# The *Salmonella* network: a surveillance scheme for *Salmonella* in the food chain: 2015 results

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**Abstract**

For 20 years, the *Salmonella* network has been centralising serotyping results for *Salmonella* isolated on a voluntary basis in the food chain, in all industries and sectors. This outbreak surveillance supplements the official inspections undertaken every year. This massive volume of data collected by ANSES confirms the trends and emerging strains reported at European level. All origins combined, S. Typhimurium and its monophasic variants as well as S. Enteritidis are the main isolated strains. For many years, *Salmonella* has been a major microbiological contaminant responsible for foodborne epidemics in France and Europe. Optimising the assessment and management of the risk of salmonellosis in humans and animals requires the collection of high-quality data, over a suitable time period. In 2015, after a process was undertaken to evaluate its operations, this network launched a major campaign to modernise its analytical tools and tools for the management, interpretation, sharing and communication of information to better meet the needs expressed by the stakeholders and users of this surveillance system. In addition to being tested for their serovar, the *Salmonella* isolated through this network can be characterised for their potential epidemiological link. New typing methods based on genome sequencing offer highly promising prospects in this area.

**Keywords**

*Salmonella*, Surveillance, Zoonosis, Serovar, Emergence

***Résumé***

***Le réseau* Salmonella*, un dispositif de surveillance des salmonelles sur la chaîne alimentaire : bilan 2015***

*Depuis 20 ans, le réseau* Salmonella *centralise des résultat sde sérotypage de salmonelles isolées sur la chaîne alimentaire, de manière volontaire, dans toutes les filières et tous les secteurs d'activités. Cette surveillance événementielle complète les contrôles officiels réalisés chaque année. Ce volume massif de données collectées par l'Anses confirme les tendances et les émergences rapportées en niveau européen. Toutes origines confondues, S. Typhimurium et ses variants monophasiques ainsi que S. Enteritidis demeurent majoritairement isolées.* Salmonella *est depuis de nombreuses années un contaminant microbiologique majeur à l'origine d'épidémie d'origine alimentaire en France et en Europe. L'optimisation de l'évaluation et de la gestion du risque de salmonellose chez l'homme et l'animal implique la collecte de données de qualité, dans un pas de temps adapté. À la suite d'un processus d'évaluation de son fonctionnement, ce réseau a entamé en 2015 une action profonde de modernisation de ses outils analytiques mais également de pilotage, d'interprétation, de partage et de communication de l'information pour mieux répondre aux besoins exprimés par l'ensemble des acteurs et utilisateurs de cette surveillance. Au-delà du sérovar, les salmonelles isolées dans le cadre de ce réseau peuvent être caractérisées pour leur potentiel lien épidémiologique. Les nouvelles méthodes de typage basées sur le séquençage du génome offrentdes perspectives très prometteuses dans ce domaine.*

***Mots-clés***

Salmonella*, surveillance, zoonose, sérovar, émergence*

*Salmonella* are a microbiological hazard mainly transmitted to humans through food. This hazard has been known and monitored at the local, national and international levels for many years. In 2014, *Salmonella* was in second position, behind *Campylobacter*, in the ranking of bacterial agents isolated in humans in Europe. It is also the main microbiological contaminant causing food-borne outbreaks in which the responsible agent has been confirmed (EFSA-ECDC, 2015). In France, over the 2008-2013 period, the incidence of non-typhoid *Salmonella* was estimated at 307 cases per 100,000 inhabitants (90%CI: 173–611), resulting in 4305 hospitalisations per year on average (Van Cauteren *et al.*, 2015).

The foods most commonly contaminated by *Salmonella* are poultry meat, pork and beef. While table eggs (and egg products) are very seldom contaminated, they still represent the leading cause of *Salmonella* outbreaks in Europe due to their very wide consumption and the risk of consuming these foods raw or undercooked (EFSA-ECDC, 2015). The impact of *Salmonella* on human health and the economic consequences of management measures in the various animal production sectors underline the need to identify and characterise *Salmonella* throughout the food chain, in order to control this pathogen.

## The scheme's objectives

The goal of the *Salmonella* network, created in 1997, was to provide scientific and technical support to partner laboratories in charge of detecting this pathogenic bacterium in animal and/or food matrices. The network now covers the entire country. Some partner laboratories were also located abroad. This support involved the phenotypic and even molecular characterisation of isolates with the aim of confirming the serovar and possibly distinguishing between the bacterial strains isolated. This activity generated the massive collection of descriptive data, associated with the sampling context. Given the network's stability, the relevance of monitoring isolation trends for the main serovars became increasingly obvious over time (Lailler *et al.*, 2012).

Today, this network's main objective is to detect the emergence of potentially problematic strains for public health and/or strains with a potential economic impact on animal production sectors. It aims to characterise contamination in animals, their environment, the ecosystem and foods in relation to the *Salmonella* hazard. Strains isolated by partner laboratories are submitted on a voluntary basis.

In this context, the data presented here are the results of serotyping by plate-agglutination tests only, obtained in 2015 by the ANSES

**Box.**

**Objectives**
Detection of the emergence of *Salmonella* serovars in a specific sector, monitoring of trends for every serovar isolated in the food chain, scientific and technical support for field laboratories for the characterisation of isolates.

**Programming framework**
The European regulations (Hygiene package) require *Salmonella* testing all throughout the food chain. Regulations (EC) No 178/2002 and No 2073/2005 (as amended) define the responsibilities of the various stakeholders in this chain and the microbiological safety and hygiene criteria that target, in particular, *Salmonella* in foods. In their most recent Opinions on *Salmonella*, EFSA (2010) and ANSES (2013) recommended the comprehensive serotyping of *Salmonella* isolated in the food chain to provide risk managers and assessors with accurate information.

In Europe, *Salmonella* and *Campylobacter* are considered to be the zoonotic agents responsible for most cases of zoonoses in humans *(Regulation (EC) No 2160/2003)*. To take into account the impact on animal health and health crises, which mobilise considerable financial and human resources, the competent authority defined *Salmonella* as a Category 1 health hazard for the *Gallus gallus* and *Meleagris gallopavo* animal species (Ministerial Order of 29 July 2013).

**Protocol**
- **Nature of the analysed contaminant:** *Salmonella* spp.
- **Affected products:** animal production and crops, production environments, animal feed, human food, ecosystem.
- **Stage of the food chain:** from farm to fork.
- **Definition of a "case':** isolation of *Salmonella* from a sample collected in the food chain.
- **Number of samples and sampling method:** 3465 *Salmonella* isolated as part of self-inspections, alerts, farm diagnoses and investigations (the total number of samples collected for self-inspections is unknown).
- **Sampling strategy:** random/targeted depending on the surveillance systems involved; data reporting on a voluntary basis.
- **Analytical method, nature of sampling:** potentially every matrix in the food chain. *Salmonella* testing using the methods validated by AFNOR Validation, reference method: NF EN ISO 6579-1 and NF EN ISO 6579/A1 (Annex D). *Salmonella* serotyping by agglutination: *FD CEN ISO/TR 6579-3*.

Laboratory for Food Safety. These results are associated with descriptive metadata regarding samples collected in the field. This report does not include serotyping results obtained by the network's partner laboratories (approximately two-thirds of the data centralised every year). The organisation and means implemented for this network do not currently ensure adequate responsiveness in reporting for the serotyping undertaken by partner laboratories or its integration into the network's database. In collaboration with all its partners, the network is undergoing major changes to improve this. The network is upgrading to allow responsiveness and to acquire more effective tools to meet its new surveillance objectives (see § Analysis of system's strengths and weaknesses).

# Summary of operations

## *Voluntary partner laboratories*

The *Salmonella* network is managed and coordinated by the ANSES Laboratory for Food Safety in Maisons-Alfort. The Laboratory for Food Safety is associated with the ANSES Ploufragan-Plouzané Laboratory, which acts as the *Salmonella* National Reference Laboratory (NRL), for the characterisation of *Salmonella*, all industries combined. In the framework of its reference mandate and according to Order 2015-1245 of 7 October 2015, the NRL is in charge of "providing the French State, accredited laboratories, and the platforms mentioned in

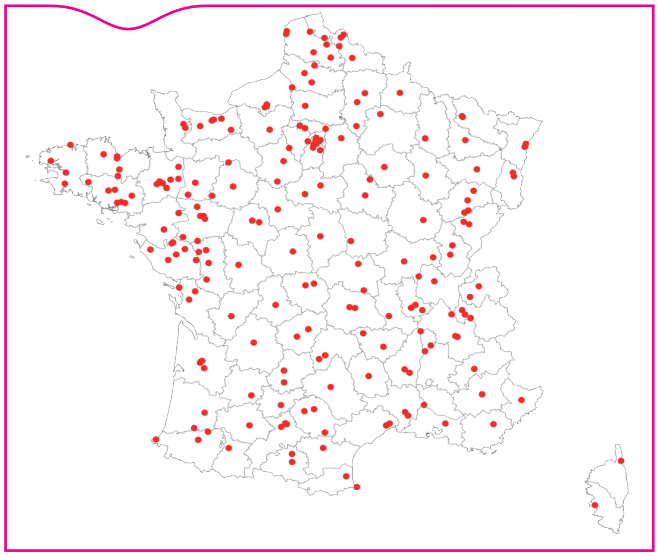

**Figure 1. Geographic distribution of the *Salmonella* network's partner laboratories in 2015**
Each red dot represents a partner laboratory. Laboratories located in French overseas territories and abroad are not shown on this map.

**Table 1. Relative significance of the various sampling contexts associated with the strains received by the Laboratory for Food Safety as part of the *Salmonella* network**

| Sampling context | Number of strains | Proportion (%) |
|---|---|---|
| Product alert | 34 | 1.0 |
| Epidemic/alert | 99 | 2.9 |
| Farm diagnosis | 288 | 8.3 |
| Monitoring (own-checks) | 3,039 | 87.7 |
| Survey | 5 | 0.1 |
| **General total** | **3,465** | **100.0** |

Sampling date between 01/01/2015 and 31/12/2015. Strains received by ANSES between 5/1/2015 and 6/6/2016

Section II of Article L. 201-14 with the scientific and technical support required for the collection, processing, accessibility, transmission and dissemination of epidemiological surveillance data. These laboratories can also provide support to other surveillance programme managers". The *Salmonella* network therefore works closely with the NRL to help it carry out this task and fulfil these requirements. In this context, the network offers a sample surveillance tool under the comprehensive management of ANSES.

The network's partners include both public and private laboratories; most of them are members of the Adliva, Aflabv and Aprolab associations. These three associations represent the following, respectively, in the *Salmonella* network:
- public departmental veterinary analysis laboratories,
- private veterinary biological analysis laboratories involved in primary production in particular,
- private environmental and food hygiene analysis laboratories.

In 2015, 131 partner laboratories sent strains and related data to the network (Figure 1). The number of strains submitted to ANSES by each partner ranged from one to 392. The sampling context associated with these strains mainly (88%) involved own-checks undertaken by professionals to monitor their activities, irrespective of the stage of the food chain (Table 1). Some strains were isolated in the framework of analyses undertaken for diagnostic purposes on farms. Less often, the *Salmonella* received were detected further to an alert, related to the contamination of a finished product, possibly during distribution, or following the occurrence of human cases of salmonellosis. Thus, the strains collected by the network were

isolated from a wide variety of matrices: from both sick animals and healthy carriers, in the farm environment, in slaughterhouses, in processing plants, and in human food and animal feed.

### *Description of the data collected*

The health status of an animal or plant involved in the processing and production of human food must be monitored to prevent pathogens such as *Salmonella* from being transmitted to humans. Partner laboratories therefore test for *Salmonella* using samples collected in all stages of the food chain: from the importing of raw materials for animal feed to food intended for consumers in their homes or in restaurants. In this context, numerous analyses are requested every year involving samples taken on farms, at the slaughterhouse, or in other stages of the food chain as part of surveillance plans and official controls or own-checks by operators.

The serotyping results integrated in the database of the *Salmonella* network are obtained either by partner laboratories or by the ANSES Laboratory for Food Safety (the only data taken into account in this article, considering the main objective related to the detection of unusual signals and emerging contamination). These results are accompanied by epidemiological data that characterise the strain:

- the country, the *département,* and if possible the town where the sample was taken,
- the sampling "site" (holding, processing plant, slaughterhouse, etc.) and date,
- the "sector" (natural ecosystem, animal feed, animal health and production, human food) and any clinical signs observed in animals,
- the "context" (surveillance, diagnosis, epidemic, product alert, etc.),
- the "sampler" (self-inspection, official sampling, etc.),
- the "sample type" (animal feed, human food, environmental sample, animal sample, etc.),
- the nature of the analysed matrix,
- identification numbers for the investigation of situations when necessary (INUAV, DAP, EDE, EGET, Food-borne outbreak no., Guidance note no., etc.).

For every strain received, a form is completed by the laboratories and the collected metadata are entered in the network's ACTEOLab (Application for the centralisation and transfer of data dedicated to the operational epidemiological surveillance of laboratories) database. Serotyping background data provided by partners are systematically verified before being included in the database. These data can be discussed on the telephone with the laboratory shipping the strains to obtain additional information. When serotyping is performed by the Laboratory for Food Safety and the result has been validated by the technical team in charge of coordinating the network, an analysis report is sent to the requesting laboratory. For strains that do not agglutinate, which cannot be serotyped using conventional methods, an alternative method is implemented by the Laboratory for Food Safety, to be able to characterise these strains (Check & Trace *Salmonella* kit by Check-Points).

These data are useful:

- to partner laboratories, which can question the *Salmonella* network's team, for example to identify the main serovar found in a given matrix or environment, or determine trends for a serovar over the years,
- to risk managers, who have information about the presence of non-regulated serovars and the emergence of certain strains to be taken into account in the regulations where appropriate,
- to partners involved in the investigation of food-borne outbreaks or product alerts related to non-compliant products placed on the market. In this case, the network's contribution consists in the transmission of reports enabling (potentially) responsible serovars and/or foods to be targeted,
- for the detection of unusual events in the food chain, through the development of dedicated statistical tools (time-series analysis in particular).

Molecular typing methods (characterisation of Typhimurium variants by PCR, MLVA, PFGE, sequencing) can also be implemented by the laboratory. These methods are able to compare strains with one another and illustrate potential links between strains isolated from various types of samples. Indeed, the probability of two strains deriving from a recent common ancestor is even higher when these strains have similar or even non-distinguishable molecular profiles. In addition to sampling information (sampling context, date and site), these methods are of particular interest for monitoring strains on a holding/in a plant or for investigating food-borne outbreaks.

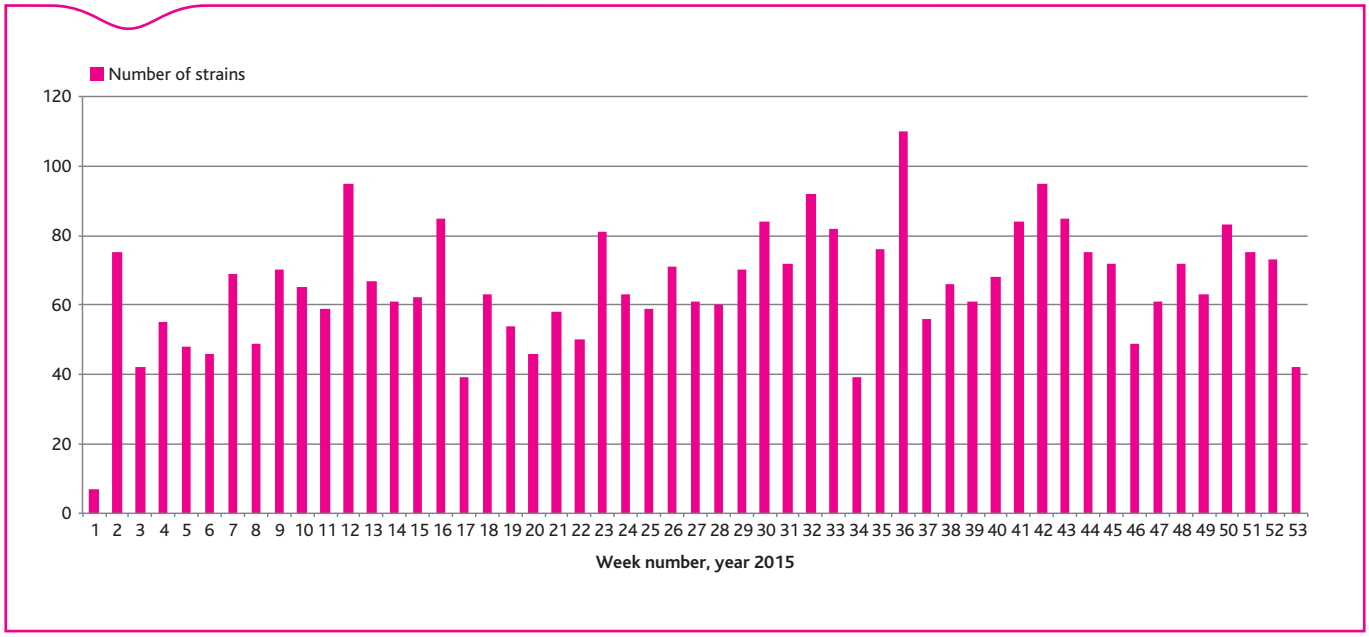


**Figure 2. Breakdown of the number of strains submitted to the Laboratory for Food Safety in the framework of the *Salmonella* network, by sampling week (average number of strains isolated and submitted to the Laboratory for Food Safety = 68 strains/week)**

**Table 2.** Main serovars of the strains received by the Laboratory for Food Safety by sector of activity, in the framework of the *Salmonella* network in 2015.

| Human food (n=1503) | Animal feed (n=619) | Animal health (n=1236) | Ecosystem (n=107) |
|---|---|---|---|
| *S.* 1,4,[5],12:i:- (224) | *S.* Livingstone (162) | *S.* Enteritidis (154) | *S.* Veneziana (17) |
| *S.* Typhimurium (135) | *S.* Cerro (113) | *S.* Livingstone (71) | *S.* 4,5,12:i:- (10) |
| *S.* Enteritidis (131) | *S.* 1,3,19:z27:- (19) | *S.* 1,4,[5],12:i:- (64) | *S.* Enteritidis (9) |
| *S.* Derby (111) | *S.* Hadar (19) | *S.* Montevideo (56) | *S.* Typhimurium (7) |
| *S.* Bredeney (98) | *S.* Mbandaka (18) | *S.* IIIb 61:k:1,5,7 (55) | *S.* Albany (6) |
| *S.* IIIb 61:k:1,5,7 (93) | *S.* Anatum (16) | *S.* Mbandaka (45) | *S.* Newport (5) |
| *S.* Dublin (66) | *S.* Havana (13) | *S.* Kottbus (42) | *S.* Bovismorbificans (4) |
| *S.* Montevideo (49) | *S.* Tennessee (13) | *S.* IIIa 48:z4,z23:- (38) | *S.* Livingstone (4) |
| *S.* Mbandaka (41) | *S.* Agona (12) | *S.* Lille (35) | *S.* London (4) |
| *S.* Infantis (38) | *S.* Newport (12) | *S.* Typhimurium (35) | *S.* Napoli (4) |
| *S.* Kentucky (28) | *S.* Indiana (11) | *S.* Llandoff (33) | *S.* Weltevreden (3) |
| *S.* Livingstone (27) | *S.* Infantis (11) | *S.* Tennessee (28) | *S.* Agona (2) |
| *S.* Newport (27) | *S.* Llandoff (10) | *S.* Give (25) | *S.* Ajiobo (2) |
| *S.* Anatum (26) | *S.* Montevideo (10) | *S.* Newport (25) | *S.* Durban (2) |
| *S.* Rissen (25) | *S.* Typhimurium (10) | *S.* Veneziana (21) | *S.* Infantis (2) |
| *S.* Kedougou (25) | *S.* 1,4,[5],12:i:- (10) | *S.* Dublin (20) | *S.* IIIb 38:r:z (2) |

# Results obtained

In 2015, the Laboratory for Food Safety serotyped 3465 strains. On average, 68 strains were received per week by the Laboratory for Food Safety, for confirmation of the serovar (Figure 2).

## *Breakdown of the isolates received by the Laboratory for Food Safety by sector and matrix type*

The inventoried strains were broken down as follows by original sector of activity: 1503 strains (43.4%) in human food, 1236 strains (35.7%) in animal health and production, 619 strains (17.8%) in animal feed, and 107 strains (3.1%) from the natural ecosystem (Table 2).

### Human food

The strains collected in this sector primarily came from the "meat products" category (815 strains, i.e. 54.2%) and the "dairy products" category (545 strains, i.e. 36.3%). Other product categories (eggs and egg products, fruits and vegetables, seafood products) each accounted for less than 2% of isolates.

Pork (302 strains), chicken (166 strains) and turkey (96 strains) meat accounted for 69.3% of the meat products for which *Salmonella* was isolated by the Laboratory for Food Safety. Isolates from sheep, cattle and duck meat accounted for 8.2%, 8.0% and 2.3% respectively. Other meat (deer, horse, goat, wild boar, goose, game, rabbit, etc.) accounted for 11.6% of the isolates from meat products received by the Laboratory for Food Safety.

Milk and cheese from cattle (114 and 189 strains) and sheep (38 and 51 strains) were the two main sources of contamination for isolates from dairy products. They accounted for 71.9% of dairy products for which *Salmonella* was isolated by the Laboratory for Food Safety.

### Animal health and production

The strains in this sector serotyped by the Laboratory for Food Safety were primarily isolated from the *Gallus gallus* species (546 strains, i.e. 44.2%), cattle (342 strains, i.e. 27.7%) and ducks (111 strains, i.e. 9.0%). Of the 546 strains isolated from *Gallus gallus*, 140 (25.6%) were isolated from laying hens and 385 (62.6%) from broiler chickens.

### Animal feed

The strains in this sector serotyped by the Laboratory for Food Safety were primarily isolated from pet food (379 strains, i.e. 61.2%). For 84 of the 619 isolates processed by the Laboratory for Food Safety (13.6%), precise information was not available; they were noted as "all animal feed'. They were followed by compound feed for poultry (43 strains, i.e. 6.9%). The Laboratory for Food Safety also serotyped 43 strains (6.9%) from seed and fruit oils (soy, rapeseed, sunflower, etc.), 35 strains (5.6%) from raw materials of animal origin, and 13 strains (2.1%) from raw materials of cereal origin (barley, maize, wheat, etc.). The other strains were divided up between various other categories.

### Ecosystem

The strains in this sector serotyped by the Laboratory for Food Safety were primarily isolated from water sources/catchments (54 strains, i.e. 50.5%) and water treatment plants (33 strains, i.e. 30.8%). Strains isolated from water distribution systems accounted for 4.7% (five strains), and eleven strains (10.3%) were identified as "other activities'.

## *Main serovars identified by the Laboratory for Food Safety*

Of the strains received by the Laboratory for Food Safety in 2015, 42 were strains that do not agglutinate (rough serovar).

### Human food

***> "Meat" category***

- Pork (n=302): the strains collected in this category belonged to 26 serovars. The three main serovars – the monophasic variants of Typhimurium (*S.* 1,4,[5],12:i:-) (43.7%), *S.* Typhimurium (17.9%) and *S.* Derby (17.9%) – accounted for 79.5% of the strains in this meat category.
- Chicken meat (n=166): *S.* Derby (14.5%), *S.* Infantis (13.7%) and *S.* Kentucky (13.3%) were the main isolated serovars out of 31 detected.
- Turkey meat (n=96): the three main serovars – *S.* Bredeney (31.3%), *S.* 1,4,[5],12:i:- (24.0%) and *S.* Brandenburg (14.6%) – accounted for 69.9% of the strains in this meat category. Fourteen serovars were found in total.
- Mutton (n=67): of the 11 serovars isolated in this meat category, the *S.* IIIb 61:k:1,5,7 serovar was the only major serovar found (64.2%).

***> "Milk and dairy products" category***

The main serovars isolated from cow's milk (n=114) were *S.* Montevideo (26.3%), *S.* Mbandaka (21.1%), *S.* Dublin (17.3%) and *S.* Enteritidis (14.0%). In total, 16 serovars were found. For cheese made from cow's milk (n=189), *S.* Enteritidis (31.2%), *S.* Dublin (21.7%), *S.* Typhimurium (14.8%) and the monophasic variants of Typhimurium (*S.* 1,4,[5],12:i:-) (9.5%) were the four main isolated serovars out of the 21 detected in this type of product.

Sheep's milk (n=38) was also occasionally a source of contamination. Over half of the isolated strains belonged to the *S.* IIIb 61:k:1,5,7 serovar (55.3%). Ten serovars were found in total. For cheese made from sheep's milk (n=51), the two main serovars found were *S.* IIIb 61:k:1,5,7 (27.4%) and *S.* IIIb 50:i:z (21.6%). For other dairy products, all types combined, *S.* Bredeney (40.5%) was the main isolated serovar of the 29 detected.

***> "Eggs and egg products" category***

The most commonly found serovar was *S.* Livingstone (35.7%) but very few of these matrices were processed by the Laboratory for Food Safety (n=28). In total, seven serovars were detected.

***> "Seafood products" category***

For seafood products (crustaceans and molluscs, n=11), nine different serovars were identified; there was therefore no major serovar.

***> "Fruits and vegetables" category***

The three most commonly isolated serovars were *S.* Typhimurium (21.4%), the monophasic variants of Typhimurium (*S.* 1,4,[5]:12:i:-) (14.3%) and *S.* Anatum (14.3%). In total, fourteen strains were isolated belonging to 10 different serovars.

**Animal health and production**

"Cattle" sector (n=342): the strains collected in the cattle sector were mainly isolated in samples from sick animals and their farm environment and belonged to 27 serovars, the main ones being *S.* Enteritidis (32.7%), *S.* Montevideo (13.5%) and *S.* Mbandaka (10.8%).

"Broiler chicken" sector (n=385): *S.* Livingstone (18.1%) and *S.* Lille (10.2%) were the two main isolated strains. It is interesting to note the wide variety of serovars (72 different serovars) detected representing these 385 strains serotyped by the Laboratory for Food Safety.

"Laying hen" sector (n=145): the most commonly isolated serovars were *S.* Enteritidis (11.4%), *S.* Havana (9.3%) and *S.* Banana (8.6%); 37 different serovars were found in total.

"Duck" sector (n=111): out of 30 identified serovars, the three main serovars isolated were *S.* Give (19.8%), *S.* Kentucky (8.1%) and *S.* 6,7:-:- (8.1%).

**Animal feed**

In this sector, pet food was the sampling category with the largest number of strains serotyped by the Laboratory for Food Safety (n=379). The *Salmonella* most frequently isolated in this sector belonged to the *S.* Livingstone (37.5%) and *S.* Cerro (28.0%) serovars, out of a total of 31 identified serovars.

**Ecosystem**

*S.* Veneziana (27.8%) was the main identified serovar out of the 25 detected for strains collected from water sources and catchments (n=54). In samples collected from water treatment plants (n=33), *S.* Albany was the most commonly isolated serovar (42.9%).

## Analysis of the system's strengths and weaknesses

The systematic serotyping of isolated strains is recommended by EFSA (2010) to enhance surveillance in the various stages of the food chain or to refine the messages provided as part of the Rapid Alert System for Food and Feed concerning the *Salmonella* hazard. Agglutination serotyping is the official typing method for *Salmonella*.

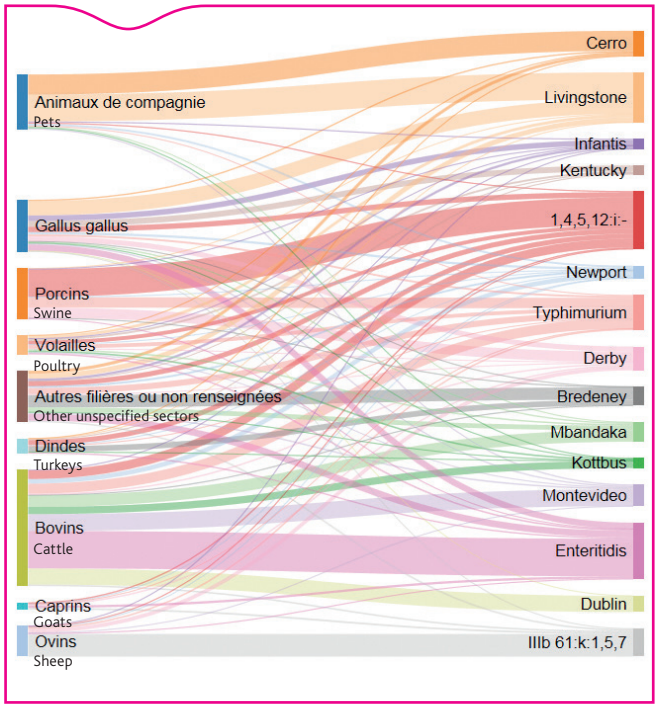


**Figure 3. Distribution of the top 15 *Salmonella* serovars (n=2100, 61%) identified from the strains sent to the Laboratory for Food Safety in the framework of the *Salmonella* network in 2015, by sampling production sector. (Sankey diagrams illustrate the relative proportion of each isolated serovar in the various production sectors)**

For uncommon or less common serovars, the isolation and identification of such strains provide valuable data for establishing a high likelihood of a relationship between strains. However, this traditional method is less relevant for the most abundant serovars found in separate sectors (monophasic variants of Typhimurium, Typhimurium, Enteritidis, Newport, Livingstone, Derby, etc.). It would be extremely beneficial to sequence the whole genome, for all or some of these serovars, to demonstrate the advantages of improving strain discrimination in preventive epidemiology. The *Salmonella* network is planning to undertake this study in 2017.

The characterisation of certain strains can be improved in response to an alert in a company or the investigation of a food-borne outbreak in order to assess the relationship between strains isolated from humans and those of non-human origin. This comparison of molecular profiles requires sound knowledge of the various strains circulating in the field that belong to the serovar in question. The network's extensive collection of strains provides access to a wide variety of isolation origins (in terms of location, time period, matrix and context) and can help confirm or refute assumptions involving epidemiological links between strains.

Data quality is ensured through the maintenance of expertise by the staff of the Laboratory for Food Safety and the network's member laboratories. Training activities on serotyping for the technicians in these laboratories are organised several times a year, but the audience remains limited (two or three people per session). In addition, every year, the Laboratory for Food Safety organises an Inter-Laboratory Proficiency Test (ILPT) in which over half of the network's partner laboratories participate and achieve satisfactory results. The aim is to assess their capacity to undertake, at the very least, the serotyping of regulated *Salmonella*. The Laboratory for Food Safety also participates in two ILPTs organised at the international level by the EU Reference Laboratory for *Salmonella* and by the World Health Organization.

As in previous years, the comparison of the annual reports prepared by the National Reference Centre (NRC) for *Salmonella* and the *Salmonella* network highlights similarities between the main

serovars isolated in the human food sector and those isolated from humans: the emergence of the monophasic variants of Typhimurium (*S*. 1,4,[5],12:i:-) since the early 2000s and the preponderance of *S*. Typhimurium and *S*. Enteritidis since the 1990s. These same serovars were the "top-3" *Salmonella* serovars identified in 2014 in Europe in these same sectors (EFSA–ECDC, 2015). More recently, based on the surveillance data collected by the *Salmonella* network and the NRC, the Kentucky serovar was provisionally included on the list of Category 1 health hazards, by Ministerial Order[1], to combat the establishment of multi-drug resistant strains during primary production in the regulated *Gallus gallus* and *Meleagris gallopavo* sectors.

The *Salmonella* network also collects data from the animal feed sector, primarily related to strains isolated from pet food, which is a potential source of human contamination by direct contact. The goal is therefore to reduce this route of animal contamination and monitor the carriage of *Salmonella* by pets, some of which are more exotic (reptiles, snakes, etc.) and are known to sometimes host several serovars without showing signs.

The scope of surveillance covered by this network is therefore very broad. However, it has some weaknesses, described below, which need to be corrected to improve its operations. It is reasonable to assume that first-line laboratories more easily determine *Salmonella* serovars they encounter on a regular basis or for which regulatory requirements are set and ILPTs are organised.

Moreover, the external assessment of the network, undertaken in 2015 using the "Oasis flash" method (Hendrikx *et al.,* 2011), underlined the lack of information regarding the representativeness of the data collected in relation to all of the *Salmonella* isolated throughout France. This surveillance system does not take into account the total number of analyses undertaken but considers only isolated strains voluntarily submitted by partners for serotyping. However, the prevalence of *Salmonella* in at-risk matrices could be estimated by enhancing the centralisation of analytical results, including negative results obtained in France.

Deadlines for the reporting of serotyping data by the network's partners to the system's central unit as well as deadlines for integration into the database must be compatible with the level of responsiveness expected by the network's users.

Furthermore, some serovars that are not commonly isolated, as well as others whose antigenic formula requires the use of uncommon sera, are probably overrepresented among the strains received by the Laboratory for Food Safety for serovar confirmation. More generally, even if laboratories are competent to perform this serotyping, a non-negligible proportion of strains isolated mainly on poultry farms (a regulated sector) are sent to the Laboratory for Food Safety, associated with the NRL, to confirm the result (for the purpose of an audit argument or to restore a client's confidence).

The network therefore needs to strengthen its actions for the development of tools facilitating the use of data and real-time communication between partners before it sets more binding reporting targets.

To be more effective, the wealth of data collected by the *Salmonella* network should be processed in near real-time in order to provide risk managers with information allowing them to anticipate the potential occurrence of human cases and plan official controls. This development is eagerly awaited, since the database is needed by the French Public Health Agency (SPF) to facilitate epidemiological investigations in the context of health alerts, which would ideally require recent analytical results, involving samples collected in a time window compatible with the timeline of cases. For this to happen, the characteristics of the suspected food matrix must also be considered: the product's shelf life, the complexity of the product's production and distribution process, etc.

1. Ministerial Order of 17 February 2015 amending Ministerial Order of 29 July 2013 on the definition of Category 1 and 2 health hazards for animal species.

The network is coordinated by a multidisciplinary team made up primarily of microbiologists and epidemiologists. Its coordinating team collaborates with the Agency's other entities to develop computing tools (database, algorithms, applications in the R-Shiny environment, etc.). Through its new tools, the network is diversifying its support for its partners and thus indirectly for professionals in the various sectors of the agri-food industry and risk assessors. Query tools are available for example to determine the nature of the most contaminated matrices for a given serovar. This information is extremely useful for guiding professionals in the management of a contamination situation. This feature, currently available only to the network's coordinating team, will soon be offered to the network's partners in return for their active participation in the health surveillance of *Salmonella* in the food chain.

This *Salmonella* surveillance system is thus undergoing major changes. Internal discussions are currently being held at ANSES on whether the means allocated to this system can meet the surveillance objectives currently set in France, in relation to the *Salmonella* hazard. The network's new operating procedures will be clarified by the end of 2016, after approval by the steering committee. The roles of all of the system's stakeholders will be specified. Through these efforts, the network is expected to strike a better balance between the acquired data (benchmarks, estimated representativeness of certain industries, etc.) and the expectations of end users (risk assessors and managers, agri-food professionals) of the information produced by the surveillance system.

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## Glossary

ADILVA: French Association of Directors and Executives of Public Veterinary Analysis Laboratories

AFLABV: French Association of Veterinary Biological Analysis Laboratories

Aprolab: Professional Association of French Analytical Laboratories

NRC: National Reference Centre

DAP: Support document for samples

EDE: Identification number for cattle farms

EGET: Identification number for fattening pig plants

ILPT: Inter-Laboratory Proficiency Test

NRL: National Reference Laboratory

EURL: European Union Reference Laboratory

MLVA: Multi-Locus VNTR Analysis

WHO: World Health Organization

PCR: Polymerase Chain Reaction

PFGE: Pulse Field Gel Electrophoresis

FCS: Food Chain Surveillance

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