

Genomic analysis of avian pathogenic *Escherichia coli*: transmission of antibiotic resistance via food chain

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Background and aims



The significance of avian pathogenic *E. coli* (APEC) in the context to increasing AMR



Genetic similarities between APEC strains from poultry and humans



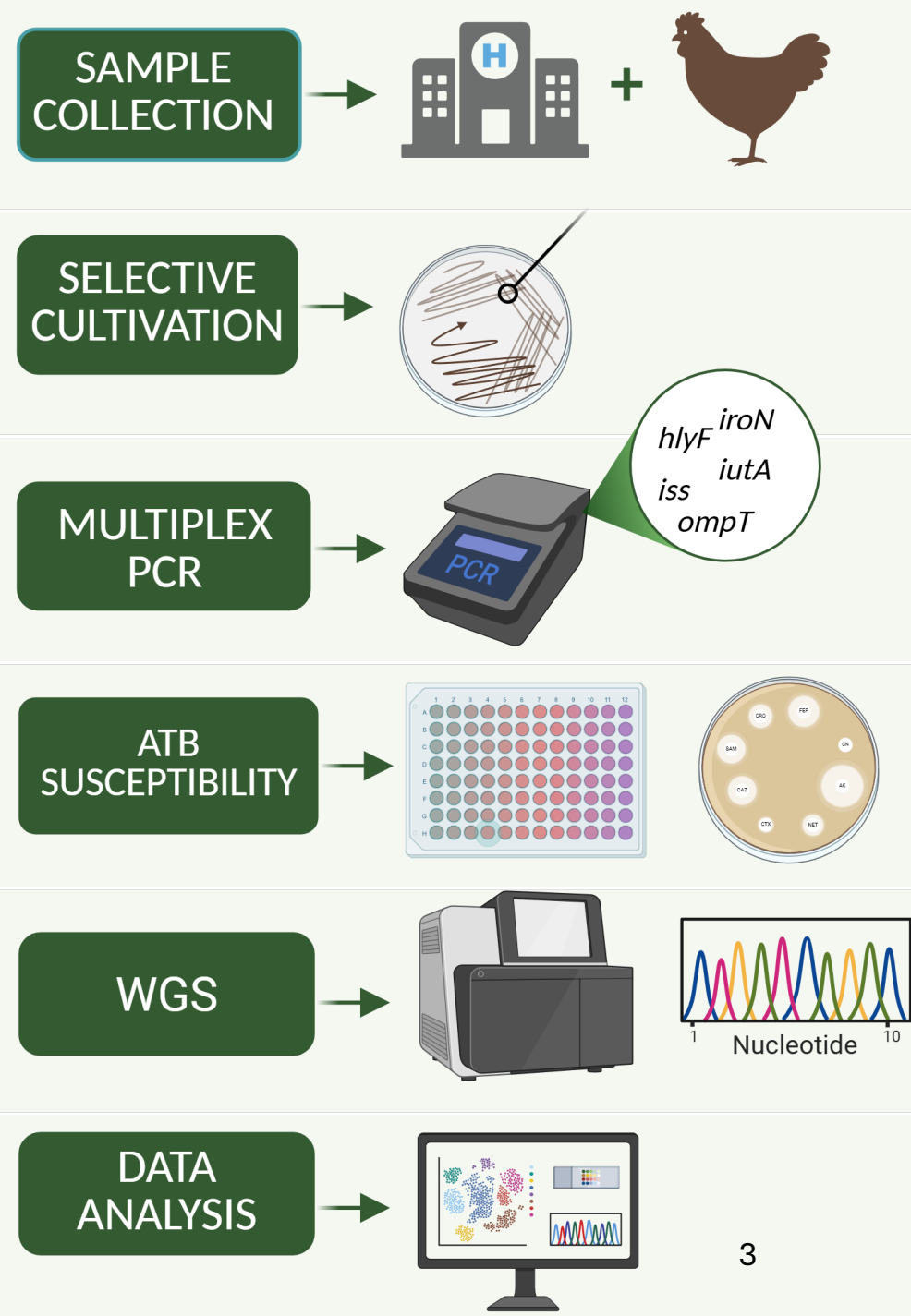
The omnipresence of APEC in humans, animals, and the environment as a challenge for the One Health concept



The aim of the study is to investigate the molecular epidemiology of APEC strains from humans and poultry and to determine which specific features they share

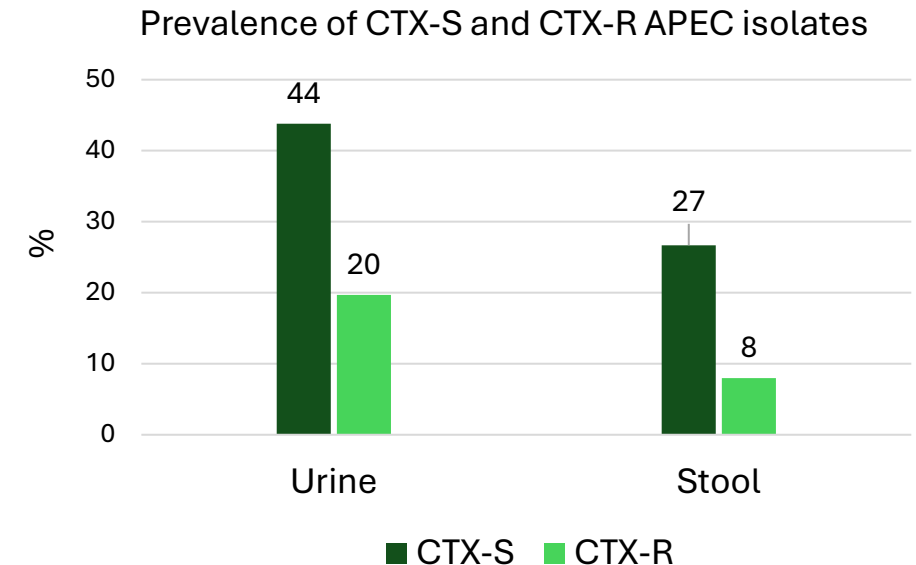
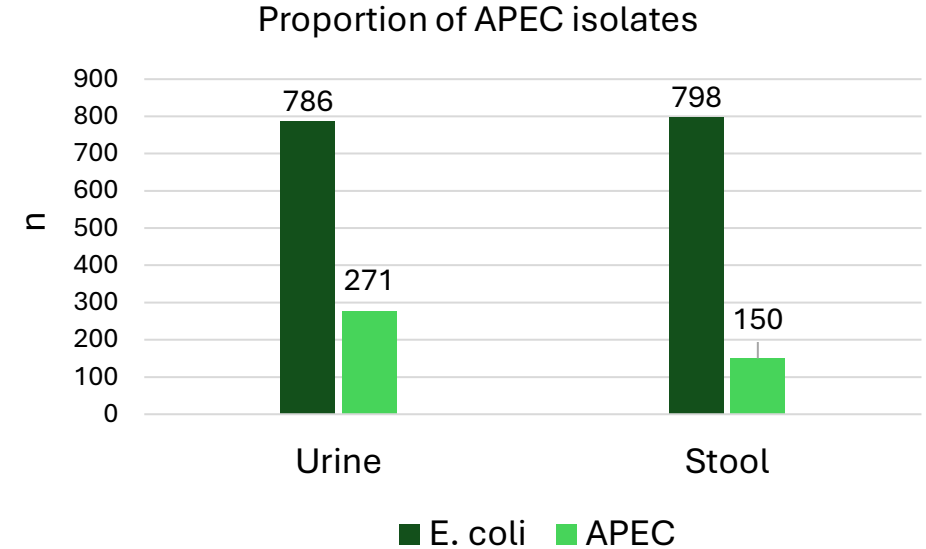
Methods

- **Human isolates** from community-acquired and hospitalized patients (urine and stool)
- **Veterinary isolates** from fresh chicken meat, appendix and cuffs of broilers, feces and swabs from domestic chickens
- Selective cultivation on plates without antibiotics and in parallel with cefotaxime (2 mg/l) to detect **cefotaxime-susceptible** (CTX-S) and **cefotaxime-resistant** (CTX-R) isolates
- Selection of APEC strains by **multiplex PCR** targeting five genes associated with this pathotype
- **Antibiotic susceptibility testing** using microdilution and disc diffusion tests
- **Whole-genome sequencing** on the Illumina platform



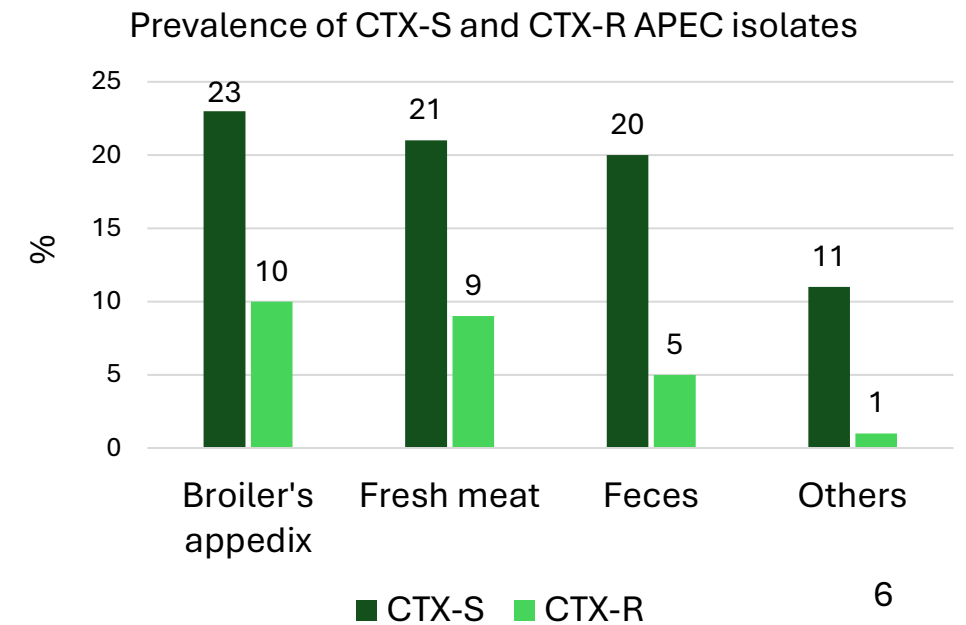
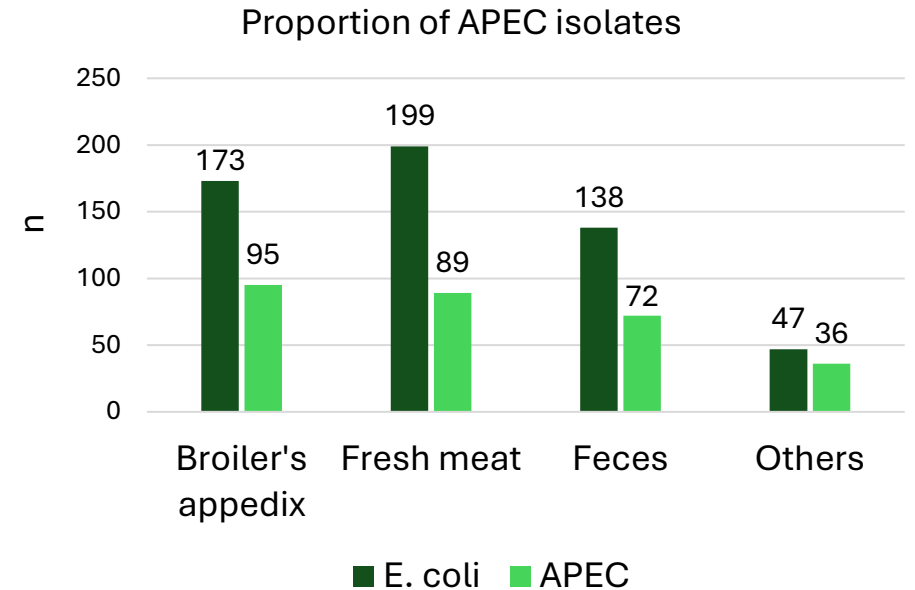
Results – human sample set

- In total, we collected **1584 isolates** from urine (n=786) and stool (n=798)
- We detected **427 APEC isolates** (27%)
- The majority (n=271) of them were from urine and were susceptible to cefotaxime (n=301)
- A representative set (n=335) of APEC isolates was sequenced
- A total of **235 genomes** were analyzed



Results – poultry sample set

- Out of **557 poultry** isolates, we identified total of **292 APEC isolates** (52%)
- Most APEC isolates were from **broiler's appendix** (n=95) and **fresh chicken meat** (n=89)
- Susceptibility to cefotaxime was observed in the majority of isolates
- A representative set (n=268) of APEC isolates was sequenced
- A total of **230 genomes** were analyzed



Sequencing data analysis

FoodQC pipeline

Trimming, QC, and assembly (SPAdes)

KmerFinder

Species identification

CSI Phylogeny + FastTree

Phylogenetic tree

MLST

Sequence types

ResFinder

Antibiotic resistance genes

Phylogenetic tree of human APEC isolates based on SNP analysis

Tree scale: 0.1

Susceptibility

- CTX-S
- CTX-R

Sample type

- Urine
- Stool

Origin type

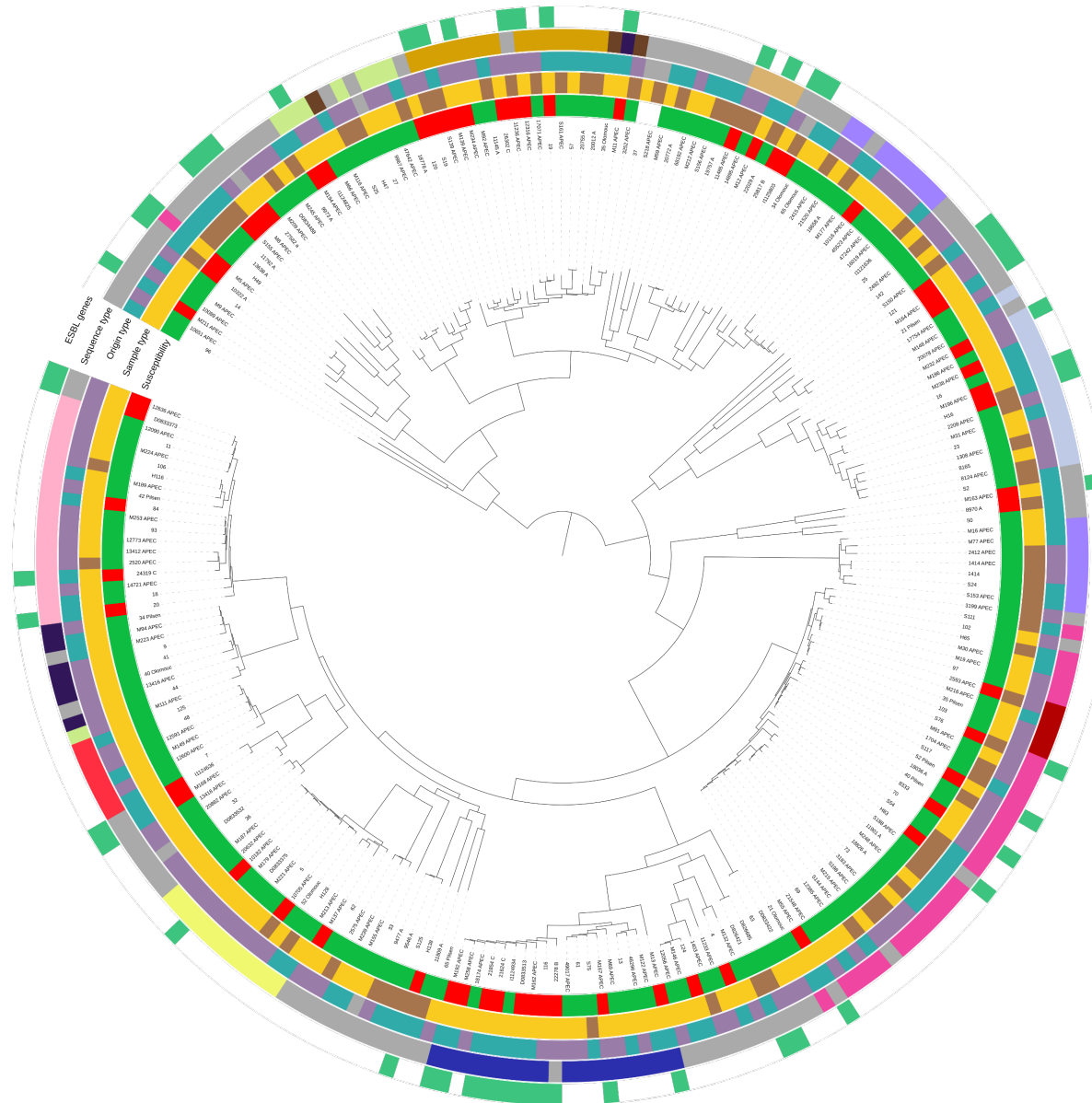
- Community
- Hospital
- Not provided

ESBL genes

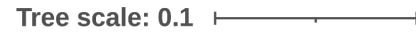
- ESBL+

Sequence type

- ST95
- ST73
- ST131
- ST69
- ST58
- ST141
- ST162
- ST88
- ST12
- ST117
- ST390
- ST80
- ST155
- ST101
- Other



Phylogenetic tree of poultry APEC isolates based on SNP analysis



Susceptibility

 CTX-S

CTX-R

Sample type

Broiler's appendix

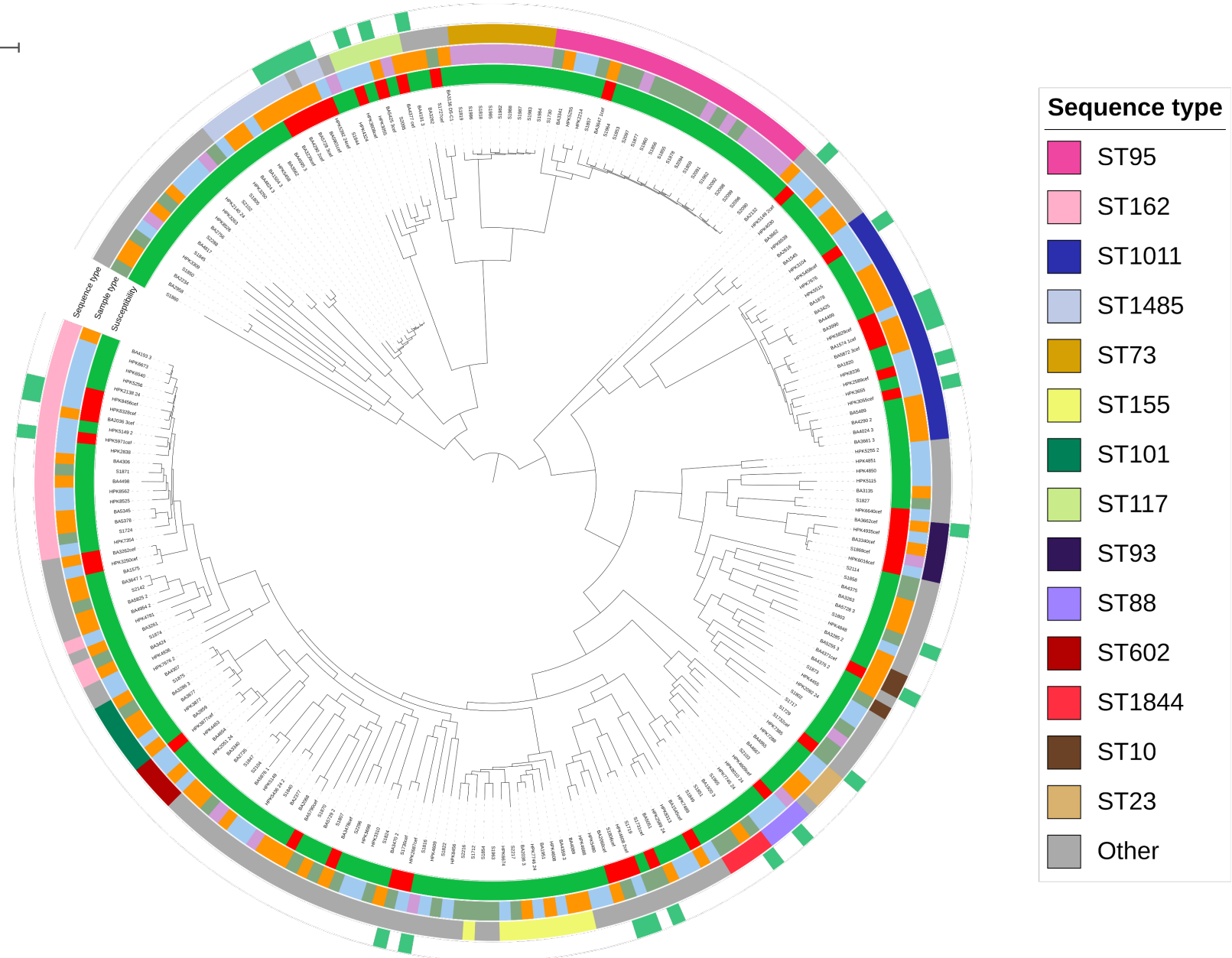
☐ Fresh chicken meat

 Feces

 Cuffs

ESBL genes

ESBL+



What's Next?

- Create a phylogenetic tree including APEC isolates from human and poultry
- Focus on the most prevalent lineages appearing in both sets (e.g. **ST95, ST73, ST162**)
- Classify isolates into **phylogroups**
- Run **VirulenceFinder**, **PlasmidFinder**, and **pMLST**
- Detect the presence of **ColV plasmids**
- Analysis and visualization of **gene synteny** (e.g. *bla*_{CTX-M-15}) using Flankophile