



**Universiteit  
Leiden**  
The Netherlands

**The emergence of Clostridium difficile ribotypes 027 and 176 with a predominance of the Clostridium difficile ribotype 001 recognized in Slovakia following the European standardized Clostridium difficile infection surveillance of 2016**

Novakova, E.; Stefkovicova, M.; Kopilec, M.G.; Novak, M.; Kotlebova, N.; Kuijper, E.; Krutova, M.

**Citation**

Novakova, E., Stefkovicova, M., Kopilec, M. G., Novak, M., Kotlebova, N., Kuijper, E., & Krutova, M. (2020). The emergence of Clostridium difficile ribotypes 027 and 176 with a predominance of the Clostridium difficile ribotype 001 recognized in Slovakia following the European standardized Clostridium difficile infection surveillance of 2016. *International Journal Of Infectious Diseases*, 90, 111-115. doi:10.1016/j.ijid.2019.10.038

Version: Publisher's Version

License: [Creative Commons CC BY-NC-ND 4.0 license](https://creativecommons.org/licenses/by-nc-nd/4.0/)

Downloaded from: <https://hdl.handle.net/1887/3181555>

**Note:** To cite this publication please use the final published version (if applicable).



## The emergence of *Clostridium difficile* ribotypes 027 and 176 with a predominance of the *Clostridium difficile* ribotype 001 recognized in Slovakia following the European standardized *Clostridium difficile* infection surveillance of 2016

Elena Novakova<sup>a</sup>, Maria Stefkovicova<sup>b,c</sup>, Maria Garabasova Kopilec<sup>b</sup>, Martin Novak<sup>d</sup>, Nina Kotlebova<sup>a</sup>, Ed Kuijper<sup>e</sup>, Marcela Krutova<sup>f,\*</sup>

<sup>a</sup> Department of Microbiology and Immunology, Comenius University, Jessenius Faculty of Medicine in Martin, Slovakia

<sup>b</sup> Department of Epidemiology, Regional Public Health Authority, Trenčín, Slovakia

<sup>c</sup> Department of Laboratory Medicine and Public Health, Faculty of Health Care, Alexander Dubcek University, Trenčín, Slovakia

<sup>d</sup> Department of Public Health, Comenius University, Jessenius Faculty of Medicine in Martin, Slovakia

<sup>e</sup> Department of Medical Microbiology, Leiden University Medical Centre, Leiden, The Netherlands

<sup>f</sup> Department of Medical Microbiology, Charles University in Prague, 2nd Faculty of Medicine and Motol University Hospital, Prague, Czech Republic

### ARTICLE INFO

#### Article history:

Received 27 September 2019

Received in revised form 25 October 2019

Accepted 29 October 2019

#### Keywords:

*Clostridium difficile* infection

Surveillance

PCR ribotype 001

PCR ribotype 176

PCR ribotype 027

Moxifloxacin reduced susceptibility

### ABSTRACT

**Aim:** To obtain standardized epidemiological data for *Clostridium difficile* infection (CDI) in Slovakia.

**Methods:** Between October and December 2016, 36 hospitals in Slovakia used the European Centre for Disease Prevention and Control (ECDC) *Clostridium difficile* infection (CDI) surveillance protocol.

**Results:** The overall mean CDI incidence density was 2.8 (95% confidence interval 1.9–3.9) cases per 10 000 patient-days. Of 332 CDI cases, 273 (84.9%) were healthcare-associated, 45 (15.1%) were community-associated, and 14 (4.2%) were cases of recurrent CDI. A complicated course of CDI was reported in 14.8% of cases ( $n = 51$ ). CDI outcome data were available for 95.5% of cases ( $n = 317$ ). Of the 35 patients (11.1%) who died, 34 did so within 30 days after their CDI diagnosis.

Of the 78 isolates obtained from 12 hospitals, 46 belonged to PCR ribotype 001 (59.0%; 11 hospitals) and 23 belonged to ribotype 176 (29.5%; six hospitals). A total of 73 isolates (93.6%) showed reduced susceptibility to moxifloxacin (ribotypes 001 and 176;  $p < 0.01$ ). A reduced susceptibility to metronidazole was observed in 13 isolates that subsequently proved to be metronidazole-susceptible when, after thawing, they were retested using the agar dilution method. No reduced susceptibility to vancomycin was found.

**Conclusions:** These results show the emergence of *C. difficile* ribotypes 027 and 176 with a predominance of ribotype 001 in Slovakia in 2016. Given that an almost homogeneous reduced susceptibility to moxifloxacin was detected in *C. difficile* isolates, this stresses the importance of reducing fluoroquinolone prescriptions in Slovak healthcare settings.

© 2019 The Author(s). Published by Elsevier Ltd on behalf of International Society for Infectious Diseases. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

### Introduction

*Clostridium difficile*, recently reclassified as *Clostridioides difficile* (Oren and Rupnik, 2018), is an important nosocomial pathogen (ECDC, 2013). In the countries of the European Union and European

Economic Area (EU/EEA), the burden of hospital-associated *C. difficile* infection (CDI) in acute care hospitals was estimated at 123 997 (95% confidence interval (CI) 61 018–284 857) cases annually between 2011 and 2012. In addition, during the European Centre for Disease Prevention and Control (ECDC) point prevalence survey of healthcare-associated infections (HAI) and antimicrobial use in European acute care hospitals, *C. difficile* was the eighth most frequently found microorganism in HAI and the most common causative agent in gastrointestinal system HAIs (ECDC, 2013).

Slovakia participated in two international studies on the incidence density of CDI in the acute healthcare setting (Bauer

\* Corresponding author at: Department of Medical Microbiology, Charles University, 2nd Faculty of Medicine and Motol University Hospital, V Uvalu 84, Prague 5, 150 06, Czech Republic.

E-mail address: [marcela.krutova@lfmotol.cuni.cz](mailto:marcela.krutova@lfmotol.cuni.cz) (M. Krutova).

et al., 2011; Davies et al., 2014). In 2008, two of the three participating hospitals provided CDI incidence density data, and the weighted mean CDI incidence density was 1.4 (range 0.0 to 2.1) CDI cases per 10 000 patient bed-days (Bauer et al., 2011). In a prospective multicentre biannual point prevalence study of CDI in hospitalized patients with diarrhoea (EUCLID), six Slovakian hospitals reported a fluctuating CDI incidence density between two reporting periods. While the incidence density of CDI was 5.3 cases per 10 000 patient bed-days between September 2011 and August 2012, the reported rates between September 2012 and August 2013 fell to 1.2 cases per 10 000 patient bed-days (Davies et al., 2014).

Before the 2016 study, the *C. difficile* isolates derived from stool samples of patients hospitalized in Slovakia were characterized in three studies performed between 2011 and 2013. All three studies were in agreement and showed a low diversity of ribotypes, except for a predominance of PCR ribotype 001 (60.1%, 85.0%, 70%) (Davies et al., 2016; Nyc et al., 2015; Freeman et al., 2018).

After the successful testing of a standardized CDI surveillance protocol in 37 European hospitals in 2013 (van Dorp et al., 2016), the ECDC started coordinating the surveillance of CDI in EU/EEA countries in 2016 (Krutova et al., 2018a). Slovakia participated, in order to obtain comparable CDI density data and information on prevailing PCR ribotypes, as well as data on antimicrobial susceptibility to the first-line CDI treatment drugs.

## Methods

### Study protocol

Between October and December 2016, a total of 36 hospitals in Slovakia participated in a national CDI surveillance. A 'light surveillance option' of the ECDC-CDI surveillance protocol (ECDC, 2015) was applied to 24 hospitals across Slovakia, with the collection of hospital aggregated numerator and denominator data and information on each CDI case. Twelve hospitals applied an 'enhanced surveillance option' that also collects microbiological data including characterization of *C. difficile* isolates (ECDC, 2015).

The mean CDI incidence density was calculated from the mean CDI incidence densities of participating hospitals. Each patient's outcome was followed until the patient was discharged or died. There was no post-discharge follow-up regarding readmission or death of the patients.

### Microbiological investigation

Testing for CDI was performed only when requested by a physician, and only unformed stool samples (taking the shape of the container) were tested in the microbiology departments of the participating hospitals. Thirty-two hospitals used a recommended multi-step testing algorithm; stool samples were tested for the presence of glutamate dehydrogenase (GDH) and toxins A/B by enzyme immunoassay (EIA), and in GDH-positive and toxins A/B-negative stool samples, the presence of toxin genes was determined by nucleic acid amplification test (NAAT) (Crobach et al., 2016). Two hospitals used only *C. difficile* toxins A/B EIA detection and two hospitals used *C. difficile* toxins A/B EIA detection with NAAT in positive samples.

### Clostridium difficile culture and characterization of isolates

Toxigenic *C. difficile*-positive stool samples sent from the 12 hospitals that followed the 'enhanced surveillance option' were cultured anaerobically on selective agar for *C. difficile* (Brazier, Oxoid). Antibiotic susceptibility of the *C. difficile* isolates was determined by Etest for the following antibiotics: metronidazole,

vancomycin, and moxifloxacin. The minimum inhibitory concentration (MIC) breakpoints for metronidazole, vancomycin (2 mg/l), and moxifloxacin (4 mg/l) were based on epidemiological cut-off values (ECOFFs) and were applied according to the European Committee on Antimicrobial Susceptibility Testing (EUCAST, version 9.0, 2019). *C. difficile* isolates showing a reduced susceptibility to metronidazole and vancomycin were retested using the agar dilution method. A capillary electrophoresis-based PCR was used for ribotyping (Fawley et al., 2015) and multiplex PCR for the detection of genes (*tcdA*, *tcdB*, *cdtA*, *cdtB*) for toxin production (A, B, and binary) (Persson et al., 2008).

## Results

### Participating hospitals

A total of 36 Slovak hospitals, covering 17 721 hospital beds and 1 100 418 patient-days, voluntarily participated in a 3-month CDI surveillance (October 2016–December 2016). Eleven (30.6%) are tertiary care institutions, 12 (33.3%) are secondary care facilities, and 13 (36.1%) are primary care institutions. Thirty-two participating hospitals (88.9%) used the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) laboratory CDI diagnosis algorithm (Crobach et al., 2016). The mean testing frequency in all 36 hospitals was 36.5 (95% CI 27.9–45.0) per 10 000 patient-days.

### Clostridium difficile infections

Patient data were collected for 332 CDI episodes. The median age of the patients was 75 years; nine patients were younger than 18 years and five of them were 2 years old or younger. One hundred and seventy-six patients were female (53.0%).

The overall mean CDI incidence density was 2.8 (95% CI 1.9–3.9) cases per 10 000 patient-days. Of 332 reported CDI cases, 273 (84.9%) were healthcare-associated (HA) with an incidence density of 2.3 (95% CI 1.8–2.7) cases per 10 000 patient-days, and 45 (15.1%) were community-associated (CA) with an incidence density of 0.4 (95% CI 0.2–0.6) cases per 10 000 patient-days. Fourteen (4.2%) of the CDI cases were classified as recurrent cases with an incidence density 0.1 (95% CI 0.02–0.2) cases per 10 000 patient-days. For HA CDIs, the origin of the infection was the same healthcare facility in 264 cases (96.7%), another hospital in five cases (1.8%), and a long-term care facility in four cases (1.5%). Eight hospitals reported zero CDI cases during the surveillance period.

A complicated course of CDI (admission for CDI from the community; admission to an intensive care unit; surgery for toxic megacolon or death) was reported in 15.4% ( $n = 51$ ) of CDIs; in three cases (0.9%), the severity of the course of the CDI was unknown. CDI outcome data were available for 317 cases (95.5%). Thirty-five patients (11.1%) died, and CDI definitely contributed to death in one case (0.3%). Thirty-four patients died within 30 days after a CDI diagnosis. The McCabe score of fatal cases indicated that nine patients (25.7%) had 'rapidly fatal' and 18 patients (51.4%) had 'ultimately fatal' underlying disease. The overall results are summarized in Table 1.

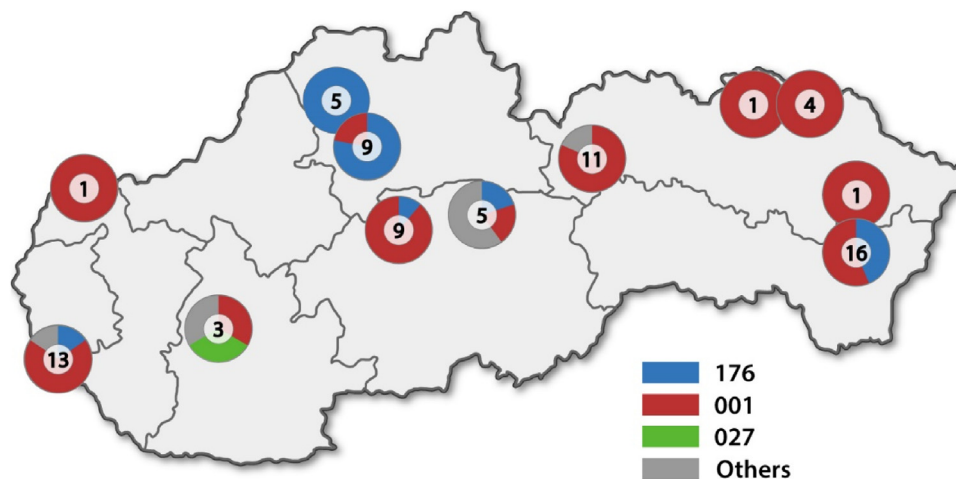
### Microbiological data

A total of 78 strains were available for further characterization. Of these, 46 isolates belonged to PCR ribotype 001 (59.0%) and 23 isolates belonged to PCR ribotype 176 (29.5%). Other PCR ribotypes identified were 017 ( $n = 3$ ; 3.8%), 020, 027, 049 and 070 ( $n = 1$ ; 1.3% each). Two ribotyping profiles remained unrecognized. The distribution of ribotypes 001 and 176 identified in Slovakian hospitals is shown in Figure 1. All 78 *C. difficile* isolates were

**Table 1**  
Results from CDI surveillance in Slovakia.

	Number (%)	Mean hospital incidence density (95% CI)
<i>Clostridium difficile</i> infections by type, 36 hospitals, 10–12/2016		
CDI cases	332 (100)	2.8 (1.9–3.9)
Healthcare-associated CDIs	273 (84.9)	2.3 (1.8–2.7)
Community-associated CDIs	45 (15.1)	0.4 (0.2–0.6)
Recurrent CDI	14 (4.2)	0.1 (0.02–0.2)
Complicated course	51 (15.4)	
Death (data for 317 cases, 95.5%)	35 (11.1)	
30-day mortality	34 (10.7)	
Characterization of <i>C. difficile</i> isolates (n = 78, 100%), 12 hospitals, 10–12/2016		
Ribotype 001	46 (59.0)	
Ribotype 176	23 (29.5)	
Others (017 n = 3; 020, 027, 049, 070 n = 1 each; unrecognized n = 2)	9 (11.5)	
Binary toxin genes positive (027, 176, and one unrecognized)	25 (32.1)	
Moxifloxacin reduced susceptibility (017, 027, 176 (100%) and 001 (97.8%))	73 (93.6)	

CDI, *Clostridium difficile* infection; CI, confidence interval.



**Figure 1.** Distribution of Slovak hospitals providing stool samples for *Clostridium difficile* culture. The pie charts show the representation of *C. difficile* ribotypes 001, 027, and 176 identified per hospital. The numbers in the centre represent the number of *C. difficile* isolates cultured for molecular characterization.

positive for the *tcdB* gene and 25 isolates (32.1%; ribotypes 027, 176, and one unrecognized profile) also carried genes for binary toxin (*cdtA*, *cdtB*).

A total of 73 isolates (93.6%) showed reduced susceptibility to moxifloxacin (MIC  $\geq$  32 mg/l; ribotypes 176 n = 23/23, 001 n = 45/46, 017 n = 3/3, 027 n = 1/1). A reduced susceptibility to metronidazole (MIC 8–256 mg/l) was observed in 13 isolates (ribotypes 001 n = 9, 017 n = 1, 020 n = 1, 027 n = 1, 176 n = 1), which subsequently were found to be metronidazole-susceptible when retested using the agar dilution method after thawing of *C. difficile* isolates. No reduced susceptibility to vancomycin was observed. The overall results are summarized in Table 1.

## Discussion

In 2016, the mean hospital CDI incidence density in 20 EU/EEA countries (579 surveillance periods from 556 hospitals) was 3.19 cases per 10 000 patient-days (ECDC, 2018). The Slovak CDI incidence density data of 2.8 cases per 10 000 patient-days (36 hospitals) is lower; however, the mean testing frequency in Slovakia of about 8.8 tests per 10 000 patient-days is lower than the European mean (45.3 vs. 36.5 tests per 10 000 patient-days). Interestingly, eight Slovak hospitals reported zero CDI cases during the 3-month surveillance period. The reason for the suboptimal testing frequency in Slovakia may be because not all diarrhoeal

stool samples from hospitalized patients were screened for the presence of toxigenic *C. difficile*, since only physician-requested testing of stool samples for CDI were included in the study (Davies et al., 2014; Alcalá et al., 2012).

In 2012, two studies reported the ribotyping data of the Slovak *C. difficile* isolates, and *C. difficile* ribotypes 027 and/or 176 were not detected (Davies et al., 2016; Nyc et al., 2015). In contrast, ribotype 001 was identified as predominant in four CDI studies within the period 2012 to 2017 (Davies et al., 2016; Nyc et al., 2015; Freeman et al., 2018; Krehelova et al., 2019) and moreover clonal relatedness of ribotype 001 isolates was confirmed in hospital and between hospitals by multilocus variable number tandem repeats analysis and whole-genome sequencing (Nyc et al., 2015; Krehelova et al., 2019; Eyre et al., 2018).

Although the occurrence of ribotype 001 is endemic in Slovakia, the emergence of ribotypes 027 and 176 in a Slovak healthcare setting is reported for the first time in this CDI surveillance period (October 2016–December 2016). Identified CDI cases of ribotype 027 (n = 1) and ribotype 176 (n = 23) were located in six hospitals, but it should be noted that ribotyping data were available for only 12 out of the 36 hospitals. Ribotype 176 is suggested to be related to ribotype 027, because they belong to the same multilocus sequence type (ST1/clade 2) and express a similar proteome profile (Knetsch et al., 2012; Dresler et al., 2017). Importantly for laboratory diagnostics, ribotypes 027 and 176 shared the molecular markers

(binary toxin gene(s) *cdtA/cdtB* and the specific deletion at position 117 of *tcdC* gene) that are used in commercial tests for the differentiation of ribotype 027 and other ribotypes (Krutova et al., 2018b).

The CDI epidemiology patterns found in this study, the predominance of ribotypes 001 and 176, is similar to that reported in the Czech Republic in 2014 (Krutova et al., 2016), a country that neighbours Slovakia. Interestingly, in Hungary and Poland, countries that also share a border with Slovakia, a high occurrence of ribotype 176 CDIs and a predominance of ribotype 027 were reported in October–December 2014 and 2011–2013 (Tóth et al., 2016; Pituch et al., 2015). Moreover, recent data from South-Eastern Europe captured an outbreak of ribotype 176 CDIs in a Croatian hospital in 2015 (Rupnik et al., 2016). In Slovakia, ongoing CDI surveillance, including ribotyping of *C. difficile* isolates, is needed in order to monitor further the development of CDI epidemiology and the possible emergence of newly recognized epidemic ribotypes such as ribotype 018 in France and Italy (Berger et al., 2019; Gateau et al., 2019).

Antimicrobial susceptibility testing identified a reduced susceptibility to metronidazole in fresh *C. difficile* cultures by Etest, but this was not confirmed after thawing of *C. difficile* isolates and retesting with the agar dilution method. The same phenomenon, when an initial metronidazole-resistant *C. difficile* isolate becomes susceptible after thawing or after serial passages, has been described in *C. difficile* isolates from Spain and Canada (Peláez et al., 2008; Martin et al., 2008). Moreover, variations in MICs using different methods and culture media for metronidazole susceptibility testing have been shown (Baines et al., 2008).

During the surveillance period, only five isolates were susceptible to moxifloxacin. The reduced susceptibility to moxifloxacin identified in ribotypes 001, 017, 027, and 176 was also demonstrated in European *C. difficile* isolates collected during the ClosER study between July 2011 and July 2014 (Freeman et al., 2018) and in national Polish and Czech studies on *C. difficile* ribotype 176 isolates (Lachowicz et al., 2015; Krutova et al., 2015). In the United Kingdom, falls in the incidence of fluoroquinolone-resistant *C. difficile* were observed after the use of fluoroquinolone was restricted (Dingle et al., 2017), even though the numbers of fluoroquinolone-susceptible *C. difficile* remained stable; however, it is probable that other factors also contributed to the stabilizing of CDI epidemiology in the UK, such as the optimizing of laboratory diagnostics, active CDI surveillance, and the availability of ribotyping in several laboratories.

Antimicrobial stewardship is an important key component in the prevention of CDI in acute healthcare settings (Tschudin-Sutter et al., 2018). Except for fluoroquinolones, antimicrobial stewardship should focus on 4C antibiotics (ciprofloxacin/fluoroquinolones, clindamycin, co-amoxiclav, and cephalosporins). A reduction in prescribing could reduce the incidence of multi-drug-resistant ribotypes, e.g., 001 and 027 (Lawes et al., 2017).

In conclusion, the results of standardized CDI surveillance in Slovakia showed a similar CDI incidence density but a lower testing frequency compared to standardized European CDI surveillance data. Microbiological investigations revealed the emergence of the *C. difficile* ribotype 176 with the predominance of ribotype 001. Given that an almost homogeneous reduced susceptibility to moxifloxacin was detected in *C. difficile* isolates, this stresses the importance of antibiotic stewardship that focuses primarily on reducing fluoroquinolone prescriptions in Slovak healthcare settings.

## Funding

The characterization of *C. difficile* isolates was supported by MH CZ–DRO, University Hospital Motol, Prague, Czech Republic

00064203. The ribotyping of *C. difficile* isolates with unrecognized CE-ribotyping profile was supported by ECDC-framework service contract ECDC/2016/016 (OJ/05/11/2015-PROC/2015/029).

## Ethical approval

For this type of study, formal consent was not required.

## Conflict of interest

The authors declare that they have no conflicts of interest.

## Acknowledgements

We would like to thank the following: the Regional Public Health Authority, Trenčín for coordinating the CDI surveillance in 2016; the Comenius University Jessenius, Faculty of Medicine in Martin, Slovakia for conducting the microbiological part of the surveillance; and the Department of Medical Microbiology, Motol University Hospital, Prague, Czech Republic for the characterization of the *C. difficile* isolates. We would also like to thank all members of the ESCMID Study Group for *Clostridioides difficile* (ESGCD) for their active contribution to the development and publication of the guidance documents for CDI diagnostics, prevention, surveillance, and treatment.

## References

- Alcalá L, Martín A, Marín M, Sánchez-Somolinos M, Catalán P, Peláez T, et al. The undiagnosed cases of *Clostridium difficile* infection in a whole nation: where is the problem?. *Clin Microbiol Infect* 2012;18(7):E204–13, doi:http://dx.doi.org/10.1111/j.1469-0691.2012.03883.x.
- Baines SD, O'Connor R, Freeman J, Fawley WN, Harmanus C, Mastrantonio P, et al. Emergence of reduced susceptibility to metronidazole in *Clostridium difficile*. *J Antimicrob Chemother* 2008;62(5):1046–52, doi:http://dx.doi.org/10.1093/jac/dkn313.
- Bauer MP, Notermans DW, van Benthem BH, Brazier JS, Wilcox MH, Rupnik M, et al. *Clostridium difficile* infection in Europe: a hospital-based survey. *Lancet* 2011;377(9759):63–73, doi:http://dx.doi.org/10.1016/S0140-6736(10)61266-4.
- Berger FK, Gfrörer S, Becker SL, Baldan R, Cirillo DM, Frentrup M, et al. Hospital outbreak due to *Clostridium difficile* ribotype 018 (RT018) in Southern Germany. *Int J Med Microbiol* 2019;309(3–4):189–93, doi:http://dx.doi.org/10.1016/j.ijmm.2019.03.001.
- Crobach MJ, Planche T, Eckert C, Barbut F, Terveer EM, Dekkers OM, et al. European Society of Clinical Microbiology and Infectious Diseases: update of the diagnostic guidance document for *Clostridium difficile* infection. *Clin Microbiol Infect* 2016;22 Suppl 4:S63–81, doi:http://dx.doi.org/10.1016/j.cmi.2016.03.010.
- Davies KA, Longshaw CM, Davis GL, Bouza E, Barbut F, Barna Z, et al. Underdiagnosis of *Clostridium difficile* across Europe: the European, multicentre, prospective, biannual, point-prevalence study of *Clostridium difficile* infection in hospitalised patients with diarrhoea (EUCLID). *Lancet Infect Dis* 2014;14(12):1208–19, doi:http://dx.doi.org/10.1016/S1473-3099(14)70991-0.
- Davies KA, Ashwin H, Longshaw CM, Burns DA, Davis GL, Wilcox MH, et al. Diversity of *Clostridium difficile* PCR ribotypes in Europe: results from the European, multicentre, prospective, biannual, point-prevalence study of *Clostridium difficile* infection in hospitalised patients with diarrhoea (EUCLID), 2012 and 2013. *Euro Surveill* 2016;21(29), doi:http://dx.doi.org/10.2807/1560-7917.ES.2016.21.29.30294.
- Dingle KE, Didelot X, Quan TP, Eyre DW, Stoesser N, Golubchik T, et al. Effects of control interventions on *Clostridium difficile* infection in England: an observational study. *Lancet Infect Dis* 2017;17(4):411–21, doi:http://dx.doi.org/10.1016/S1473-3099(16)30514-X.
- Dresler J, Krutova M, Fucikova A, Klimentova J, Hruzova V, Duracova M, et al. Analysis of proteomes released from in vitro cultured eight *Clostridium difficile* PCR ribotypes revealed specific expression in PCR ribotypes 027 and 176 confirming their genetic relatedness and clinical importance at the proteomic level. *Gut Pathog* 2017;9:45, doi:http://dx.doi.org/10.1186/s13099-017-0194-9.
- European Centre for Disease Prevention and Control. Point prevalence survey of healthcare-associated infections and antimicrobial use in European acute care hospitals. Stockholm: ECDC; 2013.
- European Centre for Disease Prevention and Control. European Surveillance of *Clostridium difficile* infections. Surveillance protocol version 2.2. Stockholm: ECDC; 2015.
- European Centre for Disease Prevention and Control. *Clostridium difficile* infections. ECDC. Annual epidemiological report for 2016. Stockholm: ECDC; 2018.
- Eyre DW, Davies KA, Davis G, Fawley WN, Dingle KE, De Maio N, et al. Two distinct patterns of *Clostridium difficile* diversity across Europe indicating contrasting

- routes of spread. *Clin Infect Dis* 2018;67(7):1035–44, doi:<http://dx.doi.org/10.1093/cid/ciy252>.
- Fawley WN, Knetsch CW, MacCannell DR, Harmanus C, Du T, Mulvey MR, et al. Development and validation of an internationally-standardized, high-resolution capillary gel-based electrophoresis PCR-ribotyping protocol for *Clostridium difficile*. *PLoS One* 2015;10(2):e0118150, doi:<http://dx.doi.org/10.1371/journal.pone.0118150>.
- Freeman J, Vernon J, Pilling S, Morris K, Nicholson S, Shearman S, et al. The CloSER study: results from a three-year pan-European longitudinal surveillance of antibiotic resistance among prevalent *Clostridium difficile* ribotypes, 2011–2014. *Clin Microbiol Infect* 2018;24(7):724–31.
- Gateau C, Deboscker S, Couturier J, Vogel T, Schmitt E, Muller J, et al. Local outbreak of *Clostridioides difficile* PCR-Ribotype 018 investigated by multi locus variable number tandem repeat analysis, whole genome multi locus sequence typing and core genome single nucleotide polymorphism typing. *Anaerobe* 2019; (August)102087, doi:<http://dx.doi.org/10.1016/j.anaerobe.2019.102087>.
- Knetsch CW, Terveer EM, Lauber C, Gorbalenya AE, Harmanus C, Kuijper EJ, et al. Comparative analysis of an expanded *Clostridium difficile* reference strain collection reveals genetic diversity and evolution through six lineages. *Infect Genet Evol*. 2012;12(7):1577–85, doi:<http://dx.doi.org/10.1016/j.meegid.2012.06.003>.
- Krehelova M, Nyč O, Sinajová E, Krutova M. The predominance and clustering of *Clostridioides (Clostridium) difficile* PCR ribotype 001 isolates in three hospitals in Eastern Slovakia, 2017. *Folia Microbiol (Praha)* 2019;64(1):49–54, doi:<http://dx.doi.org/10.1016/j.cmi.2017.10.008> 10.1007/s12223-018-0629-9.
- Krutova M, Matejkova J, Tkadlec J, Nyc O. Antibiotic profiling of *Clostridium difficile* ribotype 176—a multidrug resistant relative to *C. difficile* ribotype 027. *Anaerobe* 2015;36:88–90, doi:<http://dx.doi.org/10.1016/j.anaerobe.2015.07.009>.
- Krutova M, Matejkova J, Kuijper EJ, Drevinek P, Nyc O. Czech *Clostridium difficile* study group. *Clostridium difficile* PCR ribotypes 001 and 176 – the common denominator of *C. difficile* infection epidemiology in the Czech Republic, 2014. *Euro Surveill* 2016;21(29), doi:<http://dx.doi.org/10.2807/1560-7917.ES.2016.21.29.30296>.
- Krutova M, Kinross P, Barbut F, Hajdu A, Wilcox MH, Kuijper EJ, et al. How to: surveillance of *Clostridium difficile* infections. *Clin Microbiol Infect* 2018a;24(5):469–75, doi:<http://dx.doi.org/10.1016/j.cmi.2017.12.008>.
- Krutova M, Wilcox MH, Kuijper EJ. The pitfalls of laboratory diagnostics of *Clostridium difficile* infection. *Clin Microbiol Infect* 2018b;24(7):682–3, doi:<http://dx.doi.org/10.1016/j.cmi.2018.02.026>.
- Lachowicz D, Pituch H, Obuch-Woszczatyński P. Antimicrobial susceptibility patterns of *Clostridium difficile* strains belonging to different polymerase chain reaction ribotypes isolated in Poland in 2012. *Anaerobe* 2015;31:37–41, doi:<http://dx.doi.org/10.1016/j.anaerobe.2014.09.004>.
- Lawes T, Lopez-Lozano JM, Nebot CA, Macartney G, Subbarao-Sharma R, Wares KD, et al. Effect of a national 4C antibiotic stewardship intervention on the clinical and molecular epidemiology of *Clostridium difficile* infections in a region of Scotland: a non-linear time-series analysis. *Lancet Infect Dis* 2017;17(2):194–206, doi:[http://dx.doi.org/10.1016/S1473-3099\(16\)30397-8](http://dx.doi.org/10.1016/S1473-3099(16)30397-8).
- Martin H, Willey B, Low DE, Staempfli HR, McGeer A, Boerlin P, et al. Characterization of *Clostridium difficile* strains isolated from patients in Ontario, Canada, from 2004 to 2006. *J Clin Microbiol* 2008;46(9):2999–3004, doi:<http://dx.doi.org/10.1128/JCM.02437-07>.
- Nyc O, Krutova M, Liskova A, Matejkova J, Drabek J, Kuijper EJ. The emergence of *Clostridium difficile* PCR-ribotype 001 in Slovakia. *Eur J Clin Microbiol Infect Dis* 2015;34(8):1701–8, doi:<http://dx.doi.org/10.1007/s10096-015-2407-9>.
- Oren A, Rupnik M. *Clostridium difficile* and *Clostridioides difficile*: two validly published and correct names. *Anaerobe* 2018;52:125–6, doi:<http://dx.doi.org/10.1016/j.anaerobe.2018.07.005>.
- Peláez T, Cercenado E, Alcalá L, Marín M, Martín-López A, Martínez-Alarcón J, et al. Metronidazole resistance in *Clostridium difficile* is heterogeneous. *J Clin Microbiol* 2008;46(9):3028–32, doi:<http://dx.doi.org/10.1128/JCM.00524-08>.
- 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):1057–64, doi:<http://dx.doi.org/10.1111/j.1469-0691.2008.02092.x> Erratum in: *Clin Microbiol Infect*. 2009;15(3):296.
- Pituch H, Obuch-Woszczatyński P, Lachowicz D, Wulfańska D, Karpiński P, Młynarczyk G, et al. Hospital-based *Clostridium difficile* infection surveillance reveals high proportions of PCR ribotypes 027 and 176 in different areas of Poland, 2011 to 2013. *Euro Surveill* 2015;20(38), doi:<http://dx.doi.org/10.2807/1560-7917.ES.2015.20.38.30025>.
- Rupnik M, Tambic-Andrasevic A, Trajkovska Dokic E, Matas I, Jovanovic M, Pasic S, et al. Distribution of *Clostridium difficile* PCR ribotypes and high proportion of 027 and 176 in some hospitals in four South Eastern European countries. *Anaerobe* 2016;42:142–4, doi:<http://dx.doi.org/10.1016/j.anaerobe.2016.10.005>.
- Tóth J, Urbán E, Osztie H, Benczik M, Indra A, Nagy E, et al. Distribution of PCR ribotypes among recent *Clostridium difficile* isolates collected in two districts of Hungary using capillary gel electrophoresis and review of changes in the circulating ribotypes over time. *J Med Microbiol* 2016;65(10):1158–63, doi:<http://dx.doi.org/10.1099/jmm.0.000334>.
- Tschudin-Sutter S, Kuijper EJ, Durovic A, Vehreschild MJGT, Barbut F, Eckert C, et al. Guidance document for prevention of *Clostridium difficile* infection in acute healthcare settings. *Clin Microbiol Infect* 2018;24(10):1051–4, doi:<http://dx.doi.org/10.1016/j.cmi.2018.02.020>.
- van Dorp SM, Kinross P, Gastmeier P, Behnke M, Kola A, Delmée M, et al. Standardised surveillance of *Clostridium difficile* infection in European acute care hospitals: a pilot study, 2013. *Euro Surveill* 2016;21(29), doi:<http://dx.doi.org/10.2807/1560-7917.ES.2016.21.29.30293>.