

### Application of Next-Generation Sequencing in Public Health —Analysis of NDM-5-Carrying Bacteria, 2014–2017

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#### Abstract

Next-Generation Sequencing(NGS) has the advantage of high throughput sequence capacity which provides information on unlimited pathogen targets, resistance genes, as well as outbreak surveillance. In this study, we applied NGS for epidemiological surveillance on the bacterial antimicrobial resistance. From 2014 to 2017, 8 carbapenem-resistant *Enterobacteriaceae* (CRE) isolates carrying NDM-5 were identified and originated from 2 hospitals in northern Taiwan (HH and TH) and 1 from a hospital in southern Taiwan (CH), respectively. Among them, 5 isolates from HH hospital had high similarity in PFGE phylogenetic analysis, similar plasmid replicon type and size and identical NDM-5-containing contigs. Taken together, these 5 isolates were considered as epidemiologically related strains. Two isolates from TH hospital had lower similarity in PFGE phylogenetic analysis, differences in plasmid types and size. However, the NDM-5-containing contigs were identical, presumably due to the insertion sequence IS26 which is responsible to transmission of the antimicrobial-resistance genes. As of the isolate from CH hospital, the sequence of its NDM-5-containing plasmid was similar to the internationally epidemic NDM-5 plasmid,

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indicating that the plasmid might be imported. This study shares the vision on the use of NGS to provide the CRE antimicrobial-resistance information and benefit the epidemiological surveillance in the future. We recommended that CRE in Taiwan should be monitor continuously to follow the distribution and trends of antimicrobial resistant bacteria.

**Keywords:** Next-generation sequencing, NGS, CRE, NDM-5, IS26