P0701 Surveillance of GES-5 carbapenemase producing organisms in northern Osaka, Japan

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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 ling-term care facilities (LTCF) with 225 beds and six wards in our network. We succeeded control the first outbreak of bla_{GES-5} 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 Enterobacteriae) was cultured from a hospital in our network, we performed a multiplex polymerase chain reaction (PCR) to screen for carbapenemase genes, bla_{GES}, $bla_{OXA-48-like}$, bla_{IMP}, bla_{VIM}, and bla_{KPC} in Osaka Medical College Hospital (2) (Figure 1).

Pulse field gel electrophoresis was performed with *Spe*I restriction enzyme (3). The blaGES-like genes were amplified with the GES-1f (50-ATGCGCTTCATTCACGC-30) and Multi GES rev (50-TTTGTCCGT GCTCAGGAT-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 .

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 bla_{GES-5} gene.

The *aacA4* genes, an aminoglycoside-resistant gene, were also detected from MDRP isolates in LTCF (4). The PCR-amplified bla_{GES} sequences had 100% identity with bla_{GES-5} in the Genbank.

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

Figure 1

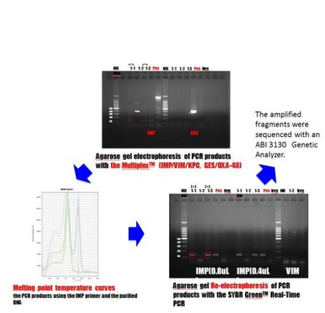


Figure 2

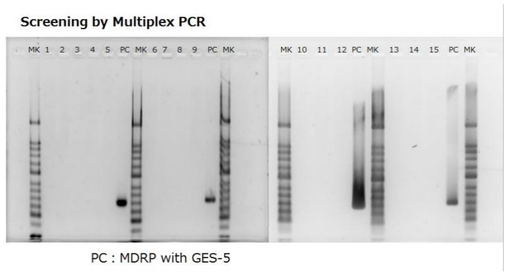
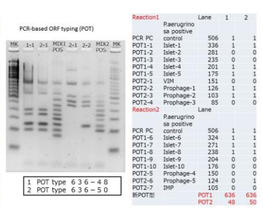


Figure 3

POT analysis of *Pseudomonas aeruginosa*

NO.	POT1	POT2	POT NO.
POT-PA-001	55	0	55-0
POT-PA-002	644	41	644-41
POT-PA-003	644	41	644-41
POT-PA-004	207	26	207-26
POT-PA-005	207	26	207-26
POT-PA-006	207	26	207-26
POT-PA-007	207	26	207-26
POT-PA-008	207	26	207-26
POT-PA-009	207	26	207-26
POT-PA-015	573	16	573-16
POT-PA-016	207	26	207-26
POT-PA-017	207	26	207-26
POT-PA-018	207	26	207-26
POT-PA-019	207	26	207-26
POT-PA-020	380	56	380-56
POT-PA-021	894	0	894-0
POT-PA-022	58	0	58-0
GES-5 (+)MDRP	207	56	207-56



Discussuion

GES-5 has been reported worldwide as a carbapenemase harboured by *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 bla_{GES-5} in other hospitals and bla_{IMP} 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.

Acknowledgements

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References

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Conflict of interest

Akira Ukimura received research funding from Pfizer Japan Inc.

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