



A *Clostridium difficile* Lineage Endemic to Costa Rican Hospitals Is Multidrug Resistant by Acquisition of Chromosomal Mutations and Novel Mobile Genetic Elements

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ABSTRACT The antimicrobial resistance (AMR) rates and levels recorded for *Clostridium difficile* are on the rise. This study reports the nature, levels, diversity, and genomic context of the antimicrobial resistance of human *C. difficile* isolates of the NAP_{CR1}/RT012/ST54 genotype, which caused an outbreak in 2009 and is endemic in Costa Rican hospitals. To this end, we determined the susceptibilities of 38 NAP_{CR1} isolates to 10 antibiotics from seven classes using Etests or macrodilution tests and examined 31 NAP_{CR1} whole-genome sequences to identify single nucleotide polymorphisms (SNPs) and genes that could explain the resistance phenotypes observed. The NAP_{CR1} isolates were multidrug resistant (MDR) and commonly exhibited very high resistance levels. By sequencing their genomes, we showed that they possessed resistance-associated SNPs in *gyrA* and *rpoB* and carried eight to nine acquired antimicrobial resistance (AMR) genes. Most of these genes were located on known or novel mobile genetic elements shared by isolates recovered at different hospitals and at different time points. Metronidazole and vancomycin remain the first-line treatment options for these isolates. Overall, the NAP_{CR1} lineage showed an enhanced ability to acquire AMR genes through lateral gene transfer. On the basis of this finding, we recommend further vigilance and the adoption of improved control measures to limit the dissemination of this lineage and the emergence of more *C. difficile* MDR strains.

KEYWORDS *Clostridium difficile*, NAP_{CR1}, multidrug resistance, comparative genomics

Clostridium difficile has attracted attention as an emerging pathogen on account of the worldwide spread of outbreak-causing strains (1), its changing epidemiology (2), and the growing incidence, severity, and health care costs associated with *C. difficile* infections (CDI) (3). Indeed, some consider that CDI have surpassed methicillin-resistant *Staphylococcus aureus* infections as the most common hospital-onset, health care facility-associated infections (4).

Partly because of the rapid spread of successful clones, such as the fluoroquinolone-resistant NAP1 strains with mutations in *gyrA* (5), but also because of the rich array of conjugative transposons (CTn), transposons (Tn), and mobilizable transposons (mobTn) that characterize some strains of this species (6), the antimicrobial resistance (AMR) rates and levels recorded for *C. difficile* are increasing around the globe (7–9).

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This worrisome issue, along with the recognized role of several antibiotics in the etiology of CDI (10) and the mobility of the gut resistome (11), justifies continuous monitoring of antimicrobial resistance in *C. difficile*, its etiology, and the mechanisms through which it spreads. To date, these issues have not been explored using whole-genome sequencing in Latin American hospitals.

Along with the epidemic strain NAP1/RT027/ST01, a novel genotype of *C. difficile* termed NAP_{CR1}/RT012/ST-54 (NAP_{CR1} variant with ribotype [RT] 012 and sequence type [ST] 54) caused an outbreak of CDI in a major Costa Rican hospital in 2009 (12). NAP_{CR1} isolates induced a severe clinical presentation, were associated with mortality and recurrence rates comparable to those of NAP1/RT027 strains, and produced a strong inflammatory reaction in animal models (12). These strains continue to circulate in several hospitals of this Central American country (13), and their closest known relative is the multidrug-resistant (MDR) strain CD630, which is also classified as RT012/ST-54 and has been claimed to carry bona fide determinants for tetracycline, erythromycin, daunorubicin, bacitracin, nogalamycin, beta-lactam, tellurite, streptogramin, and lantibiotic resistance (14).

We compared the susceptibilities to 10 antimicrobials of seven pulsed-field gel electrophoresis (PFGE) subtypes of NAP_{CR1} isolates recovered from patients with diarrhea over the past decade. This phenotypic analysis was followed by a detailed examination of whole-genome sequences (WGS) in order to determine the etiology and genomic context of the resistance phenotypes observed.

RESULTS

Antimicrobial susceptibility profiles. In Costa Rica, epidemiological surveillance of *C. difficile* is performed using pulsed-field gel electrophoresis (PFGE). We analyzed 38 NAP_{CR1} isolates with 10 different PFGE Smal patterns (Table 1) on account of their epidemic potential, high virulence, and close relationship to CD630 (Fig. 1). Although different resistance levels and patterns were seen across and within PFGE Smal patterns (Table 2), all these bacteria were resistant to 4 to 7 classes of antimicrobials and were therefore categorized as MDR (Table 2). With a single exception, all isolates were categorized as resistant to clindamycin, ciprofloxacin, levofloxacin, moxifloxacin, and chloramphenicol. Moreover, resistance rates above 85% were recorded for tetracycline (33 of 38 isolates [87%]) and rifampin (31 of 32 isolates [97%]), and 90% of the isolates studied showed diminished susceptibility to linezolid (34/38 [92%]). In contrast, roughly two-thirds of the isolates were susceptible to tigecycline (24/38 [63%]), 4 isolates had diminished susceptibility to vancomycin (11%), and none of the isolates showed resistance to metronidazole (Table 2). Across all isolates and their antimicrobial resistance (AMR) profiles, no obvious patterns of increased resistance over time could be seen in the data set.

Genotypic mapping of the observed phenotypic resistance profiles. Twenty-nine sequenced NAP_{CR1} isolates with PFGE Smal pattern 442, 447, 448, 449, 452, 487, 488, 558, or 578 had the gene encoding the ribosomal protection protein TetM carried on Tn5397 and were, accordingly, tetracycline resistant (Table 3). On the other hand, both NAP_{CR1} isolates with the Smal macrorestriction pattern 489 studied lacked Tn5397 and were susceptible to tetracycline.

All NAP_{CR1} isolates carried a single copy of *ermB*, the product of which confers resistance to clindamycin, inserted into the Tn5398 variant element that is characteristic of *C. difficile* 630Δ*erm* (Table 3; Fig. 2).

All isolates sequenced showed a Thr82Ile substitution in the *gyrA* gene, encoding DNA gyrase, as well as two *rpoB* mutations leading to the His502Asn and Arg505Lys substitutions (Table 3). The Thr82Ile mutation correlated with fluoroquinolone resistance and the other two mutations did so with rifampicin resistance.

In addition, all NAP_{CR1} WGS include two copies of the chloramphenicol acetyltransferase-carrying transposon Tn4453a inserted into homologues of the CD630_04230 and CD630_18620 helicases of CTn2 and CTn5, respectively (Table 3; Fig. 3 and 4). Accordingly, all NAP_{CR1} isolates are resistant to chloramphenicol.

TABLE 1 *Clostridium difficile* NAP_{CR1} isolates included in the study

Isolate	PFGE SmaI pattern (no. of isolates)	Hospital ^a	Yr(s) of isolation
LIBA-3147	442 (1)	HSJD	2003
LIBA-2994	447 (6)	HCG	2009
LIBA-5701		HSJD	2009
LIBA-5711		HSJD	2009
LIBA-5767		HCG	2009
LIBA-5771		CENARE	2009
LIBA-6281		HMX	2011–2012
LIBA-2784	448 (12)	HBC	2003
LIBA-2954		HMX	2009
LIBA-2991		HCG	2010
LIBA-2993		HCG	2010
LIBA-3125		HSJD	2003
LIBA-3137		HSJD	2003
LIBA-5434		HBC	2003
LIBA-5704		HSJD	2009
LIBA-5707		HSJD	2009
LIBA-5751		HMX	2009
LIBA-5774		HMX	2009
LIBA-6275		HMX	2011–2012
LIBA-3129	449 (6)	HSJD	2003
LIBA-5719		HSJD	2009
LIBA-5750		HMX	2009
LIBA-5755		HMX	2009
LIBA-5772		HSVP	2009
LIBA-6276		HMX	2011–2012
LIBA-5734	452 (1)	HSJD	2009
LIBA-2945	487 (4)	CENARE	2009
LIBA-5763		HCG	2009
LIBA-5769		HCG	2009
LIBA-5770		HCG	2009
LIBA-2992	488 (1)	HCG	2009
LIBA-5761	489 (2)	HEB	2009
LIBA-5762		HEB	2009
LIBA-3145	558 (2)	HSJD	2003
LIBA-6285		HMX	2011–2012
LIBA-3144	578 (3)	HSJD	2003
LIBA-3150		HSJD	2003
LIBA-5436		HBC	2003

^aHSJD, San Juan de Dios Hospital; HCG, Calderón Guardia Hospital; CENARE, Centro Nacional de Rehabilitación; HMX, México Hospital; HBC, Blanco Cervantes Hospital; HSVP, San Vicente de Paúl Hospital; HEB, Enrique Baltodano Hospital.

Other resistance genes and resistance-related mobile genetic elements (MGE).

Although all sequenced NAP_{CR1} isolates included a *vanG*-like cluster (data not shown), only a few isolates showed decreased vancomycin susceptibility. This incongruence has been reported previously (15).

A gene coding for a putative radical SAM protein marginally resembling the rRNA dimethyltransferase Cfr was found, along with the aminoglycoside-streptothricin resistance gene cluster *ant6-sat4-aphA-3*, in three variants of a Tn916-like element in both linezolid-resistant and linezolid-susceptible NAP_{CR1} isolates (Table 3; Fig. 5). The largest and most common variant of this MGE was shared by isolates with PFGE SmaI patterns 442, 447, 448, 449, 452, 488, 489, 558, and 578. It included two putative mobTn: one with the *cfr*-like gene mentioned above and one with a gene showing partial matches to the gene encoding the 16S rRNA methyltransferase KsgA and an adjacent sigma factor (Fig. 5). The second variant was restricted to isolates with PFGE SmaI pattern 487 and lacked the mobTn with the *ksgA*-like gene (Fig. 5), which, instead, was found inserted into a putative conjugative gene of CTn2 (CD630_04140) (Fig. 3). The third variant did not have the mobTn with the *cfr*-like gene and was unique to the NAP_{CR1} isolate with PFGE SmaI pattern 447, LIBA-5701 (Fig. 5).

Except for isolates with PFGE SmaI pattern 487, the NAP_{CR1} WGS possessed two copies of a putative mobTn element inserted into genes homologous to those encod-

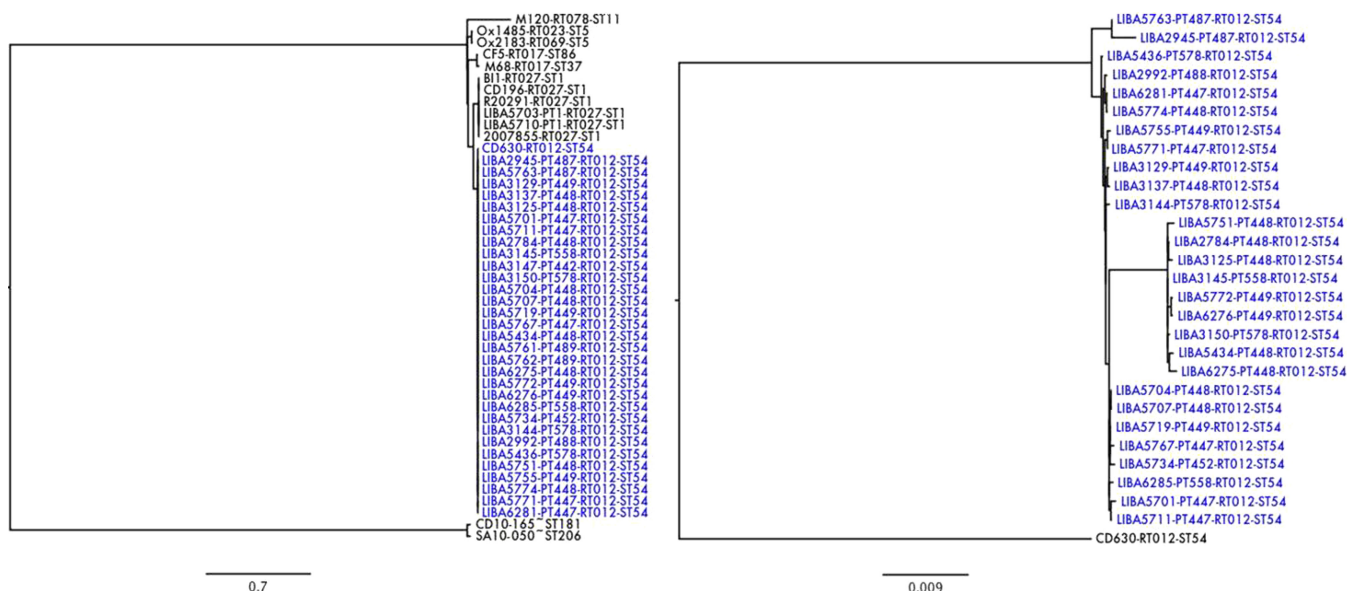


FIG 1 Despite clustering with CD630 in a core SNP tree that includes representatives of all six *C. difficile* MLST clades (left), the NAP_{CR1} isolates (highlighted in blue) can be clearly distinguished from this MDR reference strain (right). Small patterns (PT), ribotypes (RT), and sequence types (ST) are given after isolate designations when available. Bars represent the average numbers of substitutions per site.

ing transcriptional regulators CD630_02920 and CD630_31200 (Table 3; Fig. 6). This novel mobTn includes in its sequence a copy of the composite transposon Tn4001, which encodes a bifunctional aminoglycoside-modifying enzyme (AME) with both acetyltransferase and phosphotransferase functions (*aacA-aphD*) (Table 3; Fig. 6). The NAP_{CR1}-487 isolates carried another putative bifunctional aminoglycoside-modifying enzyme, but in a phage-like sequence inserted into the CD630_18620 helicase of CTn5 (Fig. 4). The latter bifunctional aminoglycoside-modifying enzyme shows 56% identity to orthologous proteins from *Campylobacter jejuni* and *C. difficile* (NCBI protein accession numbers [AGV79342.1](#) and [WP_004452859.1](#)) and is flanked by a gene encoding a protein with a GNAT acetyltransferase domain and a phosphotransferase from *C. difficile* (61% identity to NCBI protein accession number [WP_021424056.1](#)).

DISCUSSION

We have completed the first genomic study of *C. difficile* in Costa Rica to determine the underlying diversity of AMR-associated single nucleotide polymorphisms (SNPs) and genes of isolates causing disease. We showed that NAP_{CR1} isolates are noteworthy not only because of the number of classes of antibiotics to which they are resistant but also because of their high MICs, the numbers of resistance genes detected in their genomes, and the association of these AMR-related genes with multiple transmissible or potentially transmissible MGE, some of which are novel.

Tetracycline resistance in human-associated strains of *C. difficile* is commonly explained by carriage of Tn5397 or Tn916-like elements that, in addition to *tetM* variants (16), include *ermB* (17). In contrast *C. difficile* strains of swine origin have been shown to be strongly associated with *tetW* (18). In agreement with their human intestinal origin, those sequenced isolates with phenotypically confirmed tetracycline resistance carried Tn5397.

The widespread clindamycin resistance of *C. difficile* is often linked to the rRNA adenine N-6-methyltransferase encoded by *ermB*. The best-known *erm*⁺ MGE in this species is the nonconjugative mobTn Tn5398, which contains two *ermB* copies (19). Laboratory strains positive for Tn5398 may become clindamycin susceptible through the loss of one *ermB* copy, although reversion of the phenotype may also occur (20). This might be the case for our sequenced isolates, since they naturally lost one *ermB* copy but retained their phenotypic resistance to clindamycin.

TABLE 2 Antibiotic susceptibility profiles of *Clostridium difficile* NAP_{CR1} isolates

Isolate	Smal pattern	MIC ($\mu\text{g/ml}$) ^a										
		Tetracyclines		Lincosamides (CLI)	Quinolones			Nitroimidazoles (MET)	Ansamycins (RIF)	Glycopeptides (VAN)	Oxazolidinones (LIN)	Phenicolos (CHL)
		TET	TIG		CIP	LEV	MOX					
LIBA-3147	442	0.38	0.064	≥ 256	256	256	NA ^b	≤ 0.25	128	1	1	64
LIBA-2994	447	64	0.5	≥ 256	128	≥ 256	16	≤ 0.25	≥ 32	1	8	≥ 256
LIBA-5701		64	0.064	≥ 256	≥ 32	≥ 32	≥ 32	0.19	NA ^b	1	1	128
LIBA-5711		64	0.094	≥ 256	≥ 32	≥ 32	≥ 32	0.5	NA	2	1	128
LIBA-5767		64	0.125	≥ 256	128	≥ 256	16	≤ 0.25	256	1	6	≥ 256
LIBA-5771		64	0.125	≥ 256	128	≥ 256	16	1	128	2	8	≥ 256
LIBA-6281		64	0.125	≥ 256	≥ 32	≥ 32	≥ 32	≤ 0.25	≥ 32	0.75	8	≥ 256
LIBA-2784	448	64	0.125	8	≥ 32	≥ 32	≥ 32	2	NA	1	8	≥ 256
LIBA-2954		32	0.25	≥ 256	128	≥ 256	≥ 32	0.5	128	4	8	≥ 256
LIBA-2991		64	0.5	≥ 256	128	≥ 256	16	0.5	≥ 32	1	8	≥ 256
LIBA-2993		64	0.5	≥ 256	128	≥ 256	16	≤ 0.25	≥ 32	0.125	8	≥ 256
LIBA-3125		64	0.25	≥ 256	256	256	≥ 32	≤ 0.25	128	1	6	≥ 256
LIBA-3137		64	0.125	8	256	256	≥ 32	≤ 0.25	≤ 0.125	1	8	> 256
LIBA-5434		32	0.19	≥ 256	256	256	≥ 32	≤ 0.25	128	2	6	64
LIBA-5704		32	0.064	≥ 256	≥ 32	≥ 32	≥ 32	0.125	NA	1	6	64
LIBA-5707		64	0.094	≥ 256	≥ 32	≥ 32	≥ 32	0.75	NA	2	6	128
LIBA-5751		64	0.25	≥ 256	128	≥ 256	16	≤ 0.25	128	1	8	≥ 256
LIBA-5774		96	0.25	≥ 256	128	≥ 256	≥ 32	0.5	128	4	8	≥ 256
LIBA-6275		64	0.064	≥ 256	≥ 32	≥ 32	≥ 32	≤ 0.25	≥ 32	1.5	6	128
LIBA-3129	449	32	0.125	≥ 256	≥ 256	≥ 256	≥ 32	≤ 0.25	128	2	8	≥ 256
LIBA-5719		64	0.094	≥ 256	≥ 32	≥ 32	≥ 32	≤ 0.25	NA	4	6	128
LIBA-5750		64	0.5	≥ 256	128	≥ 256	16	0.5	128	1	8	≥ 256
LIBA-5755		64	0.25	≥ 256	128	≥ 256	16	0.5	128	2	8	≥ 256
LIBA-5772		64	0.125	≥ 256	128	≥ 256	16	0.5	128	1	8	≥ 256
LIBA-6276		64	0.064	≥ 256	≥ 32	≥ 32	≥ 32	≤ 0.25	≥ 32	0.75	8	64
LIBA-5734	452	0.25	0.064	≥ 256	≥ 32	≥ 32	≥ 32	≤ 0.25	NA	4	12	64
LIBA-2945	487	64	0.094	≥ 256	≥ 32	≥ 32	≥ 32	0.5	> 32	3	8	128
LIBA-5763		64	0.5	≥ 256	≥ 256	≥ 256	16	≤ 0.25	128	0.5	8	≥ 256
LIBA-5769		128	0.5	≥ 256	≥ 256	≥ 256	32	≤ 0.25	≥ 32	2	2	≥ 256
LIBA-5770		128	0.5	≥ 256	≥ 256	≥ 256	16	≤ 0.25	≥ 32	1	4	≥ 256
LIBA-2992	488	64	0.5	≥ 256	128	≥ 256	16	0.5	≥ 32	1	8	≥ 256
LIBA-5761	489	0.5	0.094	≥ 256	128	≥ 256	16	≤ 0.25	128	1	6	128
LIBA-5762		0.25	0.125	≥ 256	128	≥ 256	16	≤ 0.25	128	1	6	≥ 256
LIBA-3145	558	64	0.25	≥ 256	≥ 256	≥ 256	≥ 32	≤ 0.25	128	1	6	≥ 256
LIBA-6285		1	0.064	≥ 256	≥ 32	≥ 32	≥ 32	≤ 0.25	≥ 32	0.75	8	64
LIBA-3144	578	32	0.125	≥ 256	≥ 256	≥ 256	≥ 32	≤ 0.25	128	2	8	≥ 256
LIBA-3150		32	0.047	≥ 256	≥ 256	≥ 256	≥ 32	≤ 0.25	128	1	8	128
LIBA-5436		32	0.19	≥ 256	≥ 256	≥ 256	≥ 32	≤ 0.25	16	2	12	≥ 256

^aTET, tetracycline; TIG, tigecycline; CLI, clindamycin; CIP, ciprofloxacin; LEV, levofloxacin; MOX, moxifloxacin; MET, metronidazole; RIF, rifampin; VAN, vancomycin; LIN, linezolid; CHL, chloramphenicol. MIC values that indicate resistance or diminished susceptibility are shown in boldface. MICs were obtained with Etests or macrodilution tests.

^bNA, not assayed.

Mutations in the DNA gyrase GyrA or GyrB and in RNA polymerase subunit B (RpoB) confer resistance to fluoroquinolones and rifampin, respectively. Our NAP_{CR1} isolates share the fluoroquinolone resistance mutation Thr82Ile in GyrA, in addition to the RpoB substitutions Arg505Lys and His502Asn, known to confer high levels of resistance to rifampin on epidemic strains of *C. difficile* (21). In this regard, it is tempting to speculate that the Thr82Ile mutation in GyrA contributed to the epidemic potential shown by the NAP_{CR1} strains when they caused an outbreak in 2009.

Although all strains possessed VanG-like sequences, most remained susceptible to vancomycin. The genomic and experimental results at hand indicate that all NAP_{CR1} isolates share the same *slpA* allele, but in the future, we aim to address the cell wall structure and antibiotic binding characteristics of these isolates in order to understand the lack of congruence between genotypic and phenotypic data.

With regard to chloramphenicol resistance, this antibiotic is not widely used in human medicine, although different phenicolos are used in animal farming (F. García, personal communication). It is not known at present whether animal- and farm-associated isolates of *C. difficile* from Costa Rica carry Tn4453 or *cat* genes in other molecular contexts.

TABLE 3 Mechanisms and molecular context of the antibiotic resistance of *Clostridium difficile* NAP_{CR1} isolates from Costa Rican hospitals

Smal pattern(s) (isolate)	Resistance-associated SNP ^a	Acquired resistance gene(s)	Molecular context of acquired resistance
442, 448, 449, 452, 447, ^b 488, 558, 578	<i>gyrA</i> (Thr82Ile) <i>rpoB</i> (His502Asn Arg505Lys)	<i>tetM</i> <i>ermB</i> <i>aacA-aphD</i> <i>catD</i> <i>ant6-sat4-aphA-3-cfr</i> -like gene	Tn5397 Tn5398 variant Tn4001 inserted into putative mobTn Tn4453a inserted into CD630-CTn2 and CD630-CTn5 Putative Tn916-like CTn-A ^c
489	<i>gyrA</i> (Thr82Ile) <i>rpoB</i> (His502Asn Arg505Lys)	<i>ermB</i> <i>aacA-aphD</i> <i>catD</i> <i>ant6-sat4-aphA-3-cfr</i> -like gene	Tn5398 variant Tn4001 inserted into putative mobTn Tn4453a inserted into CD630-CTn2 and CD630-CTn5 Putative Tn916-like CTn-A ^c
487	<i>gyrA</i> (Thr82Ile) <i>rpoB</i> (His502Asn Arg505Lys)	<i>tetM</i> <i>ermB</i> <i>catD</i> Putative bifunctional <i>aac-aph</i> <i>ant6-sat4-aphA-3-cfr</i> -like gene	Tn5397 Tn5398 variant Tn4453a inserted into CD630-CTn2 and CD630-CTn5 Phage-like element Putative Tn916-like CTn-B ^c
447 (LIBA-5701)	<i>gyrA</i> (Thr82Ile) <i>rpoB</i> (His502Asn Arg505Lys)	<i>tetM</i> <i>ermB</i> <i>aacA-aphD</i> <i>catD</i> <i>ant6-sat4-aphA-3</i>	Tn5397 Tn5398 variant Tn4001 inserted into putative mobTn Tn4453a inserted into CD630-CTn2 and CD630-CTn5 Putative Tn916-like CTn-C ^c

^aThe MDR strain *C. difficile* 630 was used as a reference.

^bData shown for Smal pattern 447 here apply to all isolates with this pattern except isolate LIBA-5701.

^cThree variants of a putative Tn916-like CTn carrying the *ant6-sat4-aphA-3* cluster (designated CTn-A, CTn-B, and CTn-C) were seen among the NAP_{CR1} strains.

The WGS of the isolates sequenced in this study, in addition to carrying genes known to confer resistance to antimicrobials used in clinical therapy, also carried genes conferring resistance to antimicrobials that are not used to treat *C. difficile* but are implicated in the development of CDI. This finding suggests either that lateral DNA transfer in this lineage is very active and is independent of strong selective pressure or that such resistance is maintained because it is coselected or offers other selective advantages. This is not unexpected, considering that *C. difficile* may be part of the human gut microbiota. For instance, the rRNA methyltransferase encoded by *cfr* modifies the 23S rRNA and thereby provides protection against phenicols, lincosamides, pleuromutilins, streptogramin A antibiotics, and selected 16-membered

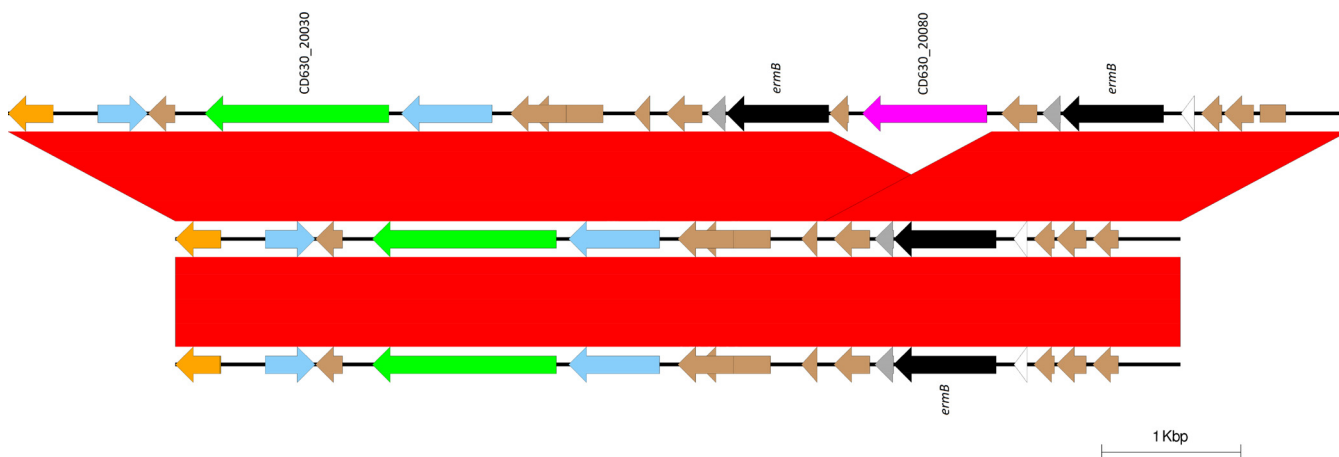


FIG 2 Relative to strain CD630 (top), the NAP_{CR1} isolates lost one copy of *ermB* and a gene coding for a hydrolase (purple) in Tn5398 (center). This variant is characteristic of strain CD630Δ*erm* (bottom). Arrows and arrowheads represent open reading frames. Black arrows represent *ermB* copies.

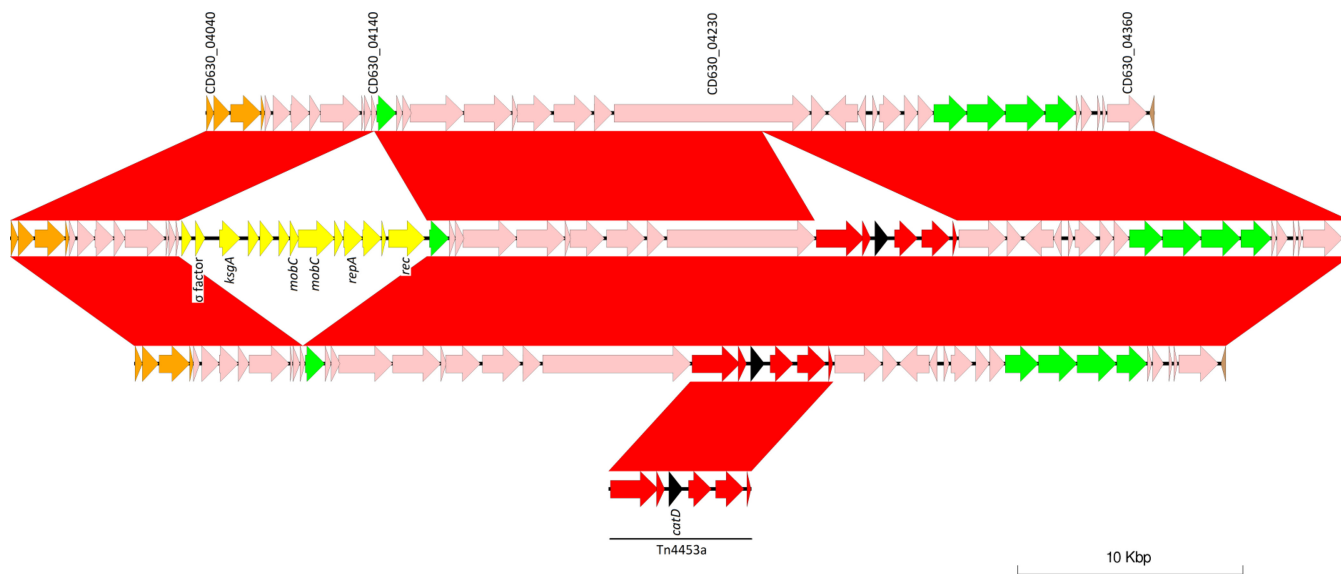


FIG 3 (Top) Two different variants of the CTn2 of strain CD630 were seen among the NAP_{CR1} isolates. (Center) In isolates with PFGE SmaI pattern 487, a mobilizable transposon with a putative 16S rRNA methyltransferase gene (*ksgA*) is inserted into CD630_04140 (yellow arrows and arrowheads). (Bottom) All of the NAP_{CR1} isolates carry a second copy of Tn4453a (red arrows), and therefore of *catD* (black arrow), inserted into homologues of the CD630_04230 helicase. *mobC*, DNA mobilization gene; *repA*, replication gene; *ksgA*, gene encoding rRNA methyltransferase; *rec*, recombinase gene.

macrolides (22). This gene has been found in Tn6218 in *C. difficile* (23). However, our NAP_{CR1} isolates, irrespective of their sensitivity to linezolid, carry a gene showing partial matches to *cfi* as part of a new Tn916-like element.

Notwithstanding the fact that aminoglycosides are not active against anaerobic bacteria, many NAP_{CR1} isolates have at least two copies of a bifunctional aminoglycoside-modifying enzyme (AME) with Aac(6') and Aph(2'') activities. This gene has already been seen in *C. difficile* as part of a novel family of transposons termed Tn6218 (24). However, we found two copies, each of which was inserted into an element that resembles a mobTn and contains Tn4001. Tn4001 was originally reported in *Staphylococcus aureus* but was later found in *Enterococcus* sp., *Enterococcus faecalis*, *Enterococcus faecium*, and *Staphylococcus epidermidis* strains from human guts (25). We found indirect evidence of

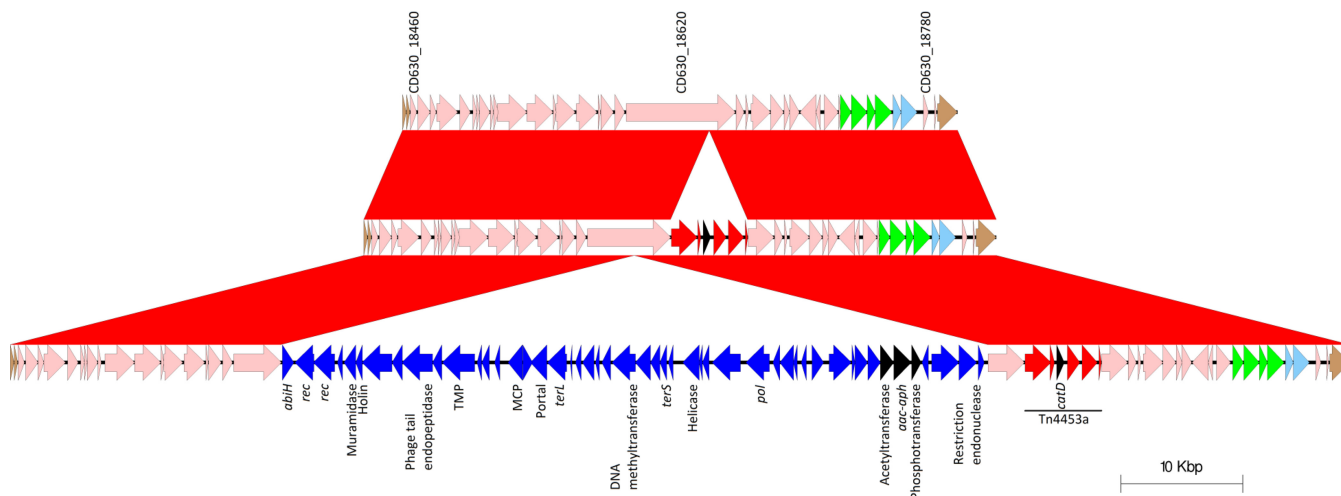


FIG 4 (Top) Two variants of the CTn5 of strain CD630 were seen among the NAP_{CR1} isolates. (Center and bottom) All isolates have the *catD* gene (black arrowhead) of Tn4453a (red arrows and arrowheads) inserted into homologues of the CD630_18620 helicase. In addition, isolates with PFGE SmaI pattern 487 have a phage-like sequence (blue arrows and arrowheads) disrupting the same helicase at another position (bottom). This phage-like element contains a cluster of three putative aminoglycoside resistance genes (black arrowheads), one of which seems to encode a bifunctional Aac-Aph enzyme. *abiH*, phage abortive infection gene; *rec*, recombinase gene; TMP, tail tape measure gene; MCP, major capsid; *terL*, terminase large-subunit gene; *terS*, terminase small-subunit gene; *pol*, DNA polymerase gene; *aac-aph*, genes encoding a bifunctional aminoglycoside acetyltransferase/phosphotransferase.

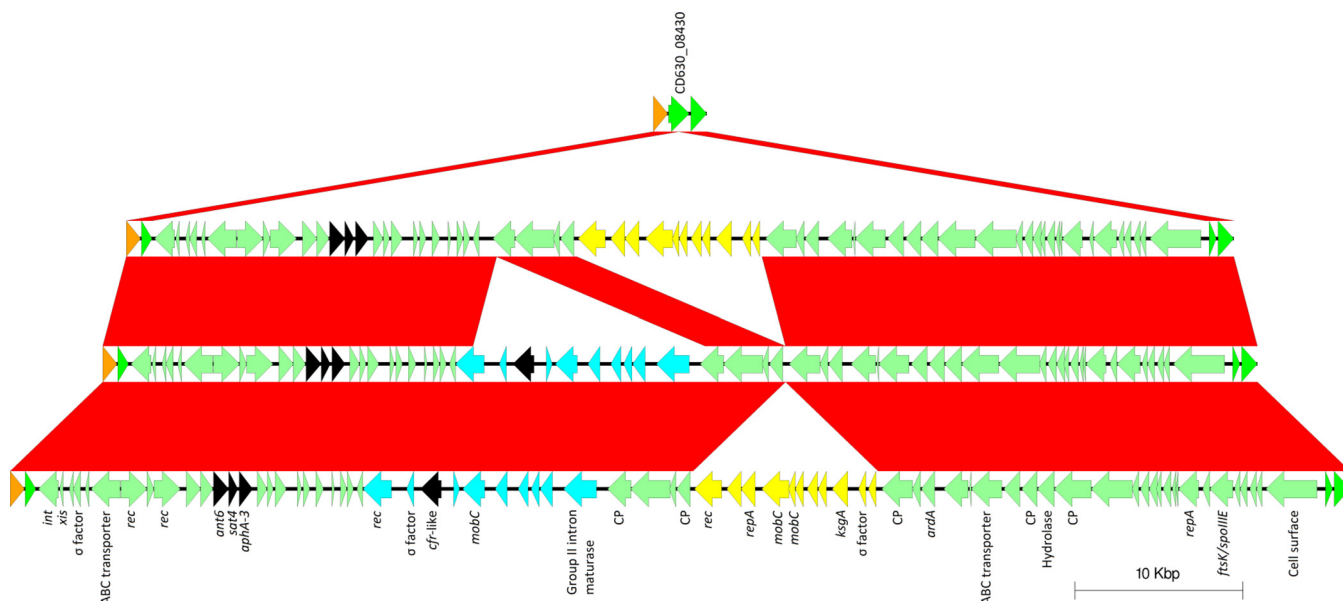


FIG 5 The NAP_{CR1} isolates have three variants of a composite Tn916-like element inserted into the putative group 1 glycosyltransferase CD630_08430 of strain CD630 (top). All three variants include an *ant6-sat4-aphA-3* aminoglycoside-streptothricin cluster (array of three black arrowheads). Two variants have a gene coding for a radical SAM enzyme showing partial matches to *cfr* in a putative mobilizable transposon (single black arrow within blue arrows and arrowheads). One of these also has the mobilizable transposon positive for the putative *ksgA* shown in Fig. 3 (yellow arrows and arrowheads), as does the variant without the *cfr*-like gene. The mobilizable transposon containing the *ksgA*-like gene is inserted into CTn2 in isolates with the PFGE Smal 487 pattern. *int*, gene encoding integrase; *xis*, gene encoding excisionase; *rec*, gene encoding recombinase; *mobC*, DNA mobilization gene; CP, conjugative gene; *repA*, replication gene; *ksgA*, gene encoding rRNA methyltransferase; *ardA*, antirestriction gene; *ftsK-spoIIIE*, DNA transporter gene.

its mobility in *C. difficile*. In a few NAP_{CR1} isolates, another allele for a bifunctional AME was seen in a putative phage as part of a gene array including genes with matches to other types of potential AMEs. This phage shows multiple features of the family *Siphoviridae* and is more closely related to phage from *Enterococcus* spp. than to cognates from *Clostridium* spp. (data not shown), suggesting that the NAP_{CR1} isolates

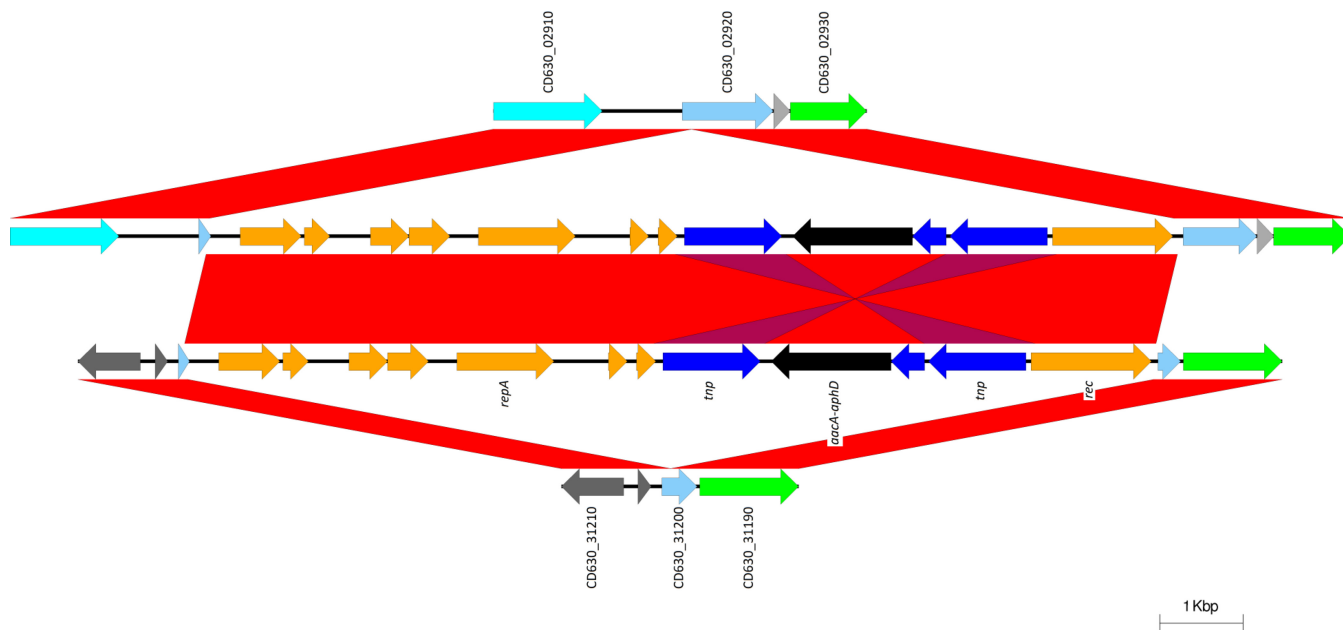


FIG 6 Except for isolates with PFGE Smal pattern 487, the NAP_{CR1} isolates have two copies of an uncharacterized MGE, each of which is inserted into a homologous gene of the putative transcriptional regulator CD630_02920 (top) or CD630_31200 (bottom). Along with other functions (orange arrows), this putative MGE includes a bifunctional *aacA-aphD* gene (black arrows) within Tn4001 (blue arrows). *repA*, replication gene; *tnp*, transposase-encoding gene; *rec*, recombinase-encoding gene.

actively exchange DNA with other intestinal *Firmicutes*. Although it has been shown that *C. difficile* phage can mediate the transduction of MGE containing AMR genes (26), if the NAP_{CR1} phage and its AME are indeed functional, this is the first report of a *C. difficile* phage with AMR genes.

The NAP_{CR1} isolates also have the aminoglycoside-streptothricin resistance gene cluster *ant6-sat4-aphA-3*, which characterizes staphylococci, *Campylobacter coli*, and *E. faecium* strains of different origins (27). In most staphylococci, the *ant6-sat4-aphA-3* array is integrated into Tn5405 (27). However, our isolates have this array inserted into a putative Tn916-like CTn related to CD630-CTn1. The chimeric nature of this composite element strongly suggests that its mobTn are functional.

In addition to these AMR genes, all of the NAP_{CR1} isolates carry three genes previously annotated in strain CD630 (14) as encoding a beta-lactamase (CD0458), a beta-lactamase regulatory protein (CD0470), and a beta-lactamase repressor (CD0471) (data not shown). Although these antibiotics are not regularly used to treat CDI, some of them clearly seem to lead to CDI (1).

In parallel to the NAP_{CR1} isolates, we performed this survey on one NAP2 strain, one NAP4 strain, one NAP6 strain, and five NAP1 strains that cocirculated in time and space. A principal-component analysis on this extended susceptibility data set clearly distinguished the profiles of NAP_{CR1} strains from those of the other genotypes (data not shown), highlighting the fact that the NAP_{CR1} strains are different. In agreement with this result, these non-NAP_{CR1} isolates lacked the MGE that characterized the NAP_{CR1} strains.

In summary, a phenotypic and genomic survey revealed that during the past decade, MDR was widespread among NAP_{CR1} isolates from various Costa Rican hospitals. This trait was due to a variety of resistance mechanisms, some of which are absent in the closely related MDR strain CD630 and also in cocirculating strains. Our results highlight the usefulness of comparative genomics in the epidemiological surveillance of antibiotic resistance, point to the need for further monitoring of circulating strains for early detection of metronidazole and vancomycin resistance, and justify further development of antibiotic-independent treatments for CDI.

MATERIALS AND METHODS

Strains and *C. difficile* isolation. A total of 38 NAP_{CR1} *C. difficile* isolates recovered from seven Costa Rican hospitals between 2003 and 2010 were studied (Table 1). These bacteria were taken from a collection maintained at the Anaerobic Bacteriology Research Laboratory of the University of Costa Rica. Without exception, they were derived from stool samples positive for *C. difficile* toxins as revealed by rapid immunochromatographic assays. For isolation, ethanol-treated samples were inoculated onto cefoxitin-cycloserine-fructose agar (CCFA; Oxoid) plates that were incubated under anaerobic conditions (90% N₂, 5% H₂, and 5% CO₂) in a Bactron II chamber. To confirm their identification, we used the Rapid ID 32A system (bioMérieux) based on preformed enzymes, a PCR targeting *tpi* (28), and, in some cases, determination of fatty acid methyl ester profiles through gas chromatography (MIDI, microbial identification system).

PFGE typing. The PFGE procedure followed was derived from a published protocol (12). Briefly, agarose plugs were prepared by mixing equal volumes of bacteria from 6- to 8-h cultures and SeaKem Gold agarose (Lonza) in 1 × Tris-EDTA buffer containing SDS (Sigma). These plugs were then incubated in a buffer composed of lysozyme, RNase A, and mutanolysin (Sigma). After overnight digestion with SmaI (Roche), DNA fragments were separated on 1% agarose gels (Bio-Rad) prepared with 0.5 × Tris borate-EDTA buffer and 50 μM thiourea (Sigma) using a CHEF-DR II system (Bio-Rad). Digitized images were analyzed with BioNumerics software (version 6.0; Applied Maths), and the resulting macrorestriction patterns were compared with those deposited in the databases of the National Microbiology Laboratory (Public Health Agency of Canada).

Antimicrobial susceptibility testing. The MICs of tetracycline (resistance breakpoint, ≥16 mg/liter), tigecycline (≥0.25 mg/liter), clindamycin (≥8 mg/liter), cefotaxime (≥64 mg/liter), ciprofloxacin (≥8 mg/liter), levofloxacin (≥8 mg/liter), moxifloxacin (≥8 mg/liter), metronidazole (≥32 mg/liter), rifampin (≥0.004 mg/liter), chloramphenicol (≥32 mg/liter), vancomycin, and linezolid were determined using Etests (bioMérieux) or macrodilution tests. These assays were repeated 2 to 3 times using independent cultures. Resistance breakpoints were set in compliance with Clinical and Laboratory Standards Institute guidelines (29) or EUCAST epidemiological cutoff values (30), when available. For vancomycin and linezolid, we categorized MICs between 4 and 8 mg/liter as indicating reduced susceptibility (31). Isolates for which linezolid MICs were >8 mg/liter were categorized as resistant. For ciprofloxacin, we used the breakpoint defined for other fluoroquinolones. According to standardized international terminology (32), MDR was defined as acquired nonsusceptibility to at least one agent in each of three or more

antimicrobial classes. The panel of antibiotics tested included drugs used in the treatment of CDI (tigecycline), the development of CDI (expanded-spectrum fluoroquinolones), front-line treatments (metronidazole, vancomycin), and alternative treatments for CDI (linezolid) and CDI relapses (rifampin).

Whole-genome sequencing and genomic analyses. WGS for 31 isolates were obtained by sequencing by synthesis using multiplexed paired-end libraries (see Table S1 in the supplemental material). Reads were first assembled into contigs using Velvet (33) or Edena (34) and were then mapped back to assembly contigs to check for misassemblies. Single nucleotide polymorphisms (SNPs) were identified using Burrows-Wheeler alignment (BWA) (35), SAMtools (36), BCFtools (37), and the genome of the MDR reference strain CD630 (NCBI nucleotide accession number [AM180355.1](https://doi.org/10.1093/nar/am180355.1)). For automated annotation, we used Prokka, version 1.11 (38), and proprietary databases containing publicly available *C. difficile* genomes from reference strains. If required, annotations were refined manually using BLAST, BLASTP, PSI-BLAST, BYPASS, PRODOM, SMART, and UniProt searches. Contig files were scanned against *C. difficile* PubMLST typing schemes using multilocus sequence typing (MLST) (39). AMR genes were identified manually, with ABRICATE and SRST2 (40), or through BLAST/BLAT searches against the CARD (41), ARDB (42), and ARG-ANNOT (43) databases. Putative lateral gene transfer events were predicted using Alien Hunter (44), PhiSpy (45), or ICEberg (46) and were verified through visual inspection of contigs ordered with Mauve (47). Core genome SNP phylogenies were done with Parsnp (48) using the genomes of the following strains: CD630 (NCBI nucleotide accession number [AM180355.1](https://doi.org/10.1093/nar/am180355.1)), 2007855 ([FN665654.1](https://doi.org/10.1093/nar/fn665654.1)), LIBA-5703 (EBI-ENA accession number [ERR467551](https://doi.org/10.1093/ebi-ena/err467551)), LIBA-5710 ([ERR467558](https://doi.org/10.1093/ebi-ena/err467558)), R20291 (NCBI nucleotide accession number [FN545816.1](https://doi.org/10.1093/nar/fn545816.1)), CD196 ([FN538970.1](https://doi.org/10.1093/nar/fn538970.1)), BI1 ([FN668941.1](https://doi.org/10.1093/nar/fn668941.1)), OX1485 (EBI-ENA accession number [ERR232375](https://doi.org/10.1093/ebi-ena/err232375)), Ox2183 ([ERR126286](https://doi.org/10.1093/ebi-ena/err126286)), M68 (NCBI nucleotide accession number [FN668375.1](https://doi.org/10.1093/nar/fn668375.1)), CF5 ([FN665652.1](https://doi.org/10.1093/nar/fn665652.1)), M120 ([FN665653.1](https://doi.org/10.1093/nar/fn665653.1)), CD10-165 ([JRHN00000000.1](https://doi.org/10.1093/nar/jrhn00000000.1)), and SA10-050 ([JRHM00000000.1](https://doi.org/10.1093/nar/jrhm00000000.1)). All genomes and genome comparisons were visualized in Artemis (49) or ACT (50). Linear comparison figures of multiple genomic loci were prepared with Easyfig (51).

Accession number(s). Sequencing data may be downloaded from the European Nucleotide Archive (study [PRJEB5034](https://doi.org/10.1093/euclid/prjeb5034)). The corresponding EBI-ENA accession numbers are [ERR467530](https://doi.org/10.1093/ebi-ena/err467530), [ERR467534](https://doi.org/10.1093/ebi-ena/err467534), [ERR467536](https://doi.org/10.1093/ebi-ena/err467536), [ERR467538](https://doi.org/10.1093/ebi-ena/err467538), [ERR467539](https://doi.org/10.1093/ebi-ena/err467539), [ERR467541](https://doi.org/10.1093/ebi-ena/err467541) to [ERR467547](https://doi.org/10.1093/ebi-ena/err467547), [ERR467550](https://doi.org/10.1093/ebi-ena/err467550), [ERR467552](https://doi.org/10.1093/ebi-ena/err467552), [ERR467555](https://doi.org/10.1093/ebi-ena/err467555), [ERR467559](https://doi.org/10.1093/ebi-ena/err467559), [ERR467565](https://doi.org/10.1093/ebi-ena/err467565), [ERR467569](https://doi.org/10.1093/ebi-ena/err467569), [ERR467578](https://doi.org/10.1093/ebi-ena/err467578), [ERR467581](https://doi.org/10.1093/ebi-ena/err467581), [ERR467586](https://doi.org/10.1093/ebi-ena/err467586) to [ERR467588](https://doi.org/10.1093/ebi-ena/err467588), [ERR467592](https://doi.org/10.1093/ebi-ena/err467592), [ERR467594](https://doi.org/10.1093/ebi-ena/err467594) to [ERR467596](https://doi.org/10.1093/ebi-ena/err467596), [ERR467601](https://doi.org/10.1093/ebi-ena/err467601), [ERR467602](https://doi.org/10.1093/ebi-ena/err467602), [ERR467607](https://doi.org/10.1093/ebi-ena/err467607), and [ERR467610](https://doi.org/10.1093/ebi-ena/err467610) (Table S1).

SUPPLEMENTAL MATERIAL

Supplemental material for this article may be found at <https://doi.org/10.1128/AAC.02054-16>.

SUPPLEMENTAL FILE 1, PDF file, 0.1 MB.

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We declare that we have no competing interests.

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