

# Genomic surveillance of *Salmonella enterica* in Lithuania

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# Genomic surveillance in Lithuania

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Sequencing facility is operational since 2023 March

48 *Salmonella sp.* clinical isolates sequenced so far

Analysis is performed using Ridom Seqsphere+

# Selection of isolates for the first pilot run

Serotype	Total	Fully sensitive	Source	Resistance		Comments
				Resistance ≥1 antimicrobial	Source	
<i>Chartres II</i>	2	0		2		
				W/SXT/TET=2	fecal	
<i>Derby</i>	4	2		2		
				AMP=1	faecal	
				AMP/W/SXT=1	urine	
<i>Enteritidis</i>	25	19		6		
				AMP=1	faecal	
				PEF=CIP=3	faecal	
				PEF=CIP/AMP=2	faecal	
<i>Hvittingfoss</i>	1	1		0		
<i>Infantis</i>	2	1		1		
				AMR/CHL/GN/PEF=CIP=1	faecal	
<i>Nakure</i>	1	0		1		
				PEF=CIP/TET=1	Blood	
<i>Paratyphi C1</i>	1	0		1		
				AMP/PEF=CIP/TET=1	faecal	
<i>Senftenberg</i>	2	1		1		
				PEF=CIP=1	faecal	
<i>Typhimurium</i>	15	4		11		
				AMP=3	faecal	
				TET=1	faecal	
				AMP/TET=3	faecal	
				AMP/TET/GN=1	faecal	
				AMP/TET/W/SXT=1	faecal	
				AMP/TET/W/SXT/CHL=1	faecal	
				AMP/TET/W/SXT/CHL/PEF=CIP=1	faecal	
<i>Typhimurium</i>	5	0		5		
				TET=1	faecal	
				AMP/TET=4	faecal	
<i>Weltevreden</i>	1	1		0		
			<b>Total</b>	<b>24</b>		

- To sequence *S. Typhimurium* and monophasic *Typhimurium* to search for the presumptive clusters;
- To detect AMR genes and to compare them with fenotypic results
- To compare serotyping results and the WGS serotype results

# Quality control

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Follows recommendations described in FWD AMR-RefLabCap WGS Protocol (8 July 2022)

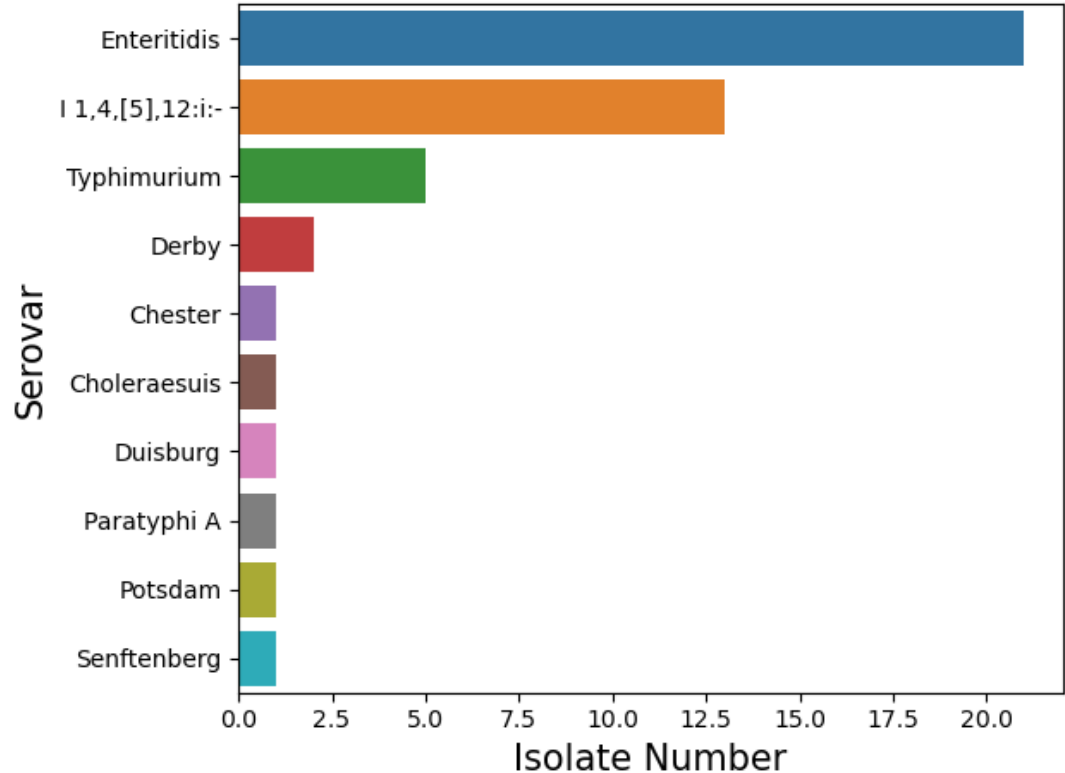
## Quality metric thresholds:

- Mash distance  $\geq 0.95$
- Reads are trimmed for average quality  $\geq 30$  in a 20 base window
- Genome coverage  $\geq 30X$
- Assembled genome size between 4.4 Mb and 5.8 Mb
- N50  $> 30000$  bp
- Less than 500 contigs
- cgMLST scheme coverage  $\geq 95\%$

# Serovar genotyping

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Enteritidis was the most abundant serovar



# Serotypes changes with WGS analyses

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- Chester
- Paratyphi A
- Potsdam
- Duisburg
- Cholerasuis



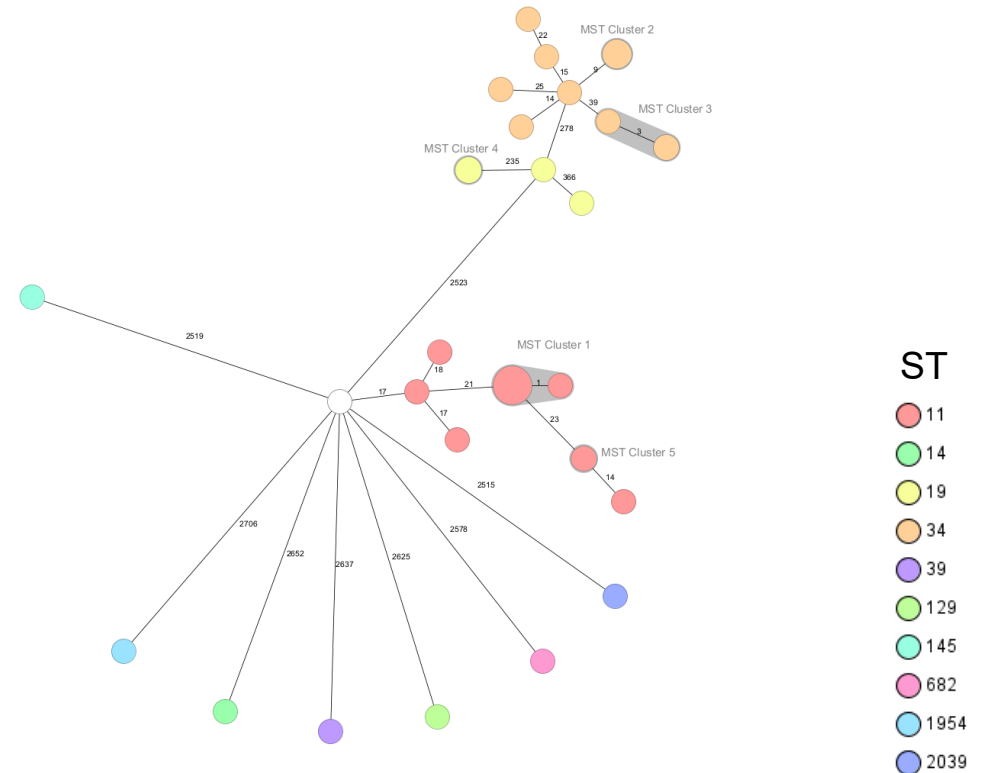
# Cluster analysis

Using *S. enterica* cgMLST v2 scheme  
from Enterobase (3002 loci)

5 AD is used as cluster threshold

5 clusters detected:

1. 14 Enteritidis isolates (ST 11)
2. 4 | 1,4,[5],12:i:- isolates (ST 34)
3. 3 | 1,4,[5],12:i:- isolates (ST 34)
4. 3 Typhimurium isolates (ST 19)
5. 2 Enteritidis isolates (ST 11)

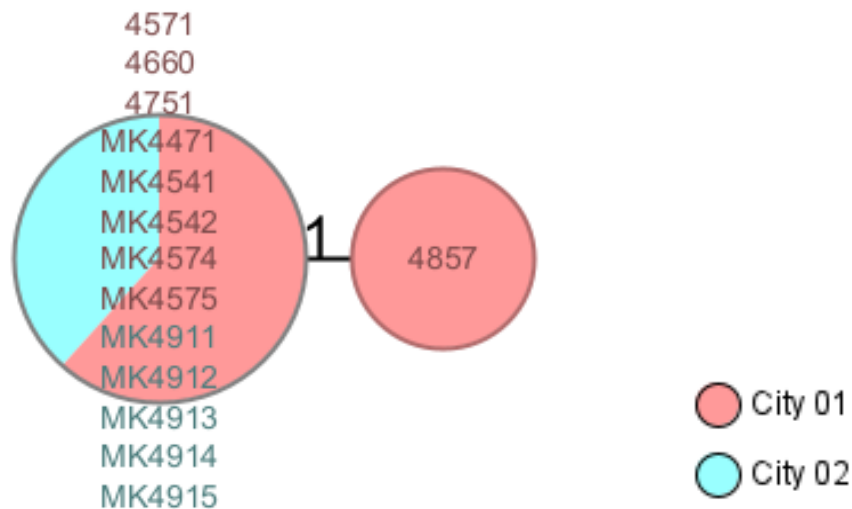




# Outbreak investigation

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WGS helped epidemiologists relate outbreak isolates from two different cities



# ST11 associated with travel to Turkey

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Sequences of Lithuanian ST11 isolates were shared on EpiPulse

4 isolates matched clusters that were related to travel to Turkey

3 of the 4 cases were confirmed to have travelled to Turkey in March 2023

# Ongoing actions

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- 100 *Salmonella* isolates sent to Contracting laboratory;
- Agreement with epidemiologists to sequencing 24 selected *Salmonella* isolates quaterly in 2024;
- To reach Agreement about clusters classification and names;
- Ongoing investigation and interpretation of AMR genes in *Salmonella spp.*

Thank you for your attention!