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Molecular epidemiology of toxigenic *Clostridium difficile isolates* in Korea

To the Editor

Clostridium difficile infection (CDI) is the commonest cause of nosocomial diarrhoea and pseudomembranous colitis [1, 2]. In their interesting article on the first nationwide study of CDI in Korea, Kim *et al.* provided an insight into the clinical characteristics of CDI in Korea [1]. In laboratory aspects of this infection, PCR ribotyping of *C. difficile* has emerged as a useful molecular tool, as it provides information about antibiotic resistance and disease severity (PCR ribotype 027), as well as helping to identify linkages and optimize management of disease outbreaks [3]. In our study of toxigenic *C. difficile* in Korea, we investigated the PCR ribotypes and molecular characteristics of toxigenic *C. difficile* strains isolated in a Korean hospital between October 2010 and October 2011. A toxigenic strain was defined as showing at least one positive result in an enzyme immunoassay (VIDAS *C. difficile* Toxin A & B assay, bioMérieux, France), in in-house PCR for toxins A and B, and in real-time PCR (AdvanSure CD real-time PCR kit, LG Lifesciences, Korea). From 442 clinical specimens of diarrheal stools tested for *C. difficile*, 67 toxigenic strains were identified. The remaining specimens were stored at –70 °C until required for PCR ribotype analysis, as described previously [2]. Some of these 67 toxigenic strains were included in our previous studies [4].

Table 1 shows the PCR ribotype profiles of the 67 toxigenic *C. difficile* strains showing 10 different kinds of PCR ribotypes. Ribotype 018 was the most prevalent (21/67). In previous studies, about half of the *C. difficile* strains in Korea comprised three dominant PCR ribotypes, i.e. 018, 017, and 014, while the other half comprised a broad spectrum of ribotypes. PCR ribotype 001, which is the prevalent type in Europe, was not identified in Korea in either study, whereas PCR ribotype 014 was one of the dominant strains, as in Western countries and other regions of east Asia [2, 5]. In this study, there was no PCR ribotype 027, a representative hypervirulent type. In addition, binary toxin was detected in three isolates (3/67, 4·5%) with PCR ribotypes 122, C24, and C25. Although the incidence of binary toxin in this study was slightly lower than in the previous

Table 1. *Molecular characteristics of 67 toxigenix* C. difficile *strains in this study*

Ribotypes (*n*, %)	Toxin A/B	Binary toxin gene
018* (21, 31·3%)	+/+	—
014* (12, 17·9%)	+/+	—
017* (6, 9·0%)	Partial deletion‡/+	—
015 (4)	+/+	—
159 (4)	+/+	—
012 (3)	+/+	—
163 (3)	+/+	—
002 (1)	+/+	—
106 (1)	+/+	—
122 (1)	+/+	*cdtA*(+), *cdtB*(+)
AB29† (3)	+/+	—
AB27† (2)	+/+	—
AB25† (2)	+/+	—
AB7† (1)	+/+	—
AB52† (1)	+/+	—
C24† (1)	+/+	*cdtA*(+), *cdtB*(+)
C25† (1)	+/+	*cdtA*(+), *cdtB*(+)

* These three dominant ribotypes account for 58·21% of the toxigenic *C. difficile* strains in this study.
† These findings are described using the nomenclature of Kim *et al.* [2].
‡ All six ribotype 017 strains had a 700-bp deletion in the toxin A gene.

report, we can reconfirm that isolates expressing binary toxin are not rare in Korea [2]. A partially deleted toxin A gene that could not be amplified using commercial real-time PCR was detected in six specimens (8·96%), which were all PCR ribotype 017 known to be prevalent in east Asia [4, 5]. We therefore suggest that any PCR ribotype 017 strain described as toxin A negative and B positive be examined carefully to confirm whether it really lacks the toxin A gene or has a partially deleted toxin A gene that is not detected with commercial kits, as shown here [4]. These accumulating clinical and laboratory data suggest that proper surveillance systems are needed to monitor and control this important infectious disease in Korea.

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DECLARATION OF INTEREST

None.

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