PFGE type	Isolate No.	OXA-51-like variant
01	15	OXA-65
01	16	OXA-65
01	17	OXA-65
01	14	OXA-65
02	12	OXA-91
03	03	OXA-69
04	29	OXA-69
05	24	OXA-69
05	26	OXA-69
05	25	OXA-69
06	05	OXA-68
07	06	OXA-71
07	27	OXA-71
07	04	OXA-71
12	18	OXA-64
12	23	OXA-64
12	28	OXA-64
12	19	OXA-64
12	21	OXA-64
13	07	OXA-69
10	02	OXA-66
10	09	OXA-66
10	01	OXA-66
11	08	OXA-66
08	10	OXA-64
09	13	OXA-317
14	11	OXA-90
15	20	OXA-66
15	22	OXA-66

Figure S1. PFGE analysis of 29 *A. baumannii* isolates and OXA-51-like variants identified by sequencing of *bla*$_{OXA-51-like}$ genes. A value of 87% was chosen as the threshold for clonality.

Table S1. Primers used for detection of β-lactamase genes and IS*Aba1*.

Primer name	Sequence	Target	Reference
OXA-51-likeF	TAATGCTTTGATCGGCCTTG	$bla_{OXA-51-like}$	(1)
OXA-51-likeR	TGGATTGCACTTCATCTTGG	$bla_{OXA-51-like}$	
OXA-51-like-up	TACTCTATCATTAATGAGTGC	Upstream region of $bla_{OXA-51-like}$	This study
OXA-51-like-down	GGCCTTCATGAGAAAATGGGC	Downstream region of $bla_{OXA-51-like}$	
OXA-23-likeF	GATCGGATTGGAGAACCAGA	$bla_{OXA-23-like}$	(1)
OXA-23-likeR	ATTTCTGACCGCATTTCCAT	$bla_{OXA-23-like}$	
OXA-23-down	ATGCCAATGAATGACGAAGCC	Downstream region of $bla_{OXA-23-like}$	This study
OXA-24-likeF	GGTTAGTTGGCCCCCTTAAA	$bla_{OXA-24-like}$	(1)
OXA-24-likeR	AGTTGAGCGAAAAGGGGATT	$bla_{OXA-24-like}$	
OXA-24-up	TGGCTGAAAGTGACAAATTCG	Upstream region of $bla_{OXA-24-like}$	This study
OXA-24-down	TAGACCCTATGATTAACCACG	Upstream region of $bla_{OXA-24-like}$	
OXA-58-likeF	AAGTATTGGGGCTTGTGCTG	$bla_{OXA-58-like}$	(1)
OXA-58-likeR	CCCCTCTGCGCTCTACATAC	$bla_{OXA-58-like}$	
OXA-143-F	TGGCACTTTCAGCAGTTCCT	$bla_{OXA-143-like}$	(2)
OXA-143-R	TAATCTTGAGGGGGCCAACC	$bla_{OXA-143-like}$	
OXA-143-like-for	AGTACCTATGGTAATAACCTG	$bla_{OXA-143-like}$[b]	This study
OXA-143-like-rev	AGGGGGGCCAACCAACCAGAAG	$bla_{OXA-143-like}$[b]	
ADC-F	GATACGCCTGGTAAATATTGG	bla_{ADC}	This study
ADC-R	CGAATCGGCTGATTTTCTTGG	bla_{ADC}	
GES-1-F	ATGCGCTTCATTCACGCAC	$bla_{GES-1-like}$	(3)
GES-1-R	CTATTTGTCCGTGCTCAGGA	$bla_{GES-1-like}$	
GES-1-like-up	CGATGCGTGGAGACCGAAACC	Upstream region of bla_{GES-1}	This study
GES-1-like-down	CGATTTAGCCACTCATAGAGC	Downstream region of bla_{GES-1}	
PER-A	ATGAATGTCATTATAAAAGC	$bla_{PER-1-like}$	(4)
PER-D	AATTTGGGCTTAGGGCAGAA	$bla_{PER-1-like}$	
PER-1-like-up	ATTTCAGGTAAGATACTTCGG	Upstream region of $bla_{PER-1-like}$	This study
PER-1-like-down	AACTGATAAGGTTGCCCTGCC	Downstream region of $bla_{PER-1-like}$[c]	
NDM-F[a]	CATTTGCGGGGTTTTTAATG	bla_{NDM}	This study
NDM-R	ATTGGCATAAGTCGCAATCC	bla_{NDM}	
CMY-2-like-F	AGACGTTTAACGGCGTGTTGG	$bla_{CMY-2-like}$	This study
CMY-2-like-R	GCTGGATTTCACGCCATAGGC	$bla_{CMY-2-like}$	
CMY-2-like-up	AACCGTTTGTCAACACGGTGC	Upstream region of $bla_{CMY-2-like}$	This study
CMY-2-like-down	GCAACGACGGGCAAAATGCGC	Downstream region of $bla_{CMY-2-like}$	
VEB-F	CGACTTCCATTTCCCGATGC	bla_{VEB-1}	(5)
VEB-B	GGACTCTGCAACAAATACGC	bla_{VEB-1}	
SPM-GBM-F	GGGTGGCTAAGACTATGAAGCC	bla_{SPM}	(6)
SPM-GBM-R	GCCGCCGAGCTGAATCGG	bla_{SPM}	
CTX-M-2F	ATGATGACTCAGAGCATTCG	$bla_{CTX-M-2}$	(7)
CTX-M-2R	TTATTGCATCAGAAACCGTG	$bla_{CTX-M-2}$	
CTX-M-9F	AGACGAGTGCGGTGCAGCAA	$bla_{CTX-M-9}$	This study
CTX-M-9R	GATTCTCGCCGCTGAAGCCA	$bla_{CTX-M-9}$	
CTX-M-10F	GCAGCACCAGTAAAGTGATGG	$bla_{CTX-M-10}$	(7)
CTX-M-10R	GCGATATCGTTGGTGGTACC	$bla_{CTX-M-10}$	
IS*Aba1*F	CACGAATGCAGAAGTTG	*tnpA* (IS*Aba1*)	(8)

[a] Positioned 40 bp upstream of start codon of bla_{NDM-1}

[b] Anneals to all variants of $bla_{OXA-143}$ known at the time of preparation of the manuscript

^{c} Anneals to *gts* (glutathione S-transferase) gene downstream of bla$_{PER-7}$ as found in retrotransposon ISCR1 of *A. baumannii* NM55 (9)

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