

Supplementary data

Table S1. Primers used in this study.

Primers	Gene	Sequence (5' to 3')	Size (bp.)	Usage	References
AdeR_Fw_P15	<i>adeR</i>	GTTAAGGCAATAAAAAGTTGCTT	895	Sequencing	[22]
AdeR_Rv_P16		TGGAGTAAGTGTGGAGAAATACG			
AdeS_Fw_P17	<i>adeS</i>	CTTGGTTAGGTTAGATATGGCATT	1213	Sequencing	[22]
AdeS_RV_P18		GGCGTGGGATATAGGCTAGATAA			
OXA-51 F	<i>blaOXA-51</i>	TAATGC TTT GATCGG CCT TG	353	identification	[21]
OXA-51 R		TGG ATT GCA CTT CAT CTT GG			
OXA-23-like Fw	<i>blaOXA-23-like</i>	GAT CGG ATT GGA GAA CCA GA	501	identification	[21]
OXA-23-like Rv		AAT TCT GAC CGC ATT TCC AT			
OXA-24-like Fw	<i>blaOXA-24-like</i>	GGT TAG TTG GCC CCC TTA AA	246	identification	[21]
OXA-24-like Rv		AGT TGA GCG AAA AGG GGA TT			
OXA-58-like Fw	<i>blaOXA-58-like</i>	AAG TAT TGG GGC TTG TGC TG	599	identification	[21]
OXA-58-like Rv		CCCCTC TGC GCT CTA CAT AC			
adeB_RT_F	<i>adeB</i>	GGATTATGGCGACTGAAGGA	106	qRT-PCR	[23]
adeB_RT_R		AATACTGCCGCAATACCAG			
adeG_RT_F	<i>adeG</i>	CGTAACTATGCGGTGCTCAA	92	qRT-PCR	[23]
adeG_RT_R		ATCGCGTAGTCACCAGAACC			
adeJ_RT_F	<i>adeJ</i>	CATCGGCTGAAACAGTTGAA	109	qRT-PCR	[23]
adeJ_RT_R		GCCTGACCATTACCAGCACT			
adeR_RT_F	<i>adeR</i>	ATTGATACCGGACTCATAGCG	180	qRT-PCR	This study
adeR_RT_R		TACGGTTCGCTCTAGTGCATC			
adeS_RT_F	<i>adeS</i>	CGCCGTCGTATTGAGCAAG	215	qRT-PCR	This study

Primers	Gene	Sequence (5' to 3')	Size (bp.)	Usage	References
adeS_RT_R		GTGCCGCCAAATTCTTTATTCC			
16S_RT_F	16S RNA	GACGTACTCGCAGAATAAGC	426	qRT-PCR	[24]
16S_RT_R		TTAGTCTTGCGACCGTACTC			

Table S2. Gene expression level of RND type efflux pump in 30 Thai clinical isolates of tigecycline-resistant *A. baumannii*

Isolate	Fold change in gene expression				
	<i>adeB</i>	<i>adeG</i>	<i>adeJ</i>	<i>adeR</i>	<i>adeS</i>
G560T	36.91	3.74	11.37	7.84	14.94
H1074	5.81	0.45	1.61	6.10	2.28
H1847	0.73	0.85	1.82	1.66	0.34
H222	3.69	0.73	3.67	19.28	3.21
M251	4.05	1.93	3.84	3.27	2.52
R109	7.93	2.37	3.91	9.29	6.09
R171	9.00	1.26	3.60	3.57	3.05
R215	4.37	0.54	3.00	3.16	7.98
R234	2.01	0.72	2.09	2.55	2.19
R270	44.65	1.93	4.28	4.66	9.52
R286	44.42	2.04	1.35	3.08	8.34
R291	9.54	2.65	3.65	4.39	4.86
R297	11.52	6.10	7.08	23.87	16.16
R328	55.51	2.91	8.42	45.70	14.95
R339	14.00	1.59	2.15	3.98	3.22
R380	11.18	5.99	13.26	4.62	6.56
R422	151.51	3.57	13.76	0.81	0.07
R435	2.94	1.93	12.83	9.76	6.11
R465	23.23	1.35	2.05	26.66	0.27
R494	14.10	0.86	10.67	10.38	0.97
R516	5.51	1.73	2.97	4.44	4.36
R64	2.99	0.98	3.51	3.05	1.56

Isolate	Fold change in gene expression				
	<i>adeB</i>	<i>adeG</i>	<i>adeJ</i>	<i>adeR</i>	<i>adeS</i>
R692	3.32	1.24	2.91	2.65	2.18
R72	1.65	0.93	1.46	2.15	1.54
R83	5.48	0.81	3.36	2.02	9.47
S203	9.11	4.09	4.15	5.75	4.04
S301	2.10	3.33	2.39	7.65	2.67
S330	0.40	0.29	1.16	1.90	0.64
S354	0.84	0.17	0.90	1.83	0.45
S367	2.40	0.48	2.11	2.24	1.11

Table S3 Frequency distribution of each codon in AdeR of 30 tigecycline-resistant *A. baumannii*

Amino acid substitution in AdeR	No (%) of isolates with AdeR mutation
D93V	1 (3.33)
V120I	28 (93.33)
A136V	20 (66.67)
I175L	8 (26.67)
F224L	2 (6.67)
Q225N	2 (6.67)
Frequency distribution of the 4 mutation patterns	
D93V+ V120I+ I175L (Triple mutations)	1 (3.33)
V120I+A136V (double mutations)	20 (66.67)
V120I+ I175L (double mutations)	7 (23.33)
F224L+ Q225N (double mutations)	2 (6.67)

Table S4 Frequency distribution of each codon in AdeS of 30 tigecycline-resistant *A. baumannii*

Amino acid substitution/deletion in AdeS	No (%) of isolates with AdeS mutation
S8R	2 (6.67)
E51K	1 (3.33)
D60A	2 (6.67)
C70Y	3 (10.00)
N127K	2 (6.67)
K132N	1 (3.33)
T156M	2 (6.67)
F170I	1 (3.33)
G186V	20 (66.67)
R249H	2 (6.67)
N268H	20 (66.67)
V279A	2 (6.67)
N314D	2 (6.67)
N314K	2 (6.67)
N314 del	2 (6.67)
V332M	2 (6.67)
V348I	20 (66.67)
Frequency distribution of the 14 mutation patterns	No (%) of isolates with AdeS mutation
No mutation	3 (10.00)

Amino acid substitution/deletion in AdeS	No (%) of isolates with AdeS mutation
D60A (Single mutation)	2 (6.67)
C70Y (Single mutation)	1 (3.33)
N314K (Single mutation)	2 (6.67)
G186V+ N268H+ V348I (Triple mutations)	7 (23.33)
S8R+ R249H+ V279A+ V332M (Quadruple mutations)	2 (6.67)
E51K+ G186V+ N268H+ V348I (Quadruple mutations)	1 (3.33)
T156M+ G186V+ N268H+ V348I (Quadruple mutations)	2 (6.67)
C70Y+G186V+ N268H+ V348I (Quadruple mutations)	2 (6.67)
N127K+G186V+ N268H+ V348I (Quadruple mutations)	2 (6.67)
G186V+ N268H+ N314D +V348I (Quadruple mutations)	2 (6.67)
K132N+ G186V+ N268H+ V348I (Quadruple mutations)	1 (3.33)
G186V+ N268H+ N314delete +V348I (Quadruple mutations)	2 (6.67)

Amino acid substitution/deletion in AdeS	No (%) of isolates with AdeS mutation
F170I+ G186V+ N268H+ V348I (Quadruple mutations)	1 (3.33)

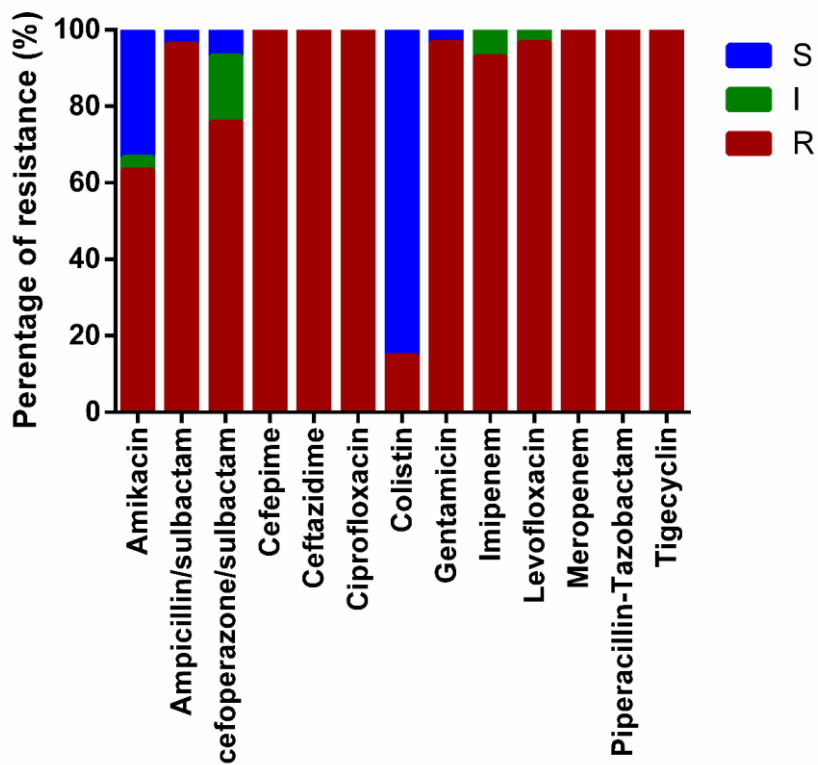


Figure S1. *In vitro* antimicrobial susceptibility profiles for 30 TRAB isolates

Abbreviations R: Resistant, I: Intermediate, S: Susceptible