

Genomic surveillance of infectious diseases

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Multi-country chocolate outbreak in Europe

- Sicken >450 patients in 17 countries in 2022
 - Recall of ~3,000 tonnes of chocolate worldwide → >60 million USD cost
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- Caused by *Salmonella* enterica Typhimurium ST34

Difficulty in strain differentiation



The classical approach

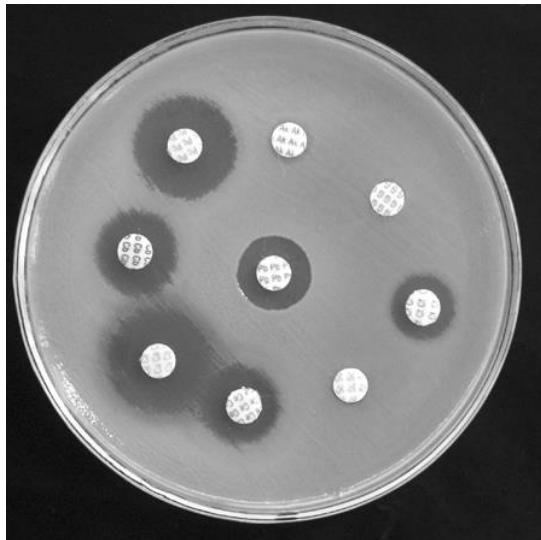
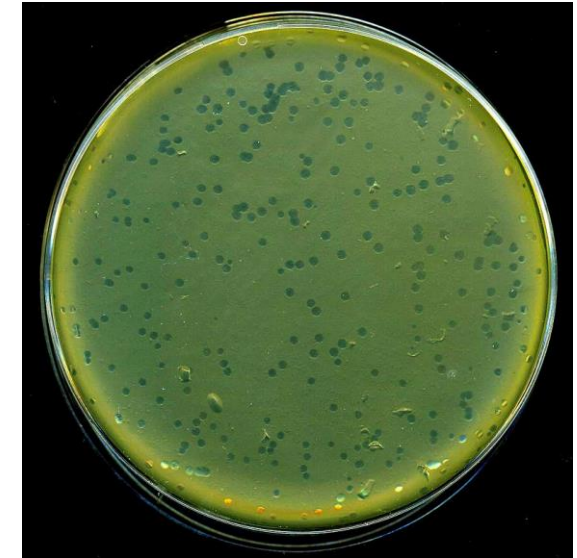
Relatedness based on:

Biochemical

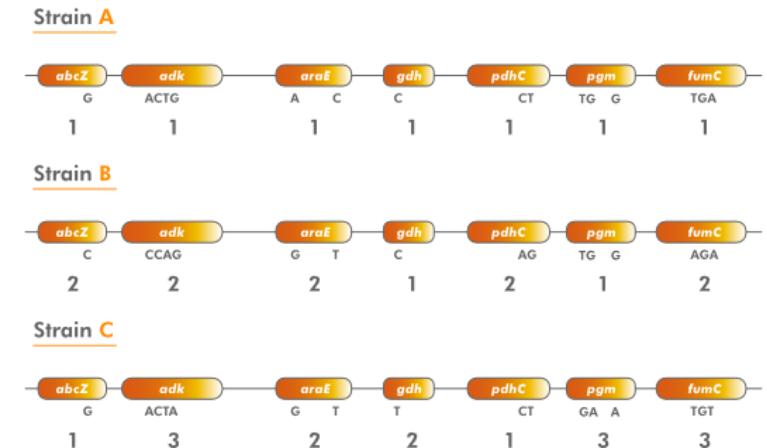
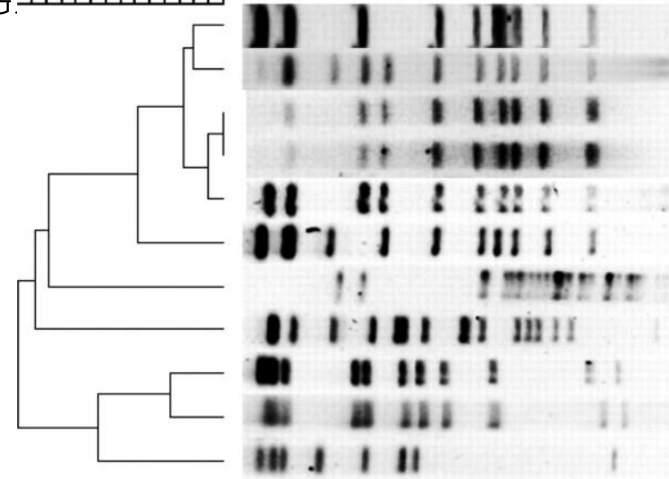
- Serotyping, phage typing
- Antibigram

Genetic

- Multilocus sequence typing (MLST)
- Pulse field gel electrophoresis (PFGE)



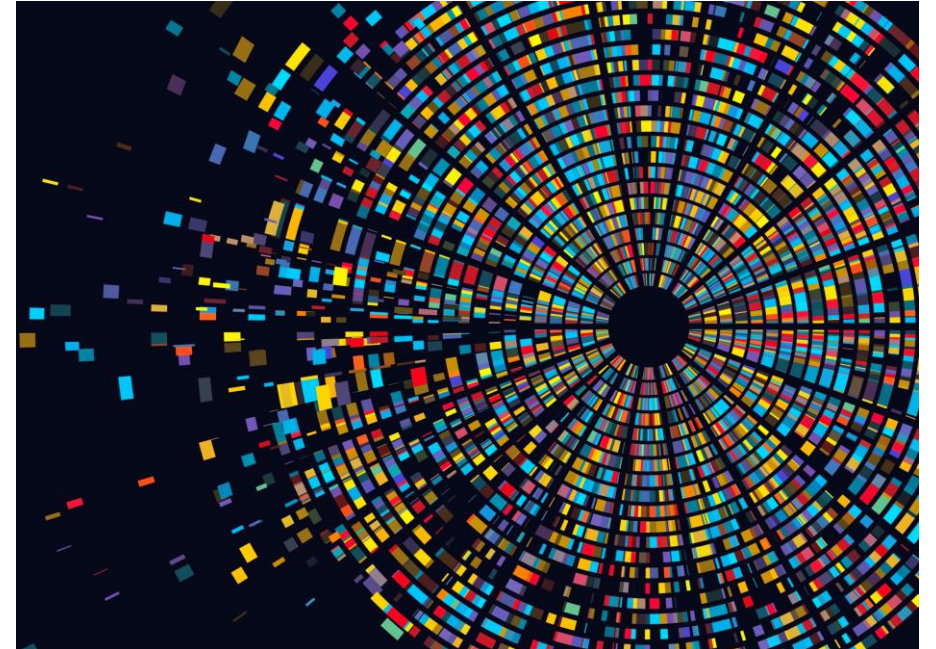
PFGE Not I
Dice Correlation



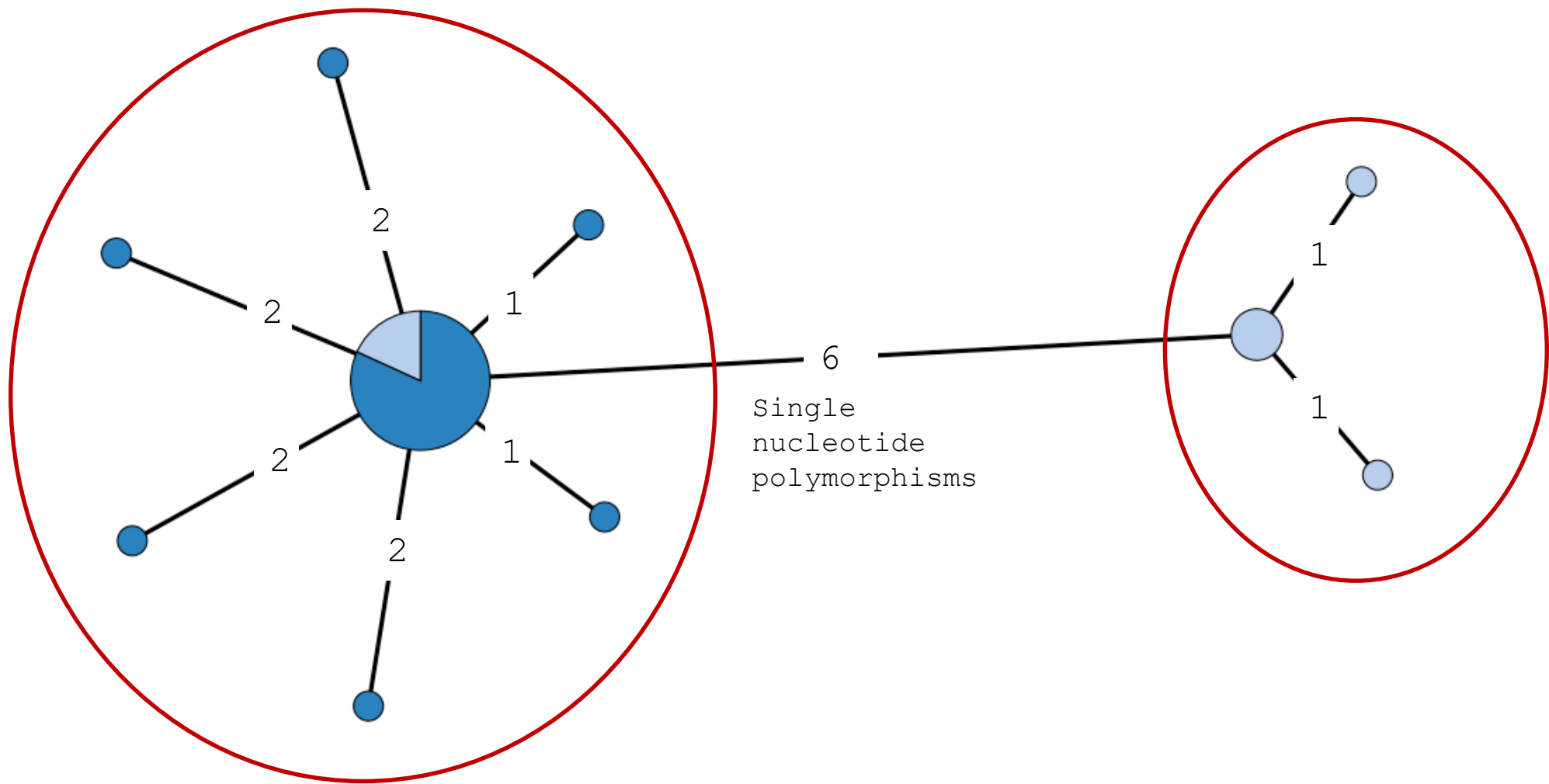
Do not offer high-resolution discriminatory power

Why genomic data?

- Highest discriminatory power
- Reflect evolutionary relationship and processes
- Include both phenotypic and non-phenotypic features
- More cost effective
- Established analysis framework



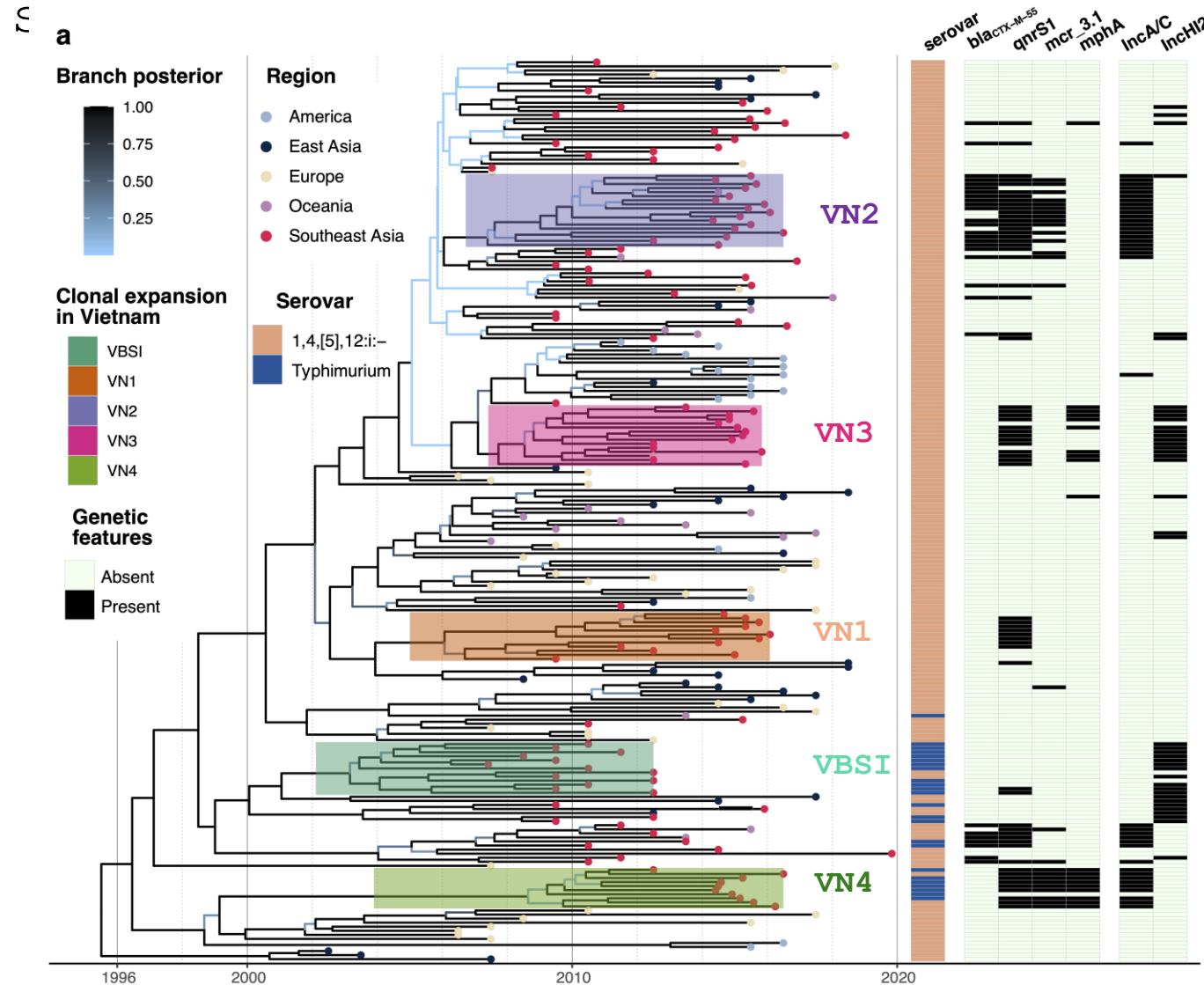
Salmonella outbreak investigation



- Human cases
- Non-human isolates (Belgian plant B)

Salmonella genomic surveillance

Salmonella ST34 is among the most common bacterial pathogens for mucoid/bloody diarrhea in children in HCMC (2014 – 2016),

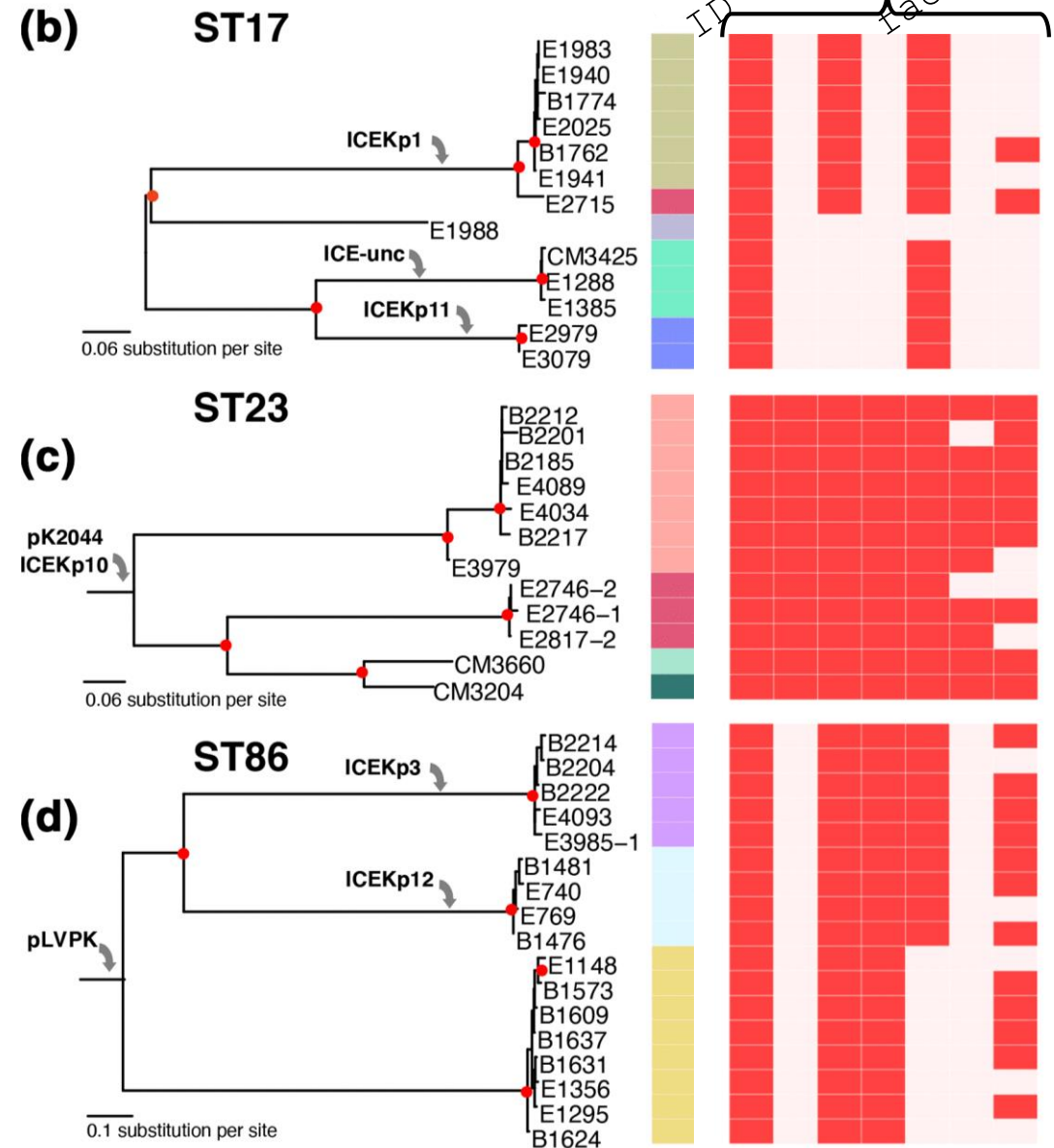
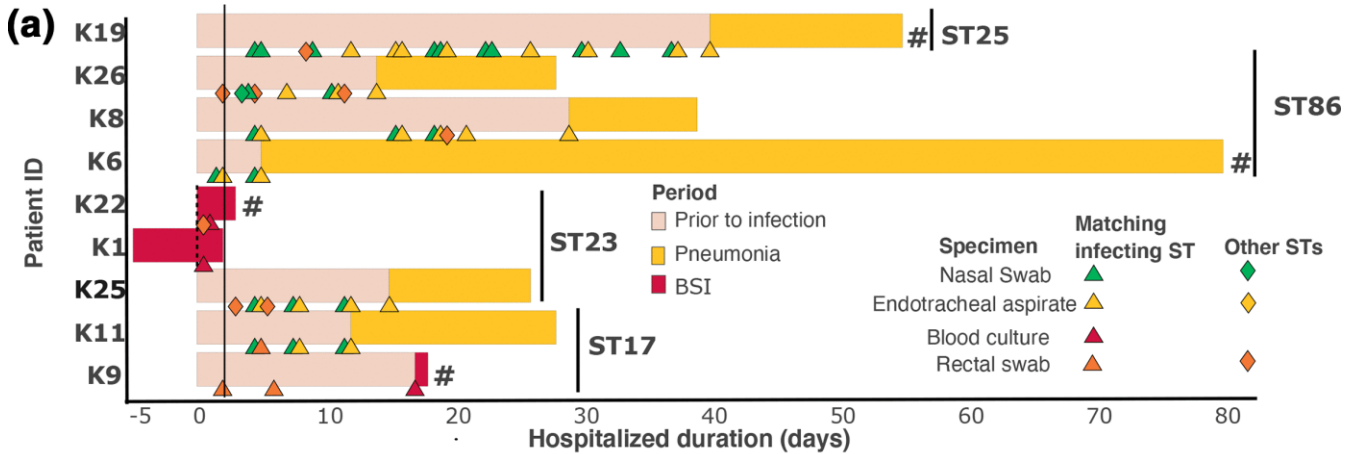


- ST34 introduced into Vietnam in at least 5 major times during 2003 – 2009

- SEA isolates carry more clinically important AMR genes (*bla*_{CTX-M-55}, *qnrS1*, *mcr3.1*, *mphA*), instigating global disseminations of MDR ST34

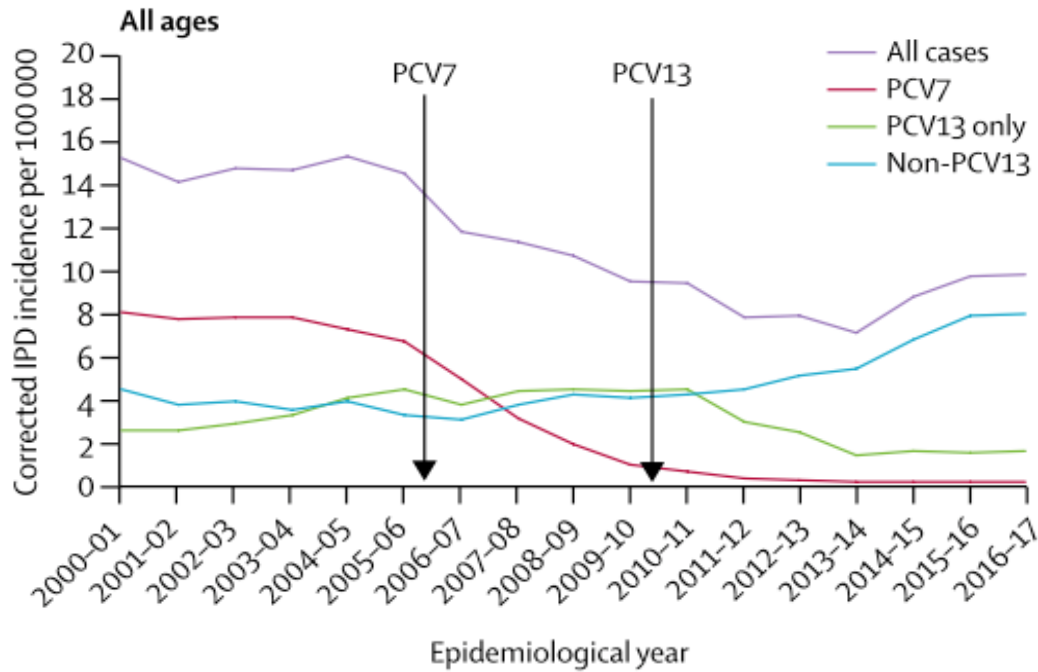
Hao Chung The et al., *Comms Biol*, 2023

Nosocomial *Klebsiella* genomics



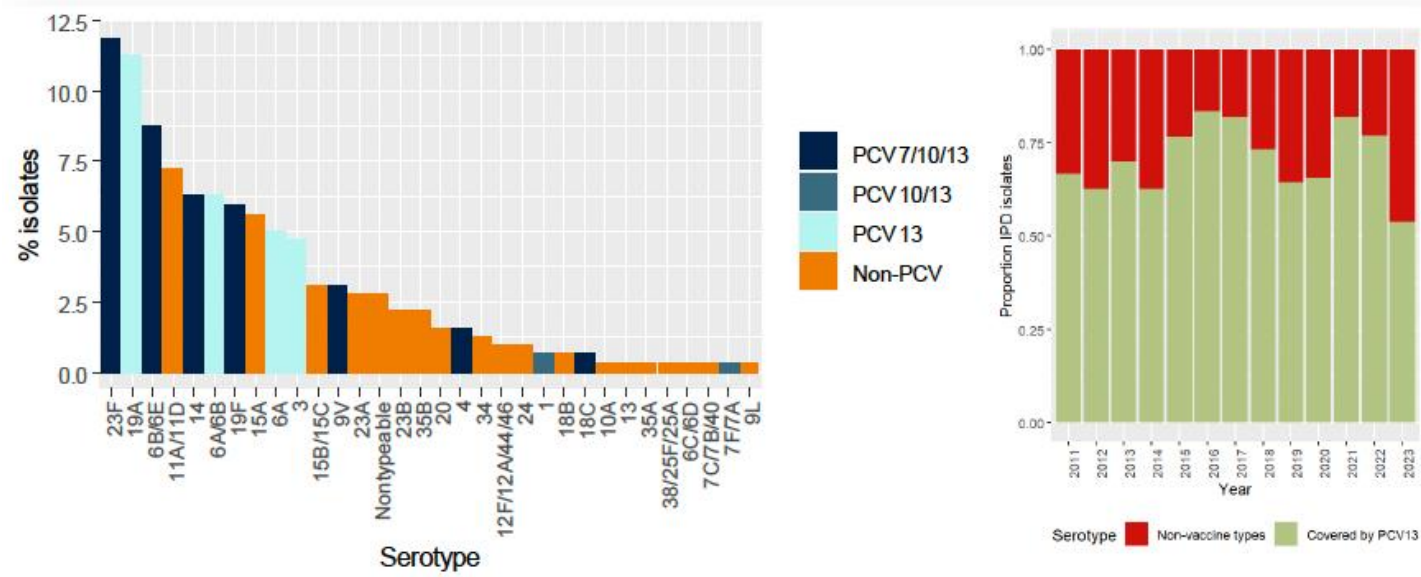
- Patients were colonized by distinct and mostly unrelated clones of *K. pneumoniae*
- Colonization leads to infections, even for hospitalized patients (**hypervirulent *K. pneumoniae***)

Genomic epidemiology to inform vaccine strategy



Trend of invasive pneumococcal disease in England and Wales

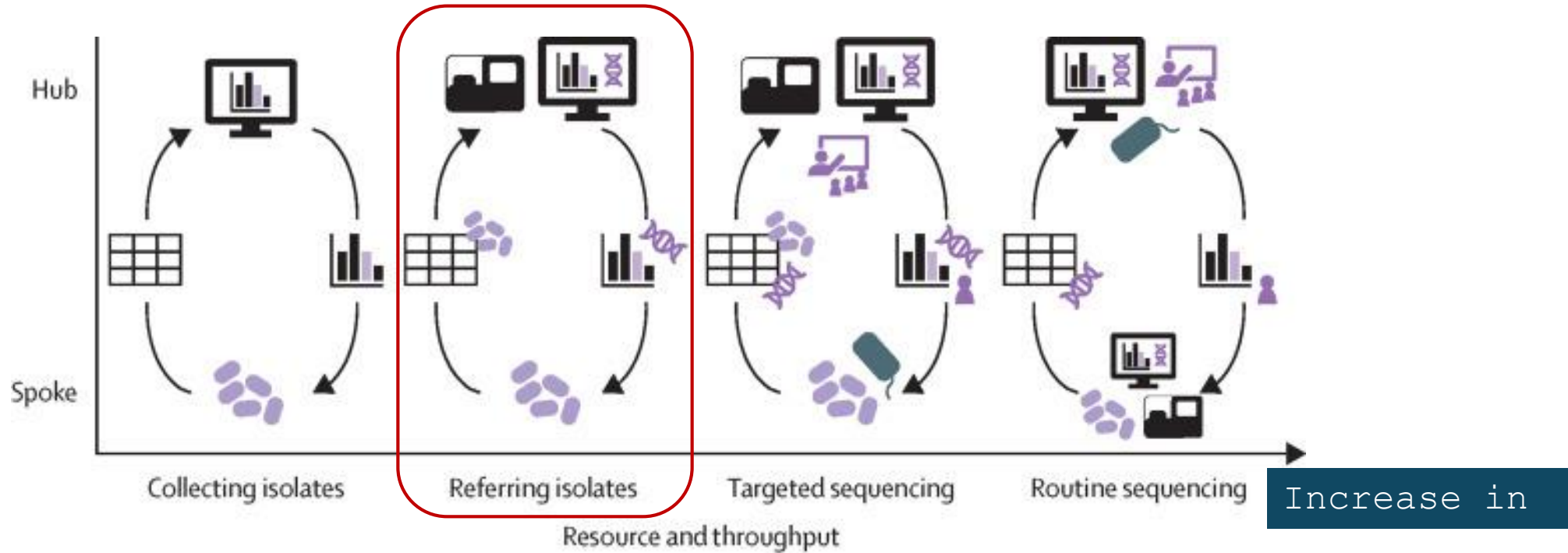
Ladhani et al., Lancet ID, 2018



Invasive pneumococcal disease from 10 hospitals in Vietnam 2011 - 2023 (n=288)

Nguyen Thi Tam et al., unpublished, 2024

Perspectives



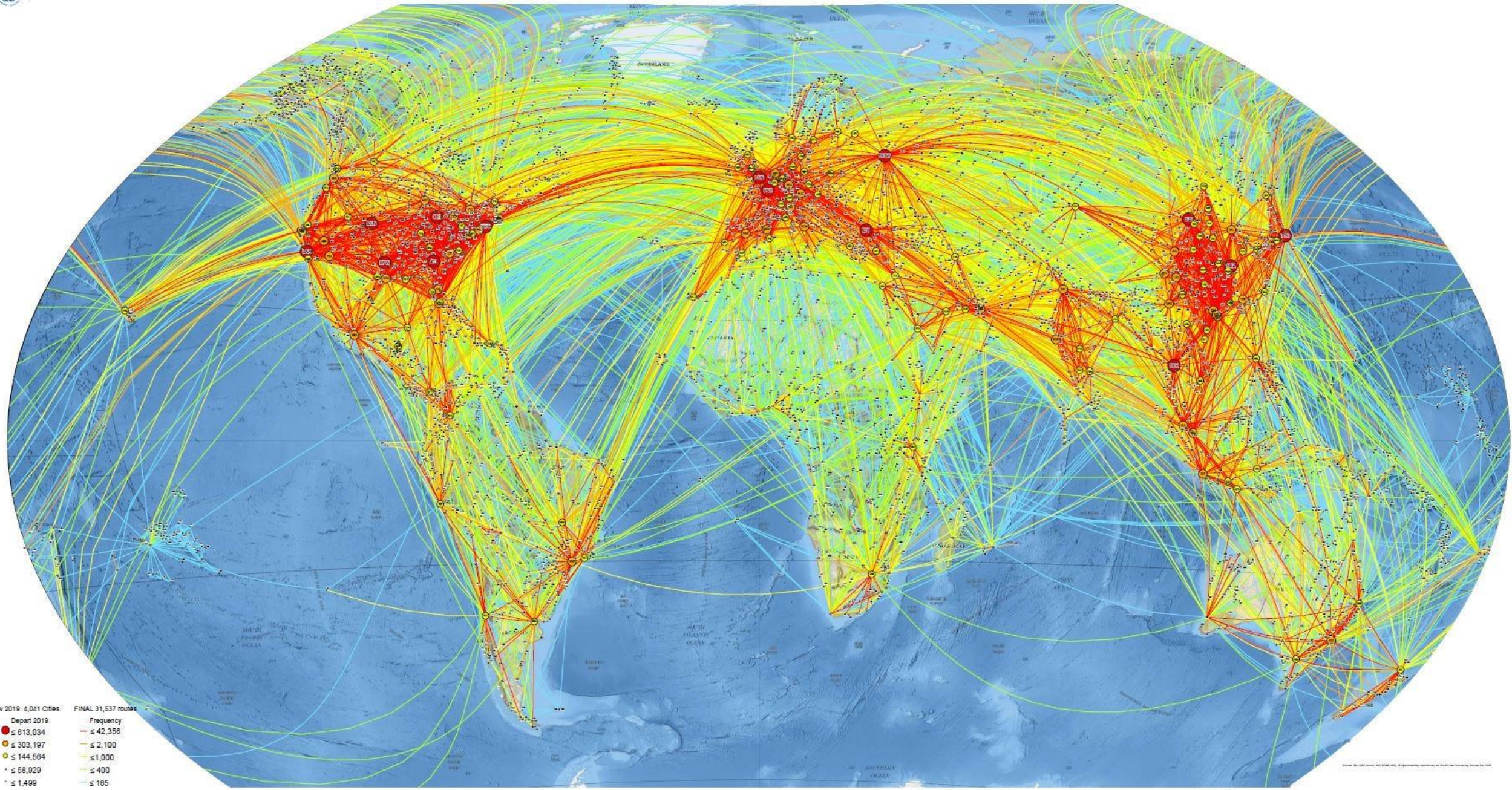
- Carbapenem-resistant Gram-negative?
- MDR Mycobacterium tuberculosis?
- Candida auris?

Isolates
 Epidemiological data
 Epidemiological analysis
 Genomic epidemiological analysis
 Data in context
 Sequence data
 Sequencer (HTP)
 Sequencer (LTP)
 Training
 Genomics trainees

Genomic surveillance is transforming public health action by providing a deeper understanding of pathogens, their evolution and circulation.

- High burden of infectious diseases and AMR
- Applicable to fungi, bacteria and viruses
- Decreasing sequencing cost with multiple platforms
- Streamlined analysis pipeline and trained workforce

- Cost of sequencing remains high per sample
- Unreliable supply chain
- Shortage of skilled analysts



Acknowledgement



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Prof. Stephen Baker



Working in partnership with

