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## Identification of *Clostridium difficile* RT078 From Patients and Environmental Surfaces in Zhejiang Province, China

To the Editor—*Clostridium difficile* has been a predominant cause of nosocomial diarrhea in North America and Europe, especially after the emergence of PCR-ribotypes 027 and 078. However, less emphasis is placed on the surveillance and control of *C. difficile* infection (CDI) in China. Li et al<sup>1</sup> isolated a novel binary toxin strain of *C. difficile* from a hospitalized

TABLE 1. The Incidence of the Binary Toxin-Positive Strains of *C. difficile* in Three Tertiary Hospitals

Hospital	Clinical Patients		Environmental Surfaces	
	No. of Isolates	No. of Binary Toxin-Positive Strains (%)	No. of Isolates	No. of Binary Toxin-Positive Strains (%)
A	33	0 (0)	2	0 (0)
B	9	2 (22)	3	1 (33)
C	19	2 (11)	32	3 (9)
Total	61	4 (7)	37	4 (11)

patient and mentioned that cases of ribotype 078 had not previously been reported in China. Here, we report 8 isolates that were identified as *C. difficile* ribotype 078 in a surveillance program in Zhejiang Province, China.

Our study was conducted at 3 tertiary hospitals (hospitals A, B, and C) from June 2013 to December 2014. A total of 98 unduplicated isolates of *C. difficile* from 61 clinical patients and 37 environmental surfaces were identified. A multiple polymerase chain reaction (multi-PCR) assay was used to amplify 16S rDNA, *tcdA*, *tcdB*, *cdtA*, and *cdtB* genes. The overall incidence of binary toxin-positive strains was 8.2%; 4 isolates (7%) were collected from patients, and 4 (11%) isolates were collected from environmental surfaces (Table 1). In hospital B, 2 (22%) of the detected binary toxin strains were obtained from patients and 1 strain (33%) was isolated from an environmental surface. In hospital C, 2 strains (11%) were identified from patients and 3 strains (9%) were obtained from environmental surfaces. No hyper-toxigenic strain was detected in hospital A. According to the *tcdC* gene sequence, all 8 isolates were identified as ribotype 078, with a mutation point at position 184 and a  $\Delta 39$ -bp deletion (Figure 1).

Previously, a few Asian countries and regions have reported the emergence of *C. difficile* ribotype 078, including Kuwait,<sup>2</sup> South Korea,<sup>3</sup> Iran,<sup>4</sup> Japan,<sup>5</sup> and Taiwan.<sup>6</sup> The present study is the first to identify ribotype 078 cases not only from patients but also from environmental surfaces in China. Compared with neighboring Japan and Korea, the prevalence of CDI in China remains unclear, mainly due to a lack of awareness in the healthcare system.<sup>7</sup> Many clinicians are accustomed to diagnosing patients with antibiotic-associated diarrhea by experience rather than by the results of stool cultures. In addition, although enzyme-linked immunosorbent assay (ELISA) has been used routinely to detect *C. difficile* in most tertiary hospitals in China, this method has a low sensitivity and does not trace the binary toxin strain. For these reasons, CDI, especially CDI caused by binary-toxin strains, may be severely underestimated in China.

China has the largest population with the trend of aging accompanied by antibiotic misuse, indicating the potential for epidemics of CDI. Medical practitioners should pay more attention to this global infection, as both *C. difficile* ribotypes

	151		STOP CODE	200
VPI10463	TGTTCTGAAG	ACCATGAGGA	GGTCATTTCT	AACCAAACAT CAGTTATAGA
6-7	TGTTCTGAAG	ACCATGAGGA	GGTCATTTCT	AATTAACAT CAGTTATAGA
14-69	TGTTCTGAAG	ACCATGAGGA	GGTCATTTCT	AATTAACAT CAGTTATAGA
N9	TGTTCTGAAG	ACCATGAGGA	GGTCATTTCT	AATTAACAT CAGTTATAGA
	201			250
VPI10463	TTCTCAAAAA	ACAGAAATAG	AAACTTTAAA	TAGCAAATTG TCTGATGCTG
6-7	TTCTCAAAAA	ACAGAAATAG	AAACTTTAAA	TAGCAAATTG TCTGATGCTG
14-69	TTCTCAAAAA	ACAGAAATAG	AAACTTTAAA	TAGCAAATTG TCTGATGCTG
N9	TTCTCAAAAA	ACAGAAATAG	AAACTTTAAA	TAGCAAATTG TCTGATGCTG
	251			300
VPI10463	AACCATGGTT	CAAAATGAAA	GACGACGAAA	AGAAAGCTAT TGAAGCTGAA
6-7	AACCATGGTT	CAAAATGAAA	GACGACGAAA	AGAAAGCTAT TGAAGCTGAA
14-69	AACCATGGTT	CAAAATGAAA	GACGACGAAA	AGAAAGCTAT TGAAGCTGAA
N9	AACCATGGTT	CAAAATGAAA	GACGACGAAA	AGAAAGCTAT TGAAGCTGAA
	301			350
VPI10463	AATCAACGTA	AAGCTGAAGA	AGCTAAAAAA	GCTGAAGAAG CTAAAAAGGC
6-7	AATCAACGTA	AAGCTGAAGA	AGCTAAAAAG	GCT-----
14-69	AATCAACGTA	AAAAAGAAGA	AGCTAAAAAG	GCT-----
N9	AATCAACGTA	AAGCTGAAA	AGCTAAAAAG	GCT-----
	351			400
VPI10463	TGAAGAACAA	CGCAAAAAAG	AAGAAGAGGA	GAAGAAAGGA TATGATACTG
6-7	-----	-----	--GAAGAAGA	GAAGAAAGGA TATGATACTG
14-69	-----	-----	--GAAGAAGA	GAAGAAAGGA TATGATACTG
N9	-----	-----	--GAAGAAGA	GAAGAAAGGA TATGATACTG

FIGURE 1. *tcdC* gene sequences of *C. difficile* ribotype 078 isolates in the study. A point mutation at position 184 and  $\Delta$ 39-bp deletion compared with wild-type strain VPI 10463 are shown.

027 and 078 have been identified in China. Routine fecal culture methods and multicenter surveillance should be introduced in hospitals to estimate the incidence of CDI and to confirm the dominant *C. difficile* strains in China.

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