

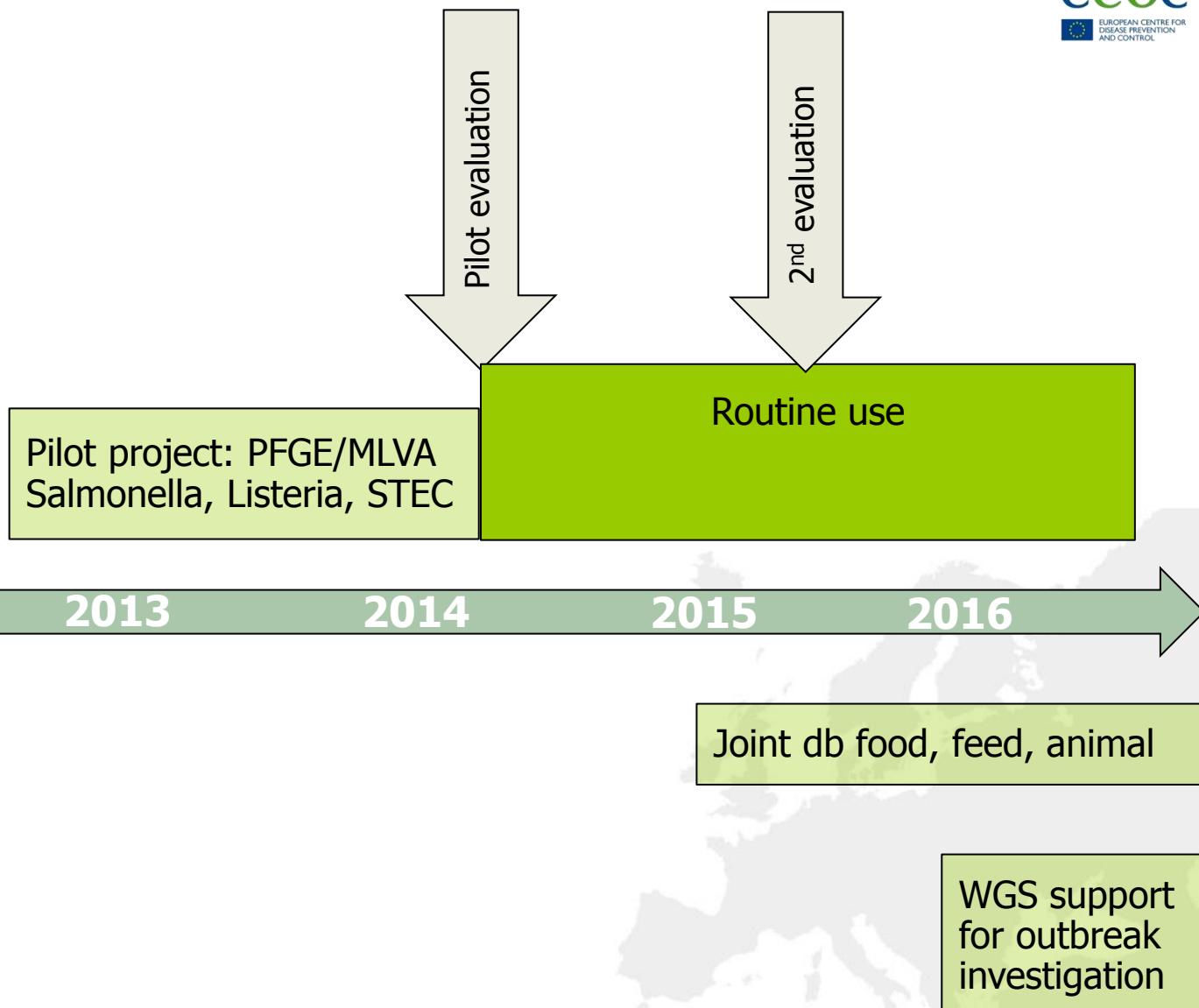


Update on VTEC molecular typing activities at ECDC

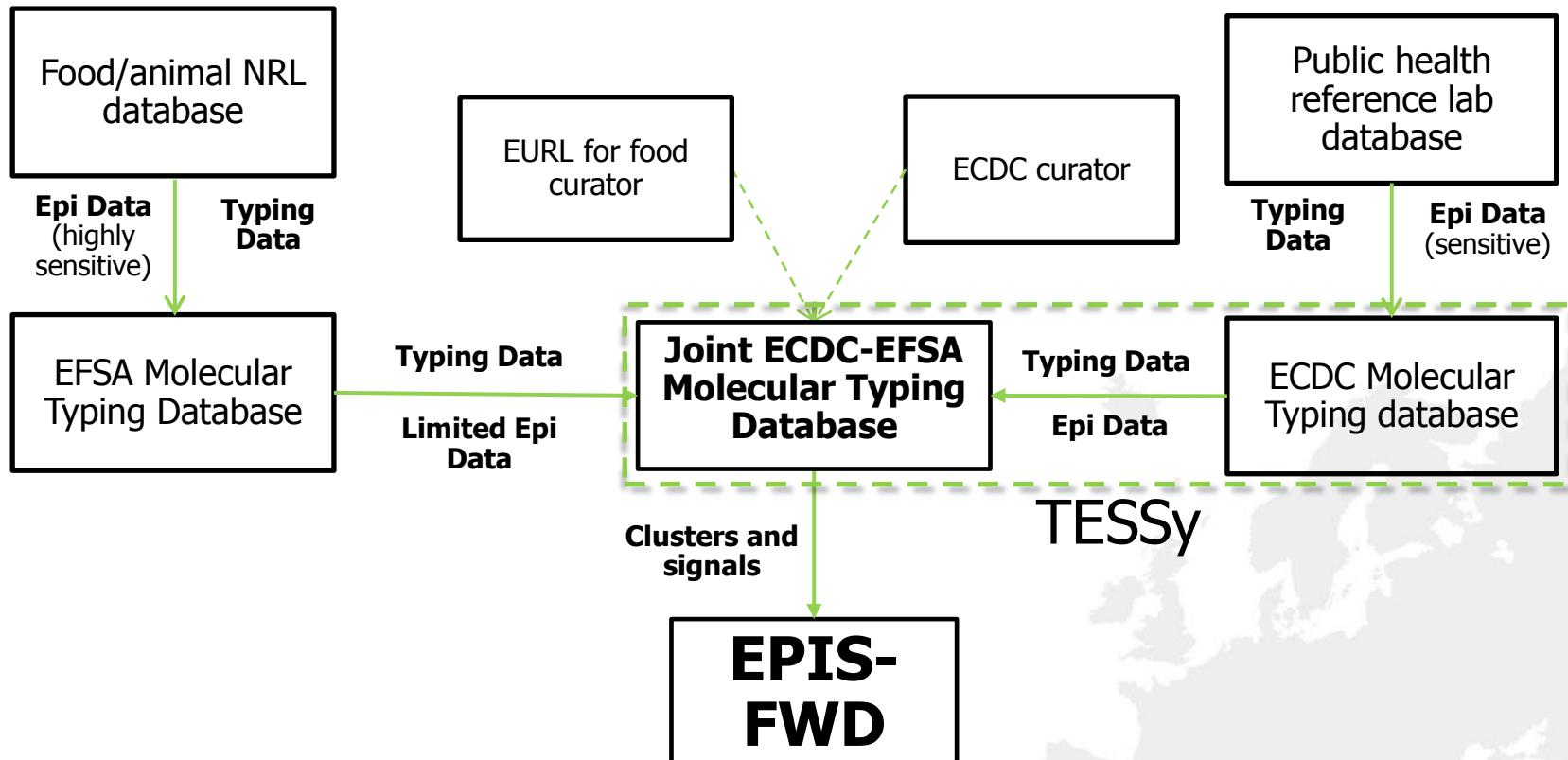
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12th Annual Workshop of the NRLs for *E. coli* in the EU
Rome, 12-13 October 2017

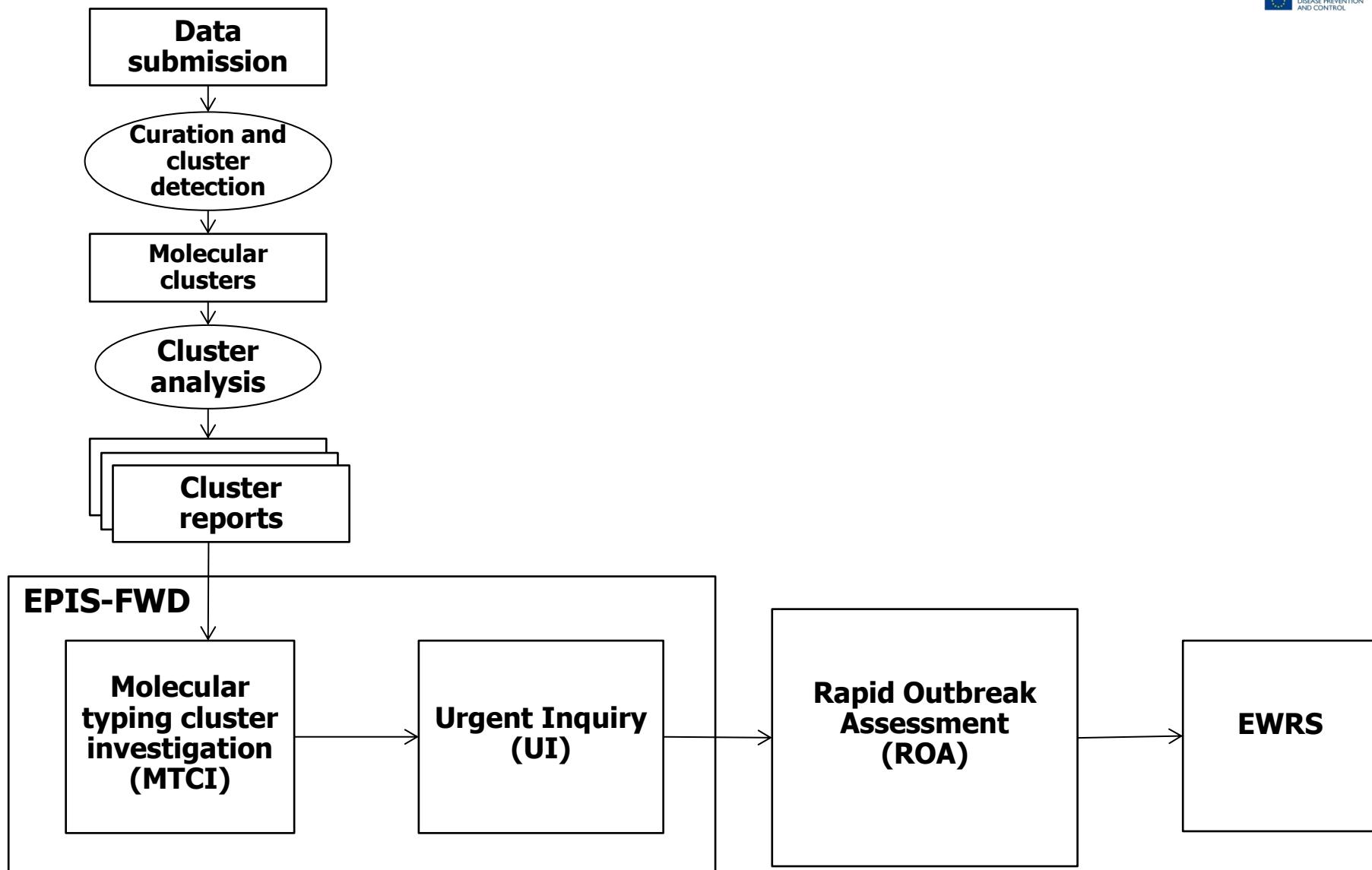
Molecular Typing, ECDC FWD activities



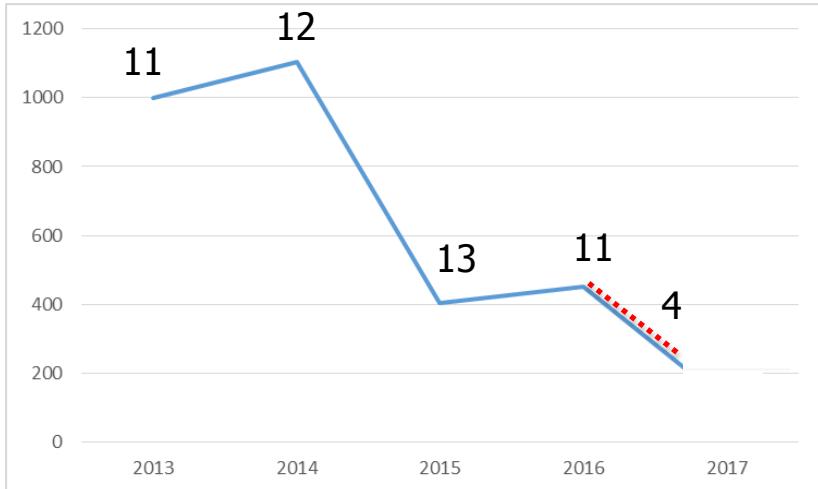
Current data flow in the joint molecular typing database



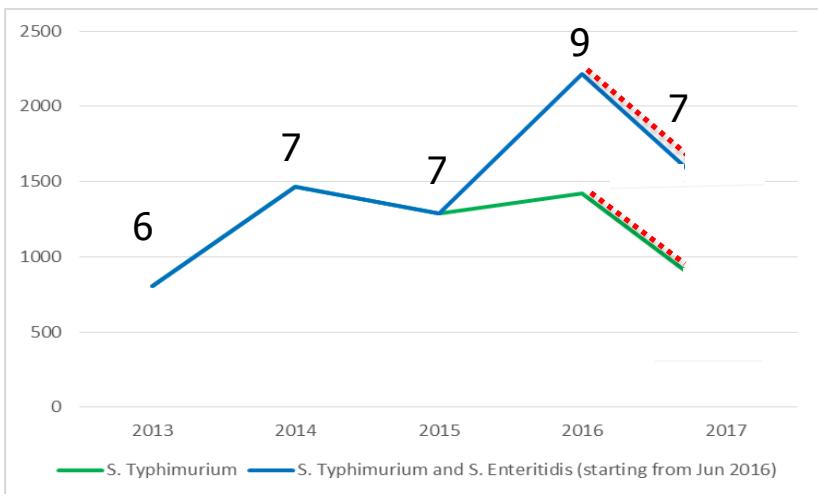
FWD cluster analysis process: From typing data to EU-level risk communication



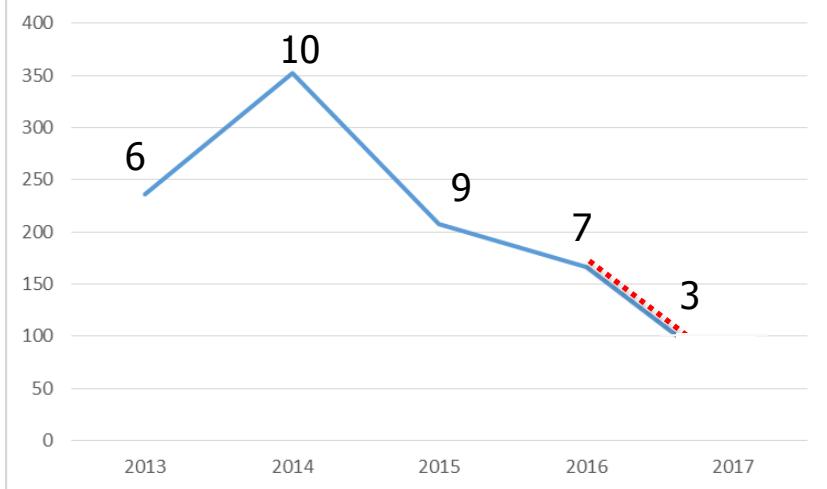
PFGE/MLVA data by year, 2013 – Sep 2017



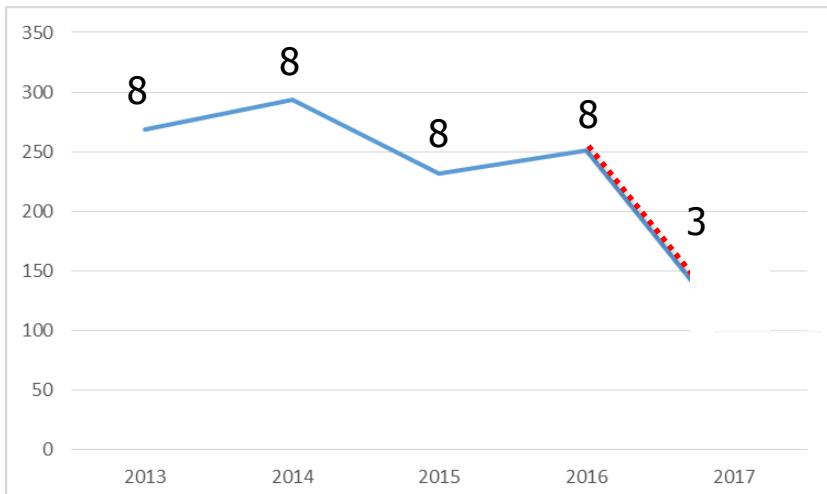
Salmonella PFGE



Salmonella MLVA



Listeria PFGE



VTEC PFGE

Note: Historical data excluded (i.e. isolates submitted to TESSy more than 16 weeks after the sampling date).

Some numbers from the human molecular typing data collection (Nov 2012-Sep 2017)

	Salmonella	Listeria	VTEC
No of isolates with typing data	37,893	2,907	1,894
...of which timely*	27%	35%	61%
Number of Member States submitting data	20	14	13
Number of detected clusters	974	119	16
Number of molecular typing cluster investigations started	261	25	2
Proportion of isolates part of multi-country cluster	37%	22%	4%
Number of non-human isolates with typing data	6	161	0

*within 112 days for Salmonella and VTEC, and 224 days for Listeria

** for which a molecular typing cluster investigation was initiated in EPIS FWD

Molecular typing in EPIS-FWD

Pathogen	Year	Total no of MTCIs	No of MTCIs escalated to UI	Proportion of UIs linked to a cluster (%)
<i>Salmonella</i>	2013	0	0	16.7
	2014	51	2	31.8
	2015	71	2	23.8
	2016	82	2	40.7
	2017	57	1	35.0
<i>Listeria</i>	2013	2	1	33.3
	2014	12	0	0
	2015	6	0	20.0
	2016	5	0	0
	2017	0	0	0
VTEC	2013	0	0	0
	2014	0	0	0
	2015	2	1	9.0
	2016	0	0	0
	2017	0	0	0

MTCI: Molecular Typing Cluster Investigation

UI: Urgent Inquiry

Main conclusions from 2015 evaluation of FWD molecular typing initiative



- Public health objectives and targets not reached
- System in place and fit for purpose
- Insufficient data coverage/timeliness for meeting objectives linked to outbreak detection
- Data quality and completeness improving but still insufficient

Outbreak investigations supported with whole genome sequencing (as of September 2017)

Support signals originating from

- EPIS-UI
- Routine molecular typing

WGS support to 21 outbreak signals since Nov 2015

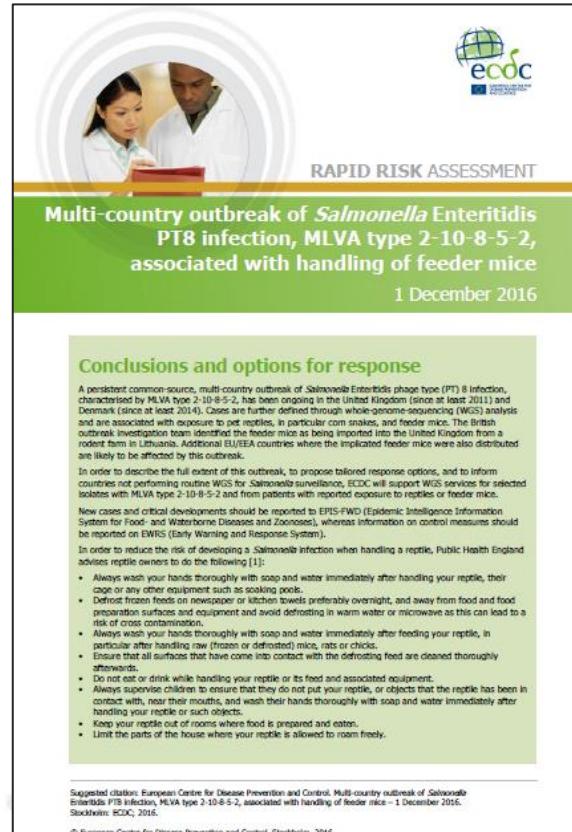
- 19 Salmonella
- 2 VTEC

Volumes

- >1000 isolates sequenced from MS
- ~900 isolates sequenced supported by ECDC

Outputs

- 18 multi-country outbreaks confirmed
- 3 multi-country outbreaks rejected
- 6 RRA/ROA prepared
- Source identified for five multi-country outbreaks



RAPID RISK ASSESSMENT

Multi-country outbreak of *Salmonella* Enteritidis PT8 infection, MLVA type 2-10-8-5-2, associated with handling of feeder mice

1 December 2016

Conclusions and options for response

A persistent common-source, multi-country outbreak of *Salmonella* Enteritidis phage type (PT) 8 infection, characterised by MLVA type 2-10-8-5-2, has been ongoing in the United Kingdom (since at least 2011) and Denmark (since at least 2014). Cases are further defined through whole-genome sequencing (WGS) analysis and are associated with exposure to pet reptiles, in particular corn snakes, and feeder mice. The British outbreak investigation team identified the feeder mice as being imported into the United Kingdom from a rodent farm in Lithuania. Additional EU/EEA countries where the implicated feeder mice were also distributed are listed.

In order to describe the full extent of this outbreak, to propose tailored response options, and to inform countries not performing routine WGS for *Salmonella* surveillance, ECDC will support WGS services for selected isolates with MLVA type 2-10-8-5-2 and from patients with reported exposure to reptiles or feeder mice. New cases and critical developments should be reported to EPIS-FWD (Epidemic Intelligence Information System for Food- and Waterborne Diseases and Zoonoses), whereas information on control measures should be reported on EWRS (Early Warning and Response System).

In order to reduce the risk of developing a *Salmonella* infection when handling a reptile, Public Health England advises reptile owners to do the following [1]:

- Always wash your hands thoroughly with soap and water immediately after handling your reptile, their cage or any other equipment such as soaking pools.
- Defrost frozen food in the microwave or paper or kitchen towels preferably overnight, and away from food and food preparation surfaces and equipment and avoid defrosting in warm water or microwave as this can lead to a risk of cross-contamination.
- Always wash your hands thoroughly with soap and water immediately after feeding your reptile, in particular after handling raw (frozen or defrosted) mice, rats or chicks.
- Ensure that all surfaces that have come into contact with the defrosting feed are cleaned thoroughly afterwards.
- Do not eat or drink while handling your reptile or its food and associated equipment.
- Always supervise children to ensure that they do not put your reptile, or objects that the reptile has been in contact with, near their mouths, and wash their hands thoroughly with soap and water immediately after handling your reptile or such objects.
- Keep your reptile out of rooms where food is prepared and eaten.
- Limit the parts of the house where your reptile is allowed to roam freely.

Supported citation: European Centre for Disease Prevention and Control. Multi-country outbreak of *Salmonella* Enteritidis PT8 infection, MLVA type 2-10-8-5-2, associated with handling of feeder mice - 1 December 2016. Stockholm: ECDC; 2016.

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2017 operational objectives and applied typing methods per pathogen

ID	Operational objective	<i>S. enterica</i>	<i>L. monocytogenes</i>	VTEC
OB.1	Regular analyses for the detection of multi-country clusters	serotyping, MLVA, PFGE*	WGS	EPIS-FWD**
OB.2	Verification of a multi-country outbreak	WGS	WGS	WGS
OB.3	Support to multi-country outbreak investigation	MLVA, WGS	WGS	WGS
OB.4	Identification of vehicle/source	PFGE***	PFGE***	PFGE***

* Method continued in 2017 until gradual expected phasing out and replacement with WGS

** In 2017, detection relies almost entirely on Urgent Inquiries and information shared in EPIS-FWD

*** Representative outbreak isolate for the purpose of finding matches in the joint ECDC-EFSA database and national food databases and contribute to data for rapid outbreak assessment

Conclusions

- Technical system for human and non-human molecular typing data submission, analysis, interpretation and communication in place
- PFGE does not work well for VTEC at EU level – rely on signals from EPIS FWD
- WGS useful for multi-country outbreak confirmation and delineation
- Strengthen epidemiological follow-up on detected molecular typing signals
 - Discussion on collection of exposure data
- Pursue investigation of human/food/feed/environment clusters detected through joint database

EC mandate terms of reference



EFSA and ECDC are requested to jointly **evaluate the possible solutions** for the collection and the analysis of WGS data for at least *L. monocytogenes*, *Salmonella*, *E. coli* by

1. **Analysing** the outcome of the **surveys on** the status of **use of WGS** of foodborne pathogens in MSs in both food and public health sectors.^a
2. Conducting a **consultation of relevant actors** and players to assess the state of the art of pipelines for collecting and analysing WGS data in Europe.
3. Involving relevant stakeholders to **assess the needs/requirements for the analysis of WGS data and their comparability and to describe roles and responsibilities**, taking into account that there are different types of WGS data (raw sequence reads, genome assemblies, wgMLST allele identifiers, strain nomenclature, phenotypic predictions), which may require interfacing with externally hosted databases and applications.
4. Preparing a **technical report** on the identification and the comparison of potential solutions for the set-up and running of a joint EFSA-ECDC pipeline for collecting and analysing WGS data, taking into account deliverables of ToRs 1,2, 3.

^aCurrent surveys: ECDC survey NMFP Survey of PH reference laboratories, 2016 EC survey on WGS capacity for non-human samples



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