Neuartige Einsichten in die Phylogenetik von ESBL-\textit{E. coli} im One Health Kontext

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Do we need a virulence gene scoring system for ESBL *E. coli* isolates?

- Multidrug resistant Gram-negative bacteria with disease potential

- **600,000** Nosocomial infections
  - **15,000** Fatal cases

- Colonization
- Clinical relevant infection

- Scoring system
Study protocol based on the One Health approach

101 *E. coli* producing Extended spectrum β-lactamases (ESBLs)

- **Human** (n = 52)
- **Animal** (n = 49)

Phylootyping
Sequence typing
Virulence genes
Resistance genes

Subset of 40 isolates (randomly chosen)

Larvicidal activity in the greater wax moth (*Galleria mellonella*)

Kaplan-Maier Cox regression
Multinominal logistic regression

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<tr>
<th>Toxins</th>
<th>Number of Operons</th>
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</table>
Classical *E. coli* phylotyping

- **A**
  - Associated with commensal phenotype

- **B1**
  - Associated with disease phenotype

- **B2**
  - Associated with disease phenotype

- **D**
  - Subclassification
    - Multi locus sequence typing (MLST)
Concatenated Multi locus sequence typing (ConMLST)

Turrientes et al. (2014)

Schmiedel et al. Manuscript in preparation
Recombination blurs *E. coli* phylogenetic groups

Concatenated Multi locus sequence typing (ConMLST)

**ConMLST PG C**

- Usually classified as PG A/B1

Sequence type (ST) 162
ConMLST phylogenetic group (conMLST PG) B1

Schmiedel *et al.* Manuscript in preparation
Larvicidal activity of *E. coli* ConMLST Phylogenetic groups in *G. mellonella*

- Each ConMLST phylogenetic group shows a different larvicidal effect
- Most larvicidal: ConMLST PG C (HR = 2.24, p < 0.001)

Schmiedel *et al.* Manuscript in preparation
Factors associated with larvicidal activity in *G. mellonella* (Cox regression)

- **iss** (HR = 2.52, p < 0.001)
- **ompT** (HR = 2.29, p < 0.001)
- **Aerobactin** (HR = 1.89, p < 0.001)

- **usp** (HR = -8.84, p < 0.001)
- **sitA** (HR = -3.18, p < 0.001)
- **kpsMT II** (HR = -2.79, p < 0.001)

Enabling serum resistance and iron acquisition

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Growth in human serum

**ConMLST PGs**

- A
- B1
- B2
- C
- D

**Optical density at 600 nm**

Log2 (time + 1) – 20 hours

**Clonal clusters**

- Other clusters
- 10
- 131
- 23

**Optical density at 600 nm**

Log2 (time + 1) – 20 hours

- Best growth in human serum: ConMLST PG C / CC 23

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Definition of a novel disease associated *E. coli* subgroup (ConMLST PG C) with properties that enable survival in the bloodstream.

Our results are supported by evidence from the literature (outbreaks with ConMLST PG C strains).

Testing and further development of the model, specifically for strains with higher risk for patients (blood culture isolates).
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