

Stein, Katharina^{1,2}. Harmanus, Céline⁶. FitzGerald, Susan^{1,2}. Roche, Fiona³. Hennessy, Sarah³. Drudy, Denise⁴. Kyne, Lorraine^{1,5}. McDermott, Sinead⁸. Burns, Karen⁸. Fitzpatrick, Fidelma^{7,8}. Kuijper, Ed⁶. Fenelon, Lynda^{1,2}.

¹University College Dublin, Ireland; ²St. Vincent's University Hospital, Dublin, Ireland; ³Health Protection Surveillance Centre, Ireland; ⁴DIT Dublin Institute of Technology, Ireland; ⁵Mater Misericordiae University Hospital, Dublin, Ireland; ⁶Leiden University Medical Centre, the Netherlands; ⁷Royal College of Surgeons in Ireland Dublin; ⁸Beaumont Hospital Dublin, Ireland

Introduction

In 2009, the first Irish national enhanced *Clostridium difficile* infection (CDI) surveillance and typing study was carried out to determine the epidemiology of CDI and the ribotype distribution of the isolated strains (1). There is no *C. difficile* reference laboratory in Ireland and therefore changing patterns of ribotype distribution over time are unknown. A second study was commenced which aimed to examine the epidemiology, ribotype distribution and presence of toxin genes of all CDI cases in Irish healthcare-facilities (HCFs) in quarter 2 in 2014 and 2015. Enhanced epidemiological information was collected by the Health Protection Surveillance Centre on all cases of CDI and compared with the ribotyping data.

Methods

- Faecal samples positive for *C. difficile* toxin or PCR positive during quarter 2 of 2014 and 2015 were included in the study
- Identification of suspected colonies by MALDI-TOF mass spectrometry
- DNA extraction with commercial extraction kit (Qiagen)
- PCR-ribotyping according to Bidet *et al.* (2) and detection of genes encoding for TcdA, TcdB, CDT, GluD and 16SrDNA according to Persson *et al.* (3)
- Ribotypes were assigned by comparison with fingerprint patterns of representatives obtained from the Leiden University Medical Centre Library, the Netherlands

References

- Burns, K., *et al.* "Clostridium difficile Infection in the Republic of Ireland: Results of a 1-Month National Surveillance and Ribotyping Project, March 2009." *Infection Control and Hospital Epidemiology* 31.10 (2010): 1085-1087
- Bidet, Philippe, *et al.* "Development of a new PCR-ribotyping method for Clostridium difficile based on ribosomal RNA gene sequencing." *FEMS Microbiology Letters* 175.2 (1999): 261-266.
- Persson S, Torpdahl M, Olsen KE: New multiplex PCR method for the detection of Clostridium difficile toxin A (tcdA) and toxin B (tcdB) and the binary toxin (cdtA/cdtB) genes applied to a Danish strain collection. *Clin Microbiol Infect* 2008, 14(11):1057-1064.

Purpose

- Investigate the PCR-ribotype distribution of *C. difficile* in Ireland
- Monitor the changing patterns over time
- Correlate ribotype to new/recurrent, HCAI/CAI and severe CDI cases

Conclusions

- Large increase in ribotype 078 and decrease in 027
- Number of CAI cases doubled from 2009 (10%) to 2015 (21%)
- Ribotype distribution varies throughout the country

Discussion

There has been a marked shift both in the most prevalent ribotypes and the epidemiological features of CDI in Ireland since 2009. Further work is required to fully explain these changes.

	Q2 2014	Q2 2015
Participating HCFs	52	52
Samples received	429	439
CD isolated	380 (89%)	408 (93%)
Distinct PCR-ribotypes	49	53
Enterotoxin A	98% (374/380)	99% (403/408)
Cytotoxin B	98% (374/380)	99% (403/408)
Binary toxin	22% (84/380)	29% (118/408)
Non-toxigenic	2% (6/380)	1% (5/408)

Table 1: Study details

	2009	2014	2015
New cases	79% (166/211)	84% (270/321)	90% (290/322)
Linked PCR-ribotypes	001 (21%) 027 (21%) 106 (20%)	078 (15%) 014/020 (13%) 015 (10%)	078 (22%) 014/020 (19%) 001 (7%)
Recurrent cases	18% (38/211)	9% (30/321)	8% (25/322)
Linked PCR-ribotypes	027 (38%) 001 (21%) 078 (17%)	078 (30%) 015 (17%) 103 (7%)	078 (40%) 014/020 (24%) 005 (8%)
HCAI	84% (176/211)	63% (201/321)	66% (214/322)
Linked PCR-ribotypes	027 (26%) 001 (23%) 106 (14%)	078 (17%) 014/020 (13%) 015 (9%)	078 (25%) 014/020 (19%) 001 (7%)
CAI	10% (21/211)	20% (63/321)	21% (67/322)
Linked PCR-ribotypes	078 (33%) 027 (17%) 106 (17%)	014/020 (14%) 015 (14%) 078 (14%)	014/020 (22%) 078 (18%) 005 (10%)
Severe cases	3% (6/211)	2% (5/321)	2% (6/322)
Linked PCR-ribotypes	001 (17%) 014 (17%) 027 (17%)	012 (28%) 015 (28%) 005 (14%)	078 (50%) 023 (33%) 015 (17%)

Table 2: New/recurrent, HCAI/CAI and severe CDI cases linked to PCR-ribotypes in 2009, 2014 & 2015

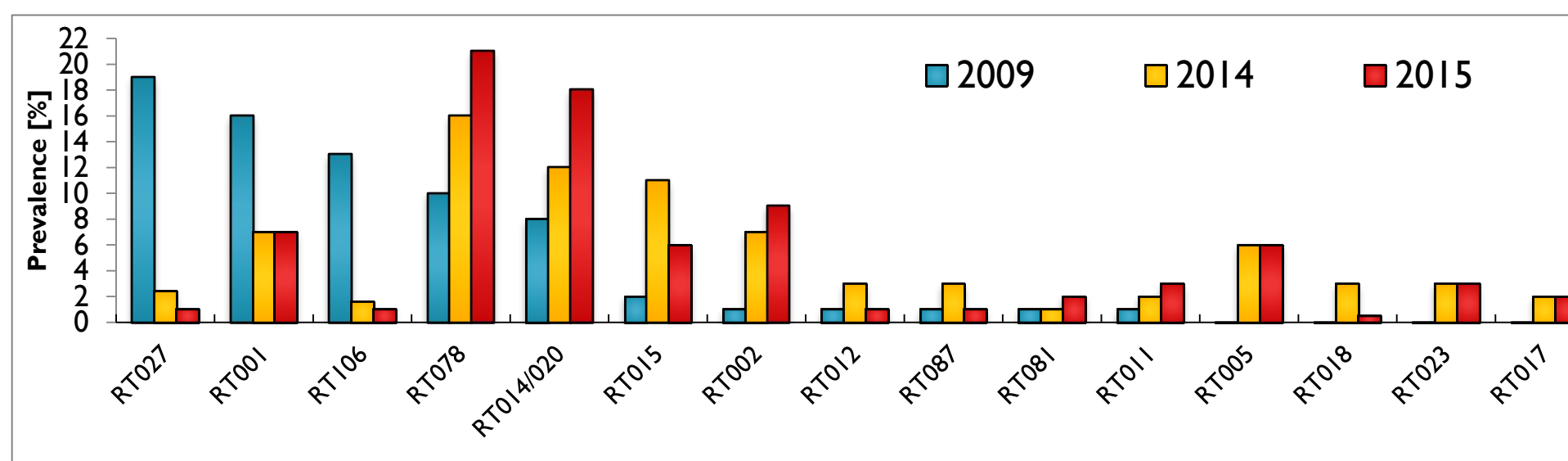


Figure 1: The prevalence of the most common PCR-ribotypes in Ireland 2009, 2014 & 2015

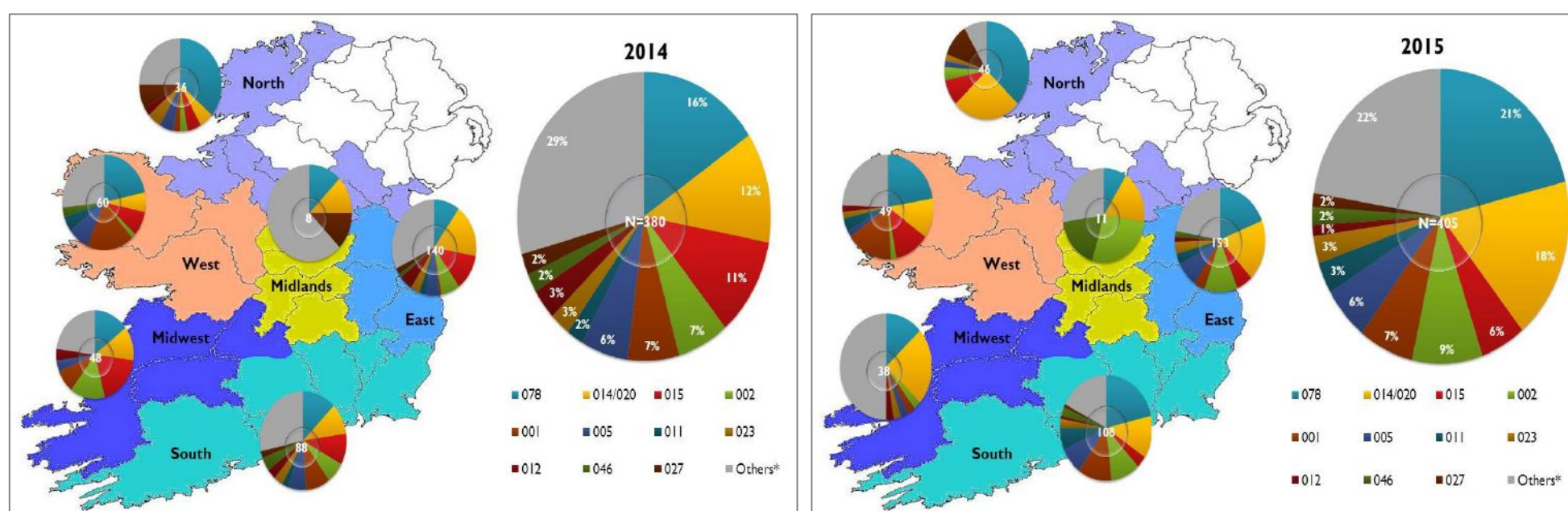


Figure 2: *C. difficile* PCR-ribotype distribution in Ireland 2014

Figure 3: *C. difficile* PCR-ribotype distribution in Ireland 2015

Results

- National HCAI-CDI incidence rate in quarter 2
2014: 2.4 cases/10,000 BDUs
2015: 2.7 cases/10,000 BDUs
- The most common PCR-ribotypes found:
2009: 027 (19%), 001 (16%), 106 (13%)
2014: 078 (16%), 014/020 (12%), 015 (11%)
2015: 078 (21%), 014/020 (18%), 002 (9%)
- Decrease of recurrent CDI
- Strains linked to recurrent CDI:
2009: 027 (38%), 001 (21%), 078 (17%)
2014: 078 (30%), 005 (17%), 103 (7%)
2015: 078 (40%), 014/020 (24%), 005 (8%)
- Increase in CAI cases
- Strains linked to CAI:
2009: 078 (33%), 027 (17%), 106 (17%)
2014: 078 (14%), 014/020 (14%), 015 (14%)
2015: 014/020 (22%), 078 (18%), 005 (10%)
- Ribotype 078 was predominantly found along the west coast of Ireland in 2014 and 2015, its numbers increased in 2015 in the south and the east
- Ribotype 014/020 was common in the east in 2014 and frequently identified in the west in 2015
- Ribotype 027 was only found in the north in 2015