Unraveling Sources and Transmission Pathways of Extended-Spectrum Beta-Lactamase Producing Enterobacterales - a One-Health Approach

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INTRODUCTION

The burden of extended-spectrum beta-lactamase producing Enterobacterales (ESBL-PE) is steadily increasing worldwide. Nevertheless, knowledge on sources, transmission pathways and contribution of horizontal gene transfer to the rapid dissemination of ESBL-PE remains elusive.

Goal: To determine diversity and migration of ESBL-PE between humans and their environment, following a "one-health"-approach.

METHODS

- This study was 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 sequencing and further core genome MLST-genotyping was applied to assess genetic relatedness.
- Plasmids, replicons and antimicrobial resistant genes were predicted.

RESULTS

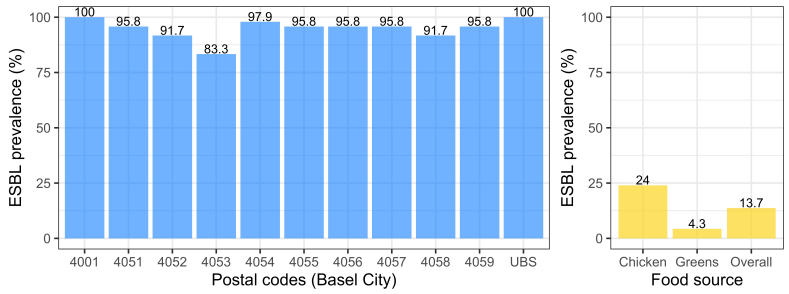
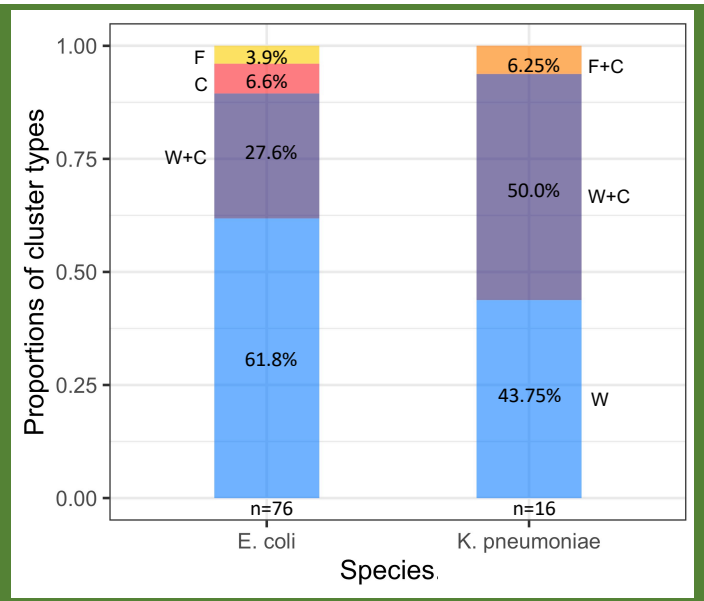


Fig. 1. Prevalence of ESBL-PE in wastewater and foodstuff. UBS – University Hospital Basel.

- Total of ESBL-PE isolates: 1079 (580 clinical, 449 from wastewater and 50 from foodstuffs).
- Most prevalent ESBL-PE: *Escherichia coli* (890 isolates, 82.5%) and *Klebsiella pneumoniae* (150 isolates, 13.9%).
- Additional ESBL-PE : *Enterobacter* sp. (13), other *Klebsiella* (11), *Citrobacter* sp. (6), *Raoultella ornithinolytica* (4), *Proteus mirabilis* (1), *Serratia fonticola (1).*



Cluster types: F-food; C-clinical, W-wastewater. Mixed clusters: W+C, F+C

- Very high **prevalence** of **ESBL-PE** in **wastewater** samples (median of **95.8%**, range 83.3 – 100) while only **13.7%** in **food** samples.
- ESBL-PE isolates from humans and their environment were **highly diverse** suggesting they originated from **genetically distinct sources**.
- **Transmission** between **foodstuffs and clinical isolates** was **rare**.

RESULTS (cont.)

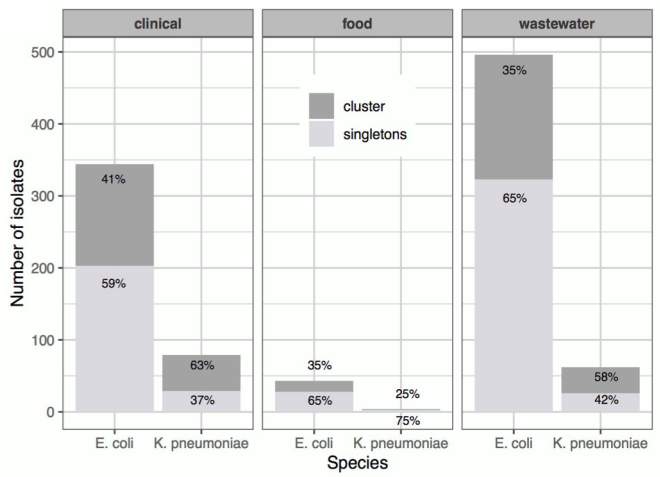


Fig. 2. Sample size stratified by compartments and bacterial species. Isolates belonging to clusters are highlighted in dark grey.

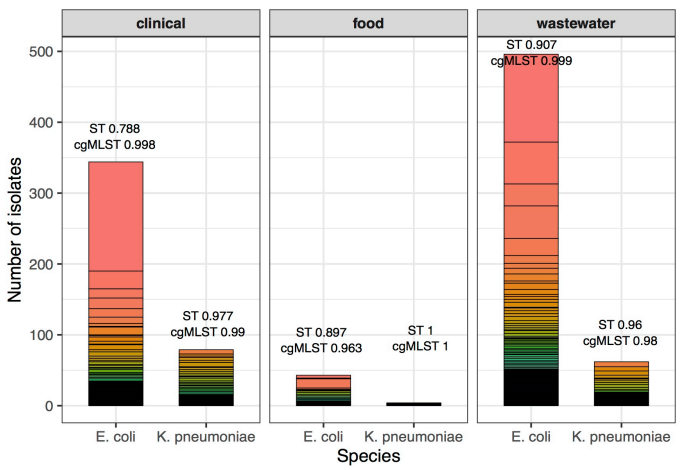


Fig. 3. Distribution of sequence types (ST) across all compartments and species. Simpson's diversity indexes are shown for ST and cgMLST classifications..

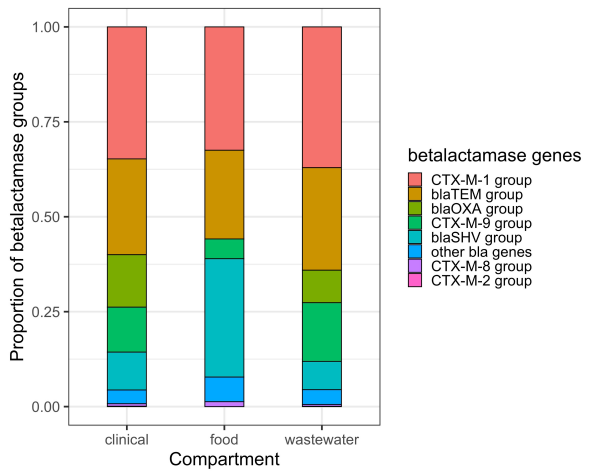


Fig. 4. Distribution of beta-lactamases encoding genes.

Table. Most abundant ESBL genes per compartment.

Compartment	ESBL gene
Clinical and wastewater	*blaCTX-M-15* and *blaCTX-M-14*
Foodstuffs	*blaCTX-M-1* and *blaSHV-12*

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