



Prospective Evaluation of the mariPOC Test for Detection of *Clostridioides difficile* Glutamate Dehydrogenase and Toxins A/B

Roosa Savolainen,^a  Juha M. Koskinen,^{b,c} Silja Mentula,^d Janne O. Koskinen,^b Suvi-Sirkku Kaukoranta^a

^aDepartment of Clinical Microbiology, Vaasa Central Hospital, Vaasa, Finland

^bArcDia International Ltd., Turku, Finland

^cFaculty of Medicine, University of Turku, Turku, Finland

^dExpert Microbiology Unit, National Institute for Health and Welfare, Helsinki, Finland

Roosa Savolainen and Juha M. Koskinen contributed equally to the manuscript. Author order was determined in order of increasing seniority.

ABSTRACT The objective of this study was to evaluate a novel automated random-access test, mariPOC CDI (ArcDia Ltd., Finland), for the detection of *Clostridioides difficile* glutamate dehydrogenase (GDH) and toxins A and B directly from fecal specimens. The mariPOC test was compared with both the GenomEra *C. difficile* PCR assay (Abacus Diagnostica Oy, Finland) and the TechLab *C. diff* Quik Chek Complete (Alere Inc.; now Abbot) membrane enzyme immunoassay (MEIA). Culture and the Xpert *C. difficile* assay (Cepheid Inc., USA) were used to resolve discrepant results. In total, 337 specimens were tested with the mariPOC CDI test and GenomEra PCR. Of these specimens, 157 were also tested with the TechLab MEIA. The sensitivity of the mariPOC test for GDH was slightly lower (95.2%) than that obtained with the TechLab assay (100.0%), but no toxin-positive cases were missed. The sensitivity of the mariPOC test for the detection of toxigenic *C. difficile* by analyzing toxin expression was better (81.6%) than that of the TechLab assay (71.1%). The analytical specificities for the mariPOC and the TechLab tests were 98.3% and 100.0% for GDH and 100.0% and 99.2% for toxin A/B, respectively. The analytical specificity of the GenomEra method was 100.0%. The mariPOC and TechLab GDH tests and GenomEra PCR had high negative predictive values of 99.3%, 98.3%, and 99.7%, respectively, in excluding infection with toxigenic *C. difficile*. The mariPOC toxin A/B test and GenomEra PCR had an identical analytical positive predictive value of 100%, providing highly reliable information about toxin expression and the presence of toxin genes, respectively.

KEYWORDS *Clostridioides difficile*, diagnostics, glutamate dehydrogenase, GDH, toxin A/B, gastrointestinal infection, acute gastroenteritis, mariPOC, CDI, *Clostridium difficile*

Clostridioides difficile infection (CDI) is the most commonly diagnosed antibiotic-associated and nosocomial cause of infectious diarrhea (1). Toxigenic *C. difficile* can cause both asymptomatic colonization (2) and symptomatic infection (3, 4). Symptoms vary from mild gastrointestinal signs to severe pseudomembranous colitis (3, 5). Toxin A (TcdA) and toxin B (TcdB), encoded by the genes *tcdA* and *tcdB*, respectively (6), cause the disease symptoms (7). Of these, TcdB has been shown to be the major virulence factor, causing damage to host cells more efficiently than TcdA (6, 8). Although toxigenic *C. difficile* is often detected in diarrheal stool samples of patients, health care-related diarrhea is common, and most cases have a noninfectious origin (9) caused, for example, by the side effects of antibiotics or other drugs (10).

Updated diagnostic guidance for CDI in Europe was released by the European Society of Clinical Microbiology and Infectious Diseases (ESCMID) in 2016 (11). The guidelines recommend algorithms for CDI testing beginning with a highly sensitive

Citation Savolainen R, Koskinen JM, Mentula S, Koskinen JO, Kaukoranta S-S. 2020. Prospective evaluation of the mariPOC test for detection of *Clostridioides difficile* glutamate dehydrogenase and toxins A/B. *J Clin Microbiol* 58:e01872-19. <https://doi.org/10.1128/JCM.01872-19>.

Editor Andrew B. Onderdonk, Brigham and Women's Hospital

Copyright © 2020 American Society for Microbiology. All Rights Reserved.

Address correspondence to Roosa Savolainen, roosa.savolainen@vshp.fi, or Juha M. Koskinen, juha.koskinen@arcdia.com.

Received 12 November 2019

Returned for modification 12 December 2019

Accepted 18 December 2019

Accepted manuscript posted online 15 January 2020

Published 25 March 2020

test, i.e., a glutamate dehydrogenase (GDH) antigen test or a nucleic acid amplification test (NAAT), followed by a clinically highly specific test, i.e., a toxin A/B test. Alternatively, GDH and toxin A/B can be tested simultaneously as the first step. Detection of GDH is highly sensitive in *C. difficile* screening, but it does not differentiate toxigenic from nontoxigenic strains. Instead, the detection of toxin A/B proteins is highly specific for CDI. The direct cell cytotoxicity assay has been traditionally considered a gold standard for the detection of toxin A/B in stool, while toxigenic culture has been regarded as the most sensitive method for the detection of viable toxigenic strains. However, both methods are time-consuming and labor-intensive and are available only in specialized laboratories. In addition, performance can vary significantly between laboratories due to a lack of standardization.

A qualitative NAAT is not recommended as a stand-alone test without a toxin A/B test because it can result in the significant overdiagnosis of CDI, especially when proper testing criteria are lacking (11–13). Overdiagnosis may result in the unnecessary use of antibiotics, hospitalization, and health care costs (14). Clinical studies have shown a positive predictive value (PPV) of approximately 50% for CDI if NAAT is used alone, without toxin A/B detection (12, 15). It has been suggested that quantitative PCR could be used as a quantification method to predict toxin positivity using low cycle threshold (C_T) values. Although there is a correlation between low C_T values and toxin positivity on a population level, similar C_T values are obtained from symptomatic CDI cases and asymptomatic individuals. Therefore, the toxin A/B test is still needed to evaluate whether the toxins are expressed (16–19).

The Infectious Diseases Society of America (IDSA) and the Society for Healthcare Epidemiology of America (SHEA) issued their corresponding updated guidelines in early 2018 (20). These guidelines do not conclude which diagnostic approach is the most optimal. However, as in the ESCMID guidelines, a two- or three-step algorithm is the most preferred method compared to NAAT alone.

In large hospital laboratories, the number of specimens received annually for CDI testing can be in the thousands. Large volumes warrant laboratory automation to serve physicians in a timely and resource-effective manner. There is a need for precise automated methods that can discriminate, together with clinical signs, asymptomatic colonization from symptomatic *C. difficile* infection (11, 20).

The mariPOC test (ArcDia International Ltd., Finland) is an automated platform for rapid multianalyte testing for acute infectious diseases. It is based on a separation-free two-photon excitation assay technique (21–23). We studied the performance of a new mariPOC CDI test. The mariPOC CDI test provides results for both GDH and toxin A/B protein antigens in the same analysis step. The test is performed by an automated analyzer with sophisticated autoverification functions, and the result can be transferred automatically to the laboratory information system. Sample pretreatment involves the simple filtration of a stool specimen suspended in a buffer. The hands-on time is a few minutes per sample, and the analyzer works in continuous-feed and walkaway modes.

(The results of this study were preliminarily presented as a poster presentation at the 6th International *C. difficile* Symposium, Bled, Slovenia, in September 2018 [24].)

MATERIALS AND METHODS

Study outline, microbiological methods, and specimens. The study was performed at Vaasa Central Hospital in Finland from May to September 2017. The hospital laboratory receives around 1,200 specimens for the detection of toxigenic *C. difficile* yearly. The specimens, which arrived consecutively in the laboratory, were collected from patients with diarrhea or from patients suspected of having CDI due to prior antibiotic treatment and/or having been exposed to *C. difficile* patients or carriers. Only samples that had a sufficient amount of native fecal specimen (unprocessed feces) in the sample container were included in the study (Fig. 1). The specimens were tested with the GenomEra *C. difficile* PCR assay (Abacus Diagnostics Oy, Finland) as part of routine diagnostics. For GenomEra, the specimens were suspended in the FecalSwab Cary-Blair collection-and-transport system (Copan Diagnostics Inc., USA). Leftover native fecal specimens were used for the study tests. In total, 337 specimens were tested with the mariPOC gastro+CDI test (ArcDia International Oy Ltd., Finland). All specimens that were positive by either the mariPOC CDI test or toxin B gene GenomEra PCR were further tested with a TechLab *C. diff* Quik Chek Complete (Alere Inc.; now Abbot) membrane enzyme immunoassay (MEIA). In addition, 110 randomly selected mariPOC- and GenomEra-negative specimens were also tested with the TechLab MEIA

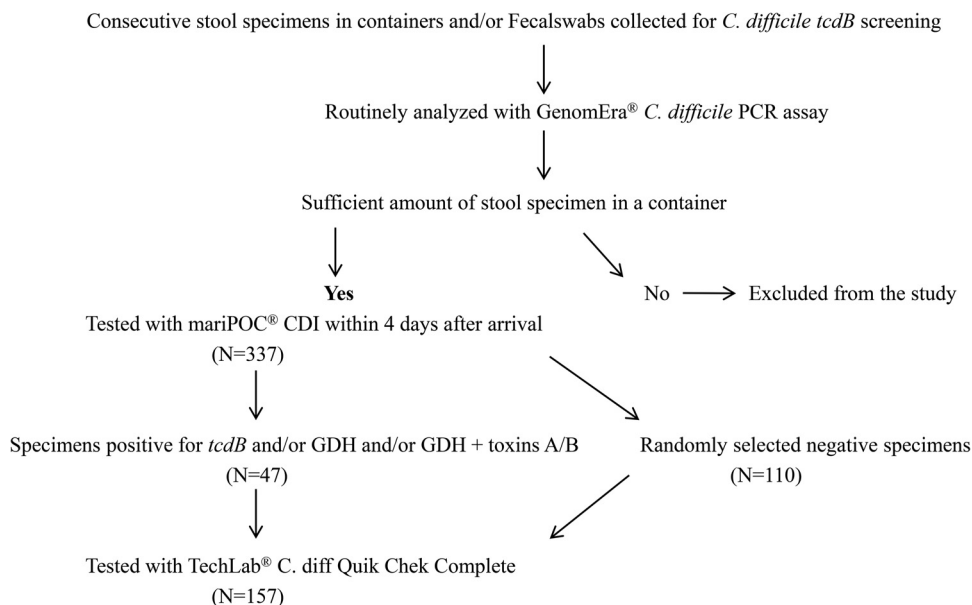


FIG 1 Study flow chart.

to study its specificity. All the tests were performed according to the manufacturers’ instructions. In the case of discrepant results, cultures on Brazier’s cycloserin-cefoxitin egg yolk (CCEY) agar plates (25) were made from specimens stored at -70°C . The culture plates were incubated under anaerobic conditions at $+36^{\circ}\text{C}$ for 2 days. Specimens that were positive only by routine GenomEra were retrospectively reanalyzed from frozen samples using another PCR method (Xpert *C. difficile*; Cepheid Inc., USA) at Seinäjoki Central Hospital (Finland).

Specimens used in the prospective study were stored at $+2^{\circ}\text{C}$ to $+8^{\circ}\text{C}$ for a maximum of 4 days prior to analysis, while the majority of the specimens (around 90%) were tested in 2 days. For longer storage, the specimens were frozen at -70°C .

Recognition of different *C. difficile* strains and cross-reactions with other *Clostridium* species with the mariPOC CDI test were studied by testing 15 *C. difficile* strains presenting different ribotypes and combinations of toxin production and 7 different *Clostridium* species (see Tables 3 and 4). Strains were obtained from the national *C. difficile* reference laboratory at the National Institute for Health and Welfare (Helsinki, Finland) and originated from either the ECDC-Leeds-Leiden collection or a local strain collection. Strains were received as a dense bacterial suspension in 0.9% NaCl harvested from brucella blood agar supplemented with hemin and vitamin K_1 . Bacteria were further diluted into mariPOC gastro sample buffer to a concentration of 5×10^7 bacteria/ml, an estimate based on the optical density at 595 nm. An absorbance value of 1 was considered to be 1×10^9 bacteria/ml.

Study definitions. True positivity was defined as a consensus in specimens’ positivity where at least two of the methods agreed (composite reference standard). A specimen was also considered to be truly GDH and/or toxin A/B protein positive when sole mariPOC or TechLab positivity was confirmed by GenomEra and/or culture. PCR was used to verify GDH positivity but not to rule it out due to the fact that nontoxigenic *C. difficile* strains express GDH. Positive findings that could not be verified by another method(s) were regarded as false positives. Information about clinical symptoms, other anamnestic information, or diagnoses were not collected. The median patient age was 64 years (range, 0 to 101 years). Specimens from patients of all ages and all forms of feces were included because these are not limiting factors when comparing the analytical performances of different methods. For the purposes of this study, toxin A/B protein-positive cases were defined as CDI cases. This definition is supported by several clinical studies (12, 15, 26–28), which state that the detection of toxin A/B protein has a high clinical PPV for CDI. Faint MEIA results (+/-) were interpreted as positive according to the manufacturer’s instructions. Only specimens that had successful PCR and mariPOC final results were included. mariPOC analysis failed for nine samples. Four of the samples were included after reanalysis, and five were excluded from the study.

RESULTS

Comparison of phenotypic methods. In total, 157 specimens were tested with mariPOC, TechLab, and GenomEra. This sample cohort consisted of specimens positive by mariPOC and/or GenomEra ($n = 47$) and randomly selected mariPOC- and GenomEra-negative specimens ($n = 110$). This was a subset of the larger cohort used for comparing phenotypic and genotypic methods (see below) and was used for direct comparison between the mariPOC and TechLab tests. In this cohort, GenomEra

TABLE 1 Performance of phenotypic assays for detection of expressed proteins in 157 fecal specimens^a

Protein	Test	No. of specimens				Sensitivity (%) (95% CI)	Specificity (%)	PPV (%) (95% CI)	NPV (%) (95% CI)
		TP	FP	TN	FN				
Toxin A/B	mariPOC	31	0	126	0	100.0 (87.8–100.0)	100.0	100.0	100.0
	TechLab	27	1	125	4	87.1 (70.2–96.4)	99.2	96.4 (79.2–99.5)	96.9 (92.6–98.7)
GDH	mariPOC	40	5	110	2	95.2 (83.8–99.4)	95.7	88.9 (77.2–95.0)	98.2 (93.4–99.5)
	TechLab	42	0	115	0	100.0 (91.6–100.0)	100.0	100.0	100.0

^aTP, true positive; FP, false positive; TN, true negative; PPV, positive predictive value; NPV, negative predictive value; CI, confidence interval.

PCR results were used only to resolve discrepant results (see Table S1 in the supplemental material). In detecting GDH, the sensitivity of mariPOC was slightly lower (95.2%) than that of TechLab (100.0%), but no toxin-positive or toxigenic cases were missed by the mariPOC test (Table 1) in this sample cohort. The two specimens that were negative with the mariPOC GDH test but positive with TechLab GDH and bacterial identification culture were negative with GenomEra PCR and with both toxin tests (samples 1 and 2). The mariPOC GDH test reported five low-positive results for which true positivity could not be verified by other methods (samples 3 to 7). The mariPOC test found all toxin A/B-positive samples in this cohort (100.0%), while the TechLab test found 87.1%. According to the PCR results, 86% (36/42) of *C. difficile* findings by GDH detection were toxigenic strains.

Comparison of methods for detection of toxigenic *C. difficile*. In total, 337 specimens were successfully tested with mariPOC and GenomEra. This larger cohort was used to determine the performance of the mariPOC test in comparison to GenomEra PCR. For the detection of toxigenic *C. difficile* strains, the sensitivities of the mariPOC and TechLab GDH tests and GenomEra PCR were 94.7%, 94.7%, and 97.4%, respectively (Table 2). The mariPOC and TechLab GDH tests missed two specimens that were positive by GenomEra PCR. One of the specimens was positive only by both of the PCR tests (GenomEra and Xpert), while the other specimen was also positive by culture. GenomEra PCR missed one case, which was GDH and toxin A/B positive by the mariPOC and TechLab tests and was also positive by culture. Another specimen from the same patient, whose positivity GenomEra PCR missed, had been positive by all methods 17 days earlier.

When comparing phenotypic and genotypic methods in order to exclude colonization with a toxigenic strain in this cohort, negative predictive values (NPVs) obtained with the mariPOC and TechLab GDH tests were 99.3% and 98.3%, respectively, which were slightly lower than the 99.7% NPV obtained by GenomEra PCR. Detailed results for the discrepant samples are shown in Table S1 in the supplemental material.

Compared with toxin B gene detection, the sensitivities of the mariPOC and TechLab toxin A/B tests were 81.6% (31/38) and 71.1% (27/38), respectively (Table 2; see the supplemental material for the discrepant samples). The mariPOC test and GenomEra PCR had the highest analytical PPV (100.0%) for toxigenic *C. difficile* (Table 2). The specificities of the mariPOC and TechLab tests presented in Table 2 are against toxin

TABLE 2 Performance of assays for detection of toxigenic strains ($n = 337$ for the mariPOC and the GenomEra tests and $n = 157$ for TechLab)^a

Protein or gene	Test	No. of specimens				Sensitivity (%) (95% CI)	Analytical specificity (%)	PPV (%) (95% CI)	NPV (%) (95% CI)
		TP	FP	TN	FN				
Toxin A/B	mariPOC	31	0	299	7	81.6 (65.7–92.3)	100.0	100.0	97.7 (95.6–98.8)
	TechLab	27	1	118	11	71.1 (54.1–84.6)	99.2	96.4 (79.1–99.5)	91.5 (86.7–94.6)
GDH	mariPOC	36	9	290	2	94.7 (82.3–99.4)	97.0	80.0 (67.7–88.4)	99.3 (97.4–99.8)
	TechLab	36	6	113	2	94.7 (82.3–99.4)	95.0	85.7 (73.3–92.9)	98.3 (93.6–99.5)
Toxin B gene	GenomEra	37	0	299	1	97.4 (86.2–99.9)	100.0	100.0	99.7 (97.7–100.0)

^aTP, true positive; FP, false positive; TN, true negative; PPV, positive predictive value; NPV, negative predictive value; CI, confidence interval.

TABLE 3 Detection of ribotypes and toxinotypes with the mariPOC CDI test

Ribotype(s)/toxinotype(s)	Toxin production	mariPOC result	
		GDH	Toxin A/B
010	Negative	+	–
033/XI	Only binary	+	–
017/VIII, 107	Only toxin B	+	+
053/0, 054, 056/XII	Toxins A and B	+	+
016, ^a 019/IX, 023/IV, 027 ^a /III, 078 ^a /V, 126/XXVIII, 176, ^a 251/III	Toxins A and B, binary	+	+

^aHypervirulent or ribotype 027-like.

gene detection and do not represent true analytical specifics for GDH because toxigenic PCR cannot be used to rule out GDH positivity. In the whole cohort, the true analytical specificities of the mariPOC toxin A/B and GDH tests were 100.0% (306/306) and 98.3% (290/295), respectively, when specimens positive by PCR only were regarded as being GDH and/or toxin A/B negative.

Recognition of *C. difficile* strains and species. The detection of different *C. difficile* strains with the mariPOC test was studied using pure cultures of bacterial strains with known toxin profiles and unified bacterial concentrations based on the optical density of the stock suspension (Table 3). The mariPOC GDH test detected all 15 *C. difficile* ribotypes studied. The mariPOC toxin A/B test detected toxins from all 13 strains carrying the *tcdA* and *tcdB* genes and was negative for the two ribotypes without the toxin gene or had only the gene for binary toxin. Quantitative results showed no clear correlation between toxin production and the strain being possibly hypervirulent. Ribotype 053 showed the highest level of toxin production, followed by ribotypes 027 and 176. Ribotypes 017, 078, and 126 showed a very low level of toxin production.

Possible cross-reactions against closely related *Clostridium* species were studied using pure-culture bacteria in a high concentration (Table 4). The mariPOC GDH test did not cross-react with any of the tested species. As expected, the mariPOC toxin A/B test detected toxins produced by *Clostridium sordellii*.

DISCUSSION

The clinical diagnosis of CDI is a physician’s decision based on clinical manifestations and laboratory findings. There are no consistent criteria for CDI based on symptoms or laboratory tests alone. Ideally, the laboratory method should help the physician by finding all relevant cases and by distinguishing asymptomatic carriage from symptomatic infection (11, 20).

We studied the performance of the novel mariPOC CDI test for the automated and rapid detection of *C. difficile* and its pathogenic toxins in comparison to the widely used MEIA and the detection of the toxin B gene by PCR. Our study was carried out in Finland, which has the highest reported CDI rate in Europe (29). An explanation for the high reporting rate could be that CDI diagnostics in the past were dominated by toxigenic culture, and currently, diagnostics based solely on NAAT are the most common routine in Finland. Accordingly, the transition from highly sensitive toxigenic culture to NAAT has not changed the reported CDI incidence in Finland (30).

TABLE 4 Detection of *Clostridium* species with the mariPOC CDI test

Species	mariPOC result	
	GDH	Toxin A/B
<i>Clostridium bifermentans</i>	–	–
<i>Clostridium innocuum</i>	–	–
<i>Clostridium novyi</i> type A	–	–
<i>Clostridium perfringens</i>	–	–
<i>Clostridium septicum</i>	–	–
<i>Clostridium sordellii</i>	–	+
<i>Clostridium sporogenes</i>	–	–

In our study, the sensitivities of the mariPOC and TechLab GDH tests were equal (both 94.7%), close to the sensitivity of GenomEra PCR (97.4%), for the detection of toxigenic *C. difficile*. The sensitivity of the mariPOC test for the detection of toxins was higher than that of the TechLab assay. In the cohort comparing just the mariPOC and the TechLab tests, the mariPOC test found all toxin-positive samples, while the TechLab test missed 12.9%. The performance of the mariPOC test compared with the TechLab assay is similar to that in a recent study by Krutova et al. (31). In the cohort comparing genotypic and phenotypic methods, the sensitivity of the mariPOC test for the detection of toxigenic *C. difficile* was 81.6%, and that of the TechLab assay was 71.1%.

The higher sensitivity of PCR than of phenotypic methods has been shown to lead to reduced clinical specificity for CDI, for example, in two large clinical studies, by Planche et al. (15) and Polage et al. (12). In our study, the background information (solid feces, repeated testing, and toxin negativity) from four patients studied suggested that six out of the seven toxigenic specimen cases (positive by PCR) that were negative by the mariPOC toxin test had a low probability for CDI.

The limitation of our study was the lack of clinical data, while our analytical results are well aligned with those reported by Planche et al. (15) and Polage et al. (12). In addition, the level of apparent sensitivity for GDH and toxin protein detection against toxin gene detection observed in our study is well in line with those of other studies reviewed recently by Crobach et al. (11). The sensitivity of GenomEra PCR has been reported to be similar to those of several other nucleic acid amplification-based methods (32, 33), thus being a valid molecular test for our comparison study. The specificity of the GenomEra PCR test in our study was better than what has previously been reported (32–34). The sensitivities obtained in our study from clinical specimens are also in line with the analytical sensitivities of the mariPOC (2018-02 user's manual) and TechLab (2016/07 user's manual) tests stated by the manufacturers: 0.7 ng/ml versus 0.8 ng/ml for GDH, 0.1 ng/ml versus 0.63 ng/ml for toxin A, and 0.1 ng/ml versus 0.16 ng/ml for toxin B, respectively.

The mariPOC and TechLab GDH tests and GenomEra PCR had high NPV values of 99.3%, 98.3%, and 99.7%, respectively, demonstrating their usefulness as primary screening tests. The mariPOC toxin A/B test and GenomEra PCR had identical analytical PPVs of 100%, providing highly reliable information about toxin expression and the presence of toxin genes, respectively. Taking together our results and ESCMID (11) and IDSA/SHEA (20) guidelines, the most obvious diagnostic approach with the mariPOC test is to screen for GDH and toxins followed by toxin B gene PCR for a toxin-negative GDH-positive specimen if clinical signs distinctly indicate CDI or in order to cohort patients. GDH/toxin screening followed by PCR was recently implemented in routine use in a Spanish hospital. The authors of that study report that this setup is cost-effective and has a high negative predictive value (35). In our study, the prevalence of toxigenic *C. difficile* in stool specimens was 11%. Our study suggests that only 2.1% or 3.3% of the samples may be needed to be analyzed by PCR if the mariPOC CDI test or TechLab C. diff Quik Chek Complete test is used for primary screening, respectively. In large-sample-volume laboratories, a high-throughput automated system is preferable. The mariPOC test system can provide this capability, as one analyzer enables random-access testing of up to 44 CDI specimens in one 8-h work shift (>5,000 per year).

One of the benefits of the mariPOC test is the optional feature of semiquantitative result reporting. The numerical result may be used to estimate the correlation between the GDH or toxin concentration and clinical outcome in prognosis (36). In our study, there were four patients where the toxin gene was detectable in feces but toxin proteins were undetectable. According to clinical studies, such cases are likely to have a low clinical PPV for severe CDI (12, 13, 37). Outside our study cohort (clinical suspicion for CDI), the mariPOC CDI test found one toxin-positive case with high toxin concentrations from specimens where the clinician suspected a non-CDI-related infection ($n = 252$). This specimen tested positive by both TechLab and GenomEra as well. Based on previous reports, such a case is likely to have a high clinical PPV for CDI (15, 26–28).

The ESCMID guidelines recommend that toxin-negative specimens should be stud-

ied for other microbial pathogens (11). The mariPOC gastro test is a multianalyte test for the detection of *Campylobacter* spp. and noro-, rota-, and adenoviruses. The mariPOC gastro+CDI combination test enables the simultaneous analysis of pathogens causing acute gastroenteritis and CDI from the same specimen. In our study, all the specimens were analyzed with the mariPOC gastro+CDI test. The gastro test found four rotavirus and one norovirus GII.4 gastroenteritis cases that routine diagnostics would have missed because the physician had suspected CDI. These patients belonged to a CDI risk group by age. The median age of these five patients was 70 years (from 40 to 87 years). It has been described in the literature, but is as yet not often implemented in clinical practice, that multianalyte diagnostic methods are needed to differentiate between CDI and viral infections because of overlapping clinical presentations (31, 38).

The mariPOC CDI test detected all studied *C. difficile* ribotypes and toxinotypes (Table 3) representing most of the known strains (39), which validates the design of the mariPOC CDI test to detect highly conserved epitopes in GDH and toxins A and B. As expected, due to the known close resemblance of *C. sordellii* and *C. difficile* toxins (40, 41), we observed a cross-reaction between the two. *C. sordellii* is a rare but highly pathogenic bacterium for which the diagnostics are challenging due to rapidly evolving severe disease. A delay in the diagnosis of *C. sordellii* infection increases mortality. Therefore, early detection of infection is important (42). Due to the otherwise high specificity of the mariPOC GDH and toxin A/B tests, the treating physician should consider the presence of a rare case of *C. sordellii* toxins if the test is positive for toxin A/B but negative for GDH.

Limitations of our study include that a composite gold standard was used instead of the traditional gold standards, and the cultures and PCRs used to resolve discrepant result were done retrospectively from frozen specimens. Freezing might have reduced the ability of bacteria to grow, or it might have degraded the nucleic acid, while GDH and toxins A and B have been shown to be robust against freezing and thawing (43). In addition, for some specimens, there were only small remains of the feces for culture testing. Thus, a positive culture confirmed positivity, but a negative culture did not necessarily exclude the possibility of true positivity. Another minor limitation is that the TechLab test was performed only on those samples that were positive by mariPOC or GenomEra as well as on a set of 110 randomly selected specimens. In theory, the TechLab assay could have found more true toxin positives from the negative sample population, but this is unlikely given the better clinical sensitivity of mariPOC, as observed in the PCR-positive sample population. Our study setup thus provides a narrower specificity confidence interval for the mariPOC than for the TechLab test, but this is justified in that the specificity of the TechLab test has been studied in previous studies, while this was the first evaluation of the mariPOC CDI test. With these limitations, our results still support the ESCMID guideline recommendation that “CDI testing should not be limited to samples with a specific physician’s request” (11).

Conclusions. In summary, high sensitivity, specificity, and throughput make the mariPOC CDI test an interesting new tool for optimizing CDI testing from fecal specimens. Testing for GDH and toxin A/B in one step with mariPOC provides a high NPV to rule out toxigenic *C. difficile* infection and a high PPV to rule in toxin expression, respectively. The seven-parameter multianalyte gastro+CDI test is an interesting tool to be considered for increasing the coverage and accuracy of diagnostics in accordance with the most recent guidelines. The automated result interpretation and random-access analysis of samples give mariPOC an advantage over other antigen detection tests. Methodological studies against cell cytotoxicity/toxigenic culture and clinical studies are needed in order to fully assess both the accuracy and clinical impact, respectively, of the mariPOC CDI test in CDI diagnosis.

SUPPLEMENTAL MATERIAL

Supplemental material is available online only.

SUPPLEMENTAL FILE 1, PDF file, 0.5 MB.

ACKNOWLEDGMENTS

We thank laboratory assistants at Vaasa Central Hospital and Jenna Mäkilä at ArcDia for her significant effort in the development of the mariPOC CDI test.

R.S. had major contributions in scientific design and execution of the studies, result analysis, scientific analysis, and writing of the manuscript. J.M.K. had major contributions in the development of the mariPOC CDI test and in scientific design, execution, and analysis of the results of the cross-reactivity studies. S.M. had major contributions in providing *Clostridium* species and revising the manuscript. J.O.K. had major contributions in the development of the mariPOC CDI test and in scientific design, execution, and analysis of the results of the cross-reactivity studies. S.-S.K. had major contributions in scientific design, scientific analysis, and revision of the manuscript.

ArcDia International Ltd. contributed to the study with the mariPOC test system and consumables. The study was partly supported by TEKES, the Finnish Funding Agency for Innovation, under the project name Get It Done!, funding decision 534/14.

J.M.K. and J.O.K. are employees of ArcDia International Ltd.

REFERENCES

- Magill SS, Edwards JR, Bamberg W, Beldavs ZG, Dumyati G, Kainer MA, Lynfield R, Maloney M, McAllister-Hollod L, Nadle J, Ray SM, Thompson DL, Wilson LE, Fridkin SK, Emerging Infections Program Healthcare-Associated Infections and Antimicrobial Use Prevalence Survey Team. 2014. Multistate point-prevalence survey of health care-associated infections. *N Engl J Med* 370:1198–1208. <https://doi.org/10.1056/NEJMoa1306801>.
- Kim KH, Fekety R, Batts DH, Brown D, Cudmore M, Silva J, Waters D. 1981. Isolation of *Clostridium difficile* from the environment and contacts of patients with antibiotic-associated colitis. *J Infect Dis* 143:42–50. <https://doi.org/10.1093/infdis/143.1.42>.
- Bartlett JG, Chang TW, Gurwith M, Gorbach SL, Onderdonk AB. 1978. Antibiotic-associated pseudomembranous colitis due to toxin-producing *Clostridia*. *N Engl J Med* 298:531–534. <https://doi.org/10.1056/NEJM197803092981003>.
- Voth DE, Ballard JD. 2005. *Clostridium difficile* toxins: mechanism of action and role in disease. *Clin Microbiol Rev* 18:247–263. <https://doi.org/10.1128/CMR.18.2.247-263.2005>.
- Hurley BW, Nguyen CC. 2002. The spectrum of pseudomembranous enterocolitis and antibiotic-associated diarrhea. *Arch Intern Med* 162:2177–2184. <https://doi.org/10.1001/archinte.162.19.2177>.
- Sullivan NM, Pellett S, Wilkins TD. 1982. Purification and characterization of toxins A and B of *Clostridium difficile*. *Infect Immun* 35:1032–1040. <https://doi.org/10.1128/IAI.35.3.1032-1040.1982>.
- Dupuy B, Sonenshein AL. 1998. Regulated transcription of *Clostridium difficile* toxin genes. *Mol Microbiol* 27:107–120. <https://doi.org/10.1046/j.1365-2958.1998.00663.x>.
- Carter GP, Chakravorty A, Pham Nguyen TA, Mileto S, Schreiber F, Li L, Howarth P, Clare S, Cunningham B, Sambol SP, Cheknis A, Figueroa I, Johnson S, Gerding D, Rood JI, Dougan G, Lawley TD, Lyras D. 2015. Defining the roles of TcdA and TcdB in localized gastrointestinal disease, systemic organ damage, and the host response during *Clostridium difficile* infections. *mBio* 6:e00551-15. <https://doi.org/10.1128/mBio.00551-15>.
- Polage CR, Solnick JV, Cohen SH. 2012. Nosocomial diarrhea: evaluation and treatment of causes other than *Clostridium difficile*. *Clin Infect Dis* 55:982–989. <https://doi.org/10.1093/cid/cis551>.
- Chassany O, Michaux A, Bergmann JF. 2000. Drug-induced diarrhoea. *Drug Saf* 22:53–72. <https://doi.org/10.2165/00002018-200022010-00005>.
- Crobach MJT, Planche T, Eckert C, Barbut F, Terveer EM, Dekkers OM, Wilcox MH, Kuijper EJ. 2016. European Society of Clinical Microbiology and Infectious Diseases: update of the diagnostic guidance document for *Clostridium difficile* infection. *Clin Microbiol Infect* 22:S63–S81. <https://doi.org/10.1016/j.cmi.2016.03.010>.
- Polage CR, Gyorke CE, Kennedy MA, Leslie JL, Chin DL, Wang S, Nguyen HH, Huang B, Tang Y, Lee LW, Kim K, Taylor S, Romano PS, Panacek EA, Goodell PB, Solnick JV, Cohen SH. 2015. Overdiagnosis of *Clostridium difficile* infection in the molecular test era. *JAMA Intern Med* 175:1792–1801. <https://doi.org/10.1001/jamainternmed.2015.4114>.
- Truong C, Schroeder LF, Gaur R, Anikst VE, Komo I, Watters C, McCalley E, Kulik C, Pickham D, Lee NJ, Banaei N. 2017. *Clostridium difficile* rates in asymptomatic and symptomatic hospitalized patients using nucleic acid testing. *Diagn Microbiol Infect Dis* 87:365–370. <https://doi.org/10.1016/j.diagmicrobio.2016.12.014>.
- Matta SK, Greenberg A, Singh A. 2015. Diarrhea with *Clostridium difficile*-positive stool—trick or treat: a teachable moment. *JAMA Intern Med* 175:1746–1747. <https://doi.org/10.1001/jamainternmed.2015.4792>.
- Planche TD, Davies KA, Coen PG, Finney JM, Monahan IM, Morris KA, O'Connor L, Oakley SJ, Pope CF, Wren MW, Shetty NP, Crook DW, Wilcox MH. 2013. Differences in outcome according to *Clostridium difficile* testing method: a prospective multicentre diagnostic validation study of *C difficile* infection. *Lancet Infect Dis* 13:936–945. [https://doi.org/10.1016/S1473-3099\(13\)70200-7](https://doi.org/10.1016/S1473-3099(13)70200-7).
- Dionne L, Raymond F, Corbeil J, Longtin J, Gervais P, Longtin Y. 2013. Correlation between *Clostridium difficile* bacterial load, commercial real-time PCR cycle thresholds, and results of diagnostic tests based on enzyme immunoassay and cell culture cytotoxicity assay. *J Clin Microbiol* 51:3624–3630. <https://doi.org/10.1128/JCM.01444-13>.
- Garvey MI, Bradley CW, Wilkinson MAC, Holden E. 2017. Can a toxin gene NAAT be used to predict toxin EIA and the severity of *Clostridium difficile* infection? *Antimicrob Resist Infect Control* 6:127. <https://doi.org/10.1186/s13756-017-0283-z>.
- Senchyna F, Gaur RL, Gombar S, Truong CY, Schroeder LF, Banaei N. 2017. *Clostridium difficile* PCR cycle threshold predicts free toxin. *J Clin Microbiol* 55:2651–2660. <https://doi.org/10.1128/JCM.00563-17>.
- Crobach MJT, Duzsenko N, Terveer EM, Verduin CM, Kuijper EJ. 2018. Nucleic acid amplification test quantitation as predictor of toxin presence in *Clostridium difficile* infection. *J Clin Microbiol* 56:e01316-17. <https://doi.org/10.1128/JCM.01316-17>.
- McDonald LC, Gerding DN, Johnson S, Bakken JS, Carroll KC, Coffin SE, Dubberke ER, Garey KW, Gould CV, Kelly C, Loo V, Shaklee Sammons J, Sandora TJ, Wilcox MH. 2018. Clinical practice guidelines for *Clostridium difficile* infection in adults and children: 2017 update by the Infectious Diseases Society of America (IDSA) and Society for Healthcare Epidemiology of America (SHEA). *Clin Infect Dis* 66:987–994. <https://doi.org/10.1093/cid/ciy149>.
- Hänninen P, Soini A, Meltola N, Soini J, Soukka J, Soini E. 2000. A new microvolume technique for bioaffinity assays using two-photon excitation. *Nat Biotechnol* 18:548–550. <https://doi.org/10.1038/75421>.
- Koskinen JO, Vainionpää R, Meltola NJ, Soukka J, Hänninen PE, Soini AE. 2007. Rapid method for detection of influenza A and B virus antigens by use of a two-photon excitation assay technique and dry-chemistry reagents. *J Clin Microbiol* 45:3581–3588. <https://doi.org/10.1128/JCM.00128-07>.
- Koskinen JM, Soukka JM, Meltola NJ, Koskinen JO. 2018. Microbial identification from feces and urine in one step by two-photon excitation assay technique. *J Immunol Methods* 460:113–118. <https://doi.org/10.1016/j.jim.2018.06.017>.
- Savolainen R, Koskinen JM, Koskinen JO, Suvi-Sirkku K. 2018. Evaluation of a new random-access antigen test for the detection of *Clostridium*

difficile, poster P65, p 134. Abstr 6th Int C. difficile Symp, Bled, Slovenia. http://www.icds.si/wp-content/uploads/2018/09/P069_Savolainen.pdf.

25. Brazier JS. 1993. Role of the laboratory in investigations of *Clostridium difficile* diarrhea. Clin Infect Dis 16:S228–S233. https://doi.org/10.1093/clinids/16.Supplement_4.S228.
26. Church JM, Fazio VW. 1985. The significance of quantitative results of *C. difficile* cultures and toxin assays in patients with diarrhea. Dis Colon Rectum 28:765–769. <https://doi.org/10.1007/bf02555469>.
27. Ryder AB, Huang Y, Li H, Zheng M, Wang X, Stratton CW, Xu X, Tang Y. 2010. Assessment of *Clostridium difficile* infections by quantitative detection of *tcdB* toxin by use of a real-time cell analysis system. J Clin Microbiol 48:4129–4134. <https://doi.org/10.1128/JCM.01104-10>.
28. Song L, Zhao M, Duffy DC, Hansen J, Shields K, Wungjiranirun M, Chen X, Xu H, Leffler DA, Sambol SP, Gerding DN, Kelly CP, Pollock NR. 2015. Development and validation of digital enzyme-linked immunosorbent assays for ultrasensitive detection and quantification of *Clostridium difficile* toxins in stool. J Clin Microbiol 53:3204–3212. <https://doi.org/10.1128/JCM.01334-15>.
29. Bauer MP, Notermans DW, van Benthem BHB, Brazier JS, Wilcox MH, Rupnik M, Monnet DL, van Dissel JT, Kuijper EJ, ECDIS Study Group. 2011. *Clostridium difficile* infection in Europe: a hospital-based survey. Lancet 377:63–73. [https://doi.org/10.1016/S0140-6736\(10\)61266-4](https://doi.org/10.1016/S0140-6736(10)61266-4).
30. Mentula S, Kotila S, Lyytikäinen O, Ibrahim S, Ollgren J, Virolainen A. 2017. *Clostridium difficile* infections in Finland, 2008–2015: trends, diagnostics and ribotypes. Eur J Clin Microbiol Infect Dis 36:1939–1945. <https://doi.org/10.1007/s10096-017-3017-5>.
31. Krutova M, Briksi A, Tkadlec J, Zajac M, Matejkova J, Nyc O, Drevinek P. 2019. Evaluation of a gastrointestinal pathogen panel immunoassay in stool testing of patients with suspected Clostridioides (*Clostridium*) *difficile* infection. J Clin Microbiol 57:e00710-19. <https://doi.org/10.1128/JCM.00710-19>.
32. Alcalá L, Reigadas E, Marín M, Fernández-Chico A, Catalán P, Bouza E. 2015. Comparison of GenomEra *C. difficile* and Xpert *C. difficile* as confirmatory tests in a multistep algorithm for diagnosis of *Clostridium difficile* infection. J Clin Microbiol 53:332–335. <https://doi.org/10.1128/JCM.03093-14>.
33. Paitan Y, Miller-Roll T, Adler A. 2017. Comparative performance study of six commercial molecular assays for rapid detection of toxigenic *Clostridium difficile*. Clin Microbiol Infect 23:567–572. <https://doi.org/10.1016/j.cmi.2017.02.016>.
34. Hirvonen JJ, Mentula S, Kaukoranta S. 2013. Evaluation of a new automated homogeneous PCR assay, GenomEra *C. difficile*, for rapid detection of toxigenic *Clostridium difficile* in fecal specimens. J Clin Microbiol 51:2908–2912. <https://doi.org/10.1128/JCM.01083-13>.
35. Origüen J, Corbella L, Orellana MÁ, Fernández-Ruiz M, López-Medrano F, San Juan R, Lizasoain M, Ruiz-Merlo T, Morales-Cartagena A, Maestro G, Parra P, Villa J, Delgado R, Aguado JM. 2018. Comparison of the clinical course of *Clostridium difficile* infection in glutamate dehydrogenase-positive toxin-negative patients diagnosed by PCR to those with a positive toxin test. Clin Microbiol Infect 24:414–421. <https://doi.org/10.1016/j.cmi.2017.07.033>.
36. Pollock NR. 2016. Ultrasensitive detection and quantification of toxins for optimized diagnosis of *Clostridium difficile* infection. J Clin Microbiol 54:259–264. <https://doi.org/10.1128/JCM.02419-15>.
37. Baker I, Leeming JP, Reynolds R, Ibrahim I, Darley E. 2013. Clinical relevance of a positive molecular test in the diagnosis of *Clostridium difficile* infection. J Hosp Infect 84:311–315. <https://doi.org/10.1016/j.jhin.2013.05.006>.
38. Ludwig A, Sato K, Schirmer P, Maniar A, Lucero-Obusan C, Fleming C, Ryono R, Oda G, Winters M, Holodniy M. 2013. Concurrent outbreaks of norovirus and *Clostridium difficile* in a long-term-care facility. Epidemiol Infect 141:1598–1603. <https://doi.org/10.1017/S0950268813000241>.
39. Rupnik M. 2008. Heterogeneity of large clostridial toxins: importance of *Clostridium difficile* toxinotypes. FEMS Microbiol Rev 32:541–555. <https://doi.org/10.1111/j.1574-6976.2008.00110.x>.
40. Rifkin GD, Fekety FR, Silva J. 1977. Antibiotic-induced colitis implication of a toxin neutralised by *Clostridium sordellii* antitoxin. Lancet ii:1103–1106. [https://doi.org/10.1016/S0140-6736\(77\)90547-5](https://doi.org/10.1016/S0140-6736(77)90547-5).
41. Martinez RD, Wilkins TD. 1992. Comparison of *Clostridium sordellii* toxins HT and LT with toxins A and B of *C. difficile*. J Med Microbiol 36:30–36. <https://doi.org/10.1099/00222615-36-1-30>.
42. Aldape MJ, Bryant AE, Stevens DL. 2006. *Clostridium sordellii* infection: epidemiology, clinical findings, and current perspectives on diagnosis and treatment. Clin Infect Dis 43:1436–1446. <https://doi.org/10.1086/508866>.
43. Schora DM, Peterson LR, Usacheva EA. 2018. Immunological stability of *Clostridium difficile* toxins in clinical specimens. Infect Control Hosp Epidemiol 39:434–438. <https://doi.org/10.1017/ice.2018.20>.