Surveillance of GES-5 carbapenemase producing organisms in northern Osaka, Japan

Akira Ukimura¹, Yuriko Shibata¹, Tomoyuki Yamada¹, Fumio Goto¹, Toyofumi Nakanishi 1,2, Yukimasa Ooi¹, Takashi Nakano¹
1. Osaka Medical College; Infection Control Center, 2. Osaka Medical College; Department of Clinical and Laboratory Medicine

Introduction

In Japan, cooperation among hospitals on infection control has been incentivized through additional reimbursement by the universal health insurance policy since 2012. We organized Hokusetsu Infection Control Network including 8 large well-resourced hospitals and 16 small-sized hospitals in north part of Osaka in 2012, supported by local public health centers. Multidrug-resistance Pseudomonas aeruginosa (MDRP) outbreak developed in long-term care facilities (LTCF) with 225 beds and six wards in our network. We succeeded control the first outbreak of bla₅GES producing MDRP in Japan by a range of enhanced infection control measures which were supported by local public health centers and National Institute of Infectious Diseases in Japan (1).

Purpose

As this is the first identification of GES-5 in Japan (1), we performed surveillance of GES-5 carbapenemase producing organism in our network.

Methods

Whenever carbapenem-resistant Gram-negative organism (pseudomonas aeruginosa or Enterobacteria) was cultured from a hospital in our network, we performed a multiplex polymerase chain reaction (PCR) to screen for carbapenemase genes, blaGES, blaOXA-48-like, blaIMP, blaVIM, and blaKPC in Osaka Medical College Hospital (2) (Figure 1).

Results

A total of 23 MDRP cases were identified in LTCF, and both infection and colonization were included in the case. These isolates were found to be negative in combined disc tests for MBL and KPC production (6,7). The MDRP isolates from 11 patients in LTCF were found to be indistinguishable or closely related by pulsed-field gel electrophoresis, and harboured the blaGES-5 gene.

Pulse field gel electrophoresis was performed with SpeI restriction enzyme (3). The blaGES-like genes were amplified with the GES-1F (50-ATGGCTTATTCCGC-30) and Multi GES rev (50-TTTTGCTTCG GTCAAAGAT-30) primers using standard PCR conditions (2). The amplified fragments were sequenced with an ABI 3130 Genetic Analyzer (Life Technologies, Carlsbad, CA, USA). The 826 bp sequence data (with primer sequences omitted) were analysed using the BLAST program against the GenBank database. The aac(6')-like genes, an aminoglycoside-resistant gene, were detected using PCR (4). We used effective molecular epidemiological technique based on the open-reading frame (ORF) distribution patterns detected by PCR to perform molecular epidemiological analysis of Pseudomonas aeruginosa, which is called PCR-based ORF typing (POT) (5). The present investigation was conducted as part of a public health response to an outbreak. Neither informed consent from patients nor bioethical review was required from the associated institutions.

The aacA4 genes, an aminoglycoside-resistant gene, were also detected from MDRP isolates in LTCF (4). The PCR-amplified blaGES sequences had 100% identity with blaGES in the Genbank.

Next, we analyzed 29 isolates (Pseudomonas aeruginosa: 16, Escherichia coli: 6, Klebsiella pneumonia: 3, Klebsiella oxytoca: 2, Enterobacter cloacae: 1 and Citrobacter koseri: 1), and we detected blaIMP in 6 isolates (Pseudomonas aeruginosa: 2, Escherichia coli: 3 and Klebsiella pneumonia: 2) in our network. We did not detect blaGES (Fig. 2) DNA type of MDRP was different from MDRP producing blaGES-5 in LTCF by POT method (Fig. 3).

Discussion

GES-5 has been reported worldwide as a carbapenemase harbouring Klebsiella pneumoniae, Escherichia coli, and Pseudomonas aeruginosa, however prior to the outbreak in LTCF, only GES-3 and GES-4 had been detected in Klebsiella pneumoniae in Japan.

Conclusion

There was no epidemiological link of blaGES-5 in other hospitals and blaIMP is common in our network. Cooperation among the hospitals of our network for controlling infectious diseases appeared to be effective in monitoring multi-drug-resistant organisms and reducing the risk of imported infections.

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References
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Conflict of interest

Akira Ukimura received research funding from Pfizer Japan Inc.

Akira Ukimura MD. PhD. Osaka Medical College 2-7 Daigaku-machi, Takatsuki 569-8686, Japan. E-mail: in3011@osaka-med.ac.jp