



Cluster of monophasic *Salmonella* Typhimurium with previously unseen MLVA pattern in the EU/EEA

3 September 2014

Conclusions

The recently detected 38 cases of monophasic *Salmonella* Typhimurium with MLVA profile 3-12-17-NA-211 and 3-12-18-NA-211 occurring in six Member States are likely to be part of the same cluster. Given the typing delay and the fact that not all countries are performing MLVA typing, the number of cases currently detected is most likely to be underestimated.

These two profiles emerged simultaneously in several Member States in June and July 2014, indicating a simultaneous exposure to the clonal strain at several locations within the EU. Based on limited available information from food investigations, meats are the suspected vehicle of human infection at present.

It is important to interview new cases to identify a common exposure and to report all new cases with matching MLVA typing results through the TESSy molecular surveillance service and EPIS FWD in order to assess the evolution of the cluster.

There is a need to gather information on the findings of these MLVA profiles in feed, animals, and foods (of animal origin and non-animal origin) in order to narrow the hypothesis for further epidemiological studies.

This cluster highlights the need to ensure a rapid exchange of information between the public health and food safety health authorities in order to assess the situation and the need for further epidemiological studies as quickly as possible.

Source and date of request

Internal decision at ECDC Round Table meeting on 26 August 2014.

Public health issue

Detection of multi-country clusters of monophasic *Salmonella* Typhimurium with previously unseen MLVA profiles 3-12-17-NA-211 and 3-12-18-NA-211 in June and July 2014.

Consulted experts

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Disease background information

Epidemiological background

During 2012, monophasic *Salmonella* Typhimurium was the third most frequently reported serotype in the EU/EEA countries, with 5 932 cases reported to The European Surveillance System (TESSy) [1]. Of these, 94% were reported as domestically acquired and 6% as travel-related (information provided for 1 651 cases).

The MLVA profiles 3-12-17-NA-211 and 3-12-18-NA-211 had not been reported in any of the affected EU/EEA countries before 2014.

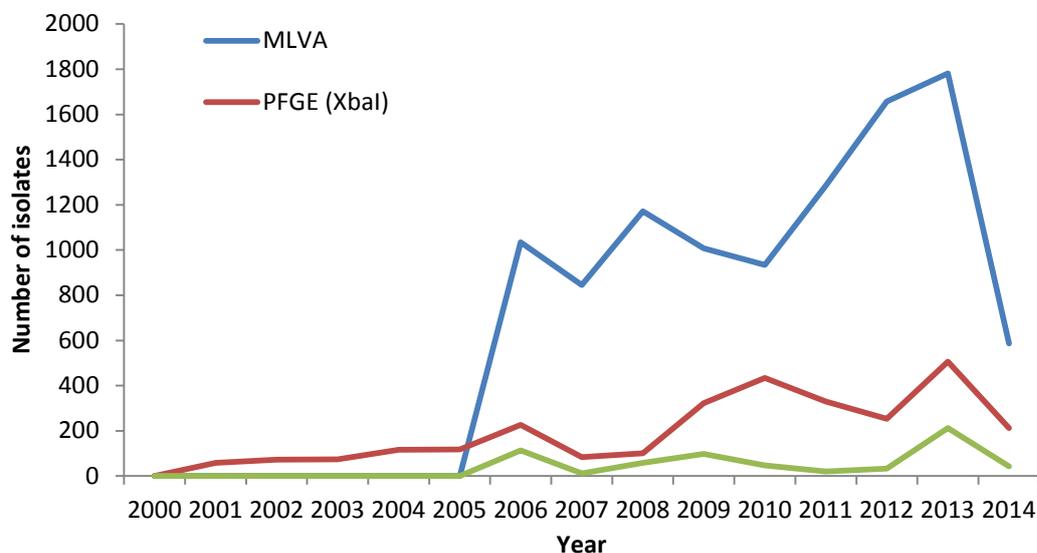
Microbiological background

Monophasic *Salmonella* Typhimurium is commonly characterised by the resistance pattern ASSuT – i.e. isolates are resistant to the four antimicrobials ampicillin, streptomycin, sulfonamides and tetracycline [2]. In 2012, about 90% of the isolates in cases reported to TESSy had this resistance pattern.

As of 29 August 2014, 22 451 isolates have been submitted to the TESSy molecular surveillance service, 12 945 (58%) of which are *Salmonella* Typhimurium. Due to the limited discriminatory power of Pulsed-Field Gel Electrophoresis (PFGE) for *S.* Typhimurium [3], ECDC recommends that *Salmonella* Typhimurium isolates be typed using the standard Multiple Locus Variable number tandem repeat Analysis (MLVA) protocol [4] which has been internationally validated. ECDC supported the Member States in implementing the protocol during 2010–2011. The protocol was published on the ECDC website in 2011 [5] and was supported by External Quality Assessment (EQA) schemes in 2012–2013.

Figure 1 shows that since 2006, MLVA has been the dominant typing method for *Salmonella* Typhimurium in the data submitted to the TESSy molecular surveillance service.

Figure 1. Number of *S.* Typhimurium isolates submitted to the TESSy molecular surveillance service by 29 August 2014, per year of sampling and per typing method (n=12 945)



Event background information

A monophasic *S. Typhimurium* cluster with a previously unseen MLVA profile, 3-12-17-NA-211, was detected through the TESSy molecular surveillance service on 4 August 2014. On 18 August, a second cluster with a closely-related, but previously unseen MLVA profile, 3-12-18-NA-211, was detected raising the question of whether the reported isolates with these two profiles were part of the same cluster. The three countries involved, Denmark, Norway and Sweden, had not identified human cases presenting with these MLVA profiles in the past.

On 22 August 2014, ECDC launched an urgent inquiry to ascertain whether other Member States had identified cases with these MLVA patterns. Three countries, Finland, Germany and the Netherlands, confirmed having identified cases with the two MLVA profiles for the first time ever in 2014.

As of 29 August 2014, 18 cases with the MLVA type 3-12-17-NA-211 and four cases with the type 3-12-18-NA-211 have been reported to the TESSy molecular surveillance service. The cases were received at the reference laboratories in Denmark, Sweden and Norway between 23 June and 25 July 2014. Fourteen of the cases are male and eight female, with ages ranging from three to 77 years (median 43).

An additional 20 cases have been reported by Germany, Finland and the Netherlands through the Epidemic Intelligence Information System for Food- and Waterborne Diseases (EPIS-FWD). This brings the total number of cases to 38: Denmark (16), Finland (9), Germany (6), Sweden (5), Norway (1) and the Netherlands (1). Cases are either reported as domestically acquired, related to travel to other EU countries or have an unknown travel history. For detailed information on the cases see Figure 2 and Table 1 below.

Figure 2. Number of human cases of monophasic *Salmonella* Typhimurium with MLVA patterns 3-12-17-NA-211 and 3-12-18-NA-211 per week of sample received at the reference laboratory or week of sampling (n=38), EU/EEA, weeks 7 to 34, 2014

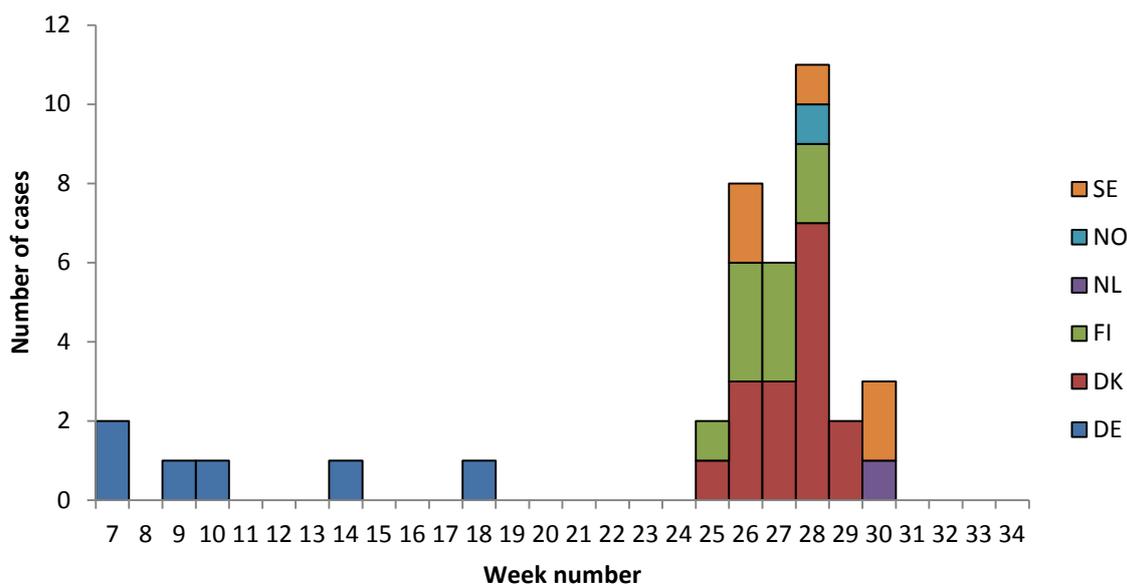


Table 1. Epidemiological and microbiological summary of the monophasic *Salmonella* Typhimurium cases reported (n=38), EU/EEA, weeks 7 to 34, 2014

	Number of cases	Dates	Anti-microbial resistance profile	Phage type	Sex ratio and age range	Travel history
Denmark	14 cases 3-12-17-NA-0211 and two cases 3-12-18-NA-0211.	Samples received at the reference laboratory between 19 June and 16 July.	Resistance to Amp, Sul and Tet (Str not tested).	-	Five females, 11 males aged 3–73 years.	Five cases have no travel history, others unknown.
Finland	Nine cases 3-12-17-NA-0211.	Sampling dates from 19 June and 10 July.	Eight are resistant to Amp, Str, Sul and Tet.	DT 120	Six males, three females aged 3–59 years.	Five domestic, one linked with travel to Spain and three unknown.
Germany	Five cases 3-12-17-NA-0211 and one case 3-12-18-NA-0211.	Dates of isolation from 10 February to 29 April.	Resistance to Amp, Str, Sul and Tet.	Five are phage type DT120 and one is DT193.	Three male, three female. Ages range from 5–32 years.	-
The Netherlands	One case 3-12-17-NA-0211.	Notified on 22 July 2014.	Resistance to Amp, Sul and Tet (Str not tested).	-	Female, 39 years old.	No travel history.
Norway	One case of 3-12-17-NA-0211.	Sample received at the reference laboratory on 9 July 2014.	Resistance to Amp and Tet (Sul and Str not tested).	-	Male, 46 years old.	Travel history to Denmark
Sweden	Three cases 3-12-17-NA-0211 and two cases 3-12-18-NA-0211.	Samples received at the reference laboratory between 27 June and 25 July 2014.	-	-	Three females, two males. Ages range from 18–77 years.	Three cases domestic, one case with travel history to Denmark, one to Greece.

Amp – ampicillin; Str – streptomycin; Sul – sulfonamides; Tet – tetracyclines

The antimicrobial resistance pattern seems to be the common one for monophasic *S. Typhimurium*, ASSuT, identified in Finland and Germany and only partially tested in Denmark and the Netherlands (ASuT, not tested for streptomycin) and Norway (AT, not tested for sulfonamides and tetracycline).

A few cases have been interviewed but no common vehicle of infection has been identified. On 25 June 2014, Denmark identified a typing match based on MLVA and antimicrobial resistance in meat that was sold in Denmark as minced beef. The producer used meat from Denmark and another unknown country. The Netherlands also reported one non-human isolate with MLVA profile 3-12-17-NA-211, notified on 7 July 2014. Trace-back to the food/animal origin of this isolate is on-going.

Probabilistic assignment has been performed in the Netherlands on both Dutch strains to determine putative sources based on population genetics modelling. This has identified pigs as the most likely source of infection with 89% and 91% probability for 3-12-17-NA-211 and 3-12-18-NA-211 respectively (personal communication, L. Mughini Gras, RIVM, the Netherlands, 28 August 2014). The model used is adapted from the Asymmetric Island Model of Wilson et al [6] but has not yet been validated formally using MLVA data, so the results should be interpreted with caution.

Threat assessment for the EU

Thirty-eight cases with previously unseen and closely related MLVA patterns have been detected in six countries. A multi-country cluster encompassing these MLVA profiles emerged during June and July 2014 in several EU/EEA Member States and would suggest a common source or vehicle of infection. All cases with travel information available (18 out of 38) have been infected within the EU. Based on the limited information available, meats are the suspected vehicles of infection at present.

Isolates from August have not yet been typed in most countries and therefore further recent cases may still be identified. Since not all countries are using MLVA typing, it is possible that cases are also occurring in other countries but that their links to this cluster remain undetected.

Interviews of new cases and compilation of the information at the EU/EEA level will be useful to identify the vehicle of infection.

Conclusions

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