

3.9 Shigellosis

Summary

Number of notifications: 84
Crude incidence rate: 1.8/100,000

Shigellosis is caused by the bacterium *Shigella*. There are four species of this bacterium *S. sonnei*, *S. boydii*, *S. flexneri* and *S. dysenteriae*. *S. dysenteriae* produces a very powerful toxin that produces severe damage to the lining of the gut. The bacteria are only found in humans. Anyone can get shigellosis, but those who are at greater risk include children in child care centres and their parents, overseas travellers, institutionalized people and men who have sex with men (MSM).

Eighty four cases of shigellosis were notified in Ireland in 2016, corresponding to a crude incidence rate (CIR) of 1.8 per 100,000. This represents a decrease of 7% compared to 2015. Of 82 cases where hospitalisation status was recorded, 24 (29%) were reported as hospital in-patients. All were laboratory confirmed.

The excess of male cases compared to females was slightly lower compared to 2014 and 2015 at 1.5: 1.0 (figure 1). During 2016, cases ranged in age from 10 months to 89 years (median age=31 years). The male to female ratio was highest in the age range 25-44 years (2.5:1.0).

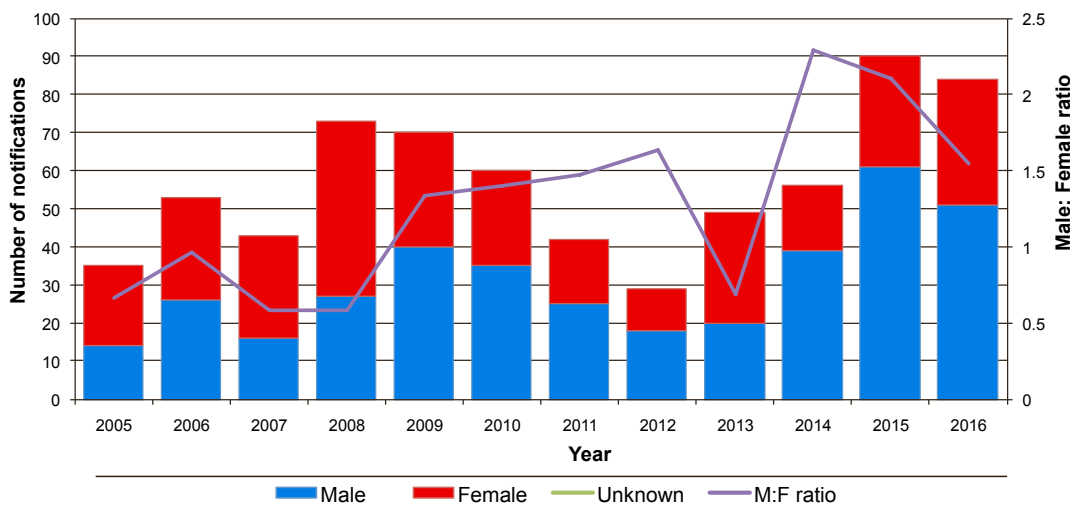


Figure 1: Annual number of notifications shigellosis by sex and year, Ireland 2004-2016 (Data source: CIDR)

Table 1: Number of *Shigella* notifications by species and country of infection, Ireland 2016

Organism	Ireland	Africa	Asia	Caribbean	South America	Unknown/Not specified	Total
<i>S. boydii</i>	1		1				2
<i>S. dysenteriae</i>			2				2
<i>S. flexneri</i>	16	2	2	0	3	4	27
<i>S. sonnei</i>	19	6	12	1	1	6	45
<i>S. species</i>	1		3	1		3	8
Total	37	8	20	2	4	13	84

Table 2: Shigellosis outbreaks 2016 (Data source: CIDR)

HSE-area	Outbreak type	Location	Transmission mode	Number ill	Serotype
HPSC	General	Community	Foodborne	14	S. sonnei
HSE-E	General	Community	Person-to-person	5	S. flexneri 2a

Information on travel history is very valuable when reviewing surveillance data for possible indigenous clusters. Data on country of infection was available for 85% of shigellosis notifications this year. Thirty-four cases were reported as being associated with foreign travel in at least 22 countries during 2016. Thirty-seven cases were reported as being acquired in Ireland (52% of known), while no country of infection information was available for 13 cases.

S. sonnei was the most common species reported (n=45), followed by *S. flexneri* (n=27), both of which were commonly associated with indigenous acquisition.

Two general shigellosis outbreaks were notified in 2016, resulting in 19 cases of illness and seven associated hospitalisations (Table 2). A small outbreak of *Shigella flexneri* 2a comprising 5 cases was reported among MSM. A foodborne outbreak comprising 14 cases of *S. sonnei* across the Republic and Northern Ireland was epidemiologically linked to consumption of pre-prepared toasted sandwiches at a restaurant chain.

More detailed typing of *Shigella* isolates can provide useful information on the relatedness of strains which is used by public health personnel to outrule/provide evidence for links between cases during investigations of case clusters. The National *Salmonella*, *Shigella* and *Listeria* Reference Laboratory (NSSLRL) provide laboratory services for speciation, serotyping, antimicrobial resistance profiling, and most recently, Whole Genome Sequencing (WGS) of *Shigella* isolates. The species/serotype and antimicrobial resistance patterns of these cases are reported in Table 3.

During 2016, almost 90% of *Shigella* isolates recovered in primary hospital laboratories were referred for typing at the NSSLRL in Galway. Speciation and antimicrobial resistance (AMR) profiling were key in defining the extent of the two general outbreaks reported in 2016, demonstrating the importance of referral of all *Shigella* isolates for typing.

Table 3: *Shigella* isolates referred to NSSLRL in 2016 by species and AMR profile

Species	Number by species	AMR profile	Number by species and AMR
<i>Shigella boydii</i>	2	none	1
		SuTTm	1
<i>Shigella dysenteriae</i>	3	ASSuTTm	1
		SuTTm	1
		SuTTmNa	1
<i>Shigella flexneri</i> 1a	1	SSuTTm	1
<i>Shigella flexneri</i> 1c	2	ASSuTTmAzst	1
		T	1
<i>Shigella flexneri</i> 2a	19	ACSAzst	1
		ACSSuTTm	5
		ACSSuTTmNaCp	1
		ACST	2
		ACSTTm	2
		ACTTmNaCp	5
		ASSuTmNaCp	2
		SSuTm	1
<i>Shigella flexneri</i> 3a	1	ACST	1
<i>Shigella flexneri</i> 3b	1	ACT	1
<i>Shigella flexneri</i> 4c	2	ACSSuTTmNaCp	1
		SuTTm	1
<i>Shigella flexneri</i> 6	1	SuTTmNaCp	1
<i>Shigella flexneri</i> X variant	1	ACST	1
<i>Shigella sonnei</i>	41	ASSuTm	1
		ASSuTTm	1
		ASSuTTmCtx	1
		ASSuTTmNa	1
		ASSuTTmNaAzst	2
		ASSuTTmNaCpAzst	1
		ASSuTTmNaGm	1
		ASuTTmNaCpAzst	1
		SSuTm	1
		SSuTTm	5
		SSuTTmNa	6
		SSuTTmNaCp	5
		Su	1
		SuTm	1
SuTTm	2		
SuTTmNa	3		
Tm	8		
Total	74	Total	74