

FWD AMR-RefLabCap in Estoni

Overview of ECDC Pilot WGS study in Estonia

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Surveillance of Salmonella & Campylobacter in Estonia

- 1
- All positive Salmonella & Campylobacter isolates/samples are sent to NRL
- 2
- Additional serotyping and AST is performed at NRL
- 3
- All isolates are stored long-term at NRL
- 4
- Sequencing is performed asap in case suspected outbreaks

1. Number of isolates

| | 2021 | 2022 | 2023 | 2024 Jan, Feb |
|------------------------|------|------|------|------------------|
| Salmonella isolates | 310 | 255 | 227 | 22 |
| Campylobacter isolates | 370 | 298 | 354 | 41 |

2. Number of isolates

| | 2021 | 2022 | 2023 |
|------------------------|------|------|------|
| Salmonella isolates | 8 | 22 | 100 |
| Campylobacter isolates | 0 | 0 | 50 |

Aim of the pilot study – to get a more sophisticated overview of the strains circulating in Estonia

ECDC SALMONELLA and CAMPYLOBACTER WGS PR

- 100 Salmonella isolates all isolates collected by mid 2
- 50 *Campylobacter* isolates representative selection of strains from mid 2023 (all *C.coli*; region, age, gender)

Laboratory capacity

- Clinical Microbiology (AST, serotyping)
- Molecular methods manual/auto extraction of genomic DNA
- WGS (sequencing temporarily outsourced in-house)





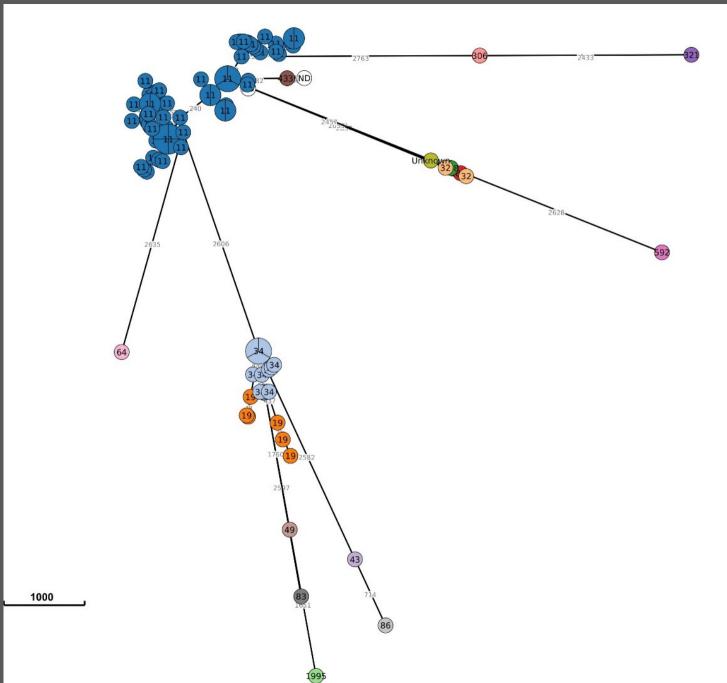


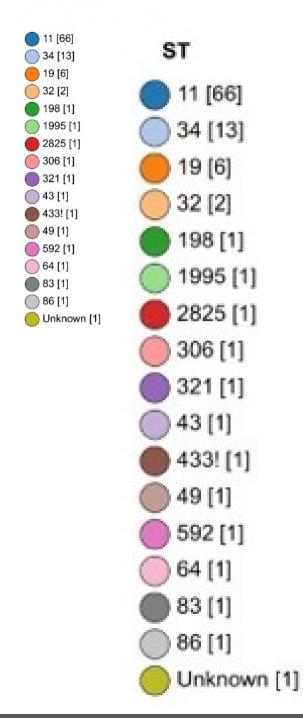


Salmonella WGS RESULTS

| | Name | Specie | s ST | Predict | Predicted | Predicted | Predicted | Gene | Sequence | Flem | Ele | Elem | Class | Subclass | % | % |
|------------|---------------|------------|----------|-----------|-------------|------------|-------------|-------------|-------------|-------|-------|-------|----------|----------|-------|-----------|
| | | Броско | | ed | serotype | | serotype | symbol | name | | men | | Ciass | Juneiuss | Cove | |
| | | | | antigeni | | profile | (Seqsero | | | subty | | subt | | | rage | to |
| | | | | c profile | ' ' | (Seqsero | 2) | | | pe | | ype | | | of | reference |
| | | | | (Seqser | | 2) | _, | | | | ,,,,, | ,,,,, | | | | sequence |
| | | | | o1) | | _, | | | | | | | | | ence | Jequence |
| ↓ ↑ | | ▼ | - | | _ | _ | _ | ~ | _ | _ | _ | _ | _ | _ | se(▼ | ~ |
| | NG-A0362_1735 | 55 Salmone | lla 11 | 9:g,m:- | Enteritidis | 9:g,m:- | Enteritidis | | | | | | | | | |
| | NG-A0362_1736 | | | 4:b:1,2 | Paratyphi B | 4:b:1,2 | | B var. L(+) | tartrate+ | | | | | | | |
| | NG-A0362_1736 | | _ | 9:g,m:- | Enteritidis | 9:g,m:- | Enteritidis | | | | | | | | | |
| | NG-A0362_1737 | | _ | 9:g,m:- | Enteritidis | 9:g,m:- | Enteritidis | | | | | | | | | |
| | NG-A0362_1737 | | | | Enteritidis | 9:g,m:- | Enteritidis | | | | | | | | | |
| 39 | NG-A0362_1738 | 29 Salmone | lla 49 | 4:z10:1,2 | 2 Haifa | 4:z10:1,2 | Haifa | | | | | | | | | |
| 40 | NG-A0362_1738 | 75 Salmone | lla 321 | 3,10:e,h | : Muenster | 3,10:e,h:1 | Muenster | | | | | | | | | |
| 41 | NG-A0362_1739 | Salmone | lla 11 | 9:g,m:- | Enteritidis | 9:g,m:- | Enteritidis | | | | | | | | | |
| 42 | NG-A0362_1740 | 32 Salmone | lla 11 | 9:g,m:- | Enteritidis | 9:g,m:- | Enteritidis | tet(A) | tetracyclir | AMR | AMR | AMR | TETRACYC | TETRACYC | 100 | 99,75 |
| 43 | | | | | | | | blaTEM-13 | broad-spe | AMR | AMR | AMR | BETA-LAC | BETA-LAC | 100 | 100 |
| 44 | | | | | | | | gyrA_D87 | l Salmonell | POINT | AMR | POIN | QUINOLOI | QUINOLO | 100 | 99,89 |
| 64 | NG-A0362_1740 | Salmone | lla 11 | 9:g,m:- | Enteritidis | 9:g,m:- | Enteritidis | | | | | | | | | |
| 65 | NG-A0362_1740 | 70 Salmone | lla 11 | 9:g,m:- | Enteritidis | 9:g,m:- | Enteritidis | | | | | | | | | |
| 66 | NG-A0362_1741 | Salmone | lla 86 | 4:b:1,2 | Paratyphi B | 4:b:1,2 | Paratyphi | В | | | | | | | | |

SALMONELLA WGS RESULTS MSTree





Campylobacter WGS RESULTS

| Name | Species | ST | Gene symbol | Sequence name |
|------------|--|------|---------------|---|
| | Campylobacter jejuni strain CJ071CC464, complete genome | | tet(O) | tetracycline resistance ribosomal protection protein Tet(O) |
| 110 710002 | cumpyiosacter jejam stram esovice to the complete genome | 101 | 50S L22 A103V | |
| | | | gyrA T86I | Campylobacter quinolone resistant GyrA |
| | | | blaOXA-193 | OXA-61 family class D beta-lactamase OXA-193 |
| NG A0262 | Campylobacter jejuni subsp. jejuni strain GB19 chromosome, complete gend | 61 | blaOXA-193 | OXA-61 family class D beta-lactamase OXA-193 |
| | | | | · |
| | Campylobacter jejuni strain CJ515CC45, complete genome | 45 | blaOXA-184 | OXA-184 family class D beta-lactamase OXA-184 |
| NG-A0362 | Campylobacter jejuni strain CJ071CC464, complete genome | 464 | 50S_L22_A103V | Campylobacter macrolide resistant 50S L22 |
| | | | gyrA_T86I | Campylobacter quinolone resistant GyrA |
| | | | blaOXA-193 | OXA-61 family class D beta-lactamase OXA-193 |
| | | | tet(O) | tetracycline resistance ribosomal protection protein Tet(O) |
| NG-A0362 | Campylobacter jejuni subsp. jejuni S3, complete genome | 2133 | blaOXA | OXA-61 family class D beta-lactamase |
| NG-A0362 | Campylobacter jejuni strain CJ071CC464, complete genome | 464 | tet(O) | tetracycline resistance ribosomal protection protein Tet(O) |
| | | | 50S_L22_A103V | Campylobacter macrolide resistant 50S L22 |
| | | | gyrA_T86I | Campylobacter quinolone resistant GyrA |
| | | | blaOXA-193 | OXA-61 family class D beta-lactamase OXA-193 |
| NG-A0362 | Campylobacter jejuni strain CJ071CC464, complete genome | 464 | 50S_L22_A103V | Campylobacter macrolide resistant 50S L22 |
| | | | gyrA_T86I | Campylobacter quinolone resistant GyrA |
| | | | blaOXA-193 | OXA-61 family class D beta-lactamase OXA-193 |
| | | | tet(O) | tetracycline resistance ribosomal protection protein Tet(O) |
| NG-A0362 | Campylobacter jejuni strain CJ071CC464, complete genome | 464 | 50S_L22_A103V | Campylobacter macrolide resistant 50S L22 |

Campylobacter WGS RESULTS MSTree ST **464** [22] 464 [22] 1055 [2] 122 [2] 1055 [2] 42 [2] 213 6461 122 [2] Unknown [2] 10044 [1] 42 [2] 1707 [1] 2066 [1] Unknown [2] 2133 [1] 2254 [1] 10044 [1] 45 [1] 583 [1] 1707 [1] 9741 1035 5-125 627 50 WH 649 61 [1] 6222 [1] 2066 [1] 6461 [1] 825 [1] 2133 [1] 827 [1] 832 [1] 2254 [1] 872 [1] 45 [1] 9741 [1] 9897 [1] 583 [1] 61 [1] 6222 [1] 6461 [1] 2254 825 [1] 827 [1] 832 [1] 500 872 [1] 9741 [1] 9897 [1]

Plans for actions

Cooperation with epidemiologists

Cooperation with vet.lab

Wider analysis on the possible clust

Reporting to EpiPulse



Thanks for listening Any Questions?

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