JOINT RAPID OUTBREAK ASSESSMENT

# Multi-country outbreak of *Salmonella* Enteritidis infections linked to Polish eggs

12 December 2017

## Conclusions and options for response

A multi-country outbreak of *Salmonella* Enteritidis linked to eggs from Poland is ongoing in the EU/EEA. Testing through whole genome sequencing (WGS) shows the isolates are part of four distinct but related genetic clusters. ECDC and EFSA are liaising with relevant authorities in the affected EU/EEA countries and the European Commission to facilitate the coordination of investigation and response measures.

From 1 February 2017 to 28 November 2017, eight EU/EEA countries have reported 196 confirmed cases of *Salmonella* Enteritidis belonging to four distinct WGS clusters, and 72 probable cases sharing one of the six *S.* Enteritidis multiple locus variable-number tandem repeat analysis (MLVA) outbreak profiles. Outbreak cases, both confirmed and probable, have been reported by Belgium, the Czech Republic, France, Luxembourg, the Netherlands, Norway, Sweden and the United Kingdom. In addition, 340 historical confirmed cases and 374 historical probable cases were reported before February 2017 by 16 countries (the previously listed eight countries plus Croatia, Denmark, Finland, Greece, Hungary, Ireland, Italy and Slovenia). The United Kingdom has reported the most cases (166 confirmed and three probable).

Additional *S.* Enteritidis cases have recently been reported by some of the above-mentioned EU countries but molecular typing results are pending.

The European outbreak case definition is based on a limited number of *S.* Enteritidis genotypes (four WGS clusters for the definition of confirmed cases and six MLVA profiles for the definition of probable cases), and is therefore extremely specific. In countries where MLVA or WGS is not undertaken routinely, additional cases are unlikely to be recognised as associated with this outbreak. An analysis of confirmed cases with a travel history to Bulgaria and Portugal in spring and summer 2017 shows that these two countries were probably affected by the outbreak.

Available evidence from epidemiological, microbiological and tracing investigations linked the cases in Sweden to consumption of eggs originating from one packing centre and two laying hen farms in Poland. The Norwegian egg product isolate was traced back to another packing centre and another laying hen farm in Poland. Information from investigations in the United Kingdom to date was not sufficient to identify the vehicle of infection for all cases, but for some cases the eggs identified as the likely source were traced back to a Polish laying hen farm. So far, no epidemiological connection has been identified between the four Polish farms and the two Polish packing centres involved in Swedish, Norwegian and British investigations. However, some food business operators involved in the event investigated in Norway, and one possibly involved in the investigations in the United Kingdom, were also implicated in the 2016 outbreak linked to Polish eggs [1]. The collection of more epidemiological information would support a more precise assessment.

---

Suggested citation: European Centre for Disease Prevention and Control and European Food Safety Authority. Multi-country outbreak of *Salmonella* Enteritidis infections linked to Polish eggs, 12 December 2017. ECDC and EFSA: Stockholm and Parma; 2017.

All *S.* Enteritidis isolates from food sampled in Sweden and Norway are closely genetically related (i.e. belonging to the same five single nucleotide polymorphism (SNP) single linkage clusters) to the strains identified in one of the human clusters included in the case definition. The isolates detected in food and environmental samples in the United Kingdom are closely related (i.e. clustered at t5 level) to the strains identified in another human cluster strain included in the case definition. No detections of *S.* Enteritidis have been reported in any farms identified in the present outbreak as the possible sources of contaminated eggs or in the holdings supplying the mentioned farms. However, some positive farms identified in the 2016 outbreak are epidemiologically or microbiologically linked to positive food sampled in Norway and the United Kingdom. This supports the hypothesis that there is persistent contamination of two or more premises with the *Salmonella* strains detected in the 2016 outbreak still circulating at the farm level in Poland.

EU/EEA countries should consider interviewing patients infected with outbreak strains of *S.* Enteritidis, following up on clusters associated with food outlets and performing appropriate investigations in food and related supply chains at those food outlets. Isolates with outbreak MLVA profiles should be sequenced. ECDC offers sequencing services for human isolates. A cluster analysis of the sequences should be performed using the Public Health England (PHE) single nucleotide polymorphisms (SNP) pipeline, as per the European outbreak case definition.

New human cases and developments on public health investigations should be reported to EPIS-FWD (Epidemic Intelligence Information System for Food- and Waterborne Diseases and Zoonoses).

Data gaps regarding food investigations in some countries have hampered the proper assessment of the epidemiological connections and microbiological contamination at primary production level and at other food business operators downstream in the food chain. Epidemiological data, especially for food/veterinary isolates, are essential to confirm the outcome of microbiological investigations. It is recommended that the involved countries carry out further epidemiological studies and tracing investigations to identify the food business operators at the source of the outbreak. Characterisation of food/veterinary isolates by WGS methods is encouraged to support the multi-country analyses. EURL *Salmonella* can provide technical support to countries' laboratories with regard to subtyping isolates from food samples.

ECDC and EFSA encourage the competent authorities in the food safety and the public health sectors in the affected EU/EEA countries and at the European level to continue sharing information on the epidemiological, microbiological and environmental investigations, including issuing relevant notifications using the Rapid Alert System for Food and Feed (RASFF) and the Early Warning and Response System (EWRS), the latter of which represents the official channel to notify cross-border threats. RASFF notifications should be completed with information on the exposure to food of related human cases, traceability information on the suspected food vehicles and WGS/MLVA results to support traceability investigations.

# Source and date of request

European Commission Directorate General for Health and Food Safety request, 10 October 2017.

# Public health issue

This document provides an assessment of the public health risk associated with a multi-country outbreak of *Salmonella* Enteritidis, which is epidemiologically and microbiologically linked to contaminated eggs from Poland, and can be characterised by at least six MLVA profiles and four clusters defined by WGS (PHE SNP analysis). A large proportion of the cases under analysis in this document have previously been presented in the update of the joint ECDC/EFSA rapid outbreak assessment published by ECDC and EFSA on 7 March 2017 'Multi-country outbreak of Salmonella Enteritidis phage type 8, MLVA profile 2-9-7-3-2 and 2-9-6-3-2 infections' [1].

# Consulted experts

ECDC experts (in alphabetical order): Saara Kotila, Taina Niskanen, Daniel Palm, Ettore Severi, Johanna Takkinen, Therese Westrell.

EFSA experts (in alphabetical order): Frank Boelaert, Domenico Deserio, Beatriz Guerra, Ernesto Liebana Criado, Olaf Mosbach-Schulz, Valentina Rizzi.

External experts representing national authorities (by alphabetical order of countries):

- Belgium: Wesley Mattheus, Sofieke Klamer (National Institute of Public Health – WIV-ISP), Vera Cantaert (Belgian Federal Agency for the Safety of the Food Chain);
- Croatia: Hunjak Blazenka (Institute of Public Health – HZJZ), Vera Katalinic-Jankovic (Ministry of Health);
- the Czech Republic: Michaela Špačková (National Institute of Public Health);
- Denmark: Steen Ethelberg (Statens Serum Institut);
- France: Nathalie Jourdan-Da Silva (Santé publique France), Simon Le Hello (Institut Pasteur);
- Hungary: Katalin Krisztalovics (Ministry of Human Capacities), Judit Pászti (Public Health Institute);
- Italy: Ida Luzzi (Istituto Superiore di Sanità);
- Luxembourg: Joël Mossong, Catherine Ragimbeau (National Health Laboratory);
- the Netherlands: Kirsten Mooijman (EU Reference Laboratory Salmonella), Eelco Franz, Ingrid Friesema, Roan Pijnacker (National Institute for Public Health and the Environment – RIVM), Judith Leblanc, Ife Slegers – Fitz-James (Food and Consumer Product Safety Authority – NVWA);
- Norway: Karin Nygård and Lin Thorstensen Brandal (Norwegian Institute of Public Health – NIPH), Margrethe Hovda Røed and Erik Løwe (Norwegian Food Safety Authority);
- Poland: Karolina Florek, Joanna Golebiowska, Krzysztof Jażdżewski (General Veterinary Inspectorate);
- Slovenia: Eva Grilc (National Institut of Public Health - NIJZ), Marija Trkov (National Laboratory of Health, Environment and Food - NLZOH);
- Sweden: Cecilia Jernberg, Linda Trönnberg (Public Health Agency of Sweden), Mats Lindblad and Karin Westholm (National Food Agency);
- the United Kingdom: Lesley Larkin, Jacquelyn McCormick, Gareth Hughes, Lara Utsi, Tim Dallman (Public Health England – PHE), Sarah Couper, John Coia (Health Protection Scotland – HPS), Paul Cook, Antonis Ampatzoglou, Drazenka Tubin-Delic, Deb Morgan, Tina Potter (Food Standards Agency).

# Disclaimer

ECDC issued this outbreak assessment document in accordance with Article 10 of Decision No 1082/13/EC and Article 7(1) of Regulation (EC) No 851/2004 establishing a European Centre for Disease Prevention and Control (ECDC), and with the contribution of the European Food Safety Authority (EFSA) in accordance with Article 31 of Regulation (EC) No 178/2002 of the European Parliament and of the Council of 28 January 2002 laying down the general principles and requirements of food law, establishing the European Food Safety Authority (EFSA) and laying down procedures in matters of food safety.

In the framework of ECDC's mandate, the specific purpose of an ECDC outbreak assessment is to present different options on a certain matter with their respective advantages and disadvantages. The responsibility on the choice of which option to pursue and which actions to take, including the adoption of mandatory rules or guidelines, lies exclusively with EU/EEA Member States. In its activities, ECDC strives to ensure its independence, high scientific quality, transparency and efficiency.

This report was written under the coordination of an internal response team at ECDC and with contributions by EFSA, as requested by the European Commission based on a mandate requesting scientific assistance of EFSA in the investigation of multinational food-borne outbreaks (Ares (2013) 2576387, Mandate M-2013-0119, 7 July 2013).

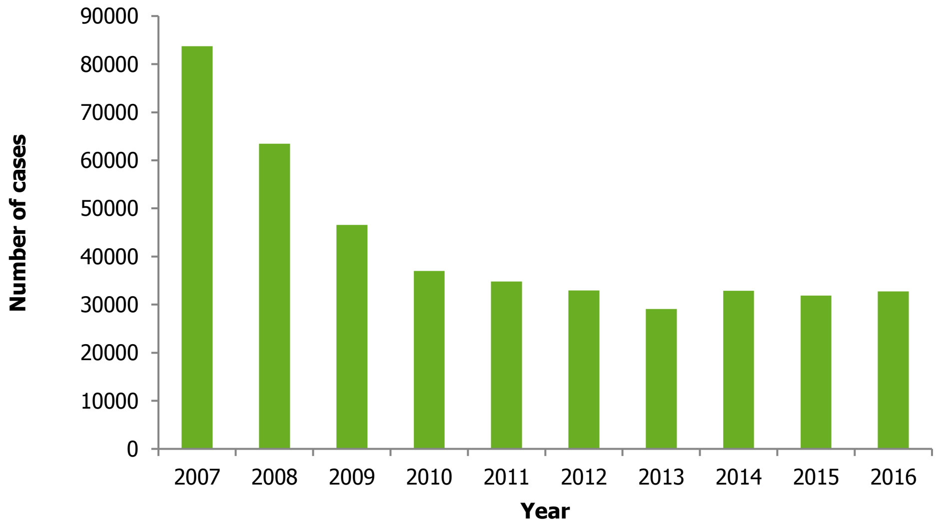
All data published in this rapid outbreak assessment are correct to the best of our knowledge on 22 November 2017. Maps and figures published do not represent a statement on the part of ECDC, EFSA or its partners on the legal or border status of the countries and territories shown.

# Disease background information

## *Salmonella* Enteritidis isolations in humans

*S.* Enteritidis is the most commonly detected serovar in cases of human non-typhoidal salmonellosis in Europe. It has declined substantially since the beginning of EU surveillance in 2007 (Figure 1), most likely as a result of successful control measures implemented under Regulation (EC) No. 2160/2003 in poultry population and measures aimed at food business operators to improve hygiene implemented under the EU Food Law, including the introduction of microbiological criteria for *Salmonella* [2].

**Figure 1. Number of confirmed cases of *Salmonella* Enteritidis by year, EU/EEA, 2007–2016**



*Source: ECDC [3]*

From 2007 to 2016, 425 057 cases of *S.* Enteritidis were reported to The European Surveillance System (TESSy) (mean number of cases per year 42 506, range 29 089 to 83 756) by 27 countries, with Germany and the Czech Republic reporting 50% of all cases. The median age for all cases with information available was 28 years (interquartile range IQR=5–49); 52% (n=218 527) were female, and 89% (n=319 650) of infections were acquired in the reporting country. Reporting dates were distributed over the year, with a peak from July to September. To date, 7 653 *S.* Enteritidis cases have been reported by 14 countries to TESSy for 2017 (data not yet published) [3].

## *Salmonella* Enteritidis MLVA profiles in TESSy

[4]EU/EEA-wide collection of *S.* Enteritidis MLVA data into TESSy using a validated scheme [4] started in June 2016. As of 23 November 2017, eight countries have submitted MLVA data for *S.* Enteritidis, including 205 *S.* Enteritidis isolates with the MLVA profile 2-9-7-3-2, the main MLVA type associated with this outbreak. In addition, 144 isolates with the outbreak-associated MLVA types (2-9-6-3-2, 2-9-10-3-2, 2-10-6-3-2, 2-10-8-3-2 and 2-11-8-3-2) have been reported (see Table 1). Besides isolate-based reporting into TESSy, additional cases with isolates of these MLVA profiles were reported to ECDC through EPIS-FWD.

**Table 1. Number of *Salmonella* Enteritidis isolates reported to TESSy with MLVA profiles identical to the outbreak case definition**

| MLVA profile | Isolates in TESSy | |
|---|---|---|
| | Number | Proportion |
| 2-9-6-3-2 | 13 | 0.3% |
| 2-9-7-3-2 | 205 | 4.7% |
| 2-9-10-3-2 | 4 | 0.1% |
| 2-10-6-3-2 | 38 | 0.9% |
| 2-10-8-3-2 | 75 | 1.7% |
| 2-11-8-3-2 | 14 | 0.3% |
| Total isolates with MLVA characterisation in TESSy | 4 400 | 100% |

# Food-borne outbreaks caused by *Salmonella* Enteritidis

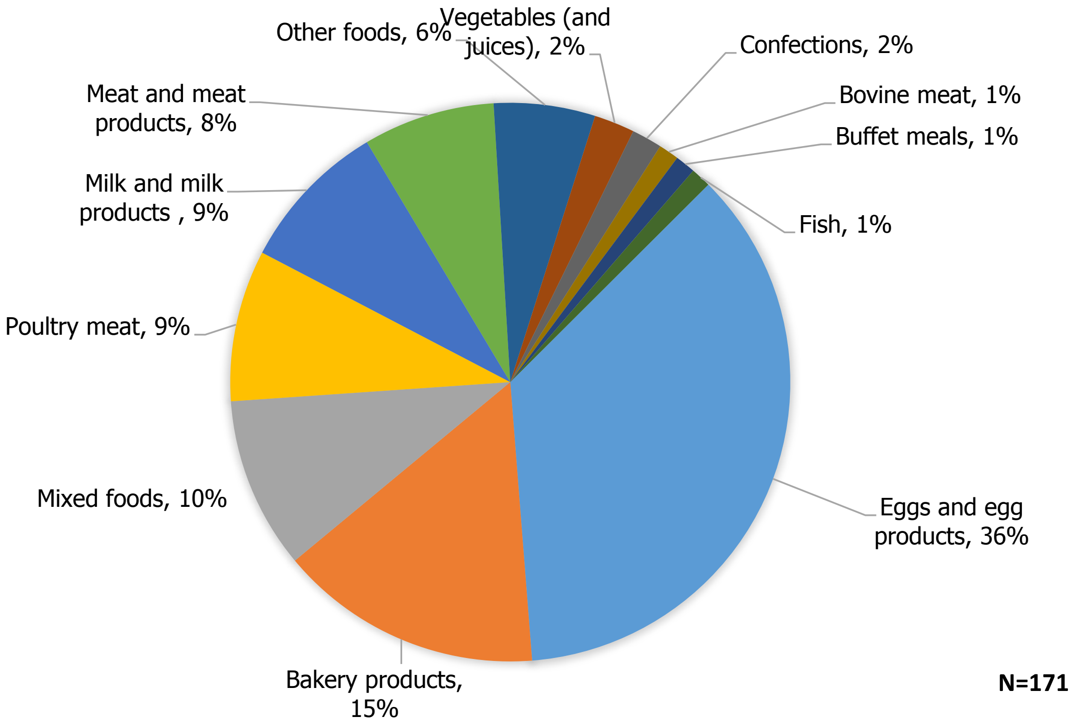
*S.* Enteritidis was the predominant serovar associated with *Salmonella* outbreaks during 2016. It was reported in 713 (66.8%) of the 1 067 reported salmonellosis outbreaks in the EU, meaning *S.* Enteritidis was the causative agent in about one in six (14.9%) of the 4 786 reported outbreaks. Food-borne outbreaks due to *S.* Enteritidis during 2016 were associated with 6 200 cases (68.4% of all 9 061 cases in *Salmonella* outbreaks) in the EU [5].

Compared with 2015, a 23.6% increase in the number of outbreaks due to *S.* Enteritidis was reported at EU-level in 2016, with 13 Member States (Austria, Belgium, Denmark, Germany, Greece, Hungary, Ireland, Italy, Latvia, Lithuania, the Netherlands, Poland and Slovakia) reporting a higher number of outbreaks than in 2015. Slovakia (n= 250) and Poland (n= 203) reported the highest number of outbreaks due to *S.* Enteritidis and reported an increase of 23.2% and 42.0% compared with 2015, respectively. A marked increase was also reported by Hungary with the 2016 number of outbreaks by *S.* Enteritidis (n=21) being almost twice the number reported for 2015. Still, considering the period 2010–2016, the overall trend of number of outbreaks of *S.* Enteritidis outbreaks decreased, at the EU-level.

For 171 of these *S.* Enteritidis food-borne disease outbreaks, evidence supporting an association with the suspected food vehicle was strong, and as in previous years, 'eggs and egg products' were the food vehicles most frequently associated with *S.* Enteritidis outbreaks.

In 2016, information on phage type was only provided for 48 food-borne outbreaks caused by *S.* Enteritidis. Nineteen of these outbreaks were due to *S.* Enteritidis PT8 and involved 552 human cases. For 12 of the 19 *S.* Enteritidis PT8 outbreaks, the evidence supporting the association with the suspected food vehicle was reported to be strong: it was associated with the consumption of 'eggs and egg products' (nine outbreaks), 'Broiler meat (*Gallus gallus*) and products thereof' (two outbreaks) and 'Bovine meat and products thereof' (one outbreak). No information on MLVA typing was reported.

Figure 2. **Distribution of food vehicles in strong-evidence food-borne outbreaks caused by *Salmonella* Enteritidis, EU, 2016 (n=171)**



*Source: The European Union summary report on trends and sources of zoonoses, zoonotic agents, and food-borne outbreaks in 2016, EFSA [5]*

*Note: Data from 171 outbreaks are included: Austria (7), Belgium (3), Croatia (4), the Czech Republic (5), Finland (1), France (17), Germany (6), Greece (3), Hungary (9), Lithuania (21), Luxembourg (1), the Netherlands (1), Poland (83), Romania (1), Slovakia (6), the United Kingdom (3). In 2016, the pre-accession country Montenegro reported 5 strong-evidence food-borne S. Enteritidis outbreaks.*

*Other foods (N=10) include: Cereal products and legumes (1), Fruits (and juices) (1), Other foods (unspecified) (5), Pig meat (1), Sheep meat (1), Unknown (1).*

# *Salmonella* Enteritidis isolations in food, animals and feed

EU/EEA countries have frequently reported *S.* Enteritidis from food and animals in the framework of the monitoring on zoonoses and zoonotic agents based on Directive 2003/99/EC [6].

From 2004 to 2016, the EU/EEA Member States reported a total of 6 908 units that were positive for *S.* Enteritidis from several food categories (Annex 1, Table 1). The main categories were meat from broilers (meat from *Gallus gallus* chickens including spent hens) (n=3 317), followed by meat from other or unspecified poultry species (n=1 222), eggs and egg products (n=1 102), meat from pigs (n=308) and other types of meat, including bovine meat, mixed and unspecified meat (n=399). *S.* Enteritidis was reported less frequently from additional food categories, such as 'fish and fishery products' (n=75), 'dairy products (including cheese) and milk' (n=34), fruits and vegetables (including 'spices and herbs' and 'sprouted seeds') (n=37) and several other foods (n=414).

In the same period, the EU/EEA Member States reported a total of 30 680 units that were positive for *S.* Enteritidis from several animal species, primarily from chickens (*Gallus gallus*) (n=25 587), followed by cattle (n=1 263), 'other or unspecified poultry or game birds' (n=651), geese (n=517), ducks (n=448), turkeys (n=413), pigs and wild boars (n=408). *S.* Enteritidis isolations were less frequently reported from other animal species. It should be clarified that reporting to the EU of *S.* Enteritidis isolates from poultry is mandatory according to EU Regulation (EC) No 2160/2003 [2] and its following amendments. This legislation obliges Member States to set up *Salmonella* National Control Programmes aimed at reducing the prevalence of *Salmonella* serovars, which are considered relevant for public health, in poultry populations. For non-poultry populations, reporting of serovar-specific data like *S.* Enteritidis is not mandatory, hence, Member States could decide not to report on *S.* Enteritidis in animal species other than poultry, which could lead to a possible reporting bias on *S.* Enteritidis in poultry populations as opposed to other animal species.

From 2004 to 2016, *S.* Enteritidis was also detected in 270 units of different feed categories: compound feedingstuffs for poultry (n=72), other or unspecified types of feedingstuffs/feed material (n=48), pet food (n=37), feed material of land animal origin (n=35), feed material of oil seed or fruit origin (n=21), feed material of marine animal origin (n=18), feed material of cereal grain origin (n=17), compound feedingstuffs for pigs (n=11) and compound feedingstuffs for cattle (n=11).

In 2016, 578 units positive for *S.* Enteritidis were reported from food of which the majority (n=275, 47.6%) was from broiler meat (meat from *Gallus gallus* chickens excluding spent hens). *S.* Enteritidis isolations from such broiler meat were provided by 12 Member States, mainly by Poland, the Czech Republic and Slovakia that reported 63.6%, 13.5% and 12.7% respectively of the total 275 *S.* Enteritidis isolations from broiler meat. In 2016, isolations of *S.* Enteritidis from eggs (n=24) and egg products (n=3) were reported by six Member States, mainly Romania, which reported 15 isolations from table eggs. Additional *S.* Enteritidis isolations from table eggs were reported by Slovakia (n=2), Bulgaria (n=2) and Hungary (n=1). Italy reported four isolates from unspecified eggs. The only isolation of *S.* Enteritidis from liquid egg products was reported by Hungary, while the Czech Republic and Romania both reported one isolate from egg products. Bosnia and Herzegovina reported eight isolates from meat from other animal species.

The majority of the 2016 *S.* Enteritidis isolations in animals (n=1 612) were obtained from fowl (*Gallus gallus*) (n=852 isolations, representing 52.9% of the total), followed by other animals (n=607; 600 isolates from foxes and six from mink both reported by Poland, and one isolate from a rodent in Switzerland), other poultry species or game birds (including ducks, geese and turkeys) (n=102) and pigs and wild boars (n=17). *S.* Enteritidis isolations were less frequently reported from several other animal species, including cattle, domestic solipeds, reptiles, cats, dogs, and other birds (Annex 1, Table 1). Out of the 852 *S.* Enteritidis isolations reported from fowl (*Gallus gallus*), 464 isolations were reported from laying hens flocks, 320 from broiler flocks and 68 isolations from breeding flocks (including parent and grandparent breeding flocks). In 2016, *S.* Enteritidis was widely isolated from fowl chickens in the EU, with the following Member States reporting the highest number of isolates: Poland (n=247), France (n=217), the Czech Republic (n=59), Germany (n=56) and Romania (n=51). Switzerland reported 13 isolates; 12 from laying hens and one from broilers.

According to Regulation 2160/2003 [2], EU Member States are subject to national control programmes for *Salmonella* in poultry populations and it is compulsory to report isolations of *S.* Enteritidis. *S.* Enteritidis isolates from breeding flocks were reported by seven EU Member States, mostly from Poland (n=26), the Netherlands (n=9) and France (n=6). Nineteen Member States and one non-EU Member State reported *S.* Enteritidis isolates from laying hen flocks; among these countries, the highest numbers of isolates from laying hen flocks were reported by Poland (n=169), France (n=69) Germany (n=54), Spain (n=30) and the Netherlands (n=24). At the EU-level, the *S.* Enteritidis flock prevalence was 1.21% in 2016, compared with 0.80% in 2015. Poland reported a *S.* Enteritidis flock prevalence of 7.15%, compared with 2.84% in 2015. In 2016, thirteen Member States reported *S.* Enteritidis from broiler flocks, with the majority of isolates reported by France (n=132), Poland (n=52), the Czech Republic (n=50) and Romania (n=45).

In 2016, 16 *S.* Enteritidis isolations in feed were reported by six Member States and one non-Member State: three isolations from compound feedingstuffs for poultry, three isolations from compound feedingstuffs for cattle, two isolations from compound feedingstuffs for pigs, three isolations from pet food, three isolations from feed material of land animal origin, and two isolates in other feedingstuffs. *S.* Enteritidis isolations from feed were reported by Belgium (n=3), the Netherlands (n=1), Latvia (n=3), Luxembourg (n=2), Spain (n=3), Croatia (n=2) and Iceland (n=2).

Information on the *S.* Enteritidis isolations reported in food, animals and feed from 2004 to 2016 are summarised in Annex 1, Table 1.

Information on phage type is usually not reported in the context of the monitoring of zoonoses and zoonotic agents in food, animals and feed based on Directive 2003/99/EC. Isolations of *S.* Enteritidis PT8 in food and animals were only provided by a few Member States in the period 2013–2016. In 2014, 22 isolations of *S.* Enteritidis PT8 were reported, 18 of which were from fowl (*Gallus gallus*), two from domestic solipeds, and two from pig meat. In 2015, only four *S.* Enteritidis PT8 isolations were reported: two isolations from broiler meat reported by Ireland and two isolations from feed reported by the United Kingdom. For 2016, 13 PT8 isolates from broiler meat and 1 PT8 isolate from mixed meat products were reported by the Czech Republic; eight PT8 isolates from laying hens flocks were reported by Austria.

Until 2012, Member States provided EFSA with isolate level information on *Salmonella* serovars and phage types from laboratories within Member States[*], in addition to monitoring data on *Salmonella* reported in the framework of Directive 2003/99/EC. During the period 2004–2012, the laboratories provided information on 239 isolations of *S.* Enteritidis PT8 from food – mainly from broiler meat (n=119), followed by eggs (n=37) – whereas only few *S.* Enteritidis PT8 isolations from other types of foods were reported. During the same period, the laboratories provided information on 1 369 *S.* Enteritidis PT8 isolations from animals, primarily fowl (*Gallus gallus*), from which 1 160 isolations were reported.

# Event background information

Following two urgent enquiries from Scotland and Netherlands regarding increases in *Salmonella* Enteritidis isolates in January and August 2016, an EU-level investigation identified a multi-country outbreak that was linked to egg production in Poland.

Using Public Health England's (PHE) in-house pipeline and nomenclature for WGS analysis, the threshold for inclusion in one of the two WGS clusters was set to ≤5 SNP difference (t5 level) to at least one other case in the cluster [7-9]. The SNP addresses at t5 level for the two WGS clusters initially part of the outbreak confirmed case definition were 1.2.3.175.175.175.% (WGS cluster_175, accession number SRR3285443) and 1.2.3.18.359.360.% (WGS cluster_360; accession number: SRR4063700). The %-sign in the SNP address represents a 'wildcard' character, i.e. it represents any number denoting the 0-SNP level, all variations of which are included for isolates clustering at the 5-SNP threshold level.

The MLVA profiles defining probable outbreak cases were MLVA profile 2-9-7-3-2 and 2-9-6-3-2.

The outbreak investigation identified a link between the outbreak of *S.* Enteritidis infections and Polish eggs. The epidemiological, microbiological and tracing investigations traced the Polish eggs back to three egg packing centres and 52 laying hen farms. Eighteen of the 52 farms were found positive for *S.* Enteritidis. Ten *S.* Enteritidis isolates from three of the 18 *Salmonella* positive farms in Poland were characterised further: eight isolates belonged to the WGS clusters identified by the case definition (cluster_175 and cluster_360), while the remaining two isolates with different SNP addresses (1.2.3.18.455.469.6307 and 1.2.3.18.455.2440.6301) clustered at t25 level with the WGS cluster_360. Of the 10 primary production isolates, seven had a MLVA profile identified by the case definition (MLVA 2-9-7-3-2), while the remaining three isolates had other MLVA profiles (2-10-6-3-2; 2-10-8-3-2; 2-11-8-3-2). Information on the other *S.* Enteritidis primary production isolates detected in the remaining 15 *S.* Enteritidis-positive Polish farms have been pending since December 2016 [1].

In March 2017, ECDC and EFSA published a joint rapid outbreak assessment describing the outbreak investigation and the control measures implemented in the previous months that led to a rapid reduction in the occurrence of cases, with only five outbreak cases reported in February 2017.

In June and September 2017, ECDC reported new increases in *S.* Enteritidis outbreak cases. Two *S.* Enteritidis isolates, from Luxembourg and Scotland, with MLVA profile 2-9-10-3-2 were found belonging to the WGS cluster_175 associated with the Polish eggs outbreak. In addition, in September 2017, Sweden launched a new urgent inquiry describing a cluster of 10 *S.* Enteritidis cases with isolates belonging to the SNP address 1.2.3.18.455.469.% (WGS cluster_469) and with MLVA profile 2-10-7-3-2 n EPIS-FWD.

---

[*] Any comparison between the reporting of *S.* Enteritidis PT8 isolations in food and animals from the laboratories and the isolations of *S.* Enteritidis collected in the framework of the Directive 2003/99/EC (as summarised in Table 1 of Annex 1) should be avoided because data are derived from two different sources and are not comparable.

An isolate from a Polish farm with this SNP address had already been detected in 2016 during the investigation of the previous outbreak [1]. The Swedish cases had consumed eggs or food items prepared with eggs. Eggs from Poland were identified as the likely source of infection.

Following these events, ECDC, EFSA and the affected EU/EEA countries broadened the European outbreak case definition to take into account all WGS clusters and MLVA profiles identified in human cases linked through the egg packing centres to the *S.* Enteritidis-positive Polish farms during the previous outbreak. The MLVA profile 2-10-7-3-2, identified in the Swedish cases in September 2017, was not included in the case definition as WGS of isolates of this type had shown that this MLVA profile had very little specificity.

The new European outbreak case definition was broadened in November 2017 and is as follows:

**A confirmed outbreak case**

- A laboratory-confirmed *Salmonella* Enteritidis case with symptoms onset on or after 1 February 2017 (date of sampling or date of receipt by the reference laboratory if date of onset is not available).

  AND

- Fulfilling the additional laboratory criterion: with a strain sharing the same t5-level SNP address as one of the defined United Kingdom outbreak clusters based on WGS analysis: 1.2.3.175.175.175.% (WGS cluster_175 – accession number SRR3285443) OR 1.2.3.18.359.360.% (WGS cluster_360 – accession number SRR4063700) OR 1.2.3.18.455.469.% (WGS cluster_469 – accession number ERR2173854) OR 1.2.3.18.455.2440.% (WGS cluster_2440 – accession number SRR4063739).

**A probable outbreak case**

- A laboratory-confirmed *Salmonella* Enteritidis case with symptoms onset on or after 1 February 2017 (date of sampling or date of receipt by the reference laboratory if date of onset is not available)

  AND

- Fulfilling the following laboratory criterion: with a strain matching the MLVA profile 2-9-7-3-2 OR 2-9-6-3-2 OR 2-9-10-3-2 OR 2-10-6-3-2 OR 2-10-8-3-2 OR 2-11-8-3-2 corresponding to the MLVA protocol with 5 loci [4].

**A historical confirmed case**

- A laboratory-confirmed *Salmonella* Enteritidis case with a strain sharing the same t5-level SNP address as one of the confirmed outbreak clusters based on WGS analysis and date of disease onset from January 2012 to January 2017 (date of sampling or date of receipt by the reference laboratory if date of onset is not available).

**A historical probable case**

- A laboratory-confirmed *Salmonella* Enteritidis case with a strain with MLVA profile 2-9-7-3-2 or 2-9-6-3-2 or 2-9-10-3-2 or 2-10-6-3-2 or 2-10-8-3-2 or 2-11-8-3-2 and date of disease onset from January 2012 to January 2017 (date of sampling or date of receipt by the reference laboratory if date of onset is not available).

**Exclusion criteria**

- Cases with travel history outside of the EU/ EEA in the seven days prior onset.
- Secondary cases defined as those confirmed cases that have had person-to-person contact with a confirmed case and no exposure to a common source.
- Cases infected with MLVA profile 2-9-6-3-2 or 2-9-7-3-2 or 2-9-10-3-2 or 2-10-6-3-2 or 2-10-8-3-2 or 2-11-8-3-2, but not sharing the t5-level SNP address as one of the confirmed outbreak WGS clusters described above.

# Epidemiological and microbiological investigation of human cases

As of 28 November 2017, 16 EU/EEA countries have reported 196 confirmed and 72 probable cases associated with this outbreak since February 2017, in addition to 340 historical confirmed cases and 374 historical probable cases reported before 1 February 2017 (Table 2). Since 1 February 2017, the United Kingdom has reported the most cases in this outbreak with 169 associated cases. Norway (n=30), Sweden (n=24), Belgium (n=23), the Netherlands (n=12), France (n=5), the Czech Republic (n=3) and Luxembourg (n=2) were also affected.

**Table 2. Number of isolates by case classification and country, EU/EEA, February 2012 to November 2017 (n=982), as of 28 November 2017**

| Country | Number of isolates | | | | |
|---|---|---|---|---|---|
| | Confirmed | Probable | Historical confirmed | Historical probable | Total |
| Belgium | 0 | 23 | 14 | 126 | **163** |
| Croatia | 0 | 0 | 4 | 0 | **4** |
| Czech Republic | 0 | 3 | 0 | 3 | **6** |
| Denmark | 0 | 0 | 6 | 2 | **8** |
| Finland | 0 | 0 | 1 | 1 | **2** |
| France | 5 | 0 | 8 | 1 | **14** |
| Greece | 0 | 0 | 0 | 2 | **2** |
| Hungary | 0 | 0 | 0 | 5 | **5** |
| Ireland | 0 | 0 | 0 | 9 | **9** |
| Italy | 0 | 0 | 1 | 19 | **20** |
| Luxembourg | 1 | 1 | 5 | 0 | **7** |
| Netherlands | 4 | 8 | 88 | 166 | **266** |
| Norway | 10 | 20 | 11 | 32 | **73** |
| Slovenia | 0 | 0 | 3 | 0 | **3** |
| Sweden | 10 | 14 | 12 | 2 | **38** |
| United Kingdom | 166 | 3 | 187 | 6 | **362** |
| **Total** | **196** | **72** | **340** | **374** | **982** |
| | **268** | | **714** | | |

The median age at infection of the 196 confirmed cases was 29 years (IQR 15–52); information on gender was available for 194 cases 100 (52%) of whom were female patients. The median age at infection of the 72 probable cases was 29 years (IQR 13-52) and 33 (46%) were in female patients. In 2017, outbreak cases peaked in September when 58 confirmed and 16 probable cases were reported (Figure 3). The 196 confirmed cases reported since 1 February 2017 belong mostly to WGS cluster_175 (105 cases, 54%) and cluster_360 (78 cases, 40%) (Figure 3). Based on the PHE WGS analysis pipeline, the minimum SNP difference between the two larger clusters, cluster_175 and cluster_360, is 70 SNPs. Cluster_360, cluster_2440 and cluster_469 fall within a 25-SNP cluster. There is a minimum SNP distance of 24 SNPs between cluster_360 and cluster_469 and a minimum of 21 SNPs between cluster_360 and cluster_2440. Within the clusters, there is a variation of 16 SNPs within cluster_175, 37 SNPs within cluster_360, 7 SNPs within cluster_2440 and 10 SNPs within cluster_469.

**Figure 3. Distribution of outbreak cases by month and case definition, EU/EEA, January 2015 to November 2017 (n=873, one historical probable case missing month of report), as of 28 November 2017**

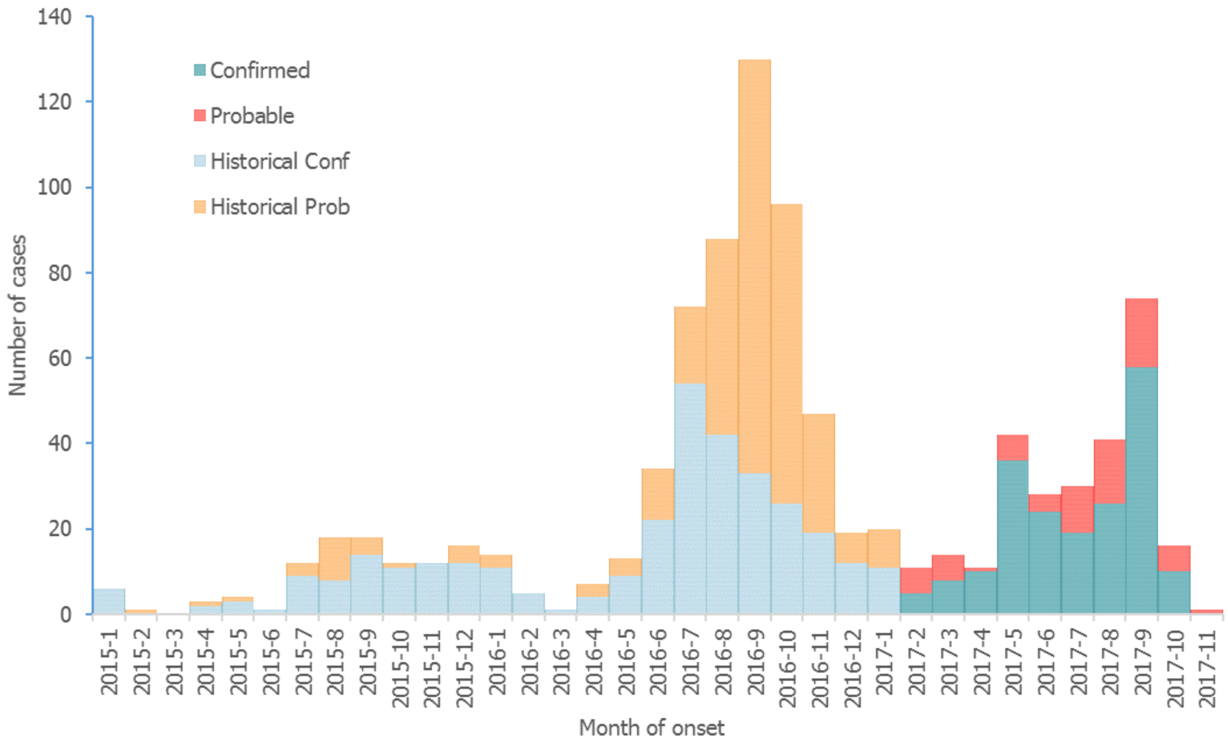
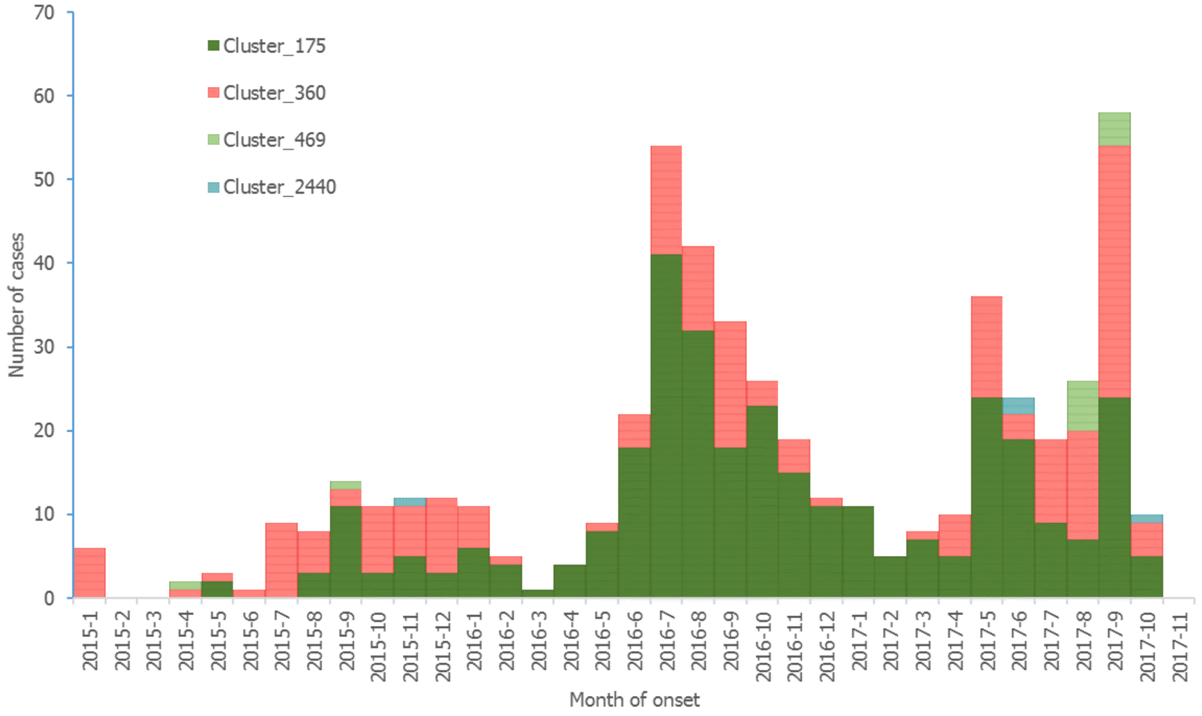


**Figure 4. Distribution of outbreak confirmed and historical confirmed cases by month and genetic cluster, EU/EEA, January 2015 to November 2017 (n=523), as of 28 November 2017**



Most confirmed and probable cases with available information on MLVA profile (n=95) have MLVA profile 2-9-7-3-2 (n=60). The remaining 35 isolates have MLVA profile 2-10-6-3-2 (n=11), 2-10-8-3-2 (n=8), 2-9-10-3-2 (n=7), 2-11-8-3-2 (n=5) and 2-9-6-3-2 (n=4).

Information on travel history within the EU/EEA was available for 125 outbreak cases, of which 33 were confirmed and 22 probable since February 2017.

Eleven confirmed and three probable cases were reported as possibly having acquired the infection while travelling in Bulgaria between June and September 2017. Nine confirmed cases were reported as having possibly been infected in Portugal between April and June 2017 (Table 3).

**Table 3. Number of cases with travel history by case classification and country of probable infection, EU/EEA, February 2012 to November 2017 (n=125), as of 28 November 2017**

| Country of probable infection | Confirmed | Probable | Historical confirmed | Historical probable | Total |
|---|---|---|---|---|---|
| Austria | 0 | 0 | 1 | 0 | **1** |
| Belgium | 0 | 0 | 3 | 0 | **3** |
| Bulgaria | 11 | 3 | 1 | 0 | **15** |
| Croatia | 0 | 0 | 0 | 8 | **8** |
| Cyprus | 0 | 0 | 1 | 1 | **2** |
| Greece | 3 | 11 | 4 | 8 | **26** |
| Hungary | 1 | 0 | 5 | 3 | **9** |
| Italy | 2 | 0 | 1 | 0 | **3** |
| Netherlands | 0 | 0 | 0 | 1 | **1** |
| Poland | 3 | 3 | 13 | 13 | **32** |
| Portugal | 9 | 0 | 2 | 0 | **11** |
| Romania | 1 | 0 | 0 | 0 | **1** |
| Spain | 2 | 3 | 1 | 0 | **6** |
| Multiple or unspecified European destinations | 1 | 2 | 2 | 2 | **7** |
| **Total** | **33** | **22** | **34** | **36** | **125** |

In September 2017, Sweden investigated a cluster of 10 *S.* Enteritidis cases with MLVA type 2-10-7-3-2. The related isolates belonged to the WGS cluster_469. The cases were reported since the beginning of August and were linked to two local outbreaks in different parts of Sweden. One of the outbreaks was associated with consumption of raw eggs in a drink. The second outbreak was associated with consumption of Béarnaise sauce made of raw eggs at a restaurant. The sauce was found positive for *S.* Enteritidis and the same MLVA and WGS-profile as the ones in the cases was identified.

In June 2017, the United Kingdom reported approximately 40 human cases with WGS profiles sharing the same t5-level SNP addresses of the case definition: 1.2.3.175.175.175.% (31 human cases) and 1.2.3.18.359.360.% (9 human cases) in EPIS FWD. All samples from these human cases were collected after 1 February 2017. Due to the close genetic relation of these strains with those identified in the previous outbreak [1], and the similar case demographics and epidemiology to the 2016 cases, the epidemiological investigations have focused on a potential vehicle(s) of infection associated with the poultry production chain. As the WGS results suggest recent cases share a common source of infection with the 2016 cases, yet do not allow inference of vehicle of infection, investigations were extended to include the whole poultry production chain including fresh shell eggs, egg products such as pasteurised liquid eggs, poultry meat and indirect poultry litter exposures. To date, the UK epidemiological investigation supports the hypothesis that class A table eggs eaten at catering premises are the primary vehicle of infection.

The Czech Republic reported three probable cases with onset in October 2017. The three cases were in patients from the Moravia-Silesian region and sampled in the frame of an investigation on a *S.* Enteritidis outbreak currently affecting the region.

# Microbiological and environmental investigations of food

This section summarises country-specific information on food and environmental investigations associated with this outbreak that has been reported to RASFF (Rapid Alert System for Food and Feed) and EPIS (Epidemic Intelligence Information System), and/or directly to EFSA by national competent authorities (up to 1 December 2017) since 1 February 2017. See Figure 5 below for details on traceability and testing.

## Sweden

Swedish human cases were first notified in RASFF 2017.1419 and EPIS UI-432. Since August 2017, Sweden reported 10 human cases of *S.* Enteritidis linked to consumption of eggs, based on information from patients' interviews, trace-back assessment and WGS analyses. The human cases that matched the confirmed case definition (SNP address 1.2.3.18.455.469.8551) declared consumption of Béarnaise sauce (four cases), table eggs (three cases) and a drink made with raw eggs (three cases). An official sample of Béarnaise sauce was taken on 29 August 2017 at restaurant A where the four cases had eaten, and tested positive for *S.* Enteritidis. The WGS profile matched the one identified in the human isolates (SNP address 1.2.3.18.455.469.8551). However, due to unavailability of the eggs used for preparing the sauce, it was not possible to identify the batch number of the eggs, hence to proceed with the traceability assessment.

The three human cases linked to the consumption of table eggs were reported in the municipalities Nybro, Virserum and Karlskrona; the consumed eggs were purchased in local stores, which bought eggs from the Swedish mobile retailer A that operates with two names and regularly receives eggs from the Polish wholesaler B. The Swedish mobile retailer A was not registered as a food business operator, and it was prohibited to continue to sell or receive eggs until registration. Concerning the three cases linked to consumption of a drink made with raw eggs, official samples on the same batch of eggs used for preparing the drink (batch A, best before date 3 September 2017) were collected at the household of the cases in Ronneby, where the three cases drank the drink, and at a local retailer. Both the samples tested negative for *S.* Enteritidis. Later, the local competent authority collected, from the same local retailer in Ronneby, a sample of eggs from another batch (batch B, best before date 2 October 2017), as they were purchased from the same Swedish company supplying the eggs used for the drink (mobile retailer A). The analytical result of this sample was positive for *S.* Enteritidis and the WGS profile was identical to the one identified in the samples from the human cases and from the sauce Béarnaise (i.e. SNP address 1.2.3.18.455.469.8551). WGS analyses confirmed that the isolates fall within the case definition. The MLVA profile identified in both food samples positive for *S.* Enteritidis (i.e. sample of the Béarnaise sauce taken at restaurant A and sample of eggs from retailer B in Ronneby) was 2-10-7-3-2.

The distribution chain of the eggs belonging to batch A and batch B in Sweden was traced back from the Swedish mobile retailer A to the Polish egg packing centre C, different from the egg packing centres involved in the previous outbreak [1]. However, due to lack of documentation on the specific batches by the Swedish mobile retailer A, it was not possible to identify whether other intermediary food business operators were involved. Nevertheless, the competent authority in Poland informed the Swedish authority that the distribution of eggs belonging to batch A and batch B in Sweden from the packing centre C involved the Polish wholesaler B. Concerning the eggs used for preparing the sauce Béarnaise, trace-back assessment was not possible due to the lack of leftover eggs and related packaging.

Further information on the trace-back of the positive food samples is included in the section on Poland.

## Norway

The RASFF 2017.0849 launched by Norway was triggered by a positive result for *S.* Enteritidis obtained from unpasteurised liquid eggs during own-check analysis performed by the Norwegian processing company A. The sample was collected on 31 May 2017 and tested positive for *S.* Enteritidis. The isolate was typed at the Norwegian Institute of Public Health as MLVA type 2-10-8-3-2 and with the SNP address 1.2.3.18.455.469.7749 (results notified on 24 October 2017). This classifies the isolate within a t5 cluster with isolates detected in the Swedish case. The eggs positive to *S.* Enteritidis were delivered from the Polish packing centre B (one of the three egg packing centres involved in the previous outbreak), with invoice dated on 30 May 2017, and the best before date 21 June 2017. The eggs came from one of the farms involved in the previous outbreak: farm E. Following the positive results, processing company A has decided to stop purchasing eggs from Poland.

Further information on the trace-back of the positive food sample is included in the section on Poland.

## United Kingdom

The epidemiological investigations related to the 155 confirmed human cases reported in the United Kingdom since 1 February 2017 have identified seven different catering premises in England. Twenty-eight cases were identified as linked through eating at the seven premises mentioned above, and information on food consumption is available for twenty-four of these. Of those twenty-four cases, sixteen reported eating class A table eggs/food made on site with class A table eggs. The eight cases who did not report consumption of eggs/dishes containing eggs ate at two of the seven catering premises that were identified to have had poor hygiene practices, and cross-contamination was considered a major contributory factor in the premises-based outbreak.

Samples of eggs/egg dishes available at the time of the inspections were taken as part of routine sampling and outbreak investigation procedures on three premises. This included 10 eggs in two pools of five from one premises sampled on 19 May, four eggs (best before date 8 September 2017) from a second premises sampled on 17 November, and a raw pooled egg mix sample from a third premises. The small sample sizes were due to limited availability of shell eggs available for testing during the inspection visits. Only one food sample at a single premises was positive for *S.* Enteritidis. This was the sample of a raw pooled egg mix and the isolate fell into the outbreak cluster 1.2.3.18.359.360.% (WGS cluster_360). No producer number was available for the eggs used in the raw pooled egg mix, and it was noted that the bowl where the raw egg mix was, had scratches, and was therefore difficult to clean. Therefore the positive result obtained at the time may have been indicative of cross-contamination or of an inadequately cleaned bowl contaminated by previous batches of eggs mixed in it.

Environmental swabs were taken on 21 July 2017 as part of routine inspection and outbreak investigation procedures at another premises, and three tested positive for *S.* Enteritidis 1.2.3.18.359.360.%. Cross-contamination was noted as a possible major contributory factor in the outbreak in these catering premises.

Four of the seven catering premises sourced eggs from the same packing centre A in United Kingdom.

Packing centre A purchased eggs for several brokers within Europe and has sourced eggs from multiple countries, including Germany, Poland, Spain, and the United Kingdom. However, the eggs on site at the time of the inspection of catering premises were generally not from the same batch/producer/supplier as those eaten by the cases. This is due to the fast turnaround time of eggs at catering establishments, the time delay in the cases becoming exposed, and the notification of the suspicion of food poisoning to public health officials. The eggs likely consumed by affected cases were only identified at one premises: eggs with best before date 8 September 2017 with negative results for *Salmonella*, supplied by packing centre A and sourced from the Polish farm A. Farm A was also involved in the Rapid Outbreak Assessment 'Multi-country outbreak of *Salmonella* Enteritidis phage type 8, MLVA profile 2-9-7-3-2 and 2-9-6-3-2 infections' [1].

# Poland

The Polish wholesaler B that was linked to the cases in Sweden distributed eggs that were packed at the Polish packing centre C, and laid in two barns of the Polish farm B, and one barn of the Polish farm C. However, the traceability system of the packing centre was not considered reliable by the Polish competent authorities, so the traceability of the eggs to these farms could not be guaranteed. Besides the mentioned barns, farm B and farm C have one more barn. This contained animals in the rearing period during the outbreak, hence there was no egg production. Farm B and farm C are located at the same postal address.

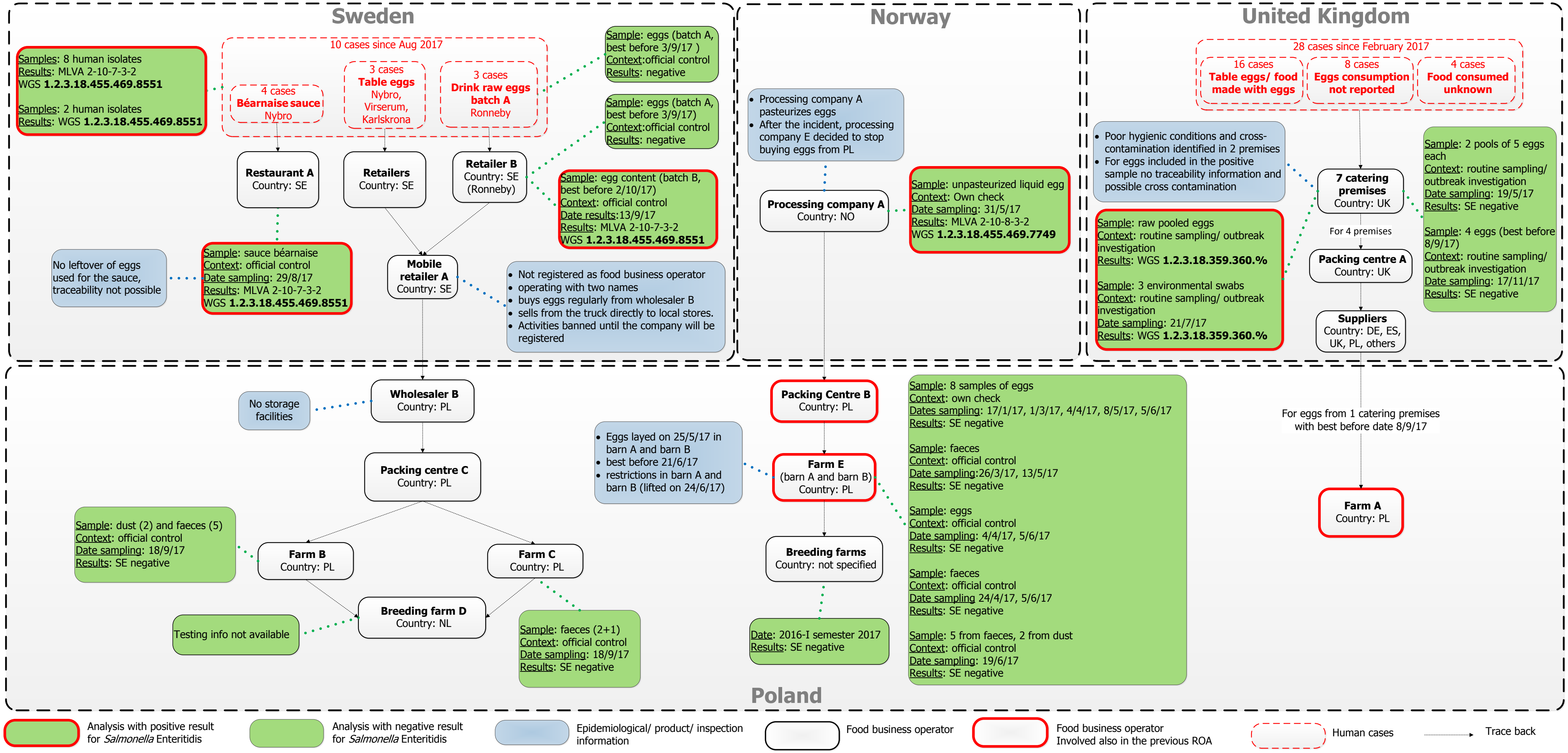
On 18 September 2017, official samples of dust and faeces were taken from the two barns of farm B, and samples of faeces from farm C. Results were negative for *S.* Enteritidis. Both farms were supplied by the Dutch breeding farm D; testing info at farm D during the current outbreak is not available.

Concerning the distribution chain connected to the Norwegian positive egg sample, the incriminated egg batch was distributed by the Polish packing centre B (also involved in the previous ROA) and originated from two barns (barn A and B) of the Polish farm E from eggs laid on 25 May 2017 (best before date 21 June 2017). Veterinary Inspector in Rawicz issued an administrative decision that banned placing eggs from barn A and barn B (from farm E), on the market, with the exception of when eggs will be used with sufficient heat treatment to inactivate microorganisms. The ban was communicated in RASFF on 21 June 2017. Official samples on eggs, faeces and dust were collected after re-population in the two barns between 17 January 2017 and 19 June 2017 and gave negative results for *S.* Enteritidis. As a consequence of these negative analytical results, the ban was lifted on 24 June 2017. The two barns (barn A and B) of the farm E were supplied by nine breeding farms that gave negative results for *S.* Enteritidis in the period 2016–first semester 2017.

The Polish packing centre B, farm A, farm E and five of the breeding farms mentioned above were also involved in the ROA 'Multi-country outbreak of *Salmonella* Enteritidis phage type 8, MLVA profile 2-9-7-3-2 and 2-9-6-3-2 infections'[1]. In particular, in the farm E during the previous outbreak an isolate of *S.* Enteritidis was detected that shares the same t5-level SNP address with the isolate detected in the egg sample in Norway, even though the barn involved in that case (barn C) was different from the barns linked to the eggs traced back from the Norwegian food (barns A and B).

In spite of the genetic closeness of the food isolates sampled in Sweden and Norway (same t5 level SNP address), no epidemiological link has yet been identified between those Polish food business operators (packing centres and farms) involved in the Swedish investigations and those involved in the Norwegian investigations.

**Figure 5. Graphical representation of traceability and testing information available in RASFF or provided by Member States to EFSA, as of 1 December 2017**



**Sweden**

Samples: 8 human isolates
Results: MLVA 2-10-7-3-2
WGS **1.2.3.18.455.469.8551**

Samples: 2 human isolates
Results: WGS **1.2.3.18.455.469.8551**

10 cases since Aug 2017

4 cases
**Béarnaise sauce**
Nybro

3 cases
**Table eggs**
Nybro,
Virserum,
Karlskrona

3 cases
**Drink raw eggs batch A**
Ronneby

Sample: eggs (batch A, best before 3/9/17 )
Context:official control
Results: negative

Sample: eggs (batch A, best before 3/9/17)
Context:official control
Results: negative

**Restaurant A**
Country: SE

**Retailers**
Country: SE

**Retailer B**
Country: SE
(Ronneby)

Sample: egg content (batch B, best before 2/10/17)
Context: official control
Date results:13/9/17
Results: MLVA 2-10-7-3-2
WGS **1.2.3.18.455.469.8551**

No leftover of eggs used for the sauce, traceability not possible

Sample: sauce béarnaise
Context: official control
Date sampling: 29/8/17
Results: MLVA 2-10-7-3-2
WGS **1.2.3.18.455.469.8551**

**Mobile retailer A**
Country: SE

- Not registered as food business operator
- operating with two names
- buys eggs regularly from wholesaler B
- sells from the truck directly to local stores.
- Activities banned until the company will be registered

**Norway**

- Processing company A pasteurizes eggs
- After the incident, processing company E decided to stop buying eggs from PL

**Processing company A**
Country: NO

Sample: unpasteurized liquid egg
Context: Own check
Date sampling: 31/5/17
Results: MLVA 2-10-8-3-2
WGS **1.2.3.18.455.469.7749**

**United Kingdom**

28 cases since February 2017

16 cases
**Table eggs/ food made with eggs**

8 cases
**Eggs consumption not reported**

4 cases
**Food consumed unknown**

- Poor hygienic conditions and cross-contamination identified in 2 premises
- For eggs included in the positive sample no traceability information and possible cross contamination

**7 catering premises**
Country: UK

Sample: raw pooled eggs
Context: routine sampling/ outbreak investigation
Results: WGS **1.2.3.18.359.360.%**

Sample: 3 environmental swabs
Context: routine sampling/ outbreak investigation
Date sampling: 21/7/17
Results: WGS **1.2.3.18.359.360.%**

For 4 premises

**Packing centre A**
Country: UK

**Suppliers**
Country: DE, ES, UK, PL, others

Sample: 2 pools of 5 eggs each
Context: routine sampling/ outbreak investigation
Date sampling: 19/5/17
Results: SE negative

Sample: 4 eggs (best before 8/9/17)
Context: routine sampling/ outbreak investigation
Date sampling: 17/11/17
Results: SE negative

For eggs from 1 catering premises with best before date 8/9/17

**Poland**

No storage facilities

**Wholesaler B**
Country: PL

**Packing centre C**
Country: PL

Sample: dust (2) and faeces (5)
Context: official control
Date sampling: 18/9/17
Results: SE negative

**Farm B**
Country: PL

**Farm C**
Country: PL

Testing info not available

**Breeding farm D**
Country: NL

Sample: faeces (2+1)
Context: official control
Date sampling: 18/9/17
Results: SE negative

- Eggs layed on 25/5/17 in barn A and barn B
- best before 21/6/17
- restrictions in barn A and barn B (lifted on 24/6/17)

**Packing Centre B**
Country: PL

**Farm E**
(barn A and barn B)
Country: PL

**Breeding farms**
Country: not specified

Date: 2016-I semester 2017
Results: SE negative

Sample: 8 samples of eggs
Context: own check
Dates sampling: 17/1/17, 1/3/17, 4/4/17, 8/5/17, 5/6/17
Results: SE negative

Sample: faeces
Context: official control
Date sampling:26/3/17, 13/5/17
Results: SE negative

Sample: eggs
Context: official control
Date sampling: 4/4/17, 5/6/17
Results: SE negative

Sample: faeces
Context: official control
Date sampling 24/4/17, 5/6/17
Results: SE negative

Sample: 5 from faeces, 2 from dust
Context: official control
Date sampling: 19/6/17
Results: SE negative

**Farm A**
Country: PL

Analysis with positive result for *Salmonella* Enteritidis
Analysis with negative result for *Salmonella* Enteritidis
Epidemiological/ product/ inspection information
Food business operator
Food business operator Involved also in the previous ROA
Human cases
Trace back

Source: RASFF or Member States (as reported to EFSA), as of 1 December 2017

# ECDC and EFSA threat assessment for the EU

A multi-country outbreak of *S.* Enteritidis associated with contaminated eggs from Poland was confirmed by epidemiological, microbiological and WGS analysis in 14 EU/EEA countries in 2016. The number of cases associated with this outbreak steadily decreased from the end of 2016 to the beginning of 2017. This was possibly due to the extended control measures implemented in Poland in the autumn 2016. However, the frequency of detection of new outbreak cases increased again after February 2017 and peaked in September. In the same month, a new cluster of cases was detected in Sweden and an association with eggs from Poland was reported.

Based on the EU outbreak case definition from November 2017, the human isolates belong to four distinct genetic clusters. Isolates belonging to these clusters were also detected during the veterinary and environmental investigations in the three farms associated with the 2016 outbreak. Data from 15 further *S.* Enteritidis-positive farms has not been included in the multi-country analysis. Following PHE nomenclature, the four clusters were given the designations 1.2.3.175.175.175. % (WGS cluster_175), 1.2.3.18.359.360.% (WGS cluster_360), 1.2.3.18.455.469.% (WGS cluster_469) and 1.2.3.18.455.2440.% (WGS cluster_2440).

The MLVA profiles associated with the four genetic clusters and denoting probable cases are 2-9-6-3-2, 2-9-7-3-2, 2-9-10-3-2, 2-10-6-3-2, 2-10-8-3-2 and 2-11-8-3-2. The European outbreak case definition is based on WGS and MLVA, and hence very specific and under-estimates the true extent of this outbreak. Only countries performing WGS and/or MLVA can identify cases linked to this outbreak, and these techniques are only used in some EU countries. In addition, a seventh MLVA type (2-10-7-3-2) identified in isolates from the Swedish cluster in September 2017 was not included in the case definition because of low discriminatory power.

The number of confirmed and probable cases increased steadily from March 2017 peaking in September 2017. The low number of cases reported in October and November 2017 is partially due to delayed reporting as several isolates from humans are still under laboratory investigation and thus case counts are likely to change in the near future.

The United Kingdom is currently the most affected country in terms of numbers of reported cases, with most cases being domestically acquired in the United Kingdom. Most of the Norwegian cases, and a good proportion of the Swedish cases were infected while travelling in other EU countries. In the last months, based on cases travel histories, Bulgaria and Portugal appear to be also affected by the outbreak. The analysis of outbreak confirmed cases with a travel history before disease onset and during the incubation period allowed the identification of the outbreak taking place in countries not performing MLVA or WGS.

The food safety authorities in Sweden, Norway, the United Kingdom and Poland carried out environmental and food investigations to identify the source of the human infections and/or of the positive food samples detected in their countries. The investigations in Sweden showed that, in those cases where traceability was feasible, the eggs linked to human cases were traced back to one packing centre and two laying hen farms in Poland. In Norway, the contaminated egg product detected at processing company level was traced back to a packing centre and a laying hen farm located in Poland but different from those identified in the Swedish assessment. Information from investigations in the United Kingdom to date has not been sufficient to identify the vehicle of infection for all human cases or the food business operators at the source of the outbreak. However, for some cases the eggs that were probably consumed were identified and traced back to a laying hen farm in Poland different from the farms identified in the Swedish and Norwegian assessments. However, so far no epidemiological links have been identified between packing centres and farms involved in the investigations in Sweden, Norway and the United Kingdom. No positive results for *S.* Enteritidis were observed in the farms identified as the possible source of contaminated eggs. There were negative results for *S.* Enteritidis at those holdings supplying the mentioned farms according to the information available.

According to the available information, some of the food business operators involved or possibly involved in the event investigated in Norway (one packing centre, one laying hen farm and five breeding farms from Poland) and the United Kingdom (one laying hen farm from Poland) were also involved in the ROA 'Multi-country outbreak of *Salmonella* Enteritidis phage type 8, MLVA profile 2-9-7-3-2 and 2-9-6-3-2 infections' [1].

All *S.* Enteritidis isolates from foods were characterised by WGS methods and matched the case definition for confirmed cases by sharing the same t5 level SNP address of the defined outbreak clusters 1.2.3.18.455.469.% (WGS cluster_469) or 1.2.3.18.359.360.% (WGS cluster_360). The two isolates from the Swedish foods (sauce Béarnaise and eggs) showed the WGS SNP address 1.2.3.18.455.469.8551 and the isolate from the Norwegian food (unpasteurised liquid eggs) had the WGS SNP address 1.2.3.18.455.469.7749. This close genetic relation between the food isolates in the two countries suggests a possible common source, even though to date no epidemiological evidence has been found. It is also interesting to observe that the WGS profile of the Norwegian food isolate (WGS cluster_469) from eggs traced back to two barns (barn A and Barn B) of the Polish farm E clustered at t5 level with an isolate detected during the previous outbreak in the same Polish farm [1], but in a different barn (barn C). This strongly suggests that *S.* Enteritidis detected in the Norwegian food isolate, and the isolate detected in the barn C of the Polish farm E in the previous outbreak are linked.

The isolate detected from raw pooled egg mix in the United Kingdom and the three isolates detected from environmental swabs at one premises in the United Kingdom shared the same t5 level SNP address within the WGS cluster_360 cluster detected in a Polish farm during the investigation of the previous outbreak. This strengthens the hypothesis that strains detected in the previous outbreak are still circulating at the farm level in Poland.

The WGS cluster_469 shares the same t25 level SNP address with the WGS cluster_360, and the t50 level SNP address with the WGS cluster_175; isolates sharing these latter clusters were mainly circulating in the previous outbreak [1], but were only detected in one food and three environmental isolates in the current event. This could suggest the presence of multiple strains circulating in the Polish farms.

Based on the current evidence, it was not possible to identify a single source of infection for the clusters of human cases for which the traceability exercise was feasible. The investigations traced back the contaminated food to packing centres and laying hen farms in Poland.

Data gaps regarding food investigations, in particular at the source of the outbreak, have hampered the proper assessment of the epidemiological connections and microbiological contamination at primary production level and at other food business operators downstream in the food chain. Epidemiological data are essential to confirm the outcome of microbiological investigations. It is recommended that the involved countries carry out further epidemiological studies and tracing investigations, to identify the food business operators at the source of the outbreak. Characterisation by WGS methods of food isolates is encouraged to support the multi-country analyses.

# References

1. European Centre for Disease Prevention and Control and European Food Safety Authority. Multicountry outbreak of Salmonella Enteritidis phage type 8, MLVA type 2-9-7-3-2 and 2-9-6-3-2 infections, 7 March 20172017. Available from: https://ecdc.europa.eu/sites/portal/files/media/en/publications/Publications/rapid-outbreak-assessment-Salmonella-Enteritidis-7-mar-2017.pdf.
2. REGULATION (EC) No 2160/2003 of the European Parliament and of the Council of 17 November 2003 on the control of salmonella and other specified food-borne zoonotic agents.2003; OJL, L325:[15 p.]. Available from: http://eur-lex.europa.eu/legal-content/EN/TXT/PDF/?uri=CELEX:32003R2160&rid=2.
3. European Centre for Disease Prevention and Control. The European Surveillance System (TESSy). 2016.
4. European Centre for Disease Prevention and Control. Laboratory standard operating procedure for multiple-locus variable-number tandem repeat analysis of *Salmonella enterica* serotype Enteritidis. Stockholm: ECDC; 2016. Available from: http://ecdc.europa.eu/en/publications/Publications/Salmonella-Enteritidis-Laboratory-standard-operating-procedure.pdf.
5. European Food Safety Authority and European Centre for Disease Prevention and Control. The European Union summary report on trends and sources of zoonoses, zoonotic agents, and food-borne outbreaks in 2016. EFSA Journal 2017; 15(12):5077[228 p.]. Available from: https://doi.org/10.2903/j.efsa.2017.5077
6. Official Journal of the European Union. Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC. 2003 12.12.2003. Report No.
7. Ashton PM, Nair S, Peters TM, Bale JA, Powell DG, Painset A, et al. Identification of Salmonella for public health surveillance using whole genome sequencing. PeerJ. 2016;4:e1752.
8. Inns T, Ashton PM, Herrera-Leon S, Lighthill J, Foulkes S, Jombart T, et al. Prospective use of whole genome sequencing (WGS) detected a multi-country outbreak of Salmonella Enteritidis. Epidemiology and infection. 2016 Oct 26:1-10.
9. Ashton P., Nair S., Peters T., Tewolde R., Day M., Doumith M., et al. Revolutionising Public Health Reference Microbiology using Whole Genome Sequencing: Salmonella as an exemplar. bioRxiv. 2015.

# Annex 1

**Table 1.** **Reported isolations of *Salmonella* Enteritidis from food, animals and feed, EU Member States and other reporting countries, 2004–2016**

| Source | No. of positive units, 2004–2010 | No. of positive units in 2011 | No. of positive units in 2012 | No. of positive units in 2013 | No. of positive units in 2014 | No. of positive units in 2015 | No. of positive units in 2016 | Total no. of positive units, 2004–2016 |
|---|---|---|---|---|---|---|---|---|
| **Food** | | | | | | | | |
| Eggs(a) | 765 | 25 | 102 | 22 | 23 | 22 | 24 | 983 |
| Egg products(b) | 94 | 7 | 7 | 4 | 3 | 1 | 3 | 119 |
| Meat from broilers | 1 451 | 107 | 298 | 499 | 551 | 136 | 275 | 3 317 |
| Meat from spent hens | 0 | | | 28 | 40 | 37 | 108 | 213 |
| Meat from turkey | 41 | | 14 | 7 | 8 | 5 | 17 | 92 |
| Meat from other poultry(c) | 739 | 84 | 37 | 7 | 4 | 18 | 28 | 917 |
| Meat from pig | 196 | 21 | 22 | 17 | 11 | 10 | 31 | 308 |
| Meat from bovine animals | 125 | 2 | 4 | 18 | 13 | 2 | 9 | 173 |
| Meat from other animal species(d) | 109 | 16 | 22 | 17 | 18 | 7 | 37 | 226 |
| Fish and fishery products(e) | 31 | 9 | 1 | 2 | | 1 | 31 | 75 |
| Dairy products (including cheeses) and milk | 20 | 1 | 1 | 5 | 3 | 3 | 1 | 34 |
| Fruits and vegetables(f) | 22 | 2 | 1 | | 4 | 8 | | 37 |
| Other food(g) | 324 | 26 | 15 | 11 | 15 | 9 | 14 | 414 |
| **Total isolations in food** | **3 917** | **300** | **524** | **637** | **693** | **259** | **578** | **6 908** |
| **Animals** | | | | | | | | |
| *Gallus gallus* (fowl) | 1 8728 | 1 381 | 1 533 | 902 | 954 | 1 237 | 852 | 25 587 |
| Ducks | 284 | 8 | 39 | 32 | 24 | 33 | 28 | 448 |
| Geese | 296 | 23 | 60 | 63 | 27 | 27 | 21 | 517 |
| Turkeys | 243 | 34 | 16 | 21 | 15 | 43 | 41 | 413 |
| Other poultry or game birds(h) | 375 | 5 | 96 | 16 | 141 | 6 | 12 | 651 |
| Other birds(i) | 59 | 7 | 4 | 3 | 2 | 4 | 1 | 80 |
| Cattle | 792 | 23 | 62 | 60 | 148 | 170 | 10 | 1 263 |
| Other ruminants(l) | 14 | 3 | 4 | 8 | | 3 | 7 | 39 |
| Pigs and wild boars | 283 | 18 | 17 | 34 | 20 | 19 | 17 | 408 |
| Domestic solipeds | 24 | 8 | 4 | 5 | 6 | 19 | 3 | 71 |
| Cats and dogs(m) | 63 | 8 | 20 | 3 | 2 | 10 | 10 | 116 |
| Reptiles | 14 | | 8 | 13 | 4 | 1 | 3 | 43 |
| Other animals(n) | 180 | 50 | 20 | 120 | 45 | 22 | 607 | 1 044 |
| **Total isolations in animals** | **21 355** | **1 568** | **1 883** | **1 280** | **1 388** | **1 594** | **1 612** | **30 680** |

| Source | No. of positive units, 2004–2010 | No. of positive units in 2011 | No. of positive units in 2012 | No. of positive units in 2013 | No. of positive units in 2014 | No. of positive units in 2015 | No. of positive units in 2016 | Total no. of positive units, 2004–2016 |
|---|---|---|---|---|---|---|---|---|
| **Feed** | | | | | | | | |
| Compound feedingstuffs for poultry | 57 | 1 | 1 | 0 | 10 | | 3 | 72 |
| Feed material of land animal origin | 26 | | 3 | 1 | 2 | | 3 | 35 |
| Pet food | 18 | 2 | 2 | | 9 | 3 | 3 | 37 |
| Feed material of oil seed or fruit origin | 12 | 4 | 1 | 3 | | 1 | | 21 |
| Feed material of marine animal origin | 13 | | | 5 | | | | 18 |
| Feed material of cereal grain origin | 12 | 2 | 2 | | | 1 | | 17 |
| Compound feedingstuffs for pigs | 6 | 1 | | 2 | | | 2 | 11 |
| Compound feedingstuffs for cattle | 7 | | | | | 1 | 3 | 11 |
| Other feedingstuffs/feed material or unspecified(o) | 33 | 1 | 6 | 0 | 0 | 6 | 2 | 48 |
| **Total isolations in feed** | **184** | **11** | **15** | **11** | **21** | **12** | **16** | **270** |
| **Total isolations (food, animals, feed)** | **25 456** | **1 879** | **2 422** | **1 928** | **2 102** | **1 865** | **2 206** | **37 858** |

*Note: Information summarised in this table is based on Directive 2003/99/EC of the European Parliament and of the Council of 17 November 2003 on the monitoring of zoonoses and zoonotic agents, amending Council Decision 90/424/EEC and repealing Council Directive 92/117/EEC.*

*(a) Eggs (2010–2016): 983 S. Enteritidis isolates distributed as follows: 887 from table eggs, 84 from liquid eggs for egg products, 12 from unspecified eggs. (b) Egg products (2010–2016): 119 S. Enteritidis isolates distributed as follows: 91 from unspecified egg products, 18 from liquid egg products, 7 from ready-to-eat egg products, 3 dried egg products. (c) 'Meat from other poultry' includes meat from ducks, geese, other poultry species and meat from unspecified poultry. (d) 'Meat from other animal species' includes 'meat from bovine animals and pig', 'meat from deer (venison)', 'meat from rabbits', 'meat from sheep', 'meat from wild boars', 'meat from wild game', 'meat from wild game – birds', 'meat from wild game – land mammals', 'meat, mixed meat', 'meat, red meat (meat from bovines, pigs, goats, sheep, horses, donkeys, bison and water buffalos)' and 'meat from other animal species or not specified'. (e) 'Fish and fishery products' includes crustaceans, fish, unspecified fishery products, live bivalve molluscs, molluscan shellfish. (f) 'Fruits and vegetables' includes vegetables, 'fruits and vegetables', 'ready-to-eat salads', sprouted seeds, and 'spices and herbs'.*

*(g) Other food includes bakery products, 'cereals and meals', 'confectionery products and pastes', 'frog legs', 'infant formula', 'sauce and dressings', sweets, 'other processed food products and prepared dishes', 'other food of non-animal origin' and 'other food'. (h) 'Other poultry or gamebirds' includes ostriches, other poultry, partridges, pheasants, pigeons, unspecified poultry, quails. (i) 'Other birds' includes canary, parrots, psittacidae and unspecified birds. (l) 'Other ruminants' includes deer, goats, sheep, 'sheep and goats'. (m) 'Cats and dogs' includes cats, dogs and the generic animal category 'pet animals, all'. (n) 'Other animals' includes badgers, bears, chinchillas, falcons, finches, fish, foxes, fur animals, guinea pigs, hedgehogs, land game mammals, leopards, lions, lynx, mice, minks, moose, rabbits, raccoon dogs, rodents, squirrels, water buffalos, wild animals, zoo animals and other animals. (o) 'Other feedingstuffs/feed material or unspecified' includes 'compound feedingstuffs for fish', 'compound feedingstuffs for fur animals', unspecified compound feedingstuffs', 'other feed material' and 'other feedingstuffs'.*