

# Multi country event of *Campylobacter* ST-464

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EURL-*Campylobacter* workshop  
Online event, September 26<sup>th</sup>, 2023



**January 2023****Event ID 2023-FWD-00011 “*Campylobacter jejuni* cluster” registered in EpiPulse**

- Reference sequence uploaded
- Matches in 4 other MS
- One MS claim imported poultry meat from another EU MS had a similar genotype

**May 2023****ECDC wanted to explore this as a multi-country event**

- Possibly engage to a Joint Notification Summary (JNS) with EFSA.

**May 11<sup>th</sup>:** EURL-*Campylobacter* contacted by EFSA, meeting is held on May 15<sup>th</sup>

**May 17<sup>th</sup>**

- EFSA informs Country officers about the upcoming exercise
- EURL-*Campylobacter* sends a letter to the NRLs on May 17<sup>th</sup> asking for:
  - Sequence data of ST-464 from isolates collected 2020 and onwards
  - Metadata
  - Background information on ST-464

**June 16th 2023**

End of call

### PubMLST

- 1391 isolates and 634 genomes of ST-464 since first submission in the year 2000 (as of May 2023)
- Among the isolates with a known source: 97 % human and chicken origin
- From all over the world
- **The closest match to the EpiPulse reference had 26 allele differences (ADs) from a human isolate from 2022**

### Literature

- The clonal complex (CC) ST-464 has been associated with both ciprofloxacin and fluoroquinolone resistance
- Appears in several national source attribution studies as a “chicken ST”

# Participation

44 NRLs in the *Campylobacter* network

20 NRLs (19 countries) with access to WGS data answered the call

10 NRLs did not have any sequence data from ST-464

8 NRLs (7 MSs, 1 third country) uploaded sequence data to the EURL-*Campylobacter*

2 NRLs had ST-464 sequence data and compared themselves with the EpiPulse reference (national collaboration) without a match

76 sequences submitted

# Sequence analysis



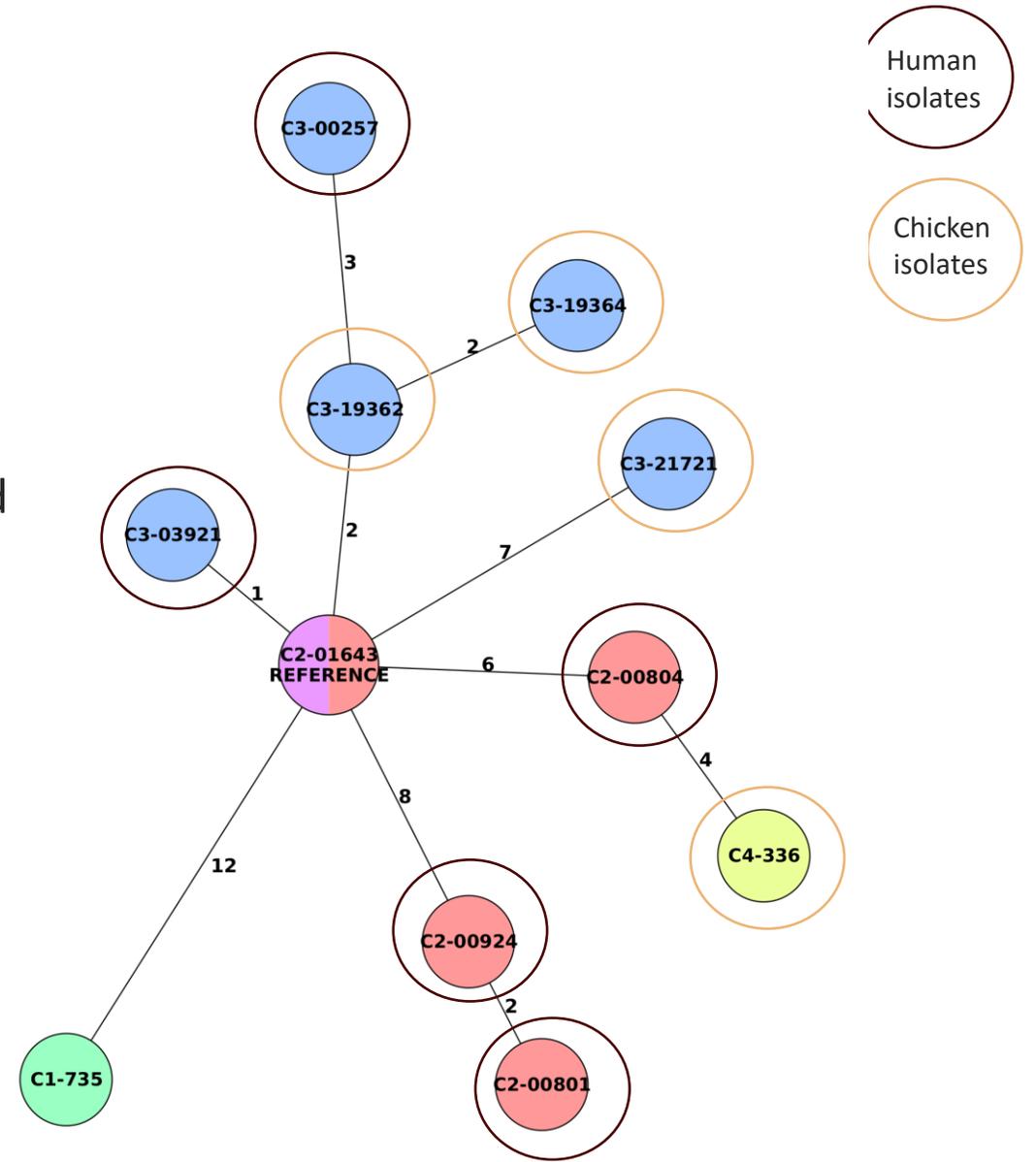
Sequences analyzed in Ridom SeqSphere+ with the 'Oxford scheme' (1343 loci) cgMLST/wgMLST.



4 NRLs had sequences that clustered with the reference genome from EpiPulse with 12 AD or less.

# Results

- 1 strain from Country 1. No metadata.
- 4 strains from Country 2. Human origin.
- 5 strains from Country 3. Two strains of human origin and three from chicken meat collected at retail – origin unknown.
- 1 strain from Country 4. Imported chicken meat.

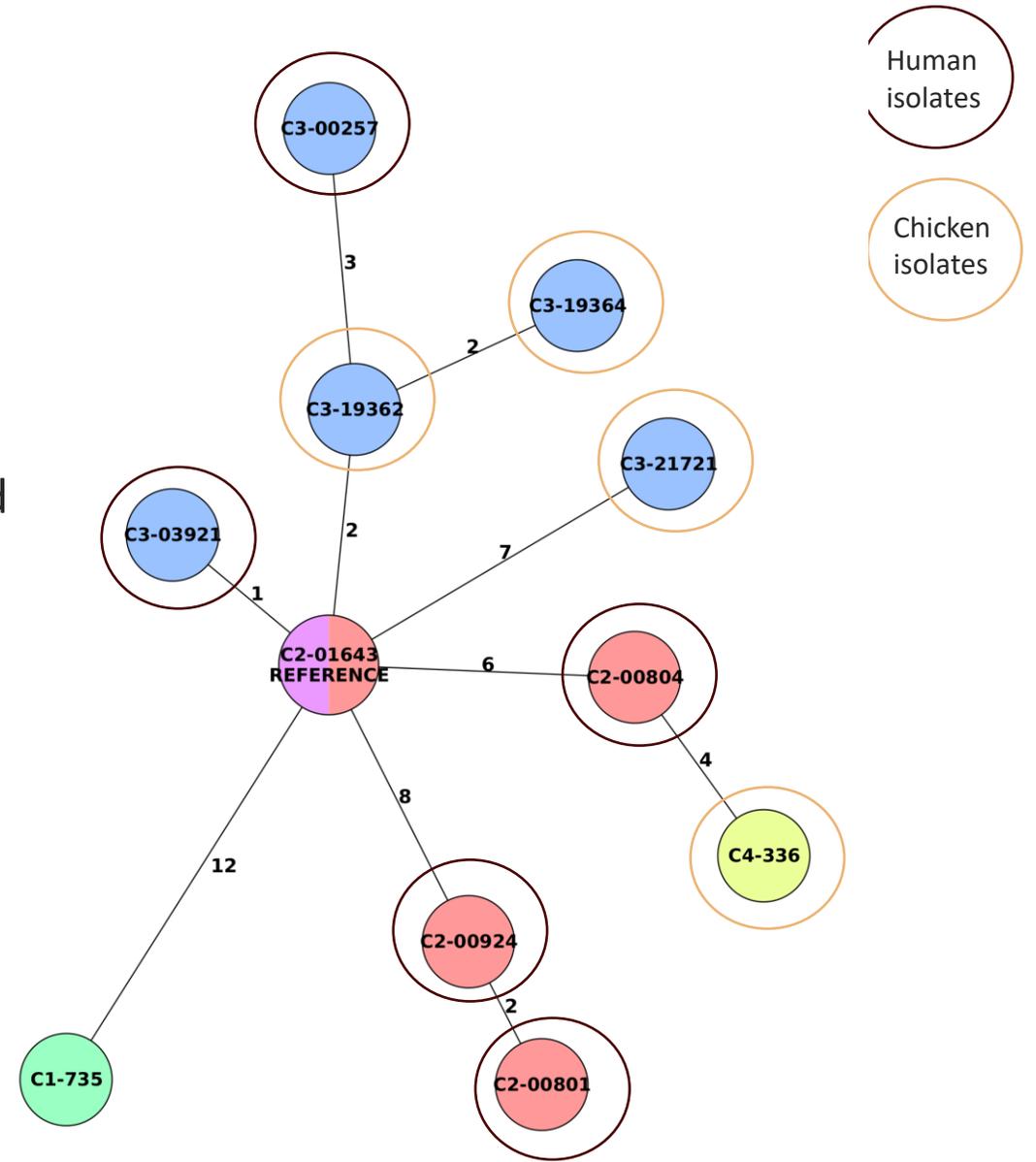


MST– 'Oxford scheme'

# Results

- 1 strain from Country 1. No metadata.
- 4 strains from Country 2. Human origin. (**April-July 2022**)
- 5 strains from Country 3. Two strains of human origin and three from chicken meat collected at retail – origin unknown. (**Feb 2021- Sept 2022**)
- 1 strain from Country 4. Imported chicken meat. (**2022**)

Reference: **2023**



MST– 'Oxford scheme'

# Comparison cgMLST and SNP-analysis

- Results displayed in distance matrices
  - Numbers are AD or SNPs
  - Ridome SeqShere/Oxford scheme
  - Snippy/EpiPulse reference genome
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- SNP-analysis with only filtering on sequence quality

	REFERENCE	C2-01643	C3-03921	C3-19362	C3-19364	C3-00257	C2-00804	C4-336	C3-21721	C2-00924	C2-00801	C1_735
REFERENCE	0	0	1	2	3	4	6	6	7	8	10	12
C2-01643	0	0	1	2	3	4	6	6	7	8	10	12
C3-03921	1	1	0	3	4	5	7	7	8	9	11	13
C3-19362	2	2	3	0	2	3	6	6	7	8	10	12
C3-19364	3	3	4	2	0	3	7	7	8	9	11	13
C3-00257	4	4	5	3	3	0	8	8	9	10	12	14
C3-00804	6	6	7	6	7	8	0	4	7	8	8	12
C4-336	6	6	7	6	7	8	4	0	7	8	10	12
C3-21721	7	7	8	7	8	9	7	7	0	9	11	13
C2-00924	8	8	9	8	9	10	8	8	9	0	2	14
C2-00801	10	10	11	10	11	12	8	10	11	2	0	16
C1_735	12	12	13	12	13	14	12	12	13	14	16	0

	C3-21721	C4-336	C2-00801	C1-735	C2-00802	C2-01643	C3-00257	C3-03921	C3-19362	C3-19364	Reference
C3-21721	0	130	98	144	141	135	136	137	135	135	136
C4-336	130	0	75	114	109	105	106	107	105	105	106
C2-00801	98	75	0	80	77	71	72	73	71	71	72
C1-735	144	114	80	0	25	15	16	17	15	15	16
C2-00802	141	109	77	25	0	16	17	18	16	16	17
C2-01643	135	105	71	15	16	0	3	2	2	2	1
C3-00257	136	106	72	16	17	3	0	5	3	3	4
C3-03921	137	107	73	17	18	2	5	0	4	4	3
C3-19362	135	105	71	15	16	2	3	4	0	2	3
C3-19364	135	105	71	15	16	2	3	4	2	0	3
Reference	136	106	72	16	17	1	4	3	3	3	0

2021 →  
→

# Comparison cgMLST and SNP-analysis

- Results displayed in distance matrices
- Numbers are AD or SNPs
- Ridome SeqShere/Oxford scheme
- Snippy/EpiPulse reference genome
- SNP-analysis with hands-on filtering  
(removal of a region with many mutations)
- Good correlation between the systems

	REFERENCE	C2-01643	C3-03921	C3-19362	C3-19364	C3-00257	C2-00804	C4-336	C3-21721	C2-00924	C2-00801	C1_735
REFERENCE	0	0	1	2	3	4	6	6	7	8	10	12
C2-01643	0	0	1	2	3	4	6	6	7	8	10	12
C3-03921	1	1	0	3	4	5	7	7	8	9	11	13
C3-19362	2	2	3	0	2	3	6	6	7	8	10	12
C3-19364	3	3	4	2	0	3	7	7	8	9	11	13
C3-00257	4	4	5	3	3	0	8	8	9	10	12	14
C3-00804	6	6	7	6	7	8	0	4	7	8	8	12
C4-336	6	6	7	6	7	8	4	0	7	8	10	12
C3-21721	7	7	8	7	8	9	7	7	0	9	11	13
C2-00924	8	8	9	8	9	10	8	8	9	0	2	14
C2-00801	10	10	11	10	11	12	8	10	11	2	0	16
C1_735	12	12	13	12	13	14	12	12	13	14	16	0

	C2-00801	C2-00802	C3-21721	C4-336	C1-735	C2-01643	C3-00257	C3-03921	C3-19362	C3-19364	Reference
C2-00801	0	18	14	18	19	10	10	12	10	10	11
C2-00802	18	0	18	20	23	14	14	16	14	14	15
C3-21721	14	18	0	18	19	10	10	12	10	10	11
C4-336	18	20	18	0	23	14	14	16	14	14	15
C1-735	19	23	19	23	0	15	15	17	15	15	16
C2-01643	10	14	10	14	15	0	2	2	2	2	1
C3-00257	10	14	10	14	15	2	0	4	2	2	3
C3-03921	12	16	12	16	17	2	4	0	4	4	3
C3-19362	10	14	10	14	15	2	2	4	0	2	3
C3-19364	10	14	10	14	15	2	2	4	2	0	3
Reference	11	15	11	15	16	1	3	3	3	3	0

# Conclusions

- Received limited background information on this ST in the call
- Patients in several (at least five) different European countries have been ill from this specific genotype
- The source is most likely chicken
- From the limited data available we cannot point out a specific country to continue the investigation
- **Complication:** this genotype seems to be a stable genetic lineage
  - How frequent are stable genetic lineages cross-country and how to deal with them?

# Lessons learnt

- Engaged network of NRLs
- Sharing metadata is very important
  - Hopefully improved once *Campylobacter* is in the One Health WGS system
- Sharing data gives us important insight about the pathogen

# Future data calls

## Through the EFSA's One Health WGS system?

Already in place for *Salmonella*, *Listeria* and *E. Coli*

- Collecting data from multiple countries simplified
- Improved sharing of metadata
- Standardized analysis pipeline
- Better understanding of cross-country behavior of *Campylobacter*

# Acknowledgements

**EURL-*Campylobacter***

Hanna Skarin

Bo Segerman

**The *Campylobacter* NRL  
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**Thank you for your attention!**



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