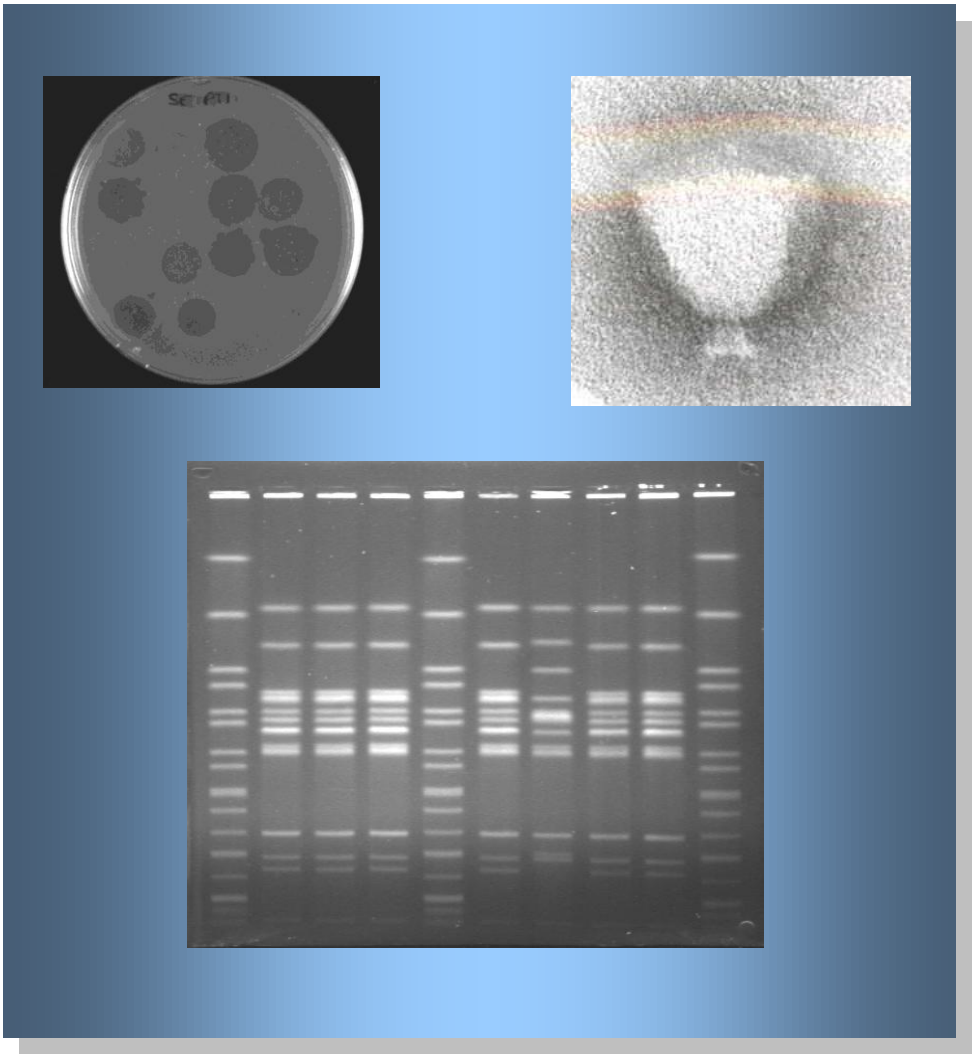
NATIONAL *SALMONELLA*, *SHIGELLA* & *LISTERIA* REFERENCE LABORATORY OF IRELAND (HUMAN HEALTH)



ANNUAL REPORT FOR 2015

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Introduction

The National *Salmonella, Shigella* & *Listeria* Reference Laboratory was established in 2000 with support from the Department of Health and Children to provide reference services related to human health. It is a public service laboratory which currently operates with 2 WTE scientific staff representing a reduction from 3 staff working in the service until 2011. The NSSLRL website is at http://www.nuigalway.ie/salmonella_lab/. The reference laboratory uses a number of phenotypic methods (serotyping, antibiotic-resistance testing and phage typing) and molecular methods (pulse-field gel electrophoresis (PFGE) and multi-locus variable number tandem repeat analysis (MLVA) and whole genome sequencing to precisely characterise *Salmonella* isolates. This process can be considered as fingerprinting of *Salmonella*. The goal of this fingerprinting is to assist relevant agencies in protecting public health by identifying and interrupting chains of transmission of *Salmonella* infection. In addition the NSSLRL provides typing services for *Shigella species* and *Listeria monocytogenes* and since the beginning of 2016 has begun to provide a very limited surveillance service for antimicrobial resistance in *Campylobacter spp.*

One of the major challenges that NSSLRL will need to address in the near future is the transformation of molecular typing methods. Whole genome sequencing is rapidly being accepted as a key method in molecular typing of pathogens and is increasingly used as a basis for international comparison of isolates within Europe. In 2016, NSSLRL is developing and applying these methods. Resources to support this transition are very limited but the transition is essential to ensure that the reference laboratory service for Ireland can benefit from and contribute to European cooperation in this field.

The Laboratory is committed to providing a high quality and timely service and has achieved accreditation to the ISO15189 standard from the Irish National Accreditation Board (INAB). The continued success of the laboratory is entirely dependent on the support of the staff in the laboratories that submit isolates for typing. My colleagues and I appreciate that the preparation, packing and dispatch of isolates is a significant burden and would like to thank you for your support over the years.

I would also like to acknowledge the support of all those agencies with whom we work closely to ensure that the service we provide works as information for action. In particular I would like to thank Galway University Hospitals, NUI Galway, the Food Safety Authority of Ireland, the Health Protection Surveillance Centre and colleagues in Public Health Departments and Environmental Health

Departments throughout the country and to acknowledge the work of colleagues in the National Reference Laboratory *Salmonella* (Food, Feed and Animal Health).

If you have any comments or questions arising from the report please feel free to contact me at the email address given below.

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Salmonella species.

In 2015, 668 isolates were submitted to the National *Salmonella, Shigella* & *Listeria* Reference Laboratory for *Salmonella* typing. When non-*Salmonella*, QC, contaminants and duplicate isolates were removed a total of 543 *Salmonella* isolates were typed. This represents a 5% increase in the number of isolates received in 2014.

There were 286 human clinical isolates, including 260 faecal isolates, 19 from blood (including 5 *S*.Typhi and 1 *S*.Paratyphi B), 2 other invasive isolates, and 5 urine isolates. *S*.Typhimurium (n = 53) and its monophasic variant 4,[5],12:i:- (n = 44) and *S*.Enteritidis (n = 72) predominated (Table 2). There was marked seasonal variation with the highest number of isolates occurring in months August to November. This coincides with the warmer months of the year and with the peak season for foreign travel (Fig.1) and may be related in part to one or both of these factors.

In some cases more than one isolate was received from a patient. For example we may have received an invasive isolate (e.g. from a blood culture) and an isolate from faeces from the same patient. Where invasive and faecal isolates come from the same patient, only the invasive isolate is recorded to avoid duplication. The average turnaround time for human isolates was 7 days (range 2-18 days). The number of human *Salmonella* isolates received is now just over half that observed when the laboratory was established in 2000 (Table 1) and has been sustained at a low level for some years. This reduction in number of isolates submitted is likely to reflect a true reduction in the incidence of human salmonellosis and represents a significant public health achievement by those agencies working in this area.

Table 1: Number of *Salmonella* isolates received in NSSLRL

Year	Human	Non-human
2015	286	257
2014	258	261
2013	345	312
2012	319	391
2011	320	381
2010	364	559
2009	364	368
2008	447	815
2007	457	653
2006	430	308
2005	357	494
2004	420	650
2003	486	634

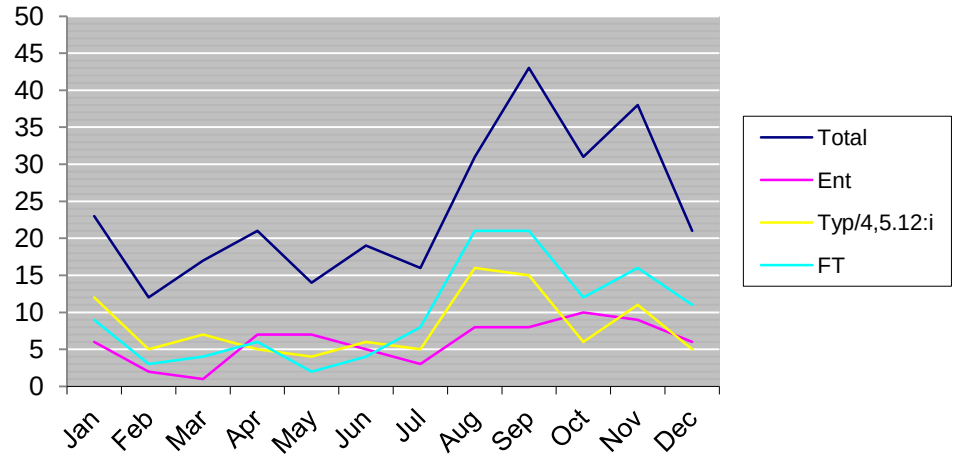
2002	394	540
2001	508	574
2000	636	21

Table 2: Top 19 serotypes of Human Isolates (including typhoidal)

Serotype	Frequency	%
Typhimurium	53	18.5
Monophasic Typhimurium[1]	44	15.4
Enteritidis	72	25.2
Infantis	8	2.8
Newport	8	2.8
Java	7	2.4
Typhi	7	2.4
Bareilly	5	1.7
Kentucky	5	1.7
Saintpaul	5	1.7
Brandenburg	4	1.4
Stanley	4	1.4
Agona	3	1.0
Bovismorbificans	3	1.0
Mbandaka	3	1.0
Napoli	3	1.0
Panama	3	1.0
Poona	3	1.0
Virchow	3	1.0
Others	43	15.0
Total	286	100

[1] The antigenic formula 4,[5],12:i:- is that of *S*. Typhimurium except that the phase 2 antigen is not expressed. These isolates are generally referred to as monophasic *S*. Typhimurium and are so called in this report.

Figure 1 Seasonal Variation in numbers of *Salmonella* isolates [1]



[1.] The line "FT (Foreign Travel)" describes the number of cases of salmonellosis for which an association with recent foreign travel was reported to NSSLRL. Reporting of recent foreign travel is likely to be incomplete.

It is important to note that there is always an interval gap between the time of onset of symptoms and date of isolate receipt in the NSSLRL. This includes time taken for patient to access doctor, taking and transporting the sample to the primary laboratory, isolation of *Salmonella*, and referral to NSSLRL. Fig 1 refers to date of receipt in the NSSLRL.

Salmonellosis non-typhoidal

S.Typhimurium and its monophasic variant.

S.Typhimurium 4,[5],12;i:2 and its monophasic variant (4,[5],12;i:-) together accounted for 33.9 % of all cases of *Salmonella*. Phage type DT193 was the most common (21.6%) phage type among human isolates in 2015. Other phage types included DT104 (6.2 %), DT120 (5.2 %) and DT104b (4.1%) and 14.4% were untypable* by the method. The proportion of isolates accounted for by phage types DT104 (6.2%) and DT104b (4.1%) has been consistently lower in recent years. In 2008 for example DT104 and DT104b each accounted for 20% of such isolates.

S.Enteritidis

S.Enteritidis accounted for 25.2% of all cases of *Salmonella*. The predominant phage types were PT21 (22.2%), PT8 (16.7%), PT1 (15.3%) and PT4 (8.3%). Approximately 1 in 10 isolates (9.7%) were untypable*.

* Does not react with typing phages.

Salmonellosis Typhi and Paratyphi

Seven isolates of *S*.Typhi and one *S*.Paratyphi B isolate were received. A history of recent travel was recorded for six of the *S*.Typhi isolates; 5 to the Indian subcontinent and one to Uganda. The *S*.Paratyphi B isolate had a history of travel to South America.

Antimicrobial resistance

More than half (53.4%) of isolates (n = 143) were susceptible to all antimicrobial agents tested. Thirty two point five percent of isolates (n = 93) were multi-drug resistant (three or more different classes of antibiotics). Of the 32.5% of isolates that were multi-drug resistant, 37.6% (n = 35) had the profile of resistance to ampicillin, streptomycin, sulphonamide and tetracycline (ASSuT) and were mainly monophasic S. Typhimurium.

Two extended spectrum beta-lactamase (ESBL) producing isolates were detected. ESBL producing isolates included a patient with travel history to Vietnam (*S*. 4,[5],12:i:- and a patient with travel to Thailand & UAE (*S*. Typhimurium). An AmpC producing *S*. Anatum isolate was received from a patient with travel to the Phillipines.

Sixty four isolates of *Salmonella* resistant to ciprofloxacin were detected (22.4%). It is worth noting that the EUCAST interpretive criteria for resistance to ciprofloxacin for *Salmonella* changed on January 1st 2014 and isolates with ciprofloxacin MIC of > 0.06 mg/l are now reported as resistant. By current EUCAST criteria therefore 15.9% (n = 55) of *Salmonella* isolates from 2013 would be considered ciprofloxacin-resistant.
High level resistance to ciprofloxacin (>2mg/l) is rare among *Salmonella* but a ciprofloxacin-resistant *S.* Kentucky clonal group has arisen and spread from North Africa in the last decade. Four such isolates were typed in the NSSLRL in 2015, 1 of which had a history of foreign travel to Australia and another to Thailand.
The NSSLRL added two new antibiotics, azithromycin and tigecycline, to its testing panel at the end of 2013, based on advice from the European Centre for Disease Prevention and Control (ECDC), to detect emerging resistances. Resistance to azithromycin was detected in isolates from 5 patients, including 1 with foreign travel to Thailand & UAE, 1 with travel to Thailand & Cambodia and 1 with travel to Africa. In 2015 no isolates exhibited tigecycline resistance.

Travel related infection

A history of recent foreign travel was recorded in 41.6 % (n = 119) of human cases of infection (Table 3). Ireland was noted as the country of infection in 46.9 % (n = 134) of cases while 11.5 % (n = 33) had no country of infection recorded. Spain, Poland and Thailand were the most commonly recorded travel destinations. *S*. Enteritidis accounted for a high proportion of isolates associated with travel to Spain (47.8%) and all the isolates from Poland (n = 9) while *S*.Stanley was strongly associated with travel to Asia (75%), i.e. 3/4 isolates. Forty one of 72 (56.9 %) *S*.Enteritidis isolates were associated with foreign travel compared to 22.7 % for *S*. Typhimurium and its monophasic variant combined. Although NSSLRL does not have access to data on the number of Irish people who travel to each country it is likely that the number of cases associated with each country is at least in part accounted for by the popularity of the country as a destination.

Table 3: Foreign travel history for *Salmonella* isolates

Continent	Country	Number
Europe (n = 50)		
	Spain	23
	Poland	9
	Italy	3
	Turkey	3
	Bulgaria	2
	Germany	2
	Czech Republic	1
	France	1
	Macedonia	1
	Malta	1
	Portugal	1
	Romania	1
	The Netherlands	1
	United Kingdom	1
Africa (n = 17)		
	Morocco	4
	Tanzania	3
	Uganda	2
	Egypt	1
	Ghana	1
	Malawi	1
	South Africa	1
	Sudan	1
	Africa*	3
Australasia (n = 44)		
	Thailand	7
	Vietnam	5
	India	4
	Pakistan	4
	Indonesia	2
	Malaysia	2
	Saudi Arabia	2
	The Philippines	2

Australia	1
Bangladesh	1
Cambodia	1
China	1
Korea	1
U.A.E.	1
Thailand & U.A.E.	3
Thailand & Cambodia	1
Vietnam & Thailand	1
New Zealand & U.A.E.	1
Asia*	4

Americas (n = 8)

Cuba	2
Brazil	1
Guatemala	1
Mexico	1
Nicaragua	1
USA	1
South America*	1

* Country not stated

Clusters

Eleven groups of related isolates involving a total of 32 isolates were identified in 2015. *S.* Typhimurium/monophasic S. Typhimurium was involved in 4 such groups (15 isolates) while *S.* Enteritidis was implicated in 4 (10 isolates). Four of these groups (8 patients) represented family outbreaks, i.e. all patients affected were from one family.

The NSSLRL liaises with the European Centre for Disease Control (ECDC) in the investigation of outbreaks that may have an international dimension. PFGE images and analysis from *Salmonella* and *Listeria* isolates are also uploaded to a centralised ECDC database where they can be compared with isolates from other countries to check for matches.

Animal Contact

A history of animal contact was recorded for 82 patients with salmonellosis including contact with turtles, birds, fish, horses, dogs and farm animals (Table 5). Dogs were the most common contact animal (n = 47) while contact with cats was less common (n = 18).

Strong links included 3 patients with *S*. Enteritidis PT21 associated with contaminated poultry, farmers (n = 2) with *S*. Dublin, and a baby with *S*. Tennessee and contact with a bearded dragon.

Although public information on the risk (particularly to children) of contact with reptiles has been circulated (http://www.fsai.ie/WorkArea/DownloadAsset.aspx?id=11207) it appears that this may not be reaching relevant sections of the population or may not have resulted in modification of risk behaviour. It may be appropriate to consider if further steps to limit exposure of children to risk of salmonellosis from contact with reptiles and other exotic pets is appropriate. In total 16 isolates of *Salmonella* (approx. 5.6 % of all human cases) were associated with contact with exotic animals although in many cases these animals may not have been the source of the infections.

Many of the patients that had a history of animal contact also had other risk factors, e.g. recent history of foreign travel, consumption of particular food products, etc. It is important to note that *Salmonella* is primarily a foodborne disease and that contact with animals such as dogs and cats is very common in the general population therefore contact with an animal species should not be taken to indicate that the animal is the likely source of infection. (A listing of associated animal contacts is provided as Appendix 1 of this report).

Non-Human isolates

The NSSLRL types non-human isolates from official food laboratories and also performs phage typing on isolates identified as *S.* Typhimurium or *S.* Enteritidis from the Central Veterinary Research Laboratory. In 2015, 257 isolates of *Salmonella* of non-human origin were submitted to the NSSLRL. This represents a decrease of 1.5 % in the number of non-human isolates received in 2014. The majority of isolates were from swine (n = 136), poultry (n = 80) and bovine (n = 19) sources. *S*. Typhimurium/monophasic *S*. Typhimurium (n = 171) and *S*.Enteritidis (n = 80) were the most prevalent serovars.

***Salmonella* serotypes and correlation with Human Infection**

***S*.Typhimurium**

S.Typhimurium and its monophasic variant 4,[5],12;i:- accounted for 66.5% of all non-human isolates and were isolated from a variety of sources predominantly swine (n = 135) but also including bovine (n = 15) and poultry (n = 6) sources. Phage types DT193 (n = 45), DT104b (n = 16), DT120/DT120 low (n = 14), DT104 (n = 8) and DT22 (n = 6) were the most common phage types from swine and 14 isolates were untypable (n = 14). Phage types DT104 (n = 3) and U310 (n = 2) were the most common phage type among bovine isolates

and 4 isolates were untypable (n = 4). Phage type DT193 (n = 2) and DT135 (n = 2) were the most common phage type among poultry isolates. As noted earlier DT193 which accounts for a high proportion of the non-human isolates of *S.* Typhimurium in Ireland is also the most common *S*. Typhimurium phage type associated with human infection.

***Salmonella* Enteritidis.**

Eighty *S*. Enteritidis isolates were received from non-human sources in the NSSRL in 2015, 73 from poultry, 3 from bovine and 4 from environmental sources. Many of the isolates were from samples from poultry flocks evaluated by in the course of an investigation by colleagues in the CVRL. Most of these isolates (61% of all S. Enteritidis received) were PT21. This was particularly true of those isolates related to the investigation referred to previously.

Antimicrobial Resistance among non-Human isolates

Antimicrobial susceptibility testing was performed on 8 of the 257 non-human isolates (249 were referred for phage typing only). Of the isolates tested 62.5% (n = 5) were susceptible to all antimicrobial agents tested while 25% (n = 2) were multi-drug resistant (three or more different classes of antibiotics).

Laboratory Contamination

False-positive *Salmonella* results due to laboratory cross-contamination are a serious problem for laboratories and can be difficult to detect. Cross contamination in a laboratory can result in inappropriate diagnosis of patient infection or in unfounded concerns regarding the safety of a food product. Detailed subtyping of isolates by the NSSLRL helps in detection and confirmation of laboratory contamination incidents (Role of Subtyping in Detecting *Salmonella* Cross Contamination in the Laboratory; BMC Microbiology: 9; 155).

We would like to reiterate our request that all laboratories involved in testing *Salmonella* from any source use *Salmonella* Nottingham NCTC 7382 as their positive control.

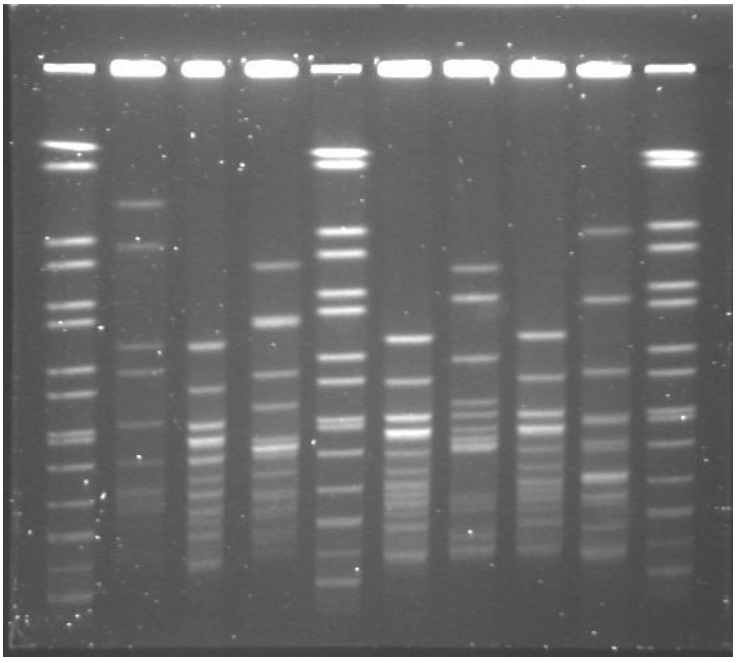
Listeria monocytogenes

Table 4: Number and serotypes of *Listeria monocytogenes* isolates from human sources received in NSSLRL

Year	Total	4b	1/2a	1/2b	1/2c
2015	19	10	8	1	0
2014	10	4	6	0	0
2013	7	6	1	0	0
2012	8	5	1	2	0
2011	6	3	3	0	0
2010	4	2	1	0	1
2009	8	4	3	0	1
2008	14	9	4	0	1
2007	12	9	2	0	1
2006	1	0	1	0	0
2005	4	3	1	0	0

Listeria monocytogenes can be subdivided into 13 different serotypes based on their combinations of O and H antigens. However serotypes 4b and the 1/2 group account for the vast majority of human infections.
Three of these isolates had been isolated in 2014 but not received in the NSSLRL until 2015.

Fig. 2 Pulse Field Gel Electrophoresis of *L.monocytogenes* isolates digested with *Apa*I



The NSSLRL received 28 *Listeria monocytogenes* isolates in 2015. These included 19 human clinical isolates; 12 from blood cultures, 4 from CSF, 1 from placental surface swab, 1 from a wound and 1 from a nasal swab. Ten of the isolates from humans typed as serotype 4b, 8 typed as serotype 1/2a and 1 typed as serotype 1/2b. The majority of the food/animal/environmental isolates serotyped as 1/2a (n = 8) and 1 isolate was serotype 4b.

The NSSLRL is working with colleagues in food and veterinary microbiology in Ireland and with colleagues in Europe towards Europe wide comparison of *L. monocytogenes* isolates. In 2015 NSSLRL contributed to an ECDC project (ELiTE) generating and comparing over 1000 whole genome sequences for *L. monocytogenes* from across the EU and EEA. To support these activities is essential that all human isolates are available for typing and we appeal for all isolates to be forwarded for typing.

Shigella species

Table 5: Number of *Shigella* isolates received in NSSLRL 2005-15

Year	Total	*sonnei*	*flexneri*	*boydii*	*dysenteriae*
2015	67	34	27	4	2
2014	45	27	18	0	0
2013	43	23	16	4	0
2012	20	12	6	2	0
2011	30	20	10	0	0
2010	39	17	18	3	0
2009	48	19	24	1	4
2008	43	22	16	5	0
2007	20	5	12	2	1
2006	20	7	12	0	1
2005	13	8	5	0	0

Shigella sonnei has only one serotype while the other *Shigella species* can be can be subdivided into a number of different serotypes and subserotypes based on their lipopolysaccharide antigens.

Figure 3 Summary of *Shigella* isolates typed in NSSLRL from 2005-15

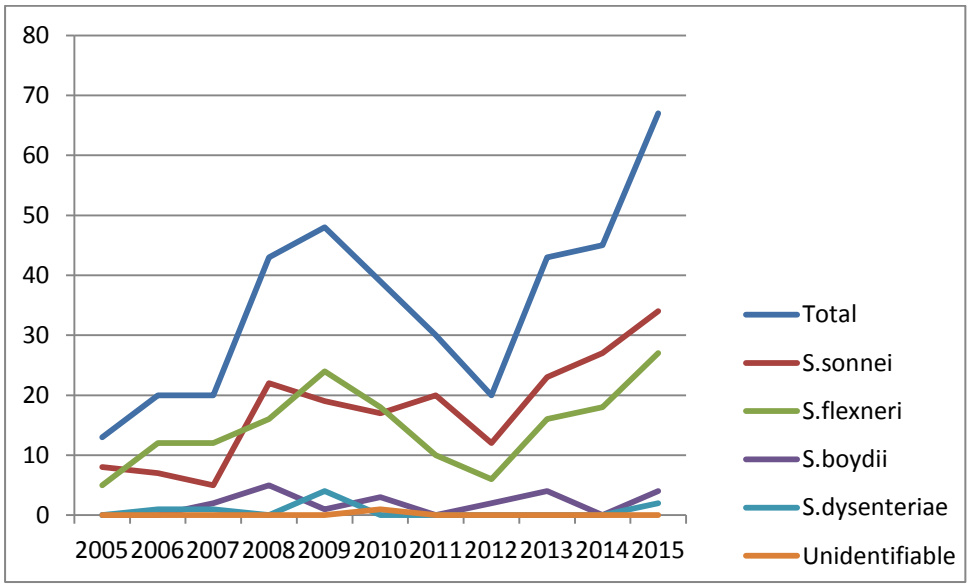
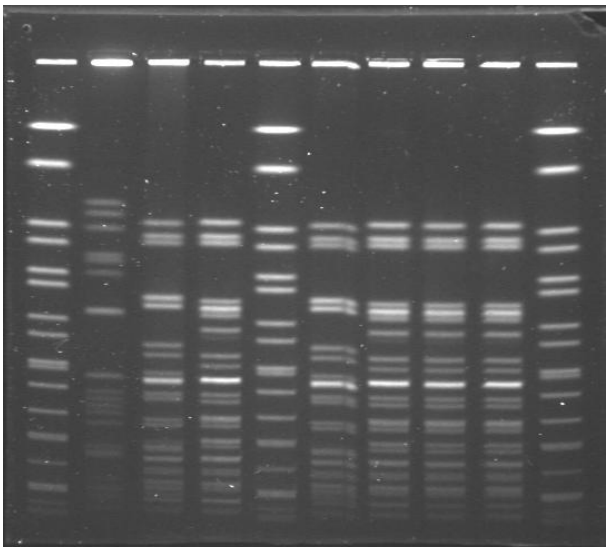


Fig. 4 Pulse Field Gel Electrophoresis image of *S.sonnei* digested with *Xba*I



Men who have sex with men (MSM) related Shigella outbreak pattern is in lanes 4, 7, 8 and 9.

A total of 95 isolates were referred to the NSSLRL in 2015 for *Shigella* typing. When non-*Shigella*, QC and duplicate isolates were removed a total of 67 *Shigella* isolates were typed. These consisted of 34 *S.sonnei* and 27 *S.flexneri*. The *S.flexneri* isolates were further divided into 1 *S.flexneri* untypable, 4 *S.flexneri* 1b, 5 *S.flexneri* 1c, 1 *S.flexneri* 2, 11 *S.flexneri* 2a, 1 *S.flexneri* 2b, 2 *S.flexneri* 3a, 1 *S.flexneri* 3b and 1 *S.flexneri* 4. This is the highest number of *Shigella species* ever submitted to the NSSLRL. It is worth noting that laboratories that have changed to use of direct molecular detection of pathogens in faces appear to have a striking increase in submission of *Shigella species* for typing. This is most likely explained by the increased sensitivity of the method compared to conventional culture. As many major laboratories have now changed to use of direct molecular detection it seems likely that the increased in *Shigella* species submitted in 2016 is related, at least in part, to improved ascertainment. An outbreak in the east of the country also contributed to the increase.

Ninety one percent of isolates (n = 61) were multi-drug resistant (three or more different classes of antibiotics). Three ESBL producing *Shigella sonnei* (travel to Belgium, Iran and Pakistan respectively) and 1 *S.dysenteriae* from a patient with travel history to Afghanistan were received in the NSSLRL in 2015 while 11 isolates were resistant to ciprofloxacin. The ciprofloxacin resistant isolates included 7 *Shigella sonnei*, 3 of which were known to be associated with travel to the Indian subcontinent, and 3 *S.flexneri* isolates with history of recent foreign travel to Asia. The proportion of *S. sonnei* isolates resistant to ciprofloxacin is a real concern given that this has increased significantly in recent years. Based on PFGE analysis many of the ciprofloxacin resistant isolates including some reported as associated with India and Ireland are very closely related suggesting relatively recent dissemination of a ciprofloxacin-resistant clonal group. In 2015 the NSSLRL worked with a group of international colleagues to further evaluate the issue of recent clonal expansion of *Shigella sonnei* and a detailed report is expected to be published in 2016. The NSSLRL added azithromycin to its antibiotic panel in October 2013 and in 2015 8/67 exhibited resistance to azithromycin. These included 3 *S.flexneri* 1c, 2 *S.flexneri* 2a, 2 *S.sonnei* and 1 *S.flexneri* untypable.

Thirty-four patients had a recorded history of recent foreign travel, including Europe (n = 7), Africa (n = 7) and Australasia (n = 18). Twenty-one patients had Ireland recorded as their country of infection while there were no details for 12 patients.

Table 6: Foreign travel history for *Shigella* isolates

Continent	Country	Number
Africa (n = 7)		
	Cape Verde	2
	Egypt	1
	Morocco	1
	Nigeria	1
	Tanzania	1
	Africa	1
Europe (n = 7)		
	U.K.	2
	Spain	2
	Belgium	1
	Germany	1
	Portugal	1
Australasia (n = 18)		
	Pakistan	6
	India	5
	Afghanistan	1
	Burma	1
	Indonesia	1
	Iran	1
	Thailand	1
	Asia	1
	Bahrain & Saudi Arabia	1
Americas (n = 2)		
	Mexico	1
	USA	1

There was a large outbreak MSM outbreak in the East of the country involving numerous *Shigella* serotypes and antibiograms which continued into 2016. These included *Shigella sonnei* SSuTTmNa (n = 9), *S. flexneri* 2a ACST (n = 5), *S. flexneri* 2a ACSSuTTmAzt (n = 2) and *S.flexneri* 1c ASSuTTmAzt (n = 3). The NSSLRL worked with public health colleagues to characterise and manage this outbreak.

NSSLRL Publications and Presentations 2015

Papers/Letters

Reptile-Associated Salmonellosis: Time for a new public health approach. Gavin, P., et al. Arch.Dis. Child. 2015 Mar;52(9): 3494-5.

Ciprofloxacin-Resistant *Shigella sonnei* Associated with Travel to India. De Lappe, N., et al. EID. 2015 May;21(5).

A proposed new bacteriophage family subfamily: "*Jerseyvirinae*". Anany, H., et al. Arch. Virol. 2015. 160:1021-1033.

Whole genome sequencing provides possible explanations for the difference in phage susceptibility among two *Salmonella* Typhimurium phage types (DT8 and DT30) associated with a single foodborne outbreak. BMC Res Notes 2015 Nov 27;8:728. doi: 10.1186/s13104-015-1687-6.

Event based surveillance of food and waterborne diseases in Europe: urgent inquiries (outbreak alerts) during 2008 to 2013. Euro Surveill 2015 Jun 25;20(25):19-28.

Case study of the use of pulsed field gel electrophoresis in the detection of a food-borne outbreak. Methods Mol Biol 2015;1301:35-40. doi: 10.1007/978-1-4939-2599-5_4.

Appendix 1.

Animal contact history or strains associated with animal contact

NSSLRL no.	Source	Sub[1].	Strain	Animal Contact
Exotic animals				
MS150002	Human	I	4,[5],12:i:- DT120	Parrot, Dog & Ponies
MS150094*	Human	I	Enteritidis PT1	Aviary
MS150136	Human	I	Java	Gerbil
MS150611	Human	I	4,[5],12:i:- U310	Hamsters
MS150095	Human	I	Typhimurium DT104	Snake
MS150096	Human	I	Thompson	Pet shops, Fish, Parrots, Dog
MS150482	Human	I	Typhimurium DT193	Tropical Fish, Guinea Pig, Cats & Pigeons
MS150467	Human	I	Kentucky	Goldfish
MS150012*	Human	I	4,[5],12:i:- DT193	Tortoises
MS150598	Human	I	Enteritidis PT8	Turtles, Parrot, Snake, Dogs
MS150650*	Human	I	Enteritidis untypable	Turtles
MS150329	Human	I	Tennessee	Bearded Dragon, Parrot, Dog & Cat
MS150230	Human	I	Typhimurium RDNC	Zoo
MS150279*	Human	I	Enteritidis PT4	Zoo
MS150541*	Human	I	Stanley	Zoo, Puppies
MS150472*	Human	I	Lomalinda	Safari animals & Dog
Farm or Food animals (including horses)				
MS150019	Human	I	Typhimurium untypable	Farm animals
MS150137	Human	I	Typhimurium untypable	Farm animals (with *Salmonella*)
MS150181	Human	I	Enteritidis PT21	Chicken farm
MS150182	Human	I	Enteritidis PT21	Chicken farm
MS150184	Human	I	Enteritidis PT21	Poultry
MS150232*	Human	I	Isangi	Chickens
MS150288	Human	I	Typhimurium U310	Chickens
MS150292	Human	I	Typhimurium U310	Chickens, Horses, Dogs
MS150110	Human	I	Typhimurium DT20a	Cows
MS150254	Human	I	Isangi	Cattle farm & Dog
MS150435	Human	I	4,[5],12:i:- DT193	Goats

MS150073	Human	I	Dublin	Farmer, visited farms
MS150315	Human	I	Dublin	Farmer
MS150566	Human	I	Typhi	Farm animals

Common companion animals

MS150057	Human	I	Typhimurium DT8	Cat
MS150366	Human	I	Enteritidis PT8	Cat
MS150427*	Human	I	Typhimurium DT104	Cat
MS150652	Human	I	Enteritidis RDNC	Cat
MS150665	Human	I	Panama	Cat
MS150135	Human	I	Typhimurium Untypable	Cat
MS150573*	Human	I	Poona	Cat
MS150646	Human	I	4,[5],12:i:- RDNC	Cat
MS150474	Human	I	Typhimurium DT120	Cat & Pigeons
MS150003	Human	I	Bovismorbificans	Dog
MS150007	Human	I	4,[5],12:i:- DT193	Dog
MS150016*	Human	I	Enteritidis PT21	Dog
MS150067	Human	I	Infantis	Dog
MS150097	Human	I	4,[5],12:i:- Untypable	Dog
MS150100	Human	I	Typhimurium DT135	Dog
MS150102	Human	I	Typhimurium RDNC	Dogs
MS150186	Human	I	Enteritidis PT21	Dog
MS150231	Human	I	Typhimurium RDNC	Puppy
MS150252	Human	I	4,[5],12:i:- DT193	Dogs
MS150253	Human	I	Typhimurium DT104b	Dog
MS150317	Human	I	Bovismorbificans	Dogs
MS150331	Human	I	Enteritidis PT21	Dog
MS150353	Human	I	Enteritidis PT1	Dog
MS150354*	Human	I	4,[5],12:i:- U323	Dog
MS150356*	Human	I	Enteritidis PT8	Dog
MS150362	Human	I	Stanley	Dog
MS150370*	Human	I	Oranienburg	Dog
MS150376	Human	I	Typhimurium RDNC	Dog
MS150377	Human	I	4,[5],12:i:- DT7	Dogs
MS150378	Human	I	4,[5],12:i:- DT193	Dog
MS150384	Human	I	Typhimurium DT120	Dog
MS150376	Human	I	Typhimurium RDNC	Dog
MS150456	Human	I	4,[5],12:i:- DT193	Dog
MS150509	Human	I	Bareilly	Dog
MS150513	Human	I	Enteritidis PT8	Dog

MS150535	Human	I	4,[5],12:i:- DT193	Dog
MS150582	Human	I	Enteritidis PT8	Dog
MS150422	Human	I	Typhimurium DT41	Dogs
MS150425*	Human	I	Unnamed (4,5,12:b:-)	Dogs
MS150433	Human	I	Bareilly	Dogs
MS150465	Human	I	4,[5],12:i:- DT20a	Dogs
MS150610*	Human	I	Thompson	Dogs
MS150310	Human	I	4,[5],12:i:- DT120	Dog & Cat
MS150318	Human	I	Typhimurium DT104b	Dogs & Cats
MS150332	Human	I	Typhimurium DT193	Dog & Cat
MS150473	Human	I	Kentucky	Dog & Cat
MS150581*	Human	I	Enteritidis PT8	Dog & Cat
MS150613*	Human	I	Enteritidis PT21	Dogs & Cat
MS150540	Human	I	4,[5],12:i:- DT193	Dog, Cat & Rabbit
MS150291	Human	I	Enteritidis RDNC	Pet animals
MS150359	Human	I	Typhimurium RDNC	Pets & Pet food
MS150187	Human	I	Enteritidis PT21	Pigeons

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1. Sub = Subspecies. There are over 2500 *Salmonella* serotypes of which approximately 60% belong to *subspecies* I. These account for about 99% of human infections. *Subspecies* I is present in both warm and cold blooded animals while the other *Salmonella subspecies* are generally associated with cold-blooded animals.

* Patient had history of recent foreign travel