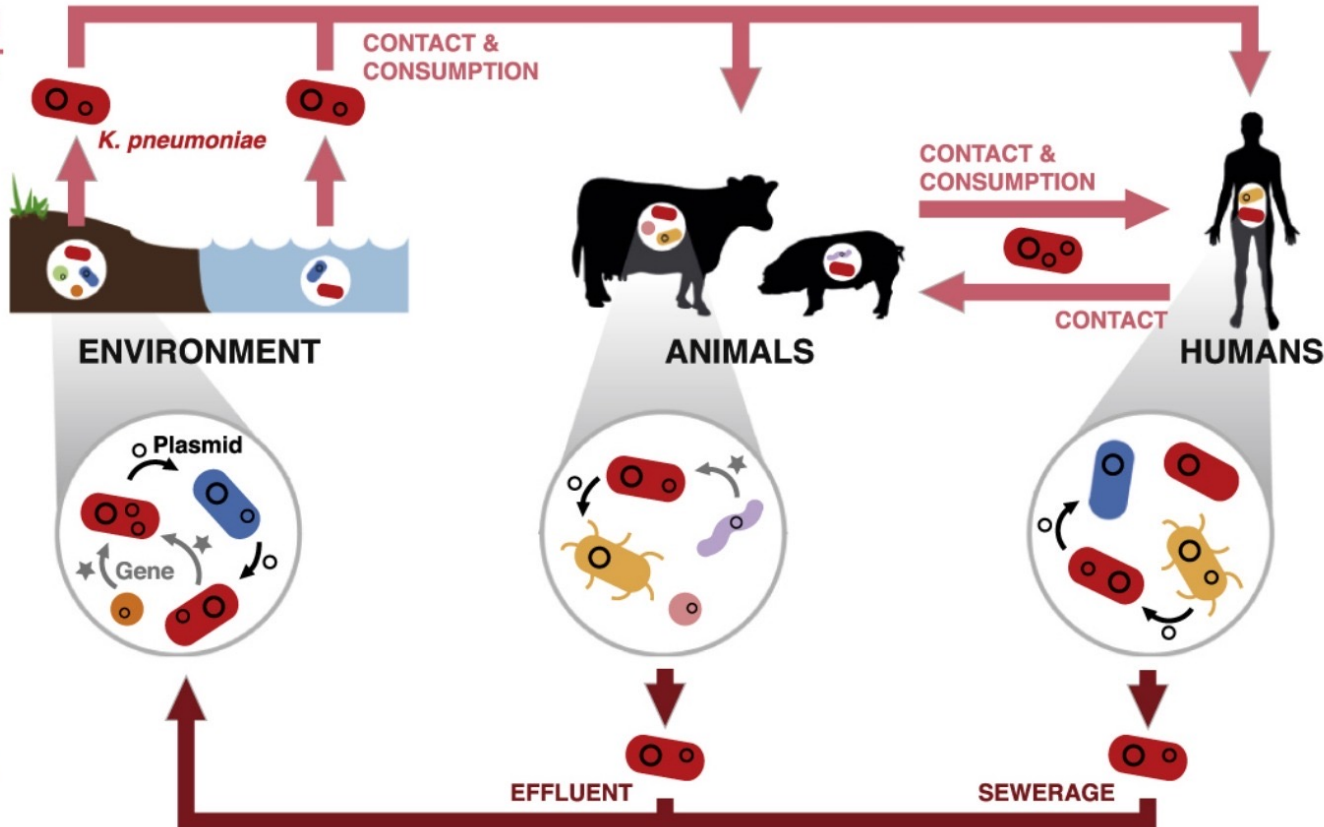
Currently: \$66B USD (0.7% global expenditure)

By 2050: \$159B USD (1.2%)

Is One Health important for *K. pneumoniae* infections?

K. pneumoniae is a key AMR trafficker

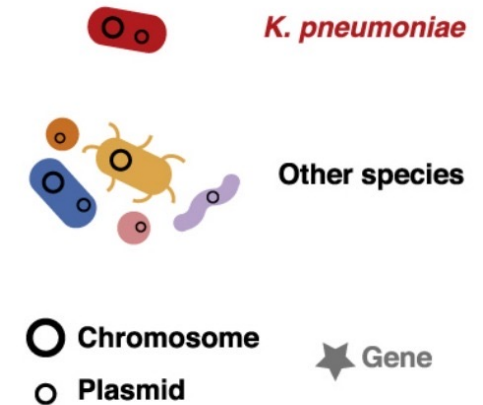
STRAIN ACQUISITION FROM ENVIRONMENT



K. pneumoniae strains acquire AMR genes and plasmids in all niches, which they can carry between niches and donate to other human pathogens.

HORIZONTAL GENE TRANSFER

STRAIN DEPOSITION IN ENVIRONMENT



Genes first detected in *K. pneumoniae* include:

***qnrAB* TEM KPC OXA-48 SHV-2 *mcr-1* CTX-M NDM CMY-1**

K. pneumoniae is a key AMR trafficker

- *K. pneumoniae* can colonise humans and animals, and has been isolated from several environmental sources
- Large accessory genome and ecological range, ability to move between ecological niches and adapt – often exchanging DNA with other bacterial species (including AMR)
- Can then “traffic” the acquired AMR genes into healthcare settings, where they can further spread in the hospital environment and among people, or to other bacterial hosts, ultimately cause opportunistic infections, that are becoming increasingly difficult to treat with accumulating AMR
- It goes both ways; *K. pneumoniae* spills back to the environment from humans, e.g. through wastewater

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K. pneumoniae is (nearly) everywhere we look

Human

- Infection
- Colonisation (12.4-87.7%)

Animals (wild & domestic)

- Pigs
- Broiler
- Turkey
- Cattle
- Horses
- Cats
- Wild boar
- Dogs
- Elephants
- Dolphins
- Catfish
- Mussels
- Oysters
- Scallops
- Prawns
- Flies

Ready-to-eat food

- Retail meat
- Cheese
- Lettuce
- Chili
- Bananas

Environment

- Hospital surfaces
- Fresh water
- Seawater
- Soil
- Sediments
- Influent and effluent wastewater

- **Examples; not a complete list**
- **Carriage rates vary**
- **Some carry AMR but not all**

References:

Calland et al, 2023. PMID: 37858320
Crippa et al, 2023. PMID: 37414963
Davies et al, 2015. PMID: 26206847
Ludden et al, 2020. PMID: 30840764
Hartanto et al, 2020. PMID: 31928427
Hetland, et al. 2025. PMID: 40296028
Huang et al, 2025. PMID: 40890500
Radisic, et al. 2022. PMID: 36521369
Thorpe et al, 2022. PMID: 36411354
Wall, et al. 2023. DOI:
10.15212/ZOONOSES-2023-0016
Zamudio, et al. 2025. PMID: 40889870

**We find *K. pneumoniae* in non-human sources...
but does it matter for human health?**

We find *K. pneumoniae* in non-human sources... but does it matter for human health?

Two examples:

- AMR genes can emerge in the environment or in animals and move to humans: the colistin resistance gene *mcr-1*
- Animal reservoirs as a source of virulence traits: the pig-associated siderophore *iuc3*

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Where do you think clinically relevant *K. pneumoniae* clones circulate most?

A large-scale genomic snapshot of *Klebsiella* spp. isolates in Northern Italy reveals limited transmission between clinical and non-clinical settings

Received: 19 July 2021

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 Check for updates

Harry A. Thorpe¹, Ross Booton², Teemu Kallonen³, Marjorie J. Gibbon⁴, Natacha Couto⁴, Virginie Passet⁵, Sebastián López-Fernández⁵, Carla Rodrigues⁵, Louise Matthews⁵, Sonia Mitchell⁶, Richard Reeve⁶, Sophia David⁷, Cristina Merla⁸, Marta Corbella⁸, Carolina Ferrari⁸, Francesco Comandatore⁹, Piero Marone⁸, Sylvain Brisse⁵, Davide Sasserà^{10,12}, Jukka Corander^{1,7,11,12} & Edward J. Feil^{4,12}✉



Population structure and antimicrobial resistance among *Klebsiella* isolates sampled from human, animal, and environmental sources in Ghana: a cross-sectional genomic One Health study

Jessica K Calland, Kaisa Haukka, Stephen W Kporde, Atanyiwoen Brusah, Marta Corbella, Cristina Merla, Ørjan Samuelsen, Edward J Feil, Davide Sasserà, Akosua B Karikari*, Courage K S Saba*, Harry A Thorpe*, Jukka Corander*

A genome-wide One Health study of *Klebsiella pneumoniae* in Norway reveals overlapping populations but few recent transmission events across reservoirs

[Marit A. K. Hetland](#) ✉, [Mia A. Winkler](#), [Håkon P. Kaspersen](#), [Fredrik Håkonsholm](#), [Ragna-Johanne Bakksjø](#), [Eva Bernhoff](#), [Jose F. Delgado-Blas](#), [Sylvain Brisse](#), [Annapaula Correia](#), [Aasmund Fostervold](#), [Margaret M. C. Lam](#), [Bjørn-Tore Lunestad](#), [Nachiket P. Marathe](#), [Niclas Raffelsberger](#), [Ørjan Samuelsen](#), [Marianne Sunde](#), [Arnfinn Sundsfjord](#), [Anne Margrete Urdahl](#), [Ryan R. Wick](#), [Iren H. Löhr](#) & [Kathryn E. Holt](#)

Limited Transmission of *Klebsiella pneumoniae* among Humans, Animals, and the Environment in a Caribbean Island, Guadeloupe (French West Indies)

Alexis Dereeper^a, Gaëlle Gruel^a, Matthieu Pot^a, David Couvin^a, Elodie Barbier^b, Sylvaine Bastian^c, Jean-Christophe Bambou^d, Moana Gelu-Simeon^e, Séverine Ferdinand^a, Stéphanie Guyomard-Rabenirina^a, Virginie Passet^f, Frederic Martino^g, Pascal Piveteau^h, Yann Reynaud^a, Carla Rodrigues^f, Pierre-Marie Roger^{ij}, Xavier Roy^k, Antoine Talarmin^a, Benoit Tressieres^l, Marc Valette^g,  Sylvain Brisse^f,  Sébastien Breurec^{a,c,j,l}

A One Health Study of the Genetic Relatedness of *Klebsiella pneumoniae* and Their Mobile Elements in the East of England

Catherine Ludden^{1,2,a}, Danesh Moradigaravand^{3,a}, Dorota Jamroz², Theodore Gouliouris^{4,5,6}, Beth Blane⁴, Plamena Naydenova⁴, Juan Hernandez-Garcia⁷, Paul Wood⁸, Nazreen Hadjirin⁷, Milorad Radakovic⁷, Charles Crawley⁵, Nicholas M. Brown^{5,6}, Mark Holmes⁷, Julian Parkhill², and Sharon J. Peacock^{1,2,4,5}

Limited Evidence of Spillover of Antimicrobial-Resistant *Klebsiella pneumoniae* from Animal/Environmental Reservoirs to Humans in Vellore, India

Jobin John Jacob¹ · V. Aravind¹ · Benjamin S. Beresford-Jones² · Y. Binesh Lal¹ · Chaitra Shankar¹ · M. Yesudoss¹ · Fiza Abdullah¹ · T. Monisha Priya¹ · Sanika Kulkarni¹ · Stephen Baker² · Balaji Veeraraghavan¹ · Kamini Walia³

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Key findings from One Health *K. pneumoniae* studies



- *K. pneumoniae* is «everywhere»
- But AMR *K. pneumoniae* is largely concentrated in human clinical isolates, particularly ESBLs and carbapenemases
- No carbapenemases found in non-clinical settings in large snapshot studies from Italy¹ or Ghana², or nationwide study from Norway⁴ – but carbapenemases have been found in (a few) animal and environmental *K. pneumoniae* samples elsewhere (including India⁴, China, Brazil, Canada⁵)
- Hypervirulence-associated clones found mainly in human settings (patients, colonisation or hospital environment), except 2 in dogs⁶, 1 cow & 1 pig⁵
- Animals, particularly pigs, reservoirs for virulence factors (*iuc3*^{1,3} and *iuc5*³)

1) Thorpe et al, 2022. PMID: 36411354
2) Calland et al, 2023. PMID: 37858320
3) Hetland, et al. 2025. PMID: 40296028

4) Jacob et al, 2024. PMID: 39531180
5) Huang et al, 2025. PMID: 40890500
6) Dereeper et al, 2022. PMID: 36094181

Key findings from One Health *K. pneumoniae* studies

- Genetic relatedness: Strain-sharing is more common within humans (especially in hospitals) than across niches, but occasional cross-niche transmission does occur ^{1,2}
- Overlap in gene pools: Large SL and pangenome overlap seen across niches, but also across countries (Norway and Ghana) ^{2,3}
- Cross-niche spread appears constrained more by geography and exposure patterns than by intrinsic *K. pneumoniae* barriers
- Geographic, socio-economic and cultural factors affect the amount of cross-niche transmission ⁴ – it is important to monitor *K. pneumoniae* in multiple settings
- Is *K. pneumoniae* food-borne? Several studies implicate food sources (as well as companion animals¹) as potential routes of human acquisition of *K. pneumoniae* – this warrants surveillance ^{5,6}

1) Thorpe et al, 2022. PMID: 36411354

2) Hetland, et al. 2025. PMID: 40296028

3) Calland et al, 2023. PMID: 37858320

4) Subbiah et al, 2020. PMID: 31932601

5) Zamudio et al, 2025. PMID: 40889870

6) Crippa et al, 2023. PMID: 37414963

We find *K. pneumoniae* in non-human sources... but does it matter for human health? **Yes**

- **The biggest AMR burden is in healthcare settings:** but non-human sources can act as reservoirs for new resistance or virulence traits
- **Rare spillovers can have big impacts:** even infrequent introductions from animals, food, or the environment can establish in humans and persist as public health problems
- **Colonisation often precedes infection:** preventing transmission and colonisation from the food chain can reduce disease burden and mortality

Implications for public health responses

- **Surveillance should go across sectors:** Extend beyond hospitals to include animals, food, and the environment
- **Policies must tackle antibiotic use everywhere:** Regulate use in livestock, agriculture, and wastewater to prevent AMR emergence and spillover
- **Mitigation requires research and coordination:** Study AMR/virulence evolution outside hospitals and align policy across human, animal, and environmental health

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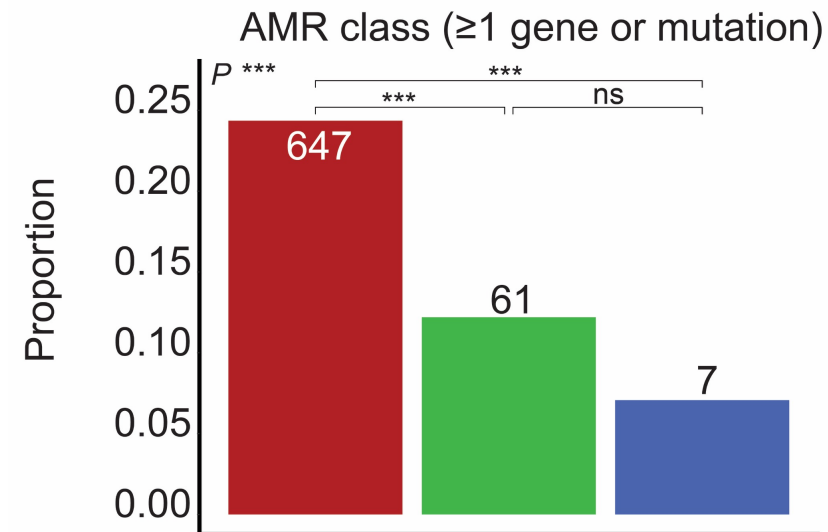
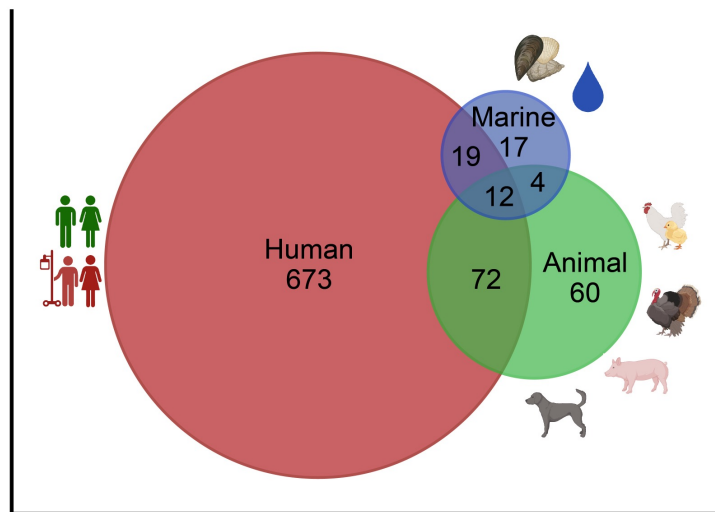
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Genomic approaches to *K. pneumoniae* surveillance

SLs, AMR, and virulence gene profiling

- Do the populations (SLs, MDR/Hv clones) overlap?
- Diversity measures (e.g. Simpson's diversity) to compare populations

A) Sharing of 857 sublineages across niches



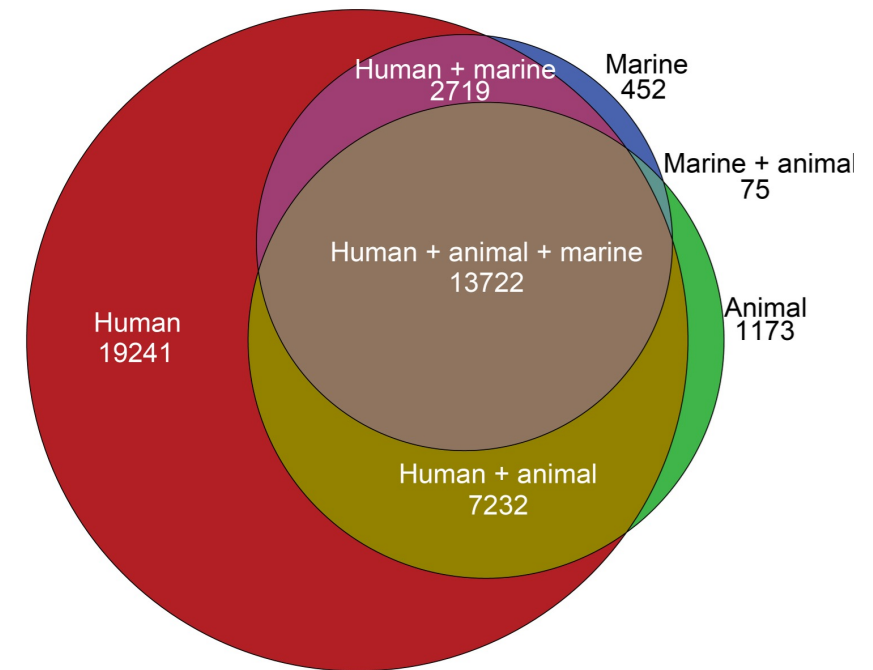
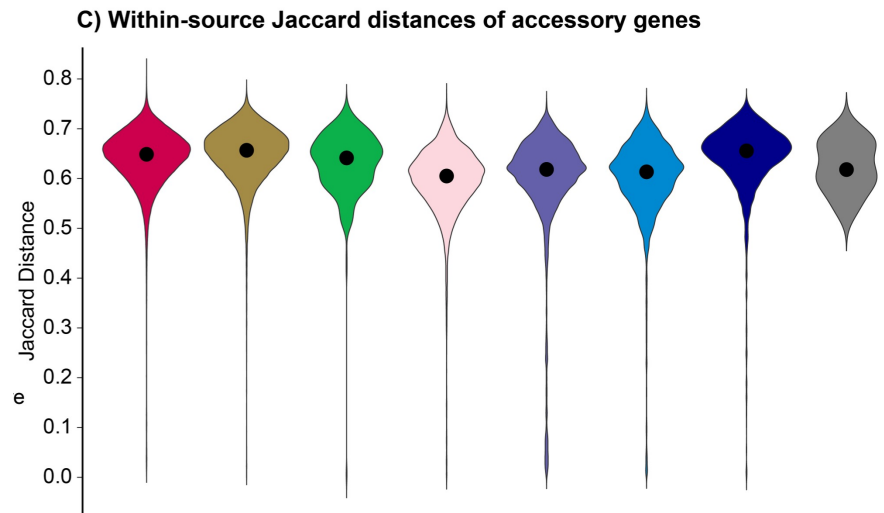
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Pangenome analysis

- Compare core vs accessory gene content between niches
- Estimate rates of gene gain/loss
- Measure gene content similarity (e.g. Jaccard distances)



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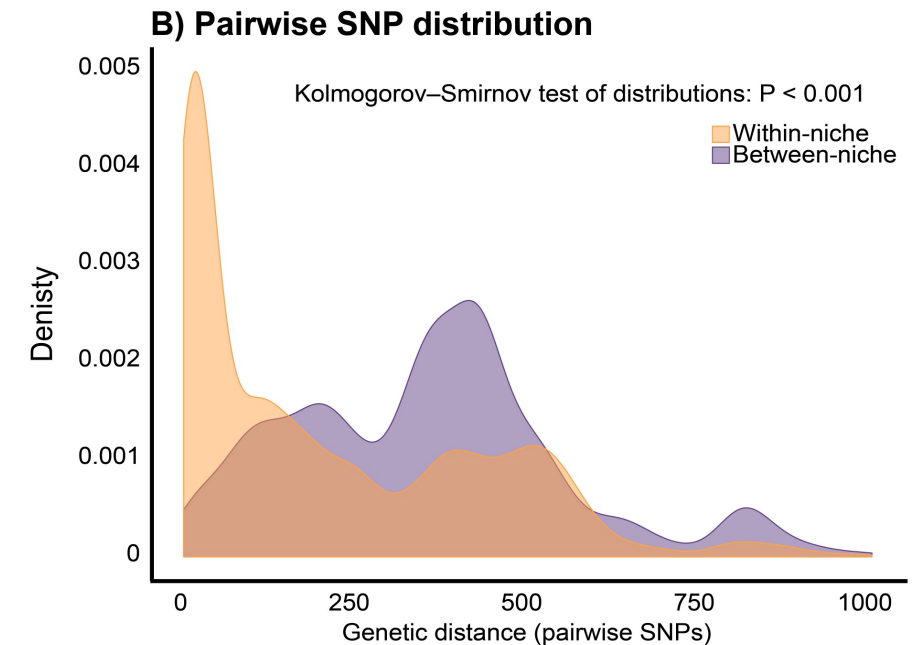
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Genetic relatedness of clones

- Pairwise SNP distances within vs between niches
- Apply thresholds to define potential strain-sharing
- Quantify how many strains show cross-niche relatedness



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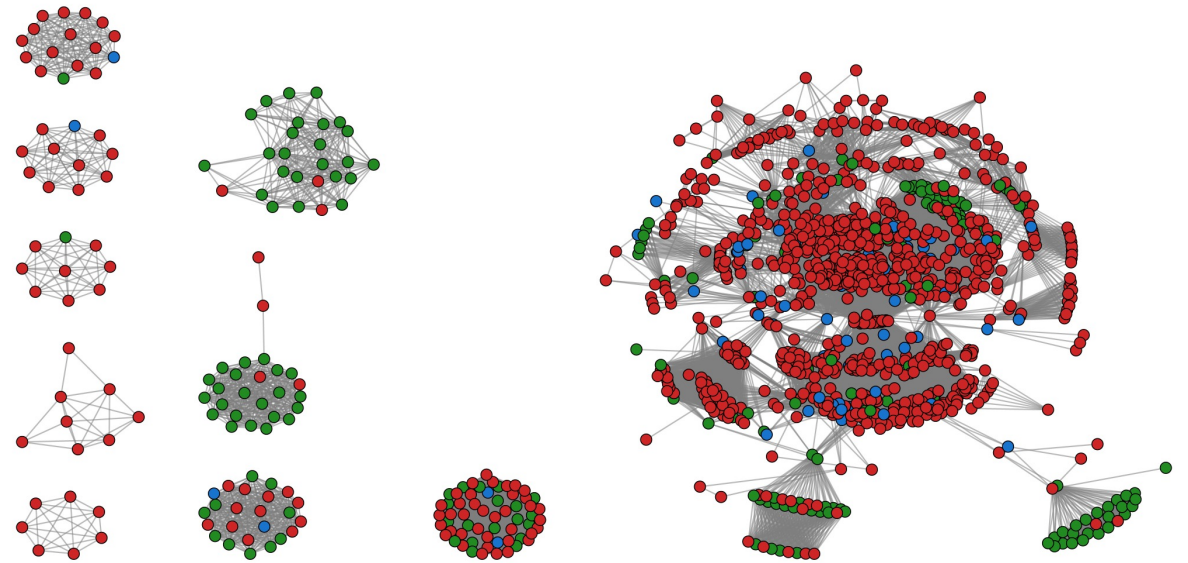
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- Cluster plasmids to track movement of AMR/virulence genes



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Genome-wide association studies (GWAS)

- Test for associations between genetic variants and traits of interest (e.g. niche, AMR, virulence)

Considerations when interpreting genomic surveillance data



- **Context matters:** When, where, and how samples are collected affects interpretation
- **Genomes alone can't prove transmission:** Must be paired with epidemiological data
- **Directionality cannot be inferred:** Identical strains may reflect unsampled hosts or a common source
- **Beware of bias and limits:** Incomplete or uneven sampling and genomic resolution can obscure the true picture

In summary

List of learning points in this session:

- One Health studies show that clinically relevant *K. pneumoniae* mostly transmits in healthcare settings; but even rare spillover events can have major public health impacts
- AMR *K. pneumoniae* is a One Health challenge: tackling it requires cross-sector surveillance, responsible antibiotic use, and coordinated policy
- Genomic tools are powerful, but must be paired with epidemiological context to understand transmission

References



- Calland et al, 2023. PMID: 37858320
- Crippa et al, 2023. PMID: 37414963
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