Clonal diversity of *Acinetobacter baumannii* clinical isolates in Myanmar: identification of novel ST1407 harbouring blaNDM-1

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Abstract

Recent *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 bla_{OXA-23}. The NDM-1 encoding gene was identified in only one isolate exhibiting novel ST1407 (a triple-locus variant of ST16).

Keywords: *Acinetobacter baumannii*, Myanmar, NDM-1, OXA-23, ST

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Acinetobacter baumannii is opportunistic pathogen with a remarkable capacity to acquire antimicrobial resistance. Global spread of carbapenem-resistant *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 multi-locus 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 *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 *Klebsiella pneumoniae* being dominant, followed by *Escherichia coli*. Forty isolates (3.1%) were identified as *Acinetobacter* species by biochemical test kit (API 20NE strip; bioMérieux), among which 25 isolates were genetically confirmed to be *A. baumannii* by PCR detection of bla_{OXA-51}-like gene [6] and sequencing of *cpn60* (one MLST locus) [2]. The most common specimen associated with *Acinetobacter spp*. was sputum, followed by wound swab and urine (Supplementary Table S1). Most Acinetobacter spp. isolates were derived from male patients of older age (>40 years) (Supplementary Table S2).

Antimicrobial susceptibility of *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 bla_{OXA-51} family were determined by PCR direct sequencing using primers designed in this study (Supplementary Table S3).

Among 25 *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 bla_{OXA-51} family, which were correlated with each of the five STs. bla_{OXA-23} was detected in all the isolates except ST23 (detection rate, 72%), and bla_{NDM-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 *A. baumannii* clinical isolates in Myanmar described the dominance of ST2 (50%), high prevalence of bla_{OXA-23} (87%) and detection of bla_{NDM-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 bla_{NDM-1}, was sporadic type but a triple-locus variant of ST16 as well as ST1480. While being a minor lineage of *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

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TABLE 1. ST, carbapenemase genes and drug resistance of *Acinetobacter baumannii* clinical isolates from North Okkalapa General Hospital, Myanmar, January to November 2018

		Carbapenemase gene (no. of isolates)			Resistance rate (%) to:				
ST (no. of isolates)	Allelic profile of ST	blaOXA-51 family	Other blaOXA	blaNDM	CAZ, CTX, GEN	IPM, MEM	AMK	DOX	Specimen (no. of isolates)
ST2 (8)	2-2-2-2-2-2-2	bla_{OXA-66} (8)	bla_{OXA-23} (8)	—	100	87.5	75	100	Sputum (5), urine (1), blood (1), suction tip (1)
ST16 (8)	7-7-2-2-8-4-4	bla_{OXA-70} (8)	bla_{OXA-23} (8)	—	100	100	37.5	87.5	Sputum (4), wound (2), pus (1), blood (1)
ST23 (7)	1-3-10-1-4-4-4	bla_{OXA-68} (7)	—	—	100	28.6	28.6	100	Sputum (4), wound (2), urine (1)
ST1406 (1)	1-3-2-1-137-4-92	$bla_{OXA-144}$ (1)	bla_{OXA-23} (1)	—	R	R	R	R	Sputum (1)
ST1407 (1)	7-190-2-2-8-82-123	$bla_{OXA-402}$ (1)	bla_{OXA-23} (1)	bla_{NDM-1} (1)	R	R	R	R	Sputum (1)
Total (25)			bla_{OXA-23} (18)	bla_{NDM-1} (1)	100	76	52	96	

For each single isolate of ST1406 and ST1407, only R (resistant) is shown. All isolates were susceptible to colistin and tigecycline.
Abbreviations: AMK, amikacin; CAZ, ceftazidime; CTX, cefotaxime; DOX, doxycycline; GEN, gentamicin; IPM, imipenem; MEM, meropenem; ST, sequence type.

countries and responsible for carbapenem resistance carrying bla_{NDM-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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