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Paper Poster Session

Emergence and worldwide outbreaks of carbapenemase-producing bacteria

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

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Background: In Japan, cooperation among hospitals for infection control has been incentivized through additional subsidies from the universal health insurance system since 2012. With support from local public health centers, we established the Hokusetsu Infection Control Network comprising eight large well-resourced hospitals and 17 small hospitals in northern Osaka in 2012. An outbreak of multidrug-resistance *Pseudomonas aeruginosa* (MDRP) occurred in the long-term care facilities (LTCF) of our network in 2013. We succeeded in controlling the first outbreak of *bla*_{GES-5}-producing MDRP in Japan by implementing a range of enhanced infection control measures, which were supported by local public health centers, Osaka Prefectural Institute of Public Health, and the National Institute of Infectious Diseases in Japan.

Materials/methods: As this was the first time GES-5 had been identified in Japan, we performed surveillance of GES-5 carbapenemase-producing organisms in our network from Feb. 2015. Whenever a carbapenem-resistant Gram-negative organism (*P. aeruginosa* or Enterobacteriaceae) was cultured from a hospital in our network, we subsequently performed multiplex polymerase chain reaction (PCR) to screen for carbapenemase genes, i.e., *bla*_{GES}, *bla*_{OXA-48-like}, *bla*_{IMP}, *bla*_{VIM}, and *bla*_{KPC}, at Osaka Medical College Hospital. Pulsed-field gel electrophoresis was performed with the *SpeI* restriction enzyme, and PCR-based open reading frame DNA typing was also performed.

Results: A total of 23 MDRP cases were identified in the LTCF, and the isolates from 11 patients were found to be indistinguishable or closely related by pulsed-field gel electrophoresis; the MDRP of these patients harbored the *bla*_{GES-5} gene. The PCR-amplified *bla*_{GES} sequences had 100% identity to the sequence of *bla*_{GES-5} in Genbank. GES-5 has been reported worldwide as a carbapenemase in *Klebsiella pneumoniae*, *Escherichia coli*, and *P. aeruginosa*; however, prior to the outbreak in the LTCF, only GES-3 and GES-4 had been detected in *K. pneumoniae* in Japan. We analyzed 29 isolates (*P. aeruginosa*: 16, *E. coli*: 6, *K. pneumoniae*: 3, *Klebsiella oxytoca*: 2, *Enterobacter cloacae*: 1, and *Citrobacter koseri*: 1) from hospitals other than the LTCF, and we detected *bla*_{IMP} in 7 isolates (*P. aeruginosa*: 2, *E. coli*: 3, and *K. pneumoniae*: 2); however, none of the other carbapenemase genes were detected. The genetic type of the MDRP found in the other hospitals was different from that of the *bla*_{GES-5}-producing MDRP found in the LTCF.

Conclusions: There was no epidemiological link between the *bla*_{GES-5}-producing MDRP found in the LTCF and carbapenem-resistant Gram-negative organisms in other hospitals in northern Osaka, Japan. We detected only *bla*_{IMP}-producing organisms in other hospitals of 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.