Update on the annual reporting of STEC in the EU and on EFSA activities for molecular typing data collection for food and animal isolates

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efsa

European Food Safety Authority

- **Annual reporting of STEC in the EU**
- EFSA activities for molecular typing data collection for food and animal isolates including WGS
- Joint ECDC – EFSA assessments on EU-wide foodborne events

Monitoring of zoonoses and FBO in the EU

- **FOOD-ANIMAL DATA**
  - **Directive 2003/99/EC on the monitoring of zoonoses and zoonotic agents**
    - Publication of the annual EU Summary Report
    - MSs have an **obligation** to report data each year
    - Mandatory data collection for:
      - 8 zoonotic agents: *Salmonella* (+ AMR), *Campylobacter* (+ AMR), *L. monocytogenes, Brucella,* tuberculosis due to *Mycobacterium bovis,* VTEC, *Trichinella, Echinococcus*
      - foodborne outbreaks (FBOs) and susceptible animal populations
- **HUMAN DATA**
  - **Decision 1082/2013/EU on serious cross-border threats to health**

EU Member States and other reporting countries

Animal, food and feed monitoring — Data Collection Framework (DCF)

Foodborne outbreaks

Communicable human diseases — The European Surveillance System (TESSy)

Scientific Network for Zoonoses Monitoring Data

FWD and EVD Networks

SCIENTIFIC REPORT

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The European Union summary report on trends and sources of zoonoses, zoonotic agents and food-borne outbreaks in 2014

European Food Safety Authority
European Centre for Disease Prevention and Control

Abstract

This report of the European Food Safety Authority and the European Centre for Disease Prevention and Control presents the results of the zoonoses monitoring activities carried out in 2014 in 32 European countries (28 Member States (MS) and four non-MS). Campylobacteriosis was the most commonly reported zoonosis with an increase in confirmed human cases in the European Union (EU)

Joint EFSA-ECDC annual EU Summary Report (EUSR) on zoonoses and food-borne outbreaks

[Available online: www.efsa.europa.eu/efsajournal]

Human zoonoses cases in EU, 2017

In the year after the 2011 outbreak, overall EU/EEA trend did not show any significant increase or decrease

1.77 cases /100,000 (IE highest notification rate = 16.6)

79.1% domestic cases (FI, SE and NO reporting the highest proportion of travel associated cases)

Table 2: Reported hospitalisation and case fatalities due to zoonoses in confirmed human cases in the EU, 2017

Disease	Number of confirmed[a]	Hospitalisation				Deaths			
	Human cases	Status available (%)	Number of reporting MS[b]	Reported hospitalised cases	Proportion hospitalised (%)	Outcome available (%)	Number of reporting MS[b]	Reported Deaths	Case Fatality (%)
Campylobacteriosis	246,158	27.6	17	20,810	30.5	72.8	16	45	0.04
Salmonellosis	91,662	43.1	14	16,796	42.5	67.8	17	156	0.25
Yersiniosis	6,823	27.1	14	616	33.4	65.5	15	3	0.07
STEC infections	6,073	41.0	18	933	37.5	66.1	21	20	0.50
Listeriosis	2,480	40.4	16	988	98.6	65.8	18	225	13.8

Serogroups in confirmed human STEC infections, 2017

O157 the most commonly reported serogroup (but steadily decreasing sing 2012)
026 decreased since 2016

O157 + O26 = 46.2%

One new serogroup (O76) entered into and three serogroups (O5, O182, O27) were dropped from the "top 20 list" in 2017.

The proportion of non-typable STEC strains increased in 2017

Table 32: Distribution of the 20 most frequent serogroups reported in confirmed cases of human STEC infections in EU/EEA, 2015–2017

Serogroup	2017			2016			2015		
	Cases	MS	%	Cases	MS	%	Cases	MS	%
O157	1,304	24	31.9	1,552	22	38.6	1,510	21	42.1
O26	582	18	14.3	671	19	16.7	537	16	15.0
NT[a]	493	11	12.1	335	12	8.3	397	10	11.1
O103	245	14	6.0	218	18	5.4	172	14	4.8
O91	179	14	4.4	149	11	4.0	114	12	3.2

STEC food and animals - methods

Analytical methods used 2017

Samples tested		proportion (%) of total samples tested by method		
Type	Number	ISO/TS 13136:2012	ISO 16654:2001 or NMKL 164:2005 or DIN 10167	Unspecified
Food	21 574	97.4	2.6	0.0
Animals	2 310	52.5	43.5	4.0

Wide adoption of standard method at EU level in Food

New aggregation rules for 2073/2005

- Data sets usable for trend watching
  - Surveillance based on Reg 2073
  - Single sampling unit
  - Appropriate sampling stage
- Other food data: only summary

	2017	2016	2015
Total number of food-borne outbreaks (including waterborne outbreaks)	48	42	69
Number of outbreak-related cases	260	735	674
Food			
Meat and meat products			
Number of sampled units	12,465	9,369	10,872
Number of reporting MS	20	18	16
Milk and milk products			
Number of sampled units	3,637	3,848	4,370
Number of reporting MS	12	12	11
Fruits and vegetables (and juices)			
Number of sampled units	2,325	1,518	1,821
Number of reporting MS	15	21	22
Animals			
Bovine animals			
Number of sampled herds	226	62	49
Number of reporting MS	4	2	2
Small ruminants			
Number of sampled herds	10	208	109
Number of reporting MS	1	8	7

- 21,574 food units tested
- 2,310 units from animals or herds or flocks tested (negative trend observed in 2016)
- Meat and meat products highest number of samples tested
- Bovine marked increase
- Increase MS reporting (=25)
- Large differences among MS in food categories sampled

8

Food category[b]	Samples tested by ISO TS 13136[c]	Any STEC	
		n[d]	%
Bovine meat	8,059	134	1.7
Ovine and goat meat	579	39	6.7
Other ruminants meat[e]	93	23	24.7
Pig meat	1,363	60	4.4
Other meat[f]	1,466	27	1.8
Mixed meat	587	13	2.2
Milk and dairy products[g]	2,322	57	2.5
Raw milk[h]	1,094	23	2.1
Fruit and vegetable	2,280	7	0.3
Seeds[i]	1,565	10	0.6
Other food	1,603	7	0.4
Total	**21,011**	**400**	**1.9**

- Food:
  - **1.8%** of the 21,574 food samples tested
  - meat samples > milk & dairy products (2.5%) > seeds (0.6%) fruit & vegetables (0.3%)
- Animals:
  - **10.6%** of the 2,310 animal samples tested
  - deer (20.1%) > 'other animals' (17.2%) > cattle (8.3%) > goat and sheep (2.9%)

STEC in sprouted seeds (reg 2073/2005)

12 MS reported sprouted seeds at retail level with <u>no positive samples</u>

4 non-compliant batches reported by 1 MS in Official samples taken at processing plant

Only 6 MS provided info on 98 single samples taken as part of official control

Table 31: STEC sprouted seeds monitoring results at retail, reporting Member States, EU, 2013–2017

Sprouted seeds	Number of reporting MS	Sample units tested	Sample units positive (%)
2013	6	444	0 (0.0%)
2014	6	481	0 (0.0%)
2015	7	576	1 (0.2%)
2016	8	344	1 (0.3%)
2017	12	786	0 (0.0%)

- <u>Serogroups</u>: < 33 % food and 52% of animals isolates
  - Food (% positive samples):

  O157 (6.2%) > O103 (2.7%) > O26 (1%) > O111 and O145 (0.75%)
  - Animals (% positive samples):

  O157 (31.5%) > O103 (2.9%) > O26 (2.5%) > O116 (1.2%) = O168 (1.2%)

- <u>Virulotype</u> for 180/401 STEC strains isolated from food
  - 50% carried the genes encoding the Stx2
  - 7.2% were stx2+; eae+ (HUS)
  - 8 stx1+; stx2+; eae+

Distribution of strong-evidence and weak-evidence food-borne and waterborne outbreaks, per causative agent, EU, 2016
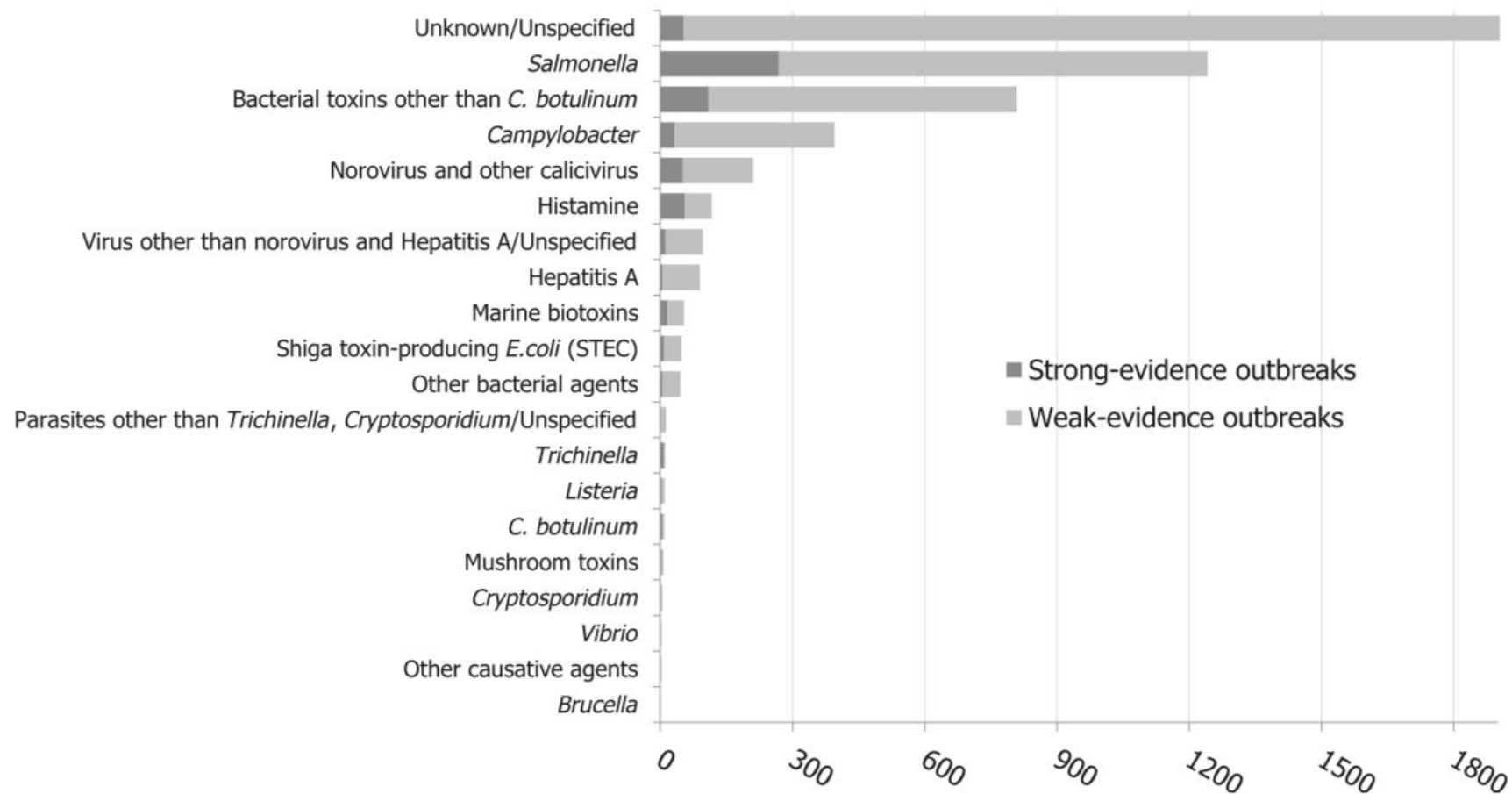
Total outbreak 5,079, strong–evidence 643

- **48 FBOs** due reported by 11 MSs 260 cases – 65 hospitalisations – 2 deaths

- 39 weak evidence

- 9 strong evidence
  - Food vehicle: Bovine meat (4), Cheese (1), Dairy products other than cheeses (1), Meat and meat products (1), Milk (2)
  - Type: All general outbreaks (but 1 N.A.)
  - Serogroup: VTEC O157 (6), VTEC O111 (1), VTEC (2)

- In addition, 1 EFTA countries reported 10 weak-evidence outbreaks (NO)
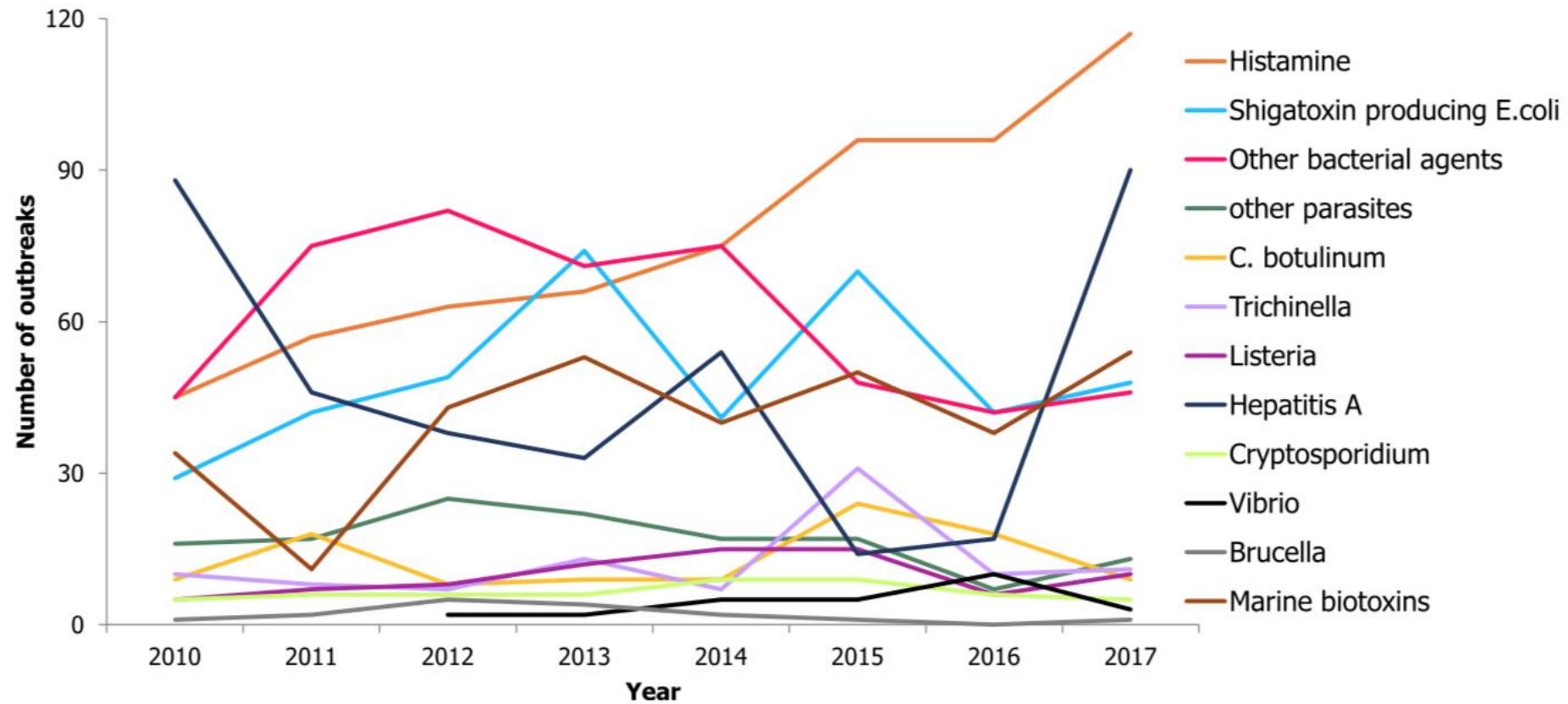
- Annual reporting of STEC in the EU
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Molecular typing data collection

Following the STEC crisis in 2011, EC sent a request to EFSA and ECDC for assistance:

➢ to collect molecular typing data (**PFGE and MLVA**) on *Salmonella*, *L. monocytogenes* and VTEC isolates from food, feed, animals and humans

➢ to perform a joint data analyses of the data in the **joint EFSA-ECDC molecular typing database**.

Food safety/ veterinary sector

Food/feed/animal in the NRL/Official lab database

Typing Data AND Epi Data (highly sensitive)

Curated Data

EFSA Molecular Typing Database

Public health sector

Human data in the Public health reference lab database

Curated Data

ECDC database (TESSy)

Joint ECDC-EFSA database

Typing Data AND Limited Set of Epi Data

Curated Data

ECDC's curator

EURLs as curators of food/feed and animal data

DATA PROVIDERS: Restricted web access depending on user rights

Status of engagement of laboratories (as of October 2019)

	Human side	Food/ veterinary side
Nominated users	All MSs	**14 MSs**[a]: AT, BE, DK, DE, ES, FI, FR, IE, IT, LU, PT, SE, SK, UK (21 labs[b])
Signature of the Collaboration Agreement	**16 MSs**: AT, CZ, DK, EE, DE, EL, HU, LV, LT, MT, NO, RO, ES, SE, NL, SK	**11 MSs**: AT, BE, DE, FI, FR, IE, IT, LU, PT, SE, SK (13 labs)
Transmission of data (excluding WGS data)	**15 MSs**: AT, BE, CZ, DK, EL, ES, FR, IE, IT, LU, NL, NO, SE, SI, UK	**9 MSs:** BE, DE, FI, FR, IE, IT, LU, SE, SK
Total number of isolates uploaded	**47,784**	**2,270**

(a): *Salmonella* and STEC: 13 MSs (all except FR) - *Listeria*: all MSs
(b): 3 different users for the 3 pathogens in AT, IE and IT, 2 users for the 3 pathogens in SK

17

Data on **food isolates** submitted per country and pathogen (as of October 2019)

Country	*L. monocytogenes*	*Salmonella*	VTEC	N. isolates submitted from EFSA DB to Joint DB
BE	326*			326
DE	152			152
FI	41			41
FR	1,186			1,186
IE	129			129
IT		91 (MLVA)	45	136
LU	118	3 (PFGE)		121
SE	26			26
SK	146	5 (PFGE)	2	153
TOTAL	2,124	99	47	2,270

* 44 isolates still to be submitted from the EFSA database to joint database

Status of engagement of laboratories

Laboratory	Mapping done	Submission
IT NRL VTEC	224 isolates	45 isolates
IT NRL Lm	Entire database (around 2000 isolates)	no submission
IT NRL *Salmonella (DCF)*	Entire database	91 isolates (MLVA)

DE: interested for outbreak cases

PT (DCF): they are interested → waiting for their feedback.

SE (*Salmonella* NRL): we provided clarification on legal aspects → waiting for their feedback.

SI: interested but they still need to sign the agreement

Prioritisation of <u>**Isolates to be typed (and then submitted**</u>**)**

Isolates identified during **multi-country outbreak investigations**

Isolates identified during **national outbreak investigations**

Isolates from food that are traded (linked to **RASFF notifications**)
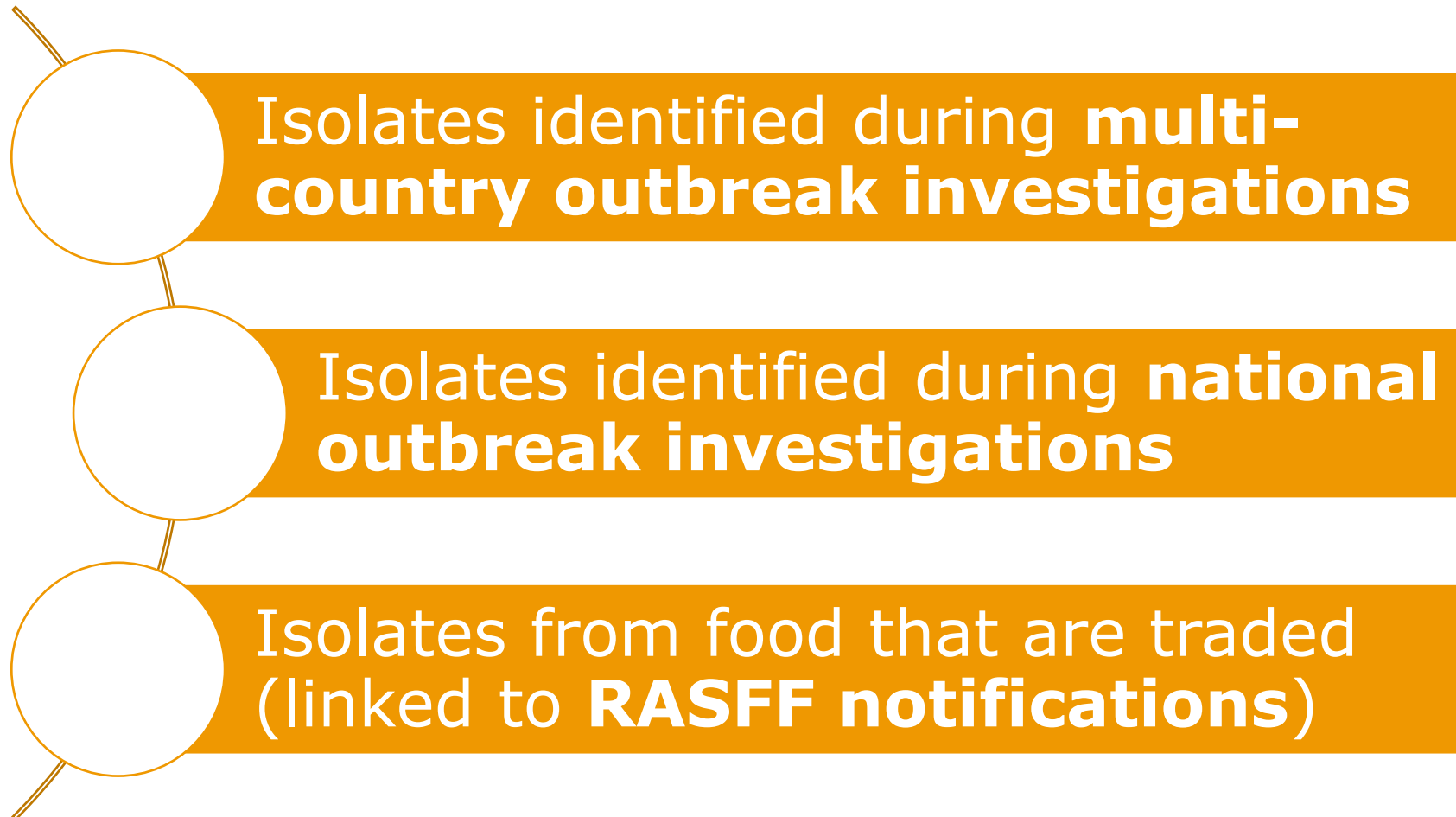
In 2017, EFSA and ECDC received a new joint mandate from EC to expand the molecular typing data collection to **Whole Genome Sequencing (WGS)** data.

TECHNICAL REPORT

APPROVED: 29 April 2019

doi:10.2903/sp.efsa.2019.EN-1337

ToR1: to analyse **outcome of ECDC and EFSA Surveys on WGS**
ToR2: to assess the **state of the art of pipelines**
ToR3: to assess **needs/requirements** for analysis
ToR4: to prepare a **Technical report**

EFSA and ECDC technical report on the collection and analysis of whole genome sequencing data from food-borne pathogens and other relevant microorganisms isolated from human, animal, food, feed and food/feed environmental samples in the joint ECDC–EFSA molecular typing database

European Centre for Disease Control (ECDC), European Food Safety Authority (EFSA), Ivo Van Walle, Beatriz Guerra, Vitor Borges, João André Carriço, Guy Cochrane, Tim Dallman, Eelco Franz, Renata Karpíšková, Eva Litrup, Michel-Yves Mistou, Stefano Morabito, Joël Mossong, Erik Alm, Federica Barrucci, Chiara Bianchi, Giancarlo Costa, Saara Kotila, Iolanda Mangone, Daniel Palm, Luca Pasinato, Joana Revez, Marc Struelens, Daniel Thomas-López and Valentina Rizzi

General conclusions from WG

- Every single solution has a substantial number of gaps due to not meeting all the critical requirements

- Scenarios would consist of a combination of solutions

- The choice among scenarios depends on other strategic or financial elements that are not under the control of the JWG

EFSA and ECDC identified '**Strategic elements**' to be used to guide the decision and are under negotiation to identify the best scenario to present to EC

Prerequisites identified by EFSA

- Develop internal bioinformatic services addressing **multiple needs** for different risk assessment domains

- Guarantee full **transparency of the analytical procedures** (following the implementation of the changes in Regulation 178/2002/EC)

- Engage more with data provider for increasing the **attractiveness of the system** and therefore the submission of data related to non-human isolates

Proposed solution

Signal detection of multi-country events based on cg/wgMLST

Two interoperating workflows

Each workflow collects and stores the data (i.e. allelic profiles and descriptive data) of the respective data domain.
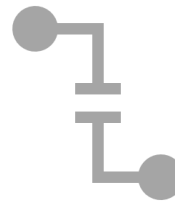
Cross-sector matches

Databases will be queried, and comparison will be performed live to the data stored, returning any matches (according to business rules)

Machine-to-machine

Automatic exchanging of **allelic profiles** and limited descriptive data as established in the Collaboration Agreement

Practical example
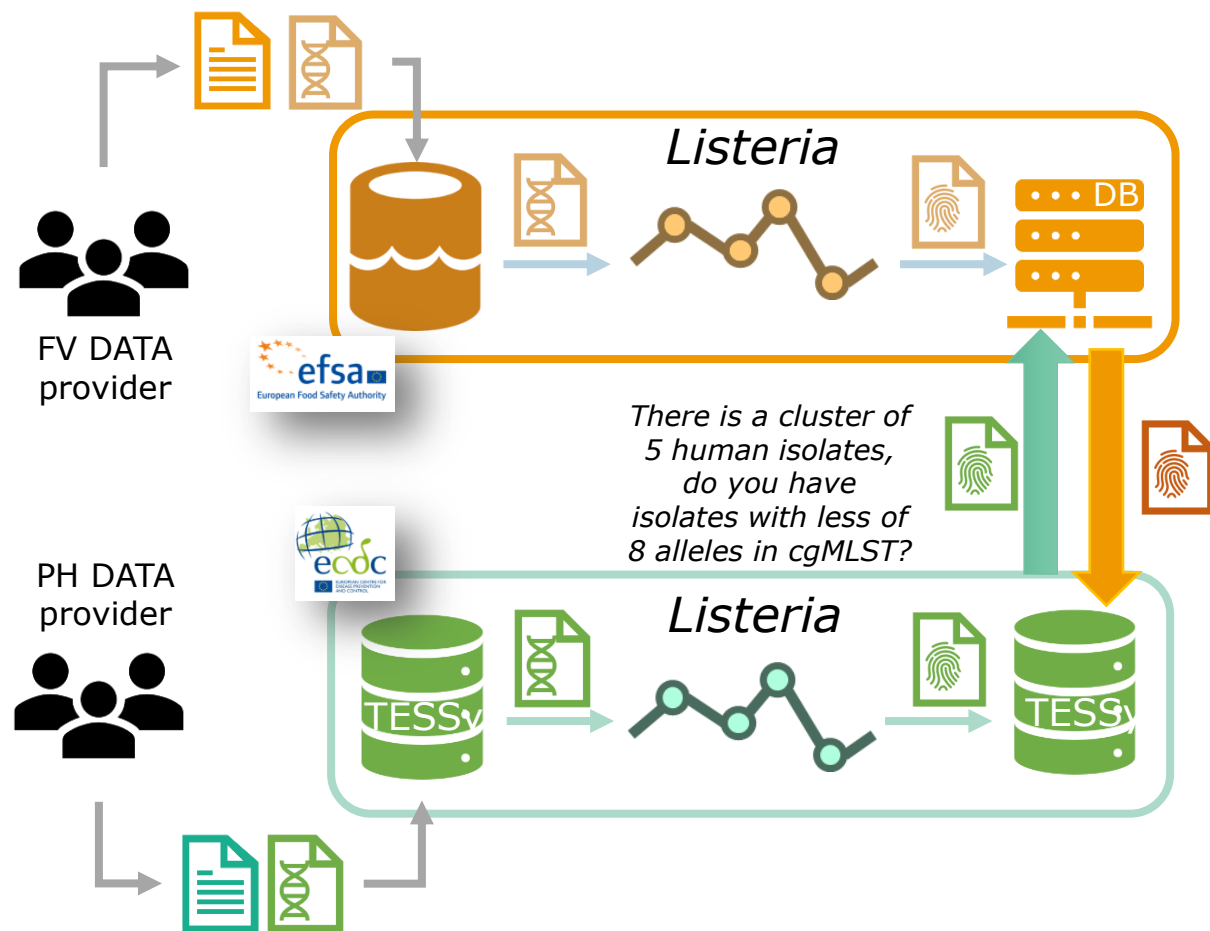
➢ **Container technology** allows sharing standard workflows

- Harmonization is ensured by sharing **identical pipeline**
- Analysis is **reproducible**

➢ **Decentralization** of the resources to data providers

- **Capacity building** at country level
- Raw can data remain at the owner level, if wished (only final results are shared)
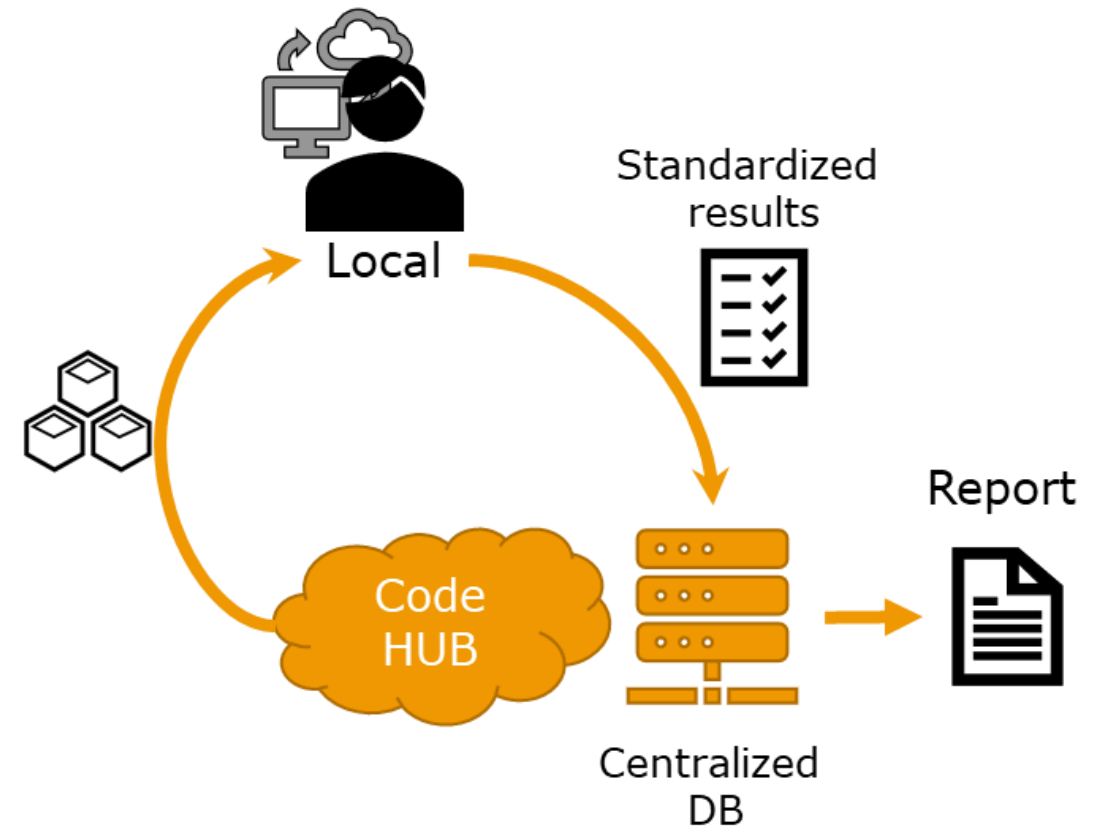
.. What do you think if only cgMLST allelic profiles need to be share?
.. Would you share data easier?

- Annual reporting of STEC in the EU
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- **Joint ECDC – EFSA assessments on EU-wide foodborne events**

Joint ECDC – EFSA assessments on EU-wide foodborne events

Joint Rapid Outbreak Assessment

- Aim: assess cross-border foodborne public health threat
- Active data collection, joint analyses
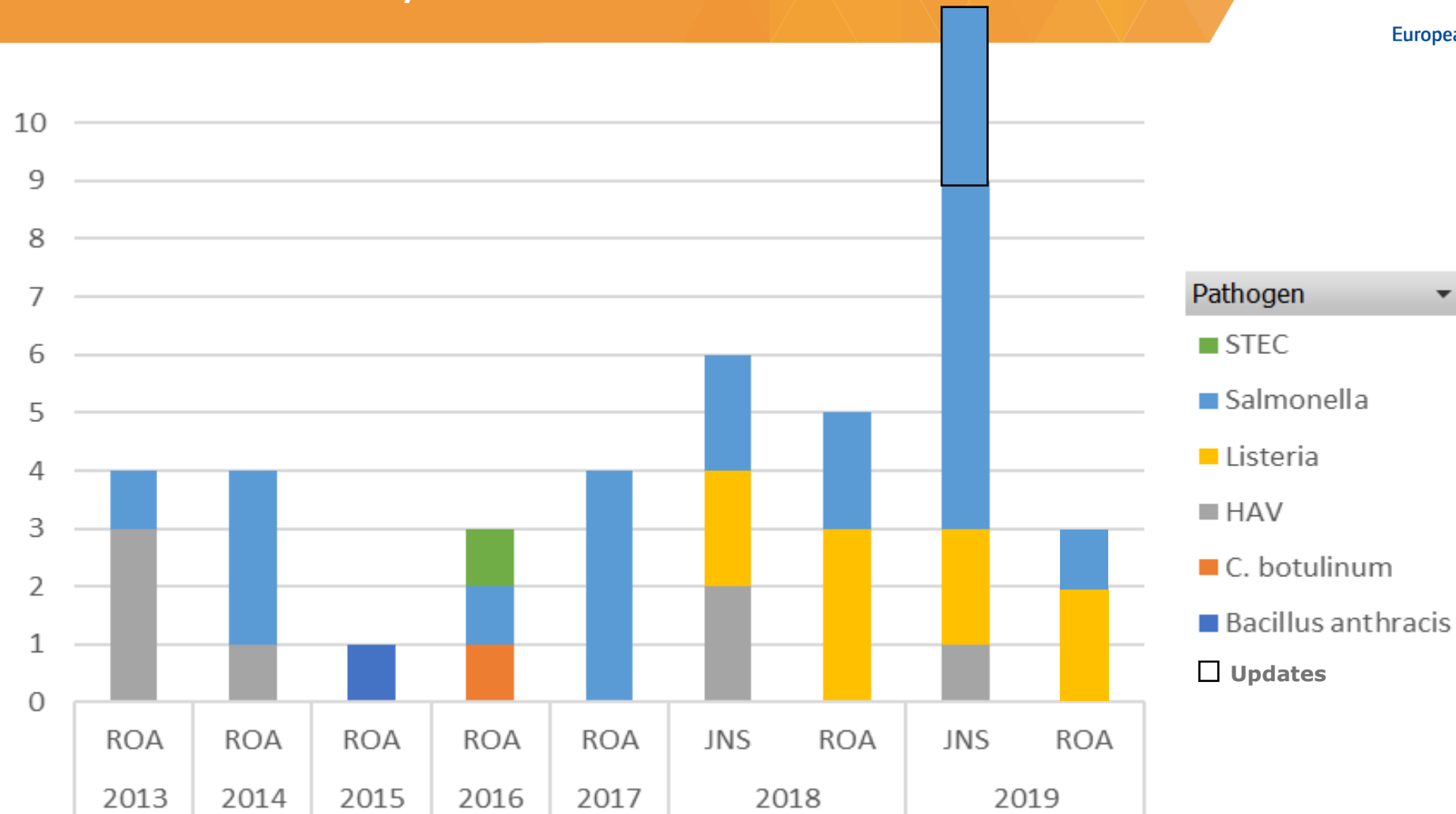- Agreed procedure

Joint Notification Summary

- Aim: immediate notification of a cross-border foodborne event to risk managers
- Based on available information
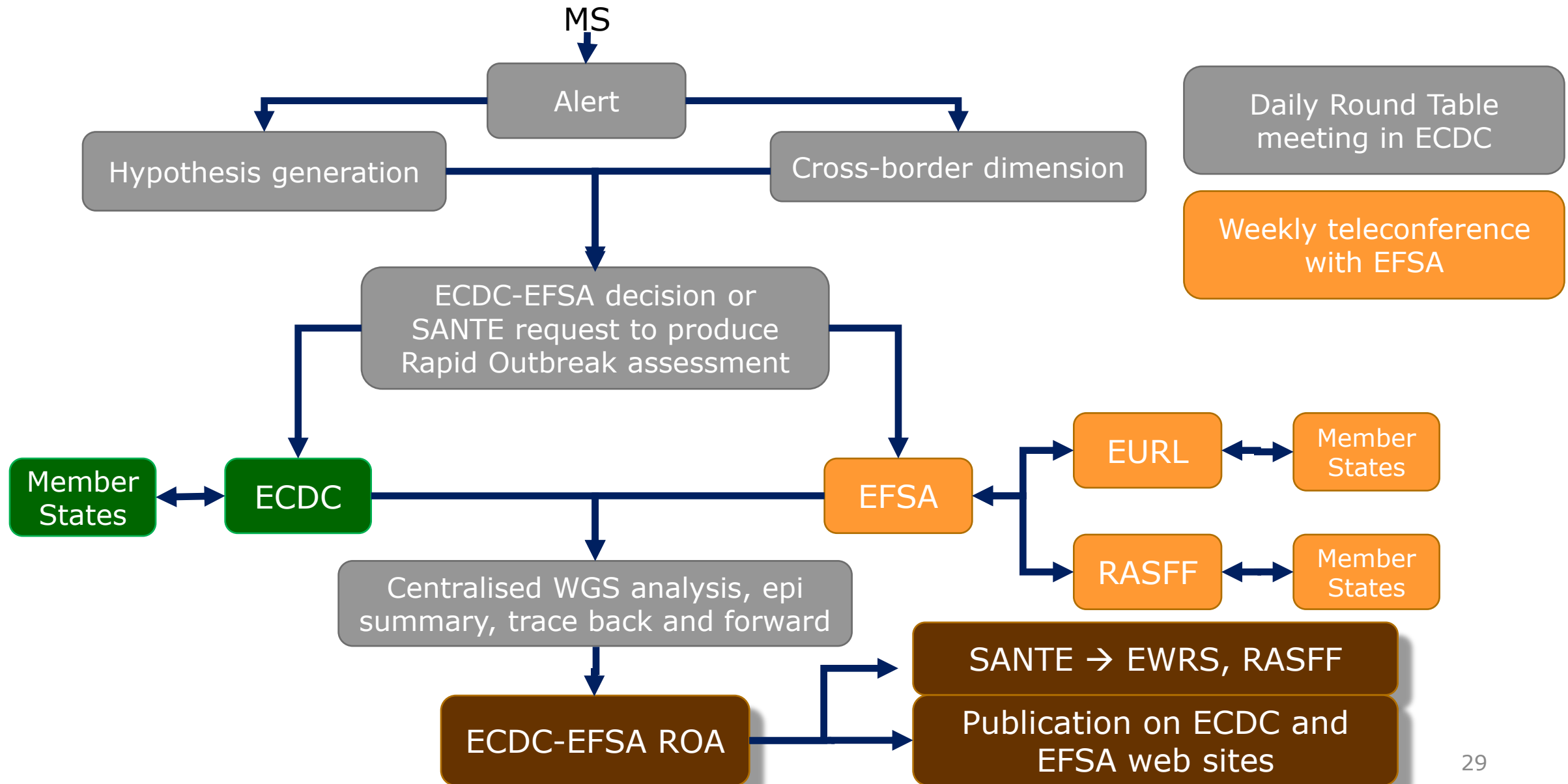
JNS = Joint Notification Summary

ROA = Rapid Outbreak Assessment

Thanks for your attention!

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Bertrand Lombard
Jean-Charles Leblanc

EURL *Salmonella*
Kirsten Mooijman

EURL *E. coli*
Stefano Morabito

EU/EEA Member States
For reporting PFGE and MLVA data

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