Clonal diversity of \textit{Acinetobacter baumannii} clinical isolates in Myanmar: identification of novel ST1407 harbouring bla\textit{NDM-1}

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Abstract

Recent \textit{Acinetobacter baumannii} clinical isolates in a teaching hospital in Myanmar comprised three major sequence types (ST2, ST16 and ST23) and two sporadic STs, showing a high resistance rate to carbapenem associated with \textit{blaOXA-23}. The NDM-1 encoding gene was identified in only one isolate exhibiting novel ST1407 (a triple-locus variant of ST16). © 2021 The Author(s). Published by Elsevier Ltd.

Keywords: \textit{Acinetobacter baumannii}, Myanmar, NDM-1, OXA-23, ST

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\textit{Acinetobacter baumannii} is opportunistic pathogen with a remarkable capacity to acquire antimicrobial resistance. Global spread of carbapenem-resistant \textit{A. baumannii} has been noted as a public health concern since 2000 as a result of intra- and inter-hospital dissemination and international transfer of resistant strains [1]. According to the Institute Pasteur scheme of multilocus sequence typing (MLST) [2], sequence type (ST) 2 is considered to be the predominant clone with carbapenem resistance globally [1,2], while other STs such as ST10, clonal complex (CC) 32 and ST589 (CC1) were also described as major lineages, depending on the country [3–5]. In Myanmar, only limited information is available regarding the clonal lineage of \textit{A. baumannii} responsible for carbapenem resistance in medical settings.

From January to November 2018, a total of 1270 bacterial isolates were recovered from clinical specimens as putative causes of infectious diseases in North Okkalapa General and Teaching Hospital, Yangon, Myanmar. Gram-negative bacteria accounted for 80.6% (1023 isolates), with \textit{Klebsiella pneumoniae} being dominant, followed by \textit{Escherichia coli}. Forty isolates (3.1%) were identified as \textit{Acinetobacter} species by biochemical test kit (API 20NE strip; bioMérieux), among which 25 isolates were genetically confirmed to be \textit{A. baumannii} by PCR detection of \textit{blaOXA-51}\textsubscript{L}-like gene [6] and sequencing of \textit{cpn60} (one MLST locus) [2]. The most common specimen associated with \textit{Acinetobacter} spp. was sputum, followed by wound swab and urine (Supplementary Table S1). Most \textit{Acinetobacter} spp. isolates were derived from male patients of older age (>$40$ years) (Supplementary Table S2).

Antimicrobial susceptibility of \textit{A. baumannii} was measured by broth microdilution test, and ST was determined as per the Institute Pasteur scheme [2]. Carbapenemase genes were detected and typed as described previously [7–9]. Nucleotide sequences of the \textit{blaOXA-51}\textsubscript{L} family were determined by PCR direct sequencing using primers designed in this study (Supplementary Table S3).

Among 25 \textit{A. baumannii} isolates, five STs were identified (Table 1), including three common STs (ST2, ST16 and ST23) and two novel STs (ST1406 and ST1407). We identified five different genotypes of the \textit{blaOXA-51}\textsubscript{L} family, which were correlated with each of the five STs. \textit{blaOXA-23} was detected in all the isolates except ST23 (detection rate, 72%), and \textit{blaNDM-1} was identified in a single isolate of ST1407. Resistance rate to carbapenem was 76%, although a lower rate was found for ST23 isolates than other STs.

A recent study of \textit{A. baumannii} clinical isolates in Myanmar described the dominance of ST2 (50%), high prevalence of \textit{blaOXA-23} (87%) and detection of \textit{blaNDM-1} in four STs (ST1, ST16, ST23 and ST109) [10]. However, in spite of the low number of isolates obtained in our study, ST2 was not dominant but rather showed isolation frequency similar to ST16 and ST23. A novel ST1407, which was assigned to one isolate harbouring \textit{blaNDM-1}, was sporadic type but a triple-locus variant of ST16 as well as ST1480. While being a minor lineage of \textit{A. baumannii}, ST16 was found in the Netherlands, the United States, Malaysia and Thailand [2,11]. ST1480 was registered as an isolate in Thailand (strain ID 4657; PubMLST, at https://pubmlst.org/). Accordingly, ST16-related clones were suggested to be potentially prevalent in South-East Asian
countries and responsible for carbapenem resistance carrying blaNDM-1. Further epidemiologic surveillance of A. baumannii and its carbapenem resistance may be necessary, particularly on ST16-related lineage in Myanmar and neighbouring countries.

Conflict of interest

None declared.

Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.nmni.2021.100847.

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