GIG CYMRU NHS WALES | Iechyd Cyhoeddus Cymru Public Health Wales

Surveillance: ***Clostridioides difficile (C. difficile)*** **PCR Ribotyping**

Report: **Annual report**

Time period: **2017/18 financial year (FY)**

Coverage: **All Wales**

Contents:

Issued by: **Public Health Wales**

Issue date: **23rd January 2019**

SUMMARY AND INTERPRETATION

This report provides a summary of the PCR ribotyping results of *Clostridioides difficile* (*C. difficile*) specimens taken in Wales during the 2017/18 financial year (FY).

Coverage
A PCR ribotype was identified for 86% of *C. difficile* specimens reported in the 2017/18 routine surveillance data. In the 6 acute heath boards (HBs) the percentage coverage ranged from 77% in Cwm Taf UHB (CT UHB) to 94% in Betsi Cadwaladr UHB (BC UHB). PCR ribotyping of all specimens was introduced in 2015/16 FY; since then the percentage of specimens PCR ribotyped has increased for all acute HBs except Cardiff and Vale UHB (C&V UHB) (although their proportion has remained >90% for the 3 FYs) and Aneurin Bevan UHB (AB UHB).

Distribution
86 distinct PCR ribotypes were identified in the 990 specimens with a ribotype; the 10 most common accounted for 71% of all sprcimens. Numbers of ribotypes by HB ranged from 19 ribotypes in 43 specimens in CT UHB to 49 ribotypes in 256 specimens in Abertawe Bro Morgannwg UHB (ABM UHB). Between 4 and 6 ribotypes accounted for approximately half of specimens in all acute HBs.

PCR ribotype 002 was most common, accounting for 15% of all specimens. 002 has been the most common for the last 3 FYs and the percentage of 002 has increased over that time. 002 was the most common PCR ribotype, or jointly the most common, in 5 of the 6 acute HBs (015 was the most common in CT UHB). The percentage of 002 has increased in all acute HBs since 2015/16, other than CT UHB. The other four most common PCR ribotypes in Wales in 2017/18 were 015, 005, 014 and 023; the percentage of all four have decreased or stayed the same since 2015/16, although 014 has increased compared to 2016/17. In addition to ribotype 002, 015 and 005 were amongst the top 5 most common ribotypes for all acute HBs. Ribotype 014 was in the top 5 most common ribotypes for all acute HBs other than CT UHB and 023 for all except ABMU HB and BCU HB. The previously common PCR ribotypes 027 and 001 both increased in 2017/18, compared to 2016/17. Increases in 027 were predominantly as a result of increases in AB UHB and CT UHB and 027 appeared in the top 5 for 2017/18 for both of these HBs.

Demographics
59% of PCR ribotyped specimens were from female patients. 68 distinct PCR ribotypes were identified in female patients and 53 in male, but the same 10 were most common, with 002 the most common for both. 80% of PCR ribotyped specimens were from patients aged over 65 years. 76 distinct PCR ribotypes were identified in patients aged over 65 years and 45 in younger patients. PCR ribotype 002 was the most common in both age groups, but there were differences in the 10 most common, with 003 and 013 replacing 027 and 018 in the younger age group. 62% of ribotyped specimens were from patients in inpatient locations. 73 distinct PCR ribotypes were identified in patients in inpatient locations and 51 in patients in non-inpatient locations, but the same 10 were most common, with 002 the most common for both.

Prior toxin negatives
21% of patients with *C. difficile* specimens reported in the 2017/18 routine surveillance data had a GDH positive, toxin negative *C. difficile* specimen within the previous 90 days. The median number of days from the toxin negative specimen to the toxin positive specimen was 10. The percentage of specimens with a prior toxin negative ranged by health board from 17% in AB UHB to 26% in C&V UHB, but may reflect local policies for retesting symptomatic patients. 002 was the most common PCR ribotype for patients with a prior toxin negative specimen, overall and in 3 of the 6 acute HBs. A higher percentage of PCR ribotype 014 was identified in patients with a prior toxin negative specimen (14%) than in those without (6%) and overall PCR ribotype 014 had the highest percentage of specimens with a prior toxin negative, at 37% of all samples of 014.

Repeat double positives
16% of patients with *C. difficile* specimens reported in the 2017/18 routine surveillance data had a GDH positive, toxin positive specimen within the 2 years prior (repeat double positive); 12% of patients had a repeat double positive specimen with the same PCR ribotype. The median time period between repeat double positives of the same PCR ribotype was 49 days, less than half that of those with different PCR ribotypes (104 days). These repeat infections could represent relapses of the original infection or reinfection with the same strain; from ribotyping information, it is not possible to determine which of these is more likely. The percentage of patients with a repeat double positive of the same PCR ribotype ranged from 7% in Hywel Dda UHB (HD UHB) to 14% in BC UHB. 015 was the most common PCR

ribotype for patients with a repeat double positive of the same PCR ribotype across Wales, but this varied by HB.

Acute hospital clusters

For surveillance purposes, cluster specimens were defined as GDH positive, toxin positive *C. difficile* specimens submitted from the same acute hospital within 28 days of each other. 37% of *C. difficile* specimens from acute hospitals reported in the 2017/18 routine surveillance data were cluster specimens, in 109 individual clusters. The median number of specimens in a cluster was 2 and the largest cluster was made up of 6 specimens. The percentage of cluster specimens by acute HB, ranged from 16% in HD UHB to 46% in ABM UHB and BC UHB and the number of clusters by acute HB ranged from 3 in CT UHB to 42 in ABM UHB. The highest number of clusters within an acute hospital was 22. Clusters were most commonly of PCR ribotype 002, which accounted for 22% (24/109) of all clusters in Wales. 002 was the most common cluster PCR ribotype for 3 (ABM UHB, BC UHB and HD UHB) of the 6 acute HBs. 67% of 002 specimens from acute hospitals in 2017/18 were part of clusters and 57% of PCR ribotype 014 samples from acute hospitals were part of clusters. Future access to whole genome sequencing results will allow us to determine whether clusters identified via this surveillance method are genotypically related, and will potentially allow us to identify genotype clusters that cross HB boundaries and have longer timescales.

Comparisons with 2017/18 *C. difficile* rates

The rate of *C. difficile* for Wales for 2017/18 was 37 per 100,000 population and ranged from 54 per 100,000 population in ABM UHB to 19 in Cwm Taf UHB.

The most common PCR ribotype in Wales was 002, which was reported in 2015 as the most prevalent UK ribotype and responsible for *C. difficile* infection in many other European countries (1). This ribotype has been shown to have increased capacity for sporulation and biofilm formation, which could enhance *C. difficile* survival and transmission early in an infection (1). A recent study on patterns of *C. difficile* spread in Europe found the observed pattern for 002 was compatible with a recent pan-European distribution and consistent with a dominant route of spread other than healthcare, although there was evidence of some within hospital clustering (2). PCR ribotype 002 was the most common PCR ribotype and increasing in all but one of the acute HBs. The highest percentages of PCR ribotype 002 were in HD UHB (18%) and ABM UHB (16%), the two HBs with the highest rates in 2017/18. PCR ribotype 002 was not the dominant PCR ribotype and only accounted for 7% of *C. difficile* in CT UHB, the acute HB with the lowest rate in 2017/18.

BC UHB and ABM UHB had the highest proportions of repeat *C. difficile* infections with the same PCR ribotype and had the third highest and first highest *C. difficile* rates respectively in 2017/18. As stated previously, these repeat infections could represent relapses of the original infection or reinfection with the same strain and it is not possible to determine which. ABM UHB and BC UHB also had the highest proportions of cluster specimens, both at 46%, and the highest numbers of clusters amongst the acute HBs (ABM – 42; BCU – 31). It is likely that repeat infections and within hospital transmissions contributed to their high rates in 2017/18 and further control measures to address the high rates may need to focus on these aspects.

HD UHB had the second highest rate in 2017/18 at 40 per 100,000 population, but the PCR ribotyping analysis suggests the pattern of transmission may be different from ABM UHB and BC UHB. The proportion of repeat *C. difficile* infections in HD UHB was the lowest in Wales (7%) and it had the lowest percentage of cluster specimens (16%) and the second lowest number of clusters (8). Whilst 002 was the dominant PCR ribotype, the second most common PCR ribotype was 078 (14%), a ribotype commonly associated with community acquisition (2). 44% of *C. difficile* from HD UHB in 2017/18 were submitted from patients in locations outside the 4 major acute hospitals. The high rate in this HB may be related to multiple community acquisitions and further control measures to address the high rate may need to focus on antimicrobial stewardship across the HB area.

Rates for both AB UHB and CT UHB increased between 2016/17 and 2017/18. The percentage of repeat *C. difficile* specimens for both was 11%. Their percentages of cluster specimens were 26% and 22% respectively, they had low numbers of clusters and more than 50% of their *C. difficile* in 2017/18 were submitted from patients in locations outside the major acute hospitals. Both HBs experienced an increase in PCR ribotype 027 over that time period (although numbers were very low in CT UHB), a ribotype associated with high levels of transmissibility and severe patient outcomes (2). Continued control of ribotype 027 via stewardship and hygiene measures is essential to maintain lower rates of *C. difficile,* as well as the application of further control measures outside acute hospital locations.

Rates of *C. difficile* in C&V UHB have continued to decrease over time since their changes in antibiotic policy, which have clearly been successful interventions. To further reduce cases in this health board, additional focus may be required on preventing within hospital transmission, since more than 40% of acute hospital samples were identified as cluster specimens using the surveillance definition and 75% of the *C. difficile* in this health board were from specimens submitted from patients within the two acute hospitals.

Future use of WGS will help to better characterise the true epidemiology of *C. difficile* in Wales to enable targeted, evidence-based and tailored interventions for each respective HB.

1. Ameh IL et al (2015). In vitro assessment of Clostridium difficile PCR ribotype 002: the most prevalent *C. difficile* ribotype in the United Kingdom. 25th European Congress on Clinical Microbiology and Infectious Diseases. Copenhagen August 2015. P1102
2. Eyre DW et al (2018). Two distinct patterns of *C. difficile* diversity across Europe indicating contrasting routes of spread. *Clinical Infectious Diseases* 2018; 67(7): 1035-44

INTRODUCTION

C. difficile remains a major cause of morbidity and mortality in Wales and continues to pose a significant challenge to our healthcare system. Although *C. difficile* rates have decreased dramatically since 2007, rates have plateaued in recent years.

A collaborative enhanced surveillance programme for *C. difficile* was instigated between Public Health Wales Health Protection and the Public Health Wales UK Anaerobe Reference Unit (UKARU) during 2014. Since April 2015, healthcare organisations in Wales have been invited to submit all laboratory confirmed double positive (GDH screen followed by detection of free toxin in stool) *C. difficile* samples to the UKARU for culture and PCR ribotyping. This replaced the previous process of storage of *C. difficile* faeces samples at local laboratories and submission of samples for ribotyping during periods of increased incidence. From 2018, this process has been further enhanced via the DIGEST pilot project, to include whole genome sequencing (WGS) of a select cohort of samples. A robust pipeline for sequencing has now been developed and we anticipate routine WGS results being available to healthcare organisations in 2019. Continuous surveillance of circulating *C. difficile* strains is critical to the early recognition of changes and more effective management of developing outbreaks, as well as identifying changes in the ecology of *C. difficile.*

This report provides a summary of the ribotyping results of specimens taken during the 2017/18 financial year (FY), but includes a wider range of analyses than previous ribotyping reports, providing an insight into what will be possible once routine WGS results of *C. difficile* specimens in Wales are available.

METHODS

General methods

Laboratory confirmed GDH positive and toxin positive (double positive) *C. difficile* faeces samples were submitted for PCR ribotyping to the UKARU via the LIMS Send Test module.

The PCR ribotyping results for 2017/18 were linked to the 2017/18 *C. difficile* routine surveillance data. The routine surveillance data was extracted from DataStore and included all double positive *C. difficile* specimens taken in an NHS healthcare facility in Wales from persons aged 2 years and over, dated by the date the specimen was received by the laboratory (specimen date) and de-duplicated using 28 days.

Linkage between the two data sets was done in the following priority order: the laboratory system accession number, patient NHS number and specimen date, or other PII (patient name, DOB) and specimen date.

PCR ribotyping results that could not be linked to a double positive *C. difficile* specimen in the routine surveillance data were excluded from further analysis. Exclusions included duplicate accession numbers, QA samples, samples from hospitals outside Wales, patients aged under 2 years, and GDH positive-toxin negative results.

Double positive *C. difficile* specimens without a PCR ribotype identified were excluded from analysis from Section 2 onwards.

Additional methods

Only specimens with an NHS number recorded were included in analysis from Section 4 onwards.

For Sections 4 and 5, analysis was carried out by patient rather than by specimen. For patients with more than one double positive specimen in a FY (identified by NHS number) only the latest specimen was included in the analysis.

Section 4 – Prior toxin negatives

Double positive *C. difficile* patients in 2017/18 were linked to GDH positive-toxin negative (toxin negative) specimens extracted from DataStore. Linkage was based on NHS number and specimen date, where the toxin negative specimen date was within 90 days prior to the double positive specimen. For patients with more than one prior toxin negative specimen, only the latest toxin negative specimen was included.

Section 5 – Repeat double positives

Double positive *C. difficile* patients in 2017/18 were linked to prior double positive specimens. Linkage was based on NHS number and specimen date, where the prior double positive specimen was within 2 years prior to the 2017/18 specimen. For patients with more than one prior double positive specimen, only the latest prior specimen was included.

Section 6 – Acute hospital clusters

Double positive *C. difficile* specimens diagnosed in an acute hospital in 2017/18 were linked to other double positive specimens of the same PCR ribotype from the same acute hospital, with specimen dates within 28 days of each other.

RESULTS

Section 1 – Coverage

Figure 1.1 All Wales, percentage of double positive *C. difficile* specimens reported in the routine surveillance data with a PCR ribotype, by FY

FY	Number of specimens	Number of specimens with a PCR ribotype	Percentage of specimens with a PCR ribotype
2015/16	1243	976	79%
2016/17	1047	864	83%
2017/18	1146	990	86%

N.B. Only specimens with a PCR ribotype were included in further analysis.

- **1146** double positive *C. difficile* specimens were reported in the 2017/18 routine surveillance data for Wales.
- **88%** (1006/1146) were submitted to the UKARU for PCR ribotyping.
- A PCR ribotype was identified for **86%** (990/1146).
- The percentage of double positive *C. difficile* specimens PCR ribotyped has increased over the last 3 FYs.

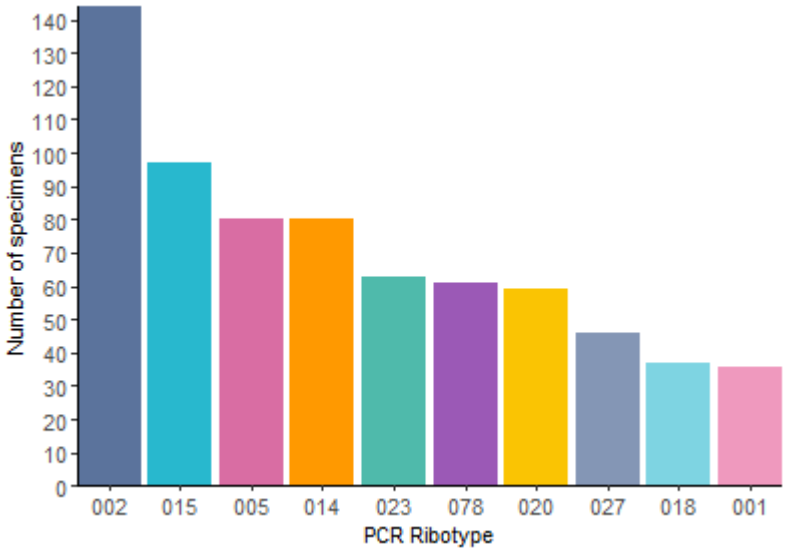
Section 2 – Distribution

Figure 2.1 All Wales, PCR ribotypes identified in double positive *C. difficile* specimens in 2017/18

N.B. The size of the font equates to the frequency of the PCR ribotype. The 10 most common PCR ribotypes have been assigned a unique colour, which is maintained throughout this report.

- **86** distinct PCR ribotypes were identified in double positive *C. difficile* specimens in Wales in 2017/18.

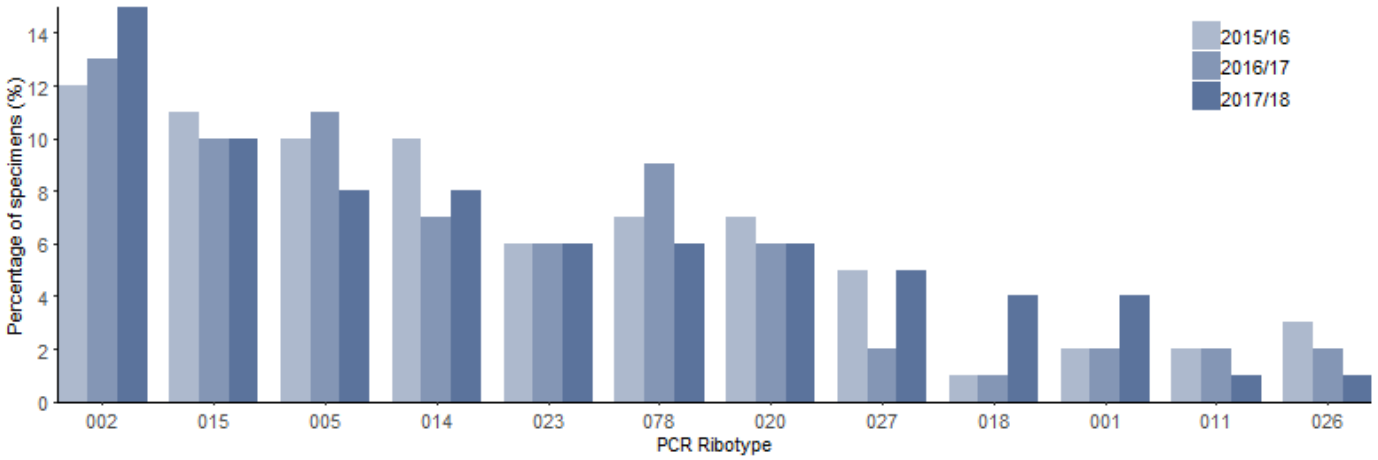
Figure 2.2 All Wales, frequency distribution of 10 most common PCR ribotypes identified in double positive *C. difficile* specimens in 2017/18



PCR ribotype	Number of specimens	Percentage of specimens
002	144	15%
015	97	10%
005	80	8%
014	80	8%
023	63	6%
078	61	6%
020	59	6%
027	46	5%
018	37	4%
001	36	4%

- **002** was the most common PCR ribotype, accounting for **15%** (144/990) of all specimens.
- The 10 most common PCR ribotypes accounted for **71%** (703/990) of all specimens.

Figure 2.3 All Wales, changes in percentage distribution of 10 most common PCR ribotypes in double positive *C. difficile* specimens in 2015/16, 2016/17 and 2017/18

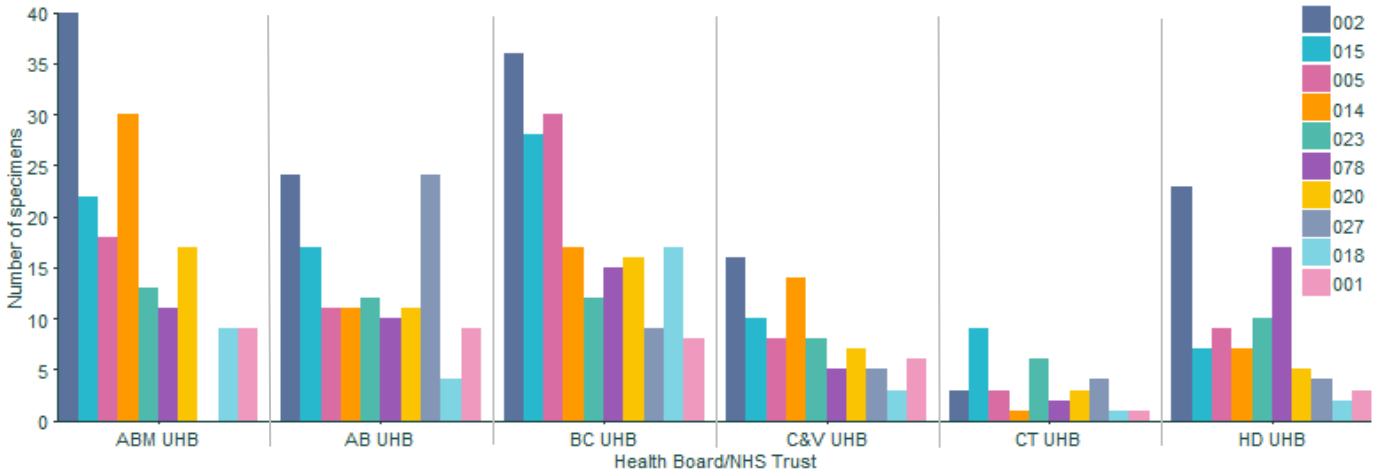


PCR ribotype	2015/16 percentage of specimens	2016/17 percentage of specimens	2017/18 percentage of specimens
002	12%	13%	15%
015	11%	10%	10%
005	10%	11%	8%
014	10%	7%	8%
023	6%	6%	6%
078	7%	9%	6%
020	7%	6%	6%
027	5%	2%	5%
018	1%	1%	4%
001	2%	2%	4%
011	2%	2%	1%
026	3%	2%	1%

N.B. In the table, red text indicates the percentage was higher than the previous FY, orange the same and green lower. Colours were applied prior to rounding.

- **002** has been the most common PCR ribotype for the last 3 FYs and the percentage of **002** has increased over that time, accounting for **12%** (113/976) in 2015/16 and **13%** (109/864) in 2016/17.
- The 3 most common PCR riboypes have remained the same for the last 3 FYs. Whilst the percentage of **002** has increased from 2015/16, the percentage of **015** and **005** has decreased.
- Increases in the percentage of **018** and **001** have put them among the 10 most common PCR ribotypes in 2017/18, replacing PCR ribotypes **026** and **011**.
- The percentage of **078** increased between 2015/16 and 2016/17, becoming the 4th most common PCR ribotype in 2016/17. In 2017/18 the percentage decreased to lower than in 2015/16.
- There was a decrease in the percentage of **027** in 2016/17, but it has increased in 2017/18 to a similar position as 2015/16.

Figure 2.4 All Wales, frequency distribution of 10 most common PCR ribotypes in double positive *C. difficile* specimens in 2017/18, by acute health board



N.B. The 10 most common PCR ribotypes for each individual health board/NHS trust are shown in the health board/NHS trust results sections of this report.

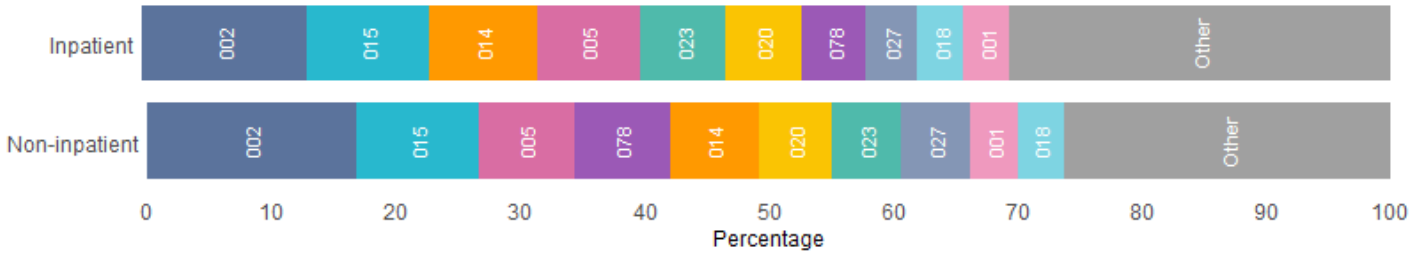
- Of the 10 most common PCR ribotypes in Wales in 2017/18, **002** was the most common in 5 of the 6 acute HBs and **015** was the most common in 1 HB.

Figure 2.5 Most common PCR ribotypes in double positive *C. difficile* specimens in 2017/18, by acute health board

HB	PCR Ribotype
ABM UHB	002
AB UHB	002 & 027
BC UHB	002
C&V UHB	002
CT UHB	015
HD UHB	002

- **002** was the most common PCR ribotype in 4 of the 6 acute HBs, and was joint top with **027** in 1 HB. **015** was the most common PCR ribotype in the remaining acute HB.

Figure 2.6 All Wales, percentage distribution of PCR ribotypes in double positive *C. difficile* specimens in 2017/18, by type of healthcare location of diagnosis

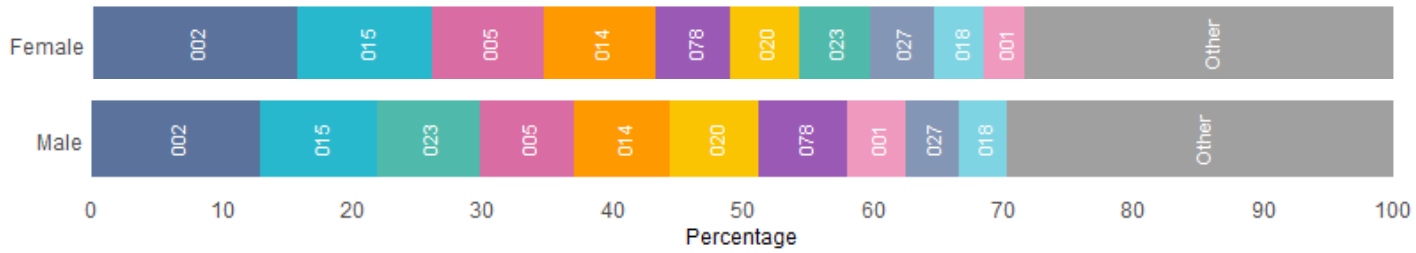


N.B. The 10 most common PCR ribotypes for each location type are shown in colour.

- **62%** (614/990) of PCR ribotyped double positive *C. difficile* specimens in Wales in 2017/18 were taken in inpatient healthcare locations.
- There were **73** distinct PCR ribotypes in specimens taken in inpatient locations and **51** in non-inpatient locations.
- The same 10 PCR ribotypes were most common for both location types.
- **002** was the most common PCR ribotype in both location types, accounting for **13%** (81/614) in inpatient locations and **17%** (63/376) in non-inpatient.
- **014** and **023** were more common in inpatient locations and **078** in non-inpatient.

Section 3 – Demographics

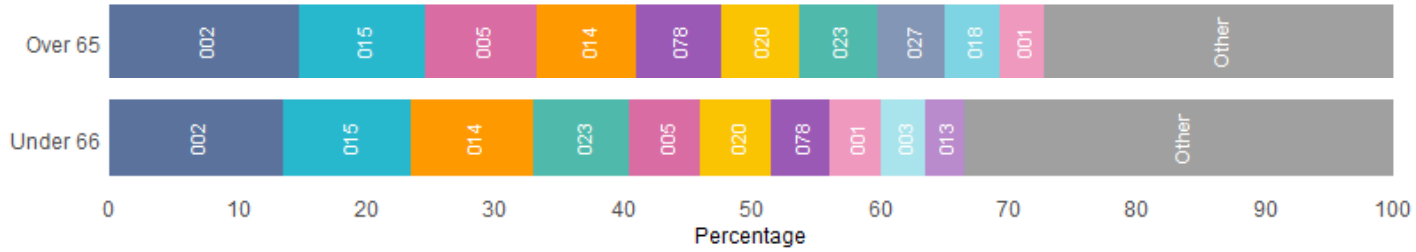
Figure 3.1 All Wales, percentage distribution of PCR ribotypes in double positive *C. difficile* specimens in 2017/18, by patient sex



N.B. The 10 most common PCR ribotypes for each sex are shown in colour.

- **59%** (580/990) of PCR ribotyped double positive *C. difficile* specimens in Wales in 2017/18 were from female patients.
- There were **68** distinct PCR ribotypes in female patients and **53** in male.
- The same 10 ribotypes were most common in both sexes.
- **002** was the most common PCR ribotype in both sexes, accounting for **16%** (91/580) in females and **13%** (53/410) in males.
- **023** was more common in males than females.

Figure 3.2 All Wales, percentage distribution of PCR ribotypes in double positive *C. difficile* specimens in 2017/18, by patient age group



N.B. The 10 most common PCR ribotypes for each age group are shown in colour.

- **80%** (790/990) of PCR ribotyped double positive *C. difficile* specimens in Wales in 2017/18 were from patients aged over 65.
- There were **76** distinct PCR ribotypes in the over 65 age group and **45** in younger patients.
- The same 10 PCR ribotypes were most common in the over 65 age group as for Wales as a whole. In younger patients, **003** and **013** replaced **027** and **018** in the 10 most common PCR ribotypes.
- **002** was the most common PCR ribotype in both age groups, accounting for **15%** (117/790) in the over 65 age group and **14%** (27/200) in younger patients.
- **005** and **078** were more common in the over 65 age group and **023** was more common in younger patients.

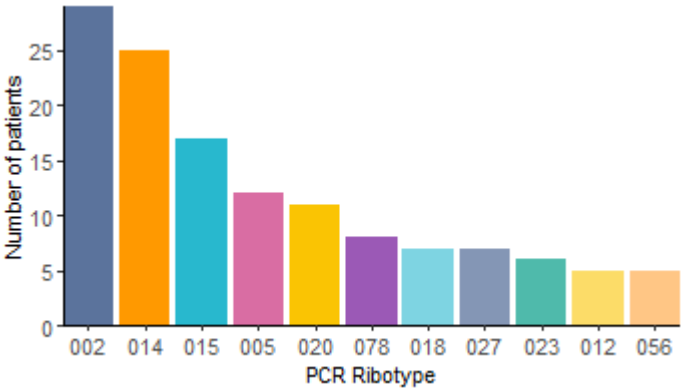
Section 4 – Prior toxin negatives

This section examines patients with a GDH positive-toxin negative (toxin negative) specimen within the 90 days prior to their 2017/18 double positive *C. difficile* specimen.

- **847** patients with a PCR ribotyped double positive *C. difficile* specimen in 2017/18 were included in the data.
- **21%** (178/847) of these patients had a prior toxin negative specimen within 90 days of their double positive specimen.

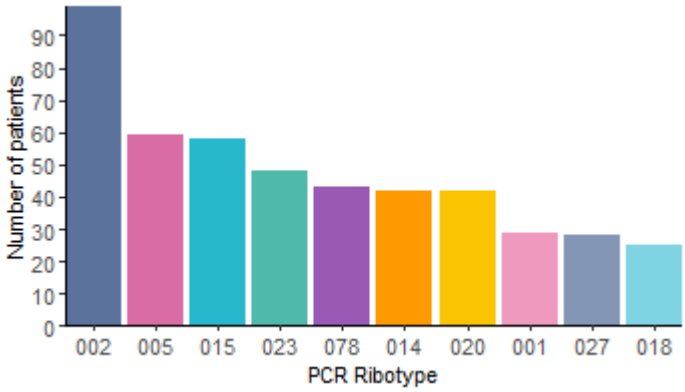
Figure 4.1 All Wales, frequency distribution of 10 most common PCR ribotypes for patients with a double positive *C. difficile* specimen in 2017/18 with and without a prior toxin negative specimen within 90 days

With a prior toxin negative



PCR ribotype	Number of patients	Percentage of patients
002	29	16%
014	25	14%
015	17	10%
005	12	7%
020	11	6%
078	8	4%
018	7	4%
027	7	4%
023	6	3%
012	5	3%
056	5	3%

Without a prior toxin negative



PCR ribotype	Number of patients	Percentage of patients
002	99	15%
005	59	9%
015	58	9%
023	48	7%
078	43	6%
014	42	6%
020	42	6%
001	29	4%
027	28	4%
018	25	4%

N.B. There were multiple PCR ribotypes in 10th position.

- There were **42** distinct PCR ribotypes for patients with a prior toxin negative and **74** in those without.
- **002** was the most common PCR ribotype for patients who had a double positive specimen in Wales in 2017/18, whether or not they had a prior toxin negative specimen.
- **002** accounted for **16%** (29/178) of patients with a prior toxin negative specimen and **15%** (99/669) of those without.
- The percentage of **014** was higher for those with a prior toxin negative specimen (**14%** (25/178)) than for those without (**6%** (42/669)).
- The percentage of **023** was higher for those without a prior toxin negative specimen (**7%** (48/669)) than for those with (**3%** (6/178)).

Figure 4.2 All Wales, percentage of patients with a double positive *C. difficile* specimen in 2017/18 and a prior toxin negative specimen within 90 days and most common PCR ribotype, by acute HB

HB	Percentage of patients with a prior toxin negative	Most common PCR ribotype for patients with a prior toxin negative
ABM UHB	24%	002
AB UHB	17%	002
BC UHB	18%	015
C&V UHB	26%	014
CT UHB	23%	015 & 020
HD UHB	22%	002

- The percentage of patients with a prior toxin negative specimen by acute HB, ranged from **17%** (AB UHB) to **26%** (C&V UHB).
- **002** was the most common PCR ribotype for patients with a prior toxin negative specimen in **3** out of the 6 acute HBs. The other most common PCR ribotypes by acute HB were **014**, **015** and **020.**

Figure 4.3 All Wales, percentage of patients with a double positive *C. difficile* specimen in 2017/18 and a prior toxin negative specimen within 90 days, by PCR ribotype

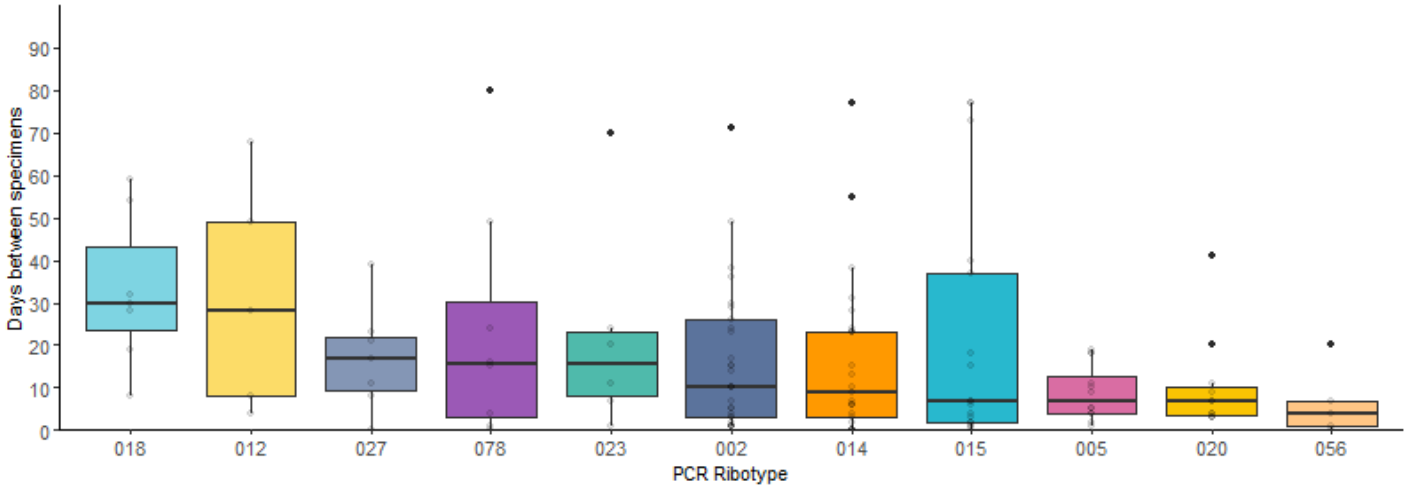
PCR ribotype	Number of patients with a double positive	Number of patients with a prior toxin negative	Percentage of patients with a prior toxin negative
014	67	25	37%
002	128	29	23%
015	75	17	23%
020	53	11	21%
005	71	12	17%

N.B. Only the 5 most common PCR ribotypes for patients with a prior toxin negative specimen are shown, as data is less meaningful for PCR ribotypes that occur infrequently.

- Of the 5 most common PCR ribotypes for patients with a prior toxin negative, **014** had the highest percentage of patients with a prior toxin negative specimen, accounting for **37%** (25/67) of all patients who had PCR ribotype **014** in 2017/18.

Figure 4.4 All Wales, days between specimens for patients with a double positive *C. difficile* specimen in 2017/18 and a prior toxin negative specimen within 90 days, by PCR ribotype

The chart shows the median number of days as a black horizontal line within the box. The upper and lower limits of the box indicate the 25th and 75th percentile. The whiskers extend to 1.5 times the interquartile range. Outliers are shown as black dots.



PCR ribotype	Median days	Mean days	Range of days	Number of patients
018	30	33	8-59	7
012	28	31	4-68	5
027	17	17	0-39	7
078	16	24	0-80	8
023	16	22	1-70	6
002	10	18	1-71	29
014	9	16	0-77	25
015	7	22	0-77	17
005	7	9	1-19	12
020	7	10	3-41	11
056	4	6	0-20	5

N.B. Only the 10* most common PCR ribotypes for patients with a prior toxin negative specimen are shown, as data is less meaningful for PCR ribotypes that occur infrequently. *There were multiple PCR ribotypes in 10th position.

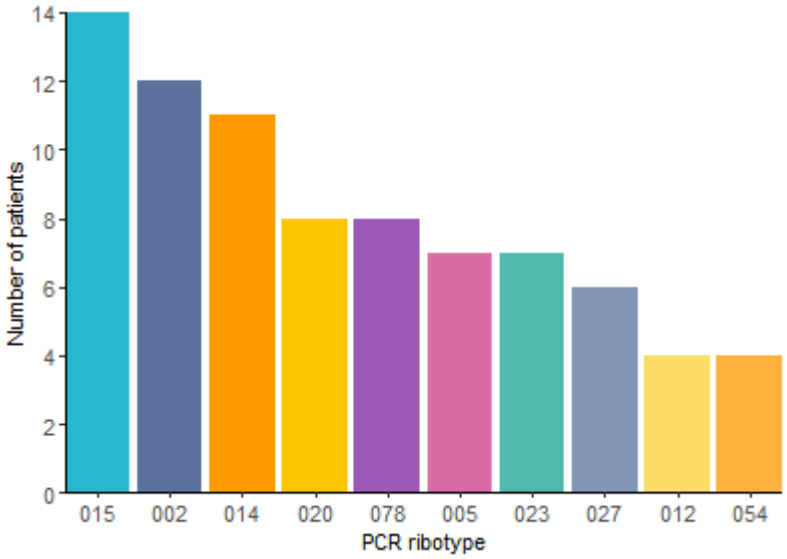
- The median number of days between double positive specimens and a prior toxin negative was **10** days, ranging from **1** to **80**. The average number of days was **18**.
- Of the 10 most common PCR ribotypes for patients with a prior toxin negative, **018** had the highest (30) median number of days between specimens and **056** the lowest (4).

Section 5 – Repeat double positives

This section examines patients in Wales with a double positive *C. difficile* specimen in 2017/18 and a prior double positive specimen within 2 years.

- **847** patients with a PCR ribotyped double positive *C. difficile* specimen in 2017/18 were included in the data.
- **16%** (135/847) of patients had a double positive specimen within the 2 years prior to their 2017/18 double positive specimen (repeat double positive).
- **12%** (101/847) of patients had a repeat double positive specimen with the same PCR ribotype (13 prior double positive specimens without a PCR ribotype were excluded).
- There were **23** distinct PCR ribotypes for patients with a repeat double positive specimen with the same PCR ribotype (repeat PCR ribotype).

Figure 5.1 All Wales, frequency distribution of 10 most common PCR ribotypes for patients with a double positive *C. difficile* specimen in 2017/18 and a double positive specimen with the same PCR ribotype within the 2 years prior



PCR ribotype	Number of patients	Percentage of patients
015	14	14%
002	12	12%
014	11	11%
020	8	8%
078	8	8%
005	7	7%
023	7	7%
027	6	6%
012	4	4%
054	4	4%

- **015** was the most common PCR ribotype for patients with a repeat PCR ribotype, accounting for **14%** (14/101).

Figure 5.2 All Wales, percentage of patients with a double positive *C. difficile* specimen in 2017/18 and a double positive specimen with the same PCR ribotype within the 2 years prior, and most common PCR ribotype, by acute HB

HB	Percentage of patients with a repeat PCR ribotype	Most common PCR ribotype for patients with a repeat PCR ribotype
ABM UHB	13%	002 & 014
AB UHB	11%	027
BC UHB	14%	002
C&V UHB	11%	014
CT UHB	11%	015
HD UHB	7%	078

- The percentage of patients with a repeat PCR ribotype by acute HB, ranged from **7%** (HD UHB) to **14%** (BC UHB).
- The most common PCR ribotypes for patients with a repeat PCR ribotype varied by acute HB.

Figure 5.3 All Wales, percentage of patients with a double positive *C. difficile* specimen in 2017/18 and a double positive specimen with the same PCR ribotype within the 2 years prior, by PCR ribotype

PCR Ribotype	Number of patients with a double positive in 2017/18	Number of patients with a repeat PCR ribotype	Percentage of patients with a repeat PCR ribotype
015	75	14	19%
014	67	11	16%
078	51	8	16%
020	53	8	15%
002	128	12	9%

N.B. Only the 5 most common PCR ribotypes for patients with a repeat PCR ribotype are shown, as data is less meaningful for PCR ribotypes that occur infrequently.

- Of the 5 most common PCR ribotypes for patients with a repeat PCR ribotype, **015** had the highest percentage of patients with a repeat PCR ribotype, accounting for **19%** (14/75) of all patients who had PCR ribotype **015** in 2017/18.

Figure 5.4 All Wales, days between specimens for patients with a double positive *C. difficile* specimen in 2017/18 and a double positive specimen within the 2 years prior, by commonality of PCR ribotype

	Median days	Mean days	Range of days	Number of patients
Different PCR ribotype	104	194	31-686	21
Repeat PCR ribotype	49	62	29-378	101

- The median number of days between repeat double positive specimens was shorter for those with the same PCR ribotype (median = 49 days) than for those with different PCR ribotypes (median=104 days).

Figure 5.5 All Wales, days between specimens for patients with a double positive *C. difficile* specimen in 2017/18 and a double positive specimen with the same PCR ribotype within the 2 years prior, by PCR ribotype

PCR ribotype	Median days	Mean days	Range of days	Number of patients
002	62	80	31-278	12
078	59	98	44-378	8
015	44	54	29-158	14
020	44	47	29-69	8
014	43	46	30-70	11

N.B. Only the 5 most common PCR ribotypes for patients with a repeat PCR ribotype are shown, as data is less meaningful for PCR ribotypes that occur infrequently.

- Of the 5 most common PCR ribotypes for patients with a repeat PCR ribotype, **002** had the highest (62) median number of days between specimens and **014** the lowest (43).

Section 6 – Acute hospital clusters

This section examines clusters of double positive *C. difficile* specimens in Wales in 2017/18. Cluster specimens have been defined as specimens with the same PCR ribotype from the same acute hospital within 28 days of each other.

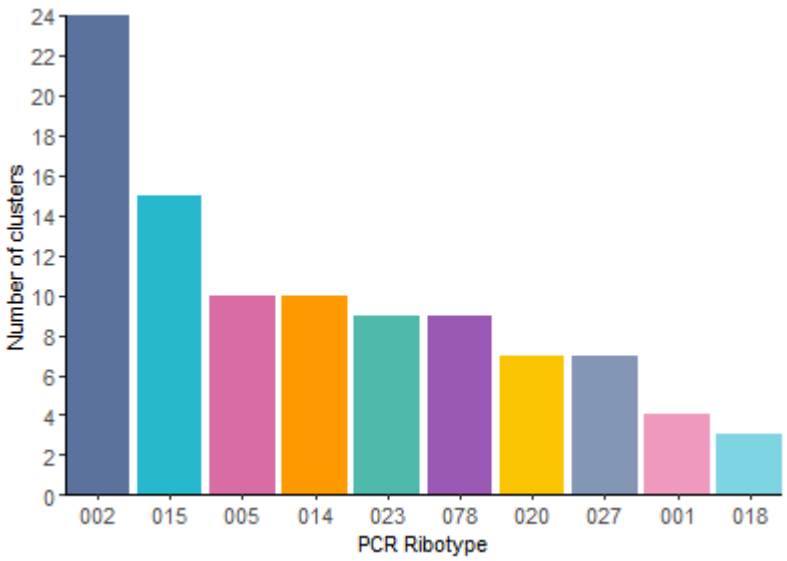
- **679** PCR ribotyped double positive *C. difficile* specimens sampled in acute hospitals in Wales in 2017/18 were included in the data.
- **37%** (254/679) of specimens in 2017/18 were cluster specimens.
- **20** of the 254 cluster specimens were repeat specimens from the same patients.
- The median number of days between cluster specimens was **13** days, ranging from **1** to **28**. The average number of days was **13**.

Figure 6.1 All Wales, double positive *C. difficile* clusters in acute hospitals in 2017/18

Median specimens	Mean specimens	Range of specimens	Number of clusters
2	2	2-6	109

- There were **109** individual clusters in acute hospitals in Wales in 2017/18.
- The largest cluster was made up of **6** specimens, the median number of specimens was 2.
- **5** of the 109 clusters had repeat specimens from the same patients.
- **20** distinct PCR ribotypes were identified in the **109** clusters.

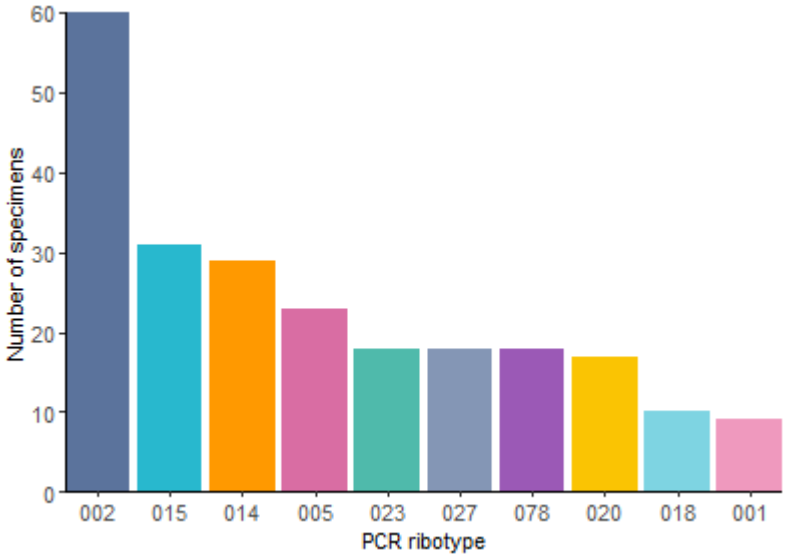
Figure 6.2 All Wales, frequency distribution of 10 most common PCR ribotypes in double positive *C. difficile* clusters in acute hospitals in 2017/18



PCR ribotype	Number of clusters	Percentage of clusters
002	24	22%
015	15	14%
005	10	9%
014	10	9%
023	9	8%
078	9	8%
020	7	6%
027	7	6%
001	4	4%
018	3	3%

- The most common clusters were of PCR ribotype **002**, accounting for **22%** (24/109) of all clusters.

Figure 6.3 All Wales, frequency distribution of 10 most common PCR ribotypes in double positive *C. difficile* cluster specimens in acute hospitals in 2017/18



PCR ribotype	Number of specimens	Percentage of specimens
002	60	24%
015	31	12%
014	29	11%
005	23	9%
023	18	7%
027	18	7%
078	18	7%
020	17	7%
018	10	4%
001	9	4%

- **002** was the most common PCR ribotype for cluster specimens, accounting for **24%** (60/254) of all 2017/18 cluster specimens.

Figure 6.4 All Wales, percentage of double positive *C. difficile* cluster specimens in acute hospitals in 2017/18 and most common PCR ribotype clusters, by acute HB

HB	Percentage of cluster specimens	Number of clusters	Most common PCR ribotype clusters
ABM UHB	46%	42	002
AB UHB	26%	10	027
BC UHB	46%	31	002
C&V UHB	42%	15	014
CT UHB	22%	3	015
HD UHB	16%	8	002

- The percentage of cluster specimens by acute HB, ranged from **16%** (HD UHB) to **46%** (ABM UHB).
- The number of clusters ranged from **3** (CT UHB) to **42** (ABM UHB).
- **002** was the most common PCR ribotype cluster in **3** out of the 6 acute HBs. The other most common PCR ribotypes by acute HB were **014**, **015** and **027.**

Figure 6.5 All Wales, percentage of double positive *C. difficile* cluster specimens in acute hospitals in 2017/18, by PCR ribotype

PCR ribotype	Number of specimens	Number of cluster specimens	Percentage of cluster specimens
002	89	60	67%
014	51	29	57%
015	70	31	44%
023	42	18	43%
005	55	23	42%

N.B. Only the 5 most common PCR ribotypes for cluster specimens are shown, as data is less meaningful for PCR ribotypes that occur infrequently.

- Of the 5 most common PCR ribotypes for cluster specimens, **002** had the highest proportion of cluster specimens, accounting for **67%** (60/89) of all **002** in acute hospitals in 2017/18.

Figure 6.6 All Wales, days between double positive *C. difficile* cluster specimens in acute hospitals in 2017/18, by PCR ribotype

PCR ribotype	Median days	Mean days	Range of days	Number of specimens
002	13	13	0-28	37
015	13	12	0-25	19
014	12	14	1-26	20
005	10	9	0-20	13
027	8	11	4-28	13

N.B. Only the 5 most common PCR ribotypes for cluster specimens are shown, as data is less meaningful for PCR ribotypes that occur infrequently.

- Of the 5 most common PCR ribotypes for patients with a repeat PCR ribotype, **002** had the highest (13) median number of days between specimens and **027** the lowest (8).