

First Report of a Cluster of Extended-Spectrum Beta-Lactamase Producing *Klebsiella pneumoniae* Sequence Type 101 Isolated from Food and Humans

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INTRODUCTION

Healthcare settings are meant to be the most important reservoir for ongoing transmission of multidrug resistant *Klebsiella pneumoniae* with only few reports pointing to the food chain as another potential source.

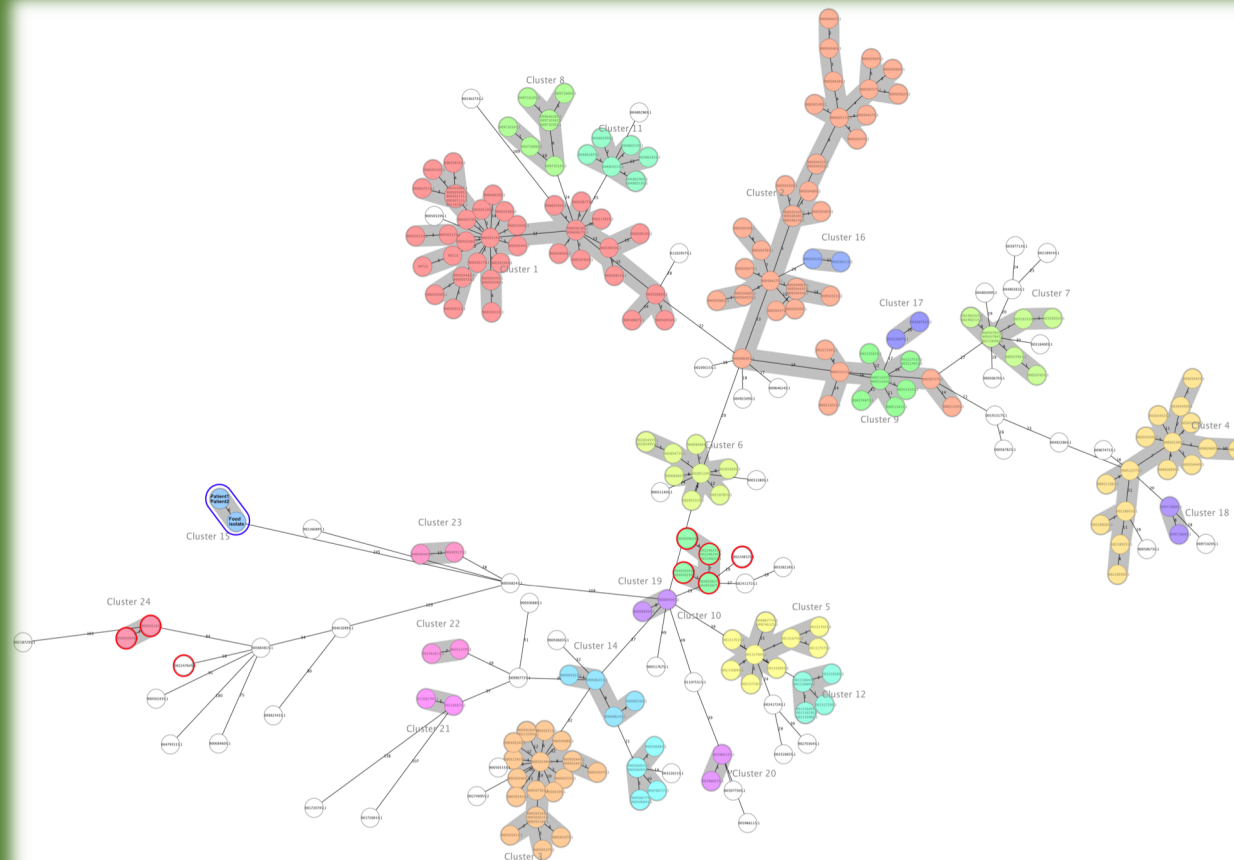
Highlight: We report the first cluster of ESBL producing *K. pneumoniae* isolates from ST101 deriving from one poultry and two clinical samples collected within the setting of a prospective study designed to determine the diversity and migration of ESBL-producing Enterobacterales (ESBL-PE) between humans and their environment.

METHODS

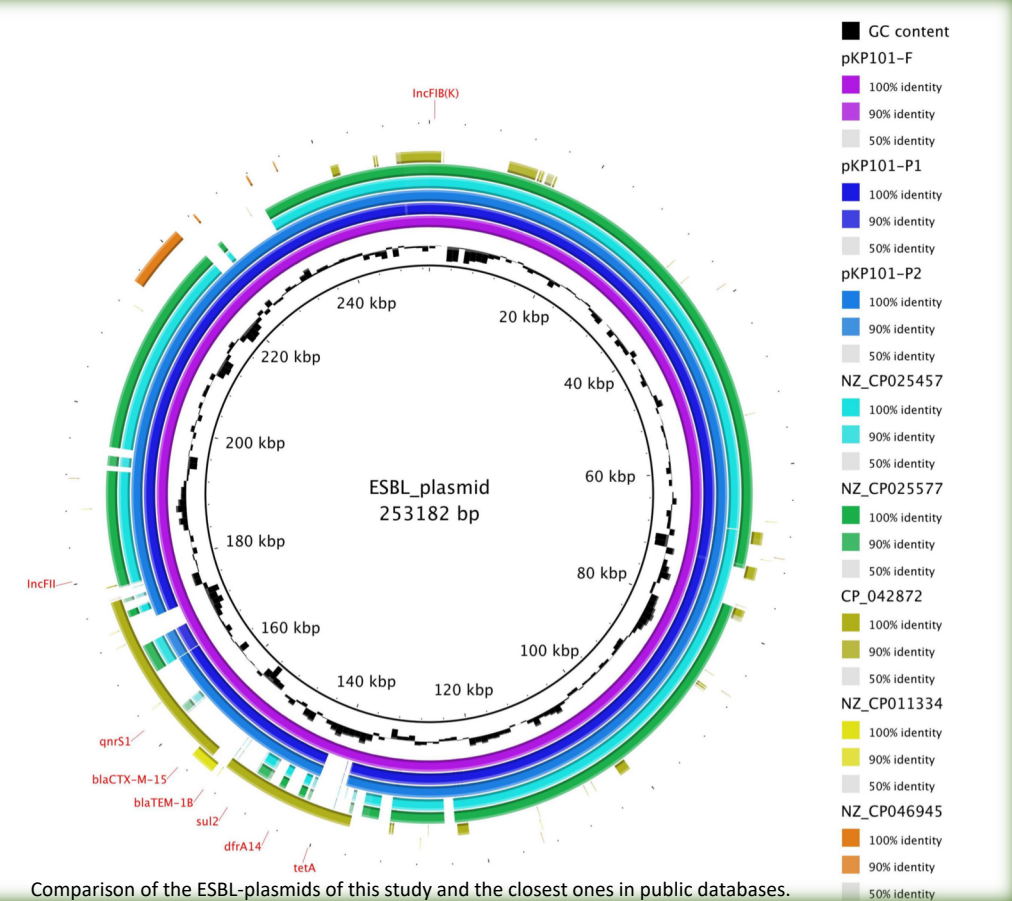
- This finding is part of a bigger study performed in the city of Basel, Switzerland, from June 2017 until May 2018.
- ESBL-PE were systematically collected from routine clinical practice, and monthly from wastewater and foodstuffs throughout the city.
- Illumina Next Seq and GridION sequencing.
- Core genome MLST-genotyping was applied to assess genetic relatedness. A cluster was defined as less than 15 allelic differences in the 2358 genes analysed.
- Resistance genes and replicons were identified in the three genomes.

RESULTS

- Mixed cluster of 3 isolates: 2 clinical (rectal swabs, July 2017) and 1 food (chicken from a supermarket in Switzerland, June 2017).
- Both patients were in Thailand together.
- To our knowledge, this is the first report of ESBL-*K. pneumoniae* ST101 in food.
- 6 allelic differences and 13 SNPs between the clinical and the food isolate. No SNPs and allelic differences between the clinical isolates.
- Chromosome of about 5.1Mb, an ESBL plasmid of 241 kb – 253 kb, and two small plasmids of 3kb and 4kb in all three isolates. ESBL-plasmids: pKP101-F in the food isolates and pKP101-P1 and pKP101-P2 in the clinical isolates.
- Shared resistant genes: *blaCTX-M-15*, *blaTEM-1B*, *sul2*, *dfrA14*, *qnrS1*, *oqxA* and *oqxB*, *fosA*, *aph(3'')-Ib*, *aph(6)-Id*, *blaSHV-28*-like gene. In addition, they also shared some metal binding and transport genes.



Minimum spanning tree of all *K. pneumoniae* ST101 isolates reported so far worldwide. Blue: mixed cluster; red: isolates from Thailand.



Comparison of the ESBL-plasmids of this study and the closest ones in public databases.

- The mixed cluster is genetically very distinct from all other ST101 isolates, suggesting they are part of a **local transmission cluster**.
- **Foodstuffs** may be an important neglected source for transmission of important outbreak clones to humans.