



325	2016	Wound	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
326	2016	Wound	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
327	2016	Urine	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
329	2016	Sputum	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	
333	2016	Wound	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	R	S	
334	2016	Blood	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
335	2016	Sputum	R	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	S	
337	2016	Sputum	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	
344	2016	CVP	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
345	2016	ETA	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
346	2016	Drain Culture	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
347	2016	Urine	R	R	R	R	R	R	R	R	R	R	R	R	S	I	R	S	S	
348	2016	Sputum	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
349	2016	Sputum	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	
354	2016	Wound	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
355	2016	ETA	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	R	I	
356	2016	Wound	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
358	2016	Urine	R	R	R	R	R	R	R	R	R	R	R	R	S	S	R	R	I	
361	2016	CVL culture	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	S
362	2016	ETA	R	R	R	R	R	R	R	R	R	R	R	R	R	I	R	S	I	
365	2016	Urine	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
366	2016	Wound	R	R	R	R	R	R	R	R	R	R	R	R	S	R	R	R	I	
367	2016	Sputum	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	
368	2016	Urine	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
369	2016	Wound	R	R	R	R	R	R	R	R	I	R	R	R	R	R	R	R	I	
371	2016	Sputum	R	R	R	R	R	R	R	R	R	R	R	R	I	R	R	R	S	
372	2016	Blood	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
373	2016	Sputum	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	S	
374	2016	Urine	R	R	R	R	R	R	R	R	I	R	R	R	R	R	R	R	I	
375	2016	Urine	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	R	I	
376	2016	Urine	R	R	R	R	R	R	R	R	I	R	R	I	R	R	R	R	I	

*(AUG) amoxicillin/clavulanic acid, (TZP) piperacillin/tazobactam, (FOX) ceftioxin, (CTX) cefotaxime, (CTC) cefotaxime/clavulanic acid, (CAZ) ceftazidime, (CZC) ceftazidime/clavulanic acid, (CPM) cefepime, (ATM) aztreonam, (IMI) imipenem, (MEM) meropenem, (ETR) ertapenem, (GN) gentamicin, (AK) amikacin, (CIP) ciprofloxacin, (STX) sulfamethoxazole/trimethoprim and (TGC) tigecycline.

R: resistant pattern, I: intermediate pattern, and S: sensitive pattern.

Table S2: Results of modified Hodge test, inhibitor-based tests and genotypic detection of investigated carbapenemases.

Isolate	Phenotypic detection of carbapenemases						Genotypic detection of carbapenemases				
	MHT	Inhibitor based test					Class A	Class B			Class D
		A	B	C	D	TEM(mm)	KPC	NDM	VIM	IMP	OXA-48
1	-	Resistance to meropenem for further comparison with other discs	+	-	-	11	-	+	+	-	-
2	-		+	-	-	12	-	+	+	+	-
6	-		+	-	-	11	-	+	+	+	-
7	-		+	-	-	6	-	+	+	+	-
8	+		-	-	-	6	-	-	-	-	+
14	-		+	-	-	6	-	+	+	-	-
16	-		+	-	-	10	-	+	-	-	-
21	-		+	-	-	8	-	-	+	+	-
24	-		+	-	-	10	-	-	+	+	-
28	+		-	-	-	6	-	-	-	-	+
31	-		+	-	-	11	-	-	+	+	-
33	-		+	-	-	13	-	-	+	-	-



97	+		+	-	-	6	-	+	+	+	-
100	+		+	-	-	6	-	+	+	-	-
102	-		-	-	-	6	-	-	+	-	+*
109	-		+	-	-	10	-	-	+	+	-
110	-		+	-	-	11	-	+	+	-	-
112	+		+	-	-	6	-	+	+	+	-
113	+		-	-	-	6	-	-	-	-	+*
117	+		+	-	-	6	-	+	+	+	+ [#]
122	+		+	-	-	12	-	+	+	+	-
125	-		+	-	-	10	-	+	+	+	-
127	+		-	-	-	6	-	-	-	-	+*
130	+		+	-	-	6	-	+	+	+	-
134	+		-	-	-	6	-	+	+	-	+*
136	+		-	-	-	6	-	-	+	-	-
137	+		-	-	-	6	-	-	-	-	-
138	-		+	-	-	10	-	+	+	+	-
139	-		+	-	-	17	-	+	+	+	-
142	+		-	-	-	6	-	-	-	-	-
143	+		+	-	-	14	-	+	-	+	-
144	-		+	-	-	14	-	+	+	-	-
145	-		+	-	-	13	-	+	+	-	-
146	-		+	-	-	12	-	+	+	-	-
147	+		-	-	-	6	-	-	+	-	-
151	+		-	-	-	6	-	-	-	-	+*
152	+		-	-	-	6	-	-	+	-	+*
300	-		+	-	-	15	-	+	+	+	-
301	+		+	-	-	12	-	+	+	+	-
302	+		+	-	-	6	-	+	+	-	-
303	-		-	-	-	6	-	-	+	-	+*
304	+		+	-	-	6	+	+	+	+	-



305	-		+	-	-	10	-	+	+	+	-
306	-		+	-	-	6	-	+	+	+	-
307	-		+	-	-	10	-	+	+	+	-
308	-		+	-	-	11	-	+	+	+	-
310	-		+	-	-	11	-	+	+	+	-
311	+		-	-	-	10	-	-	+	-	+*
312	-		+	-	-	8	-	+	+	+	-
318	-		+	-	-	6	-	+	+	+	-
319	-		+	-	-	9	-	+	+	+	-
320	-		+	-	-	11	-	+	+	+	-
321	+		+	-	-	6	-	+	+	+	-
323	+		+	-	-	6	-	+	+	+	-
324	+		-	-	-	6	-	+	+	-	+*
325	+		+	-	-	6	-	+	+	+	-
326	+		+	-	-	6	-	+	+	+	-
327	-		+	-	-	6	-	+	+	+	-
329	-		+	-	-	10	-	+	+	+	-
333	+		+	-	-	6	-	+	+	-	+ [#]
334	+		-	-	-	6	-	+	+	-	-
335	+		-	-	-	6	-	-	+	-	+*
337	-		+	-	-	18	-	+	+	+	-
344	+		-	-	-	6	-	+	+	-	-
345	-		+	-	-	14	-	+	+	+	-
346	+		-	-	-	6	-	-	-	-	+*
347	-		+	-	-	14	-	+	+	+	-
348	+		+	-	-	6	-	+	+	+	+ [#]
349	+		+	-	-	6	+	+	+	+	+ [#]
354	+		+	-	-	6	+	+	+	+	+ [#]
355	-		+	-	-	6	-	+	+	+	-
356	+		-	-	-	6	-	-	-	-	+*



antibiotics



358	-		+	-	-	12	-	+	+	+	-
361	+		+	-	-	13	-	+	+	+	-
362	-		+	-	-	18	-	+	+	+	-
365	+		-	-	-	6	-	+	+	-	-
366	-		+	-	-	6	-	+	+	+	-
367	+		+	-	-	6	-	+	+	+	-
368	-		+	-	-	9	-	+	+	+	-
369	-		+	-	-	11	-	+	+	+	-
371	+		-	-	-	6	-	+	+	+	+*
372	+		-	-	-	6	-	+	+	+	+*
373	+		-	-	-	6	-	-	+	-	+*
374	-		+	-	-	13	-	-	+	+	-
375	+		-	-	-	6	+	+	+	+	+*
376	-		+	-	-	13	-	+	+	+	-
377	+		-	-	-	6	-	+	+	+	+*
378	+		-	-	-	9	-	-	-	-	+*
379	-		+	-	-	10	-	+	+	+	-
380	-		+	-	-	16	-	+	+	+	-
381	-		+	-	-	13	-	+	+	+	-
383	+		+	-	-	6	-	+	+	+	+ [#]
385	+		-	-	-	6	-	+	+	-	+*
386	-		+	-	-	16	-	+	+	+	-
387	+		-	-	-	6	+	+	+	-	+*
388	+		-	-	-	6	-	+	+	-	-
389	-		+	-	-	11	-	+	+	+	-
391	+		+	-	-	11	-	+	-	+	-
394	+		+	-	-	6	-	+	-	+	+ [#]
396	+		-	-	-	6	-	-	+	-	-
397	+		-	-	-	6	-	+	+	-	+*
398	+		+	-	-	6	-	+	+	-	-



399	+		-	-	-	6	-	-	-	-	+
401	-		+	-	-	6	-	+	+	+	-
402	+		+	-	-	6	+	+	+	+	-
403	+		+	-	-	6	-	+	+	-	-
405	+		+	-	-	6	-	+	+	+	+#
407	+		+	-	-	8	-	+	+	-	-
409	+		-	-	-	6	-	+	+	-	+
410	+		-	-	-	6	-	-	-	-	-
411	+		+	-	-	6	-	+	+	+	-
415	+		-	-	-	8	-	-	+	-	+
416	+		+	-	-	8	-	+	+	+	-
417	+		-	-	-	6	-	+	-	-	-
418	-		+	-	-	6	-	+	+	+	-
419	+		-	-	-	6	-	-	-	-	-
420	-		+	-	-	8	-	+	+	+	-
Disc A	Meropenem 10 µg										
Disc B	Meropenem +EDTA										
Disc C	Meropenem + Phenyl boronic acid										
Disc D	Meropenem +AmpC inhibitor										
TEM	Temocillin 30 µg										
*	Results that do not comply with MβL, KPC and AmpC phenotypic detection criteria and positive genotypically for OXA-48										
#	Results that comply with MβL, KPC or AmpC phenotypic detection criteria and positive genotypically for OXA-48.										

Table S3: Simpson's Diversity Index calculations for antibiogram.

Species Type*	Antibiogram pattern			Isolates	No of individuals (n)	(n-1)	n(n-1)
	S	I	R				
AA	-	-	All investigated antimicrobials	151 & 409	2	1	2
AB	-	TGC	Remaining antimicrobials	117, 134, 152, 324, 346, 348, 354, 356, 372, 375, 385, 394, 397, 399, 405, 415.	16	15	240
AC	-	CAZ& TGC	Remaining antimicrobials	127	1	0	0
AD	-	GN& TGC	Remaining antimicrobials	311& 377	2	1	2
AE	GN& TGC	-	Remaining antimicrobials	333& 383	2	1	2
AF	TGC	-	Remaining antimicrobials	349& 373	2	1	2
AG	GN	-	Remaining antimicrobials	387	1	0	0
AH	TGC	GN	Remaining antimicrobials	371	1	0	0
AI	GN& TGC	CIP	Remaining antimicrobials	8	1	0	0
AJ	CIP	TGC	Remaining antimicrobials	303	1	0	0
AK	AK	TGC	Remaining antimicrobials	102& 113	2	1	2
AL	ATM& AK	TGC	Remaining antimicrobials	28	1	0	0
AM	AK& TGC	-	Remaining antimicrobials	335	1	0	0
AN	STX	IMI& TGC	Remaining antimicrobials	378	1	0	0
							Σ 250

* Species Type:

A: Antibiogram typing method.

(A-N): The patterns of the isolates.

Table S4: Simpson's Diversity Index calculations for ERIC-PCR.

Species Type*	No of individuals(n)	(n-1)	n(n-1)
EA (Isolates 8, 324, 354& 383)	4	3	12
EB (Isolates 117& 397)	2	1	2
EC (Isolate 335)	1	0	0
ED (Isolate 346)	1	0	0
EE (Isolates 385& 387)	2	1	2
EF (Isolates 134, 151, 303, 311, 348, 373, 399, 405, 409& 415)	10	9	90
EG (Isolates 378)	1	0	0
EH (Isolates 28& 356)	2	1	2
EI (Isolates 113)	1	0	0
EJ (Isolates 394)	1	0	0
EK (Isolates 102, 127, 152& 349)	4	3	12
EL (Isolate 333)	1	0	0
EM (Isolate 377)	1	0	0
EN (Isolate 371)	1	0	0
EO (Isolates 372)	1	0	0
EP (Isolates 375)	1	0	0
			Σ 120

* Species Type:

E: ERIC-PCR typing method.

(A-P): The patterns of the isolates.

Table S5: Simpson's Diversity Index calculations for plasmid profile analysis.

Species Type*	No of individuals (n)	(n-1)	n(n-1)
PA1	1	0	0
PA2	1	0	0
PB1	3	2	6
PB2	1	0	0
PC1	1	0	0
PC2	2	1	2
PC3	1	0	0
PC4	1	0	0
PC5	1	0	0
PC6	3	2	6
PC7	1	0	0
PC8	1	0	0
PD1	1	0	0
PD2	1	0	0
PD3	1	0	0
PD4	2	1	2
PD5	1	0	0
PE1	1	0	0
PE2	1	0	0
PE3	1	0	0
PE4	2	1	2
PE5	1	0	0
PE6	1	0	0
PE7	1	0	0
PF1	1	0	0
PG1	1	0	0
			Σ 18

*Species Type:

P: The plasmid profile analysis typing method.

(A-G): The patterns of the isolates, since:

Pattern A has one plasmid.

Pattern B has two plasmids.

Pattern C has three plasmids.

Pattern D has four plasmids.

Pattern E has five plasmids.

Pattern F has six plasmids.

Pattern G has eight plasmids.

Table S6: A comparative summing-up of SDI calculations of the three typing methods.

Isolate	Isolate Data		Isolate typing classification		
	Year	Type	Antibiogram	ERIC-PCR	Plasmid Profile analysis
8	2014	Sputum	AI	EA	PC1
28	2014	Sputum	AL	EH	PD1
102	2015	Blood	AK	EK	PE1
113	2015	Blood	AK	EI	PC2
117	2015	Urine	AB	EB	PD2
127	2015	Blood	AC	EK	PB1
134	2015	Blood	AB	EF	PC3
151	2015	Urine	AA	EF	PB1
152	2015	Urine	AB	EK	PC4
303	2016	Sputum	AJ	EF	PA2
311	2016	Sputum	AD	EF	PC6
324	2016	Urine	AB	EA	PC5
333	2016	Wound	AD	EL	PE2
335	2016	Sputum	AM	EC	PC6
346	2016	Drain Culture	AB	ED	PE6
348	2016	Sputum	AB	EF	PE3
349	2016	Sputum	AF	EK	PE4
354	2016	Wound	AB	EA	PE4
356	2016	Wound	AB	EH	PA1
371	2016	Sputum	AH	EN	PG1
372	2016	Blood	AB	EO	PE5
373	2016	Sputum	AF	EF	PF1
375	2016	Urine	AB	EP	PC6
377	2016	Sputum	AD	EM	PE6
378	2016	Urine	AN	EG	PB2
383	2016	ETA	AD	EA	PC7
385	2016	Bile culture	AB	EE	PD4
387	2016	Urine	AG	EE	PC2
394	2016	Urine	AB	EJ	PE7
397	2016	Urine	AB	EB	PD3
399	2016	Wound	AB	EF	PB1
405	2016	Sputum	AB	EF	PC8
409	2016	Urine	AA	EF	PD4
415	2016	Blood	AB	EF	PD5
Simpson's Diversity Index			0.78	0.89	0.98

Table S7: Distribution of *fimH-1* and *mrkD* adhesion genes among the carbapenem-resistant isolates.

Isolate	<i>fimH-1</i>	<i>mrkD</i>	Isolate	<i>fimH-1</i>	<i>mrkD</i>	Isolate	<i>fimH-1</i>	<i>mrkD</i>
1	-	+	302	+	+	368	+	+
2	-	+	303	+	+	369	+	+
6	-	+	304	+	+	371	+	+
7	+	+	305	+	+	372	+	+
8	+	+	306	+	+	373	+	+
14	+	+	307	+	+	374	+	+
16	+	+	308	+	+	375	+	+
21	+	+	310	+	+	376	+	+
24	+	+	311	+	+	377	+	+
28	+	+	312	+	+	378	+	+
31	+	+	318	+	+	379	+	+
33	+	+	319	+	+	380	+	+
97	+	+	320	+	+	381	+	+
100	+	+	321	+	+	383	+	+
102	+	+	323	+	+	385	+	+
109	+	+	324	+	+	386	+	+
110	+	+	325	+	-	387	+	+
112	+	+	326	+	+	388	+	+
113	+	+	327	+	+	389	+	+
117	+	+	329	+	+	391	+	+
122	+	+	333	-	+	394	+	+
125	+	+	334	+	+	396	+	+
127	+	+	335	+	+	397	+	+
130	+	+	337	+	+	398	+	+
134	+	+	344	+	-	399	+	+
136	+	+	345	+	+	401	+	+
137	+	+	346	+	+	402	-	+
138	+	+	347	+	+	403	+	+
139	+	+	348	+	+	405	-	+
142	+	+	349	+	+	407	+	+
143	+	+	354	+	+	409	-	+
144	+	+	355	+	+	410	+	+
145	+	+	356	+	+	411	+	+
146	+	+	358	+	+	415	+	+
147	+	+	361	+	+	416	+	+
151	+	+	362	+	+	417	+	+
152	+	+	365	+	+	418	-	+



300	+	+	366	+	+	419	-	+
301	+	+	367	+	+	420	+	+

Table S8: The applied antimicrobial agents, their classes, and their interpretive categories.

<u>Antimicrobial class</u>	<u>Antimicrobial agents</u>	<u>Symbol</u>	<u>Conc.</u>	<u>Interpretive Categories and Zone Diameter Breakpoints (mm)^{*A}</u>			
				S	I	R	
Penicillin Combination Agents.	Amoxicillin/Clavulanic acid	AUG	20/10 µg	≥ 18	14-17	≤ 13	
	Piperacillin/Tazobactam	TZP	100/10 µg	≥ 21	18- 20	≤ 17	
Cephems	2nd Generation Cephalosporin	Cefoxitin	FOX	30 µg	≥ 18	-	≤ 14
	3rd Generation cephalosporin	Cefotaxime	CTX	30 µg	≥ 26	23-25	≤ 22
		Cefotaxime/ Clavulanic acid	CTC	40 µg	≥ 26	23-25	≤ 22
		Ceftazidime	CAZ	30 µg	≥ 21	18-20	≤ 17
		Ceftazidime/Clavulanic acid	CZC	40 µg	≥ 21	18-20	≤ 17
4th Generation Cephalosporin	Cefepime	CPM	30 µg	≥ 25	-	≤ 18	
Carbapenems	Imipenem	IMI	10 µg	≥ 23	20-22	≤ 19	
	Meropenem	MEM	10 µg	≥ 23	20-22	≤ 19	
	Ertapenem	ETR	10 µg	≥ 22	19-21	≤ 18	
Monobactams	Aztreonam	ATM	30 µg	≥ 21	18-20	≤ 17	
Aminoglycosides	Gentamycin	GM	10 µg	≥ 15	13-14	≤ 12	
	Amikacin	AK	30 µg	≥ 17	15-16	≤ 14	
Quinolones	Ciprofloxacin	CIP	5 µg	≥ 21	16-20	≤ 15	
Folate Pathway Inhibitor.	Trimethoprim./Sulphamethoxazol	SXT	1.25/ 23.75 µg	≥ 16	11-15	≤ 10	
Protein Synthesis inhibitor	Tigecycline ^{*B}	TGC	15 µg	≥ 19	15-18	≤ 14	

*A : The interpretation of test results was according to the Clinical and Laboratory Standards Institute guidelines, CLSI (M100-S26, 2016) and further revised according to the recent edition (M100-S28, 2018).

*B: The interpretative results for tigecycline were according to the FDA criteria (http://www.accessdata.fda.gov/drugsatfda_docs/label/2009/021821s016lbl.pdf).

Table S9: Primers sequences and the expected amplicon sizes of investigated genes.

Gene	Primers Sequence (5'-3')	Expected Amplicon Size (bp)	Reference
KPC	KPC- F: 5' ATGTCACTGTATCGCCGTCT 3'	880 bp	[50]
	KPC- R: 5' TTACTGCCCGTTGACGCCCA 3'		
NDM	NDM-F: 5' GGTTTGGCGATCTGGTTTTTC 3'	621 bp	
	NDM-R: 5' CGGAATGGCTCATCACGATC 3'		
VIM	VIM-F: 5' GATGGTGTGGTTCGCATA 3'	390 bp	[51]
	VIM-R: 5' CGAATGCGCAGCACCAG 3'		
IMP	IMP-F: 5' GGAATAGAGTGGCTTAAYTCTC 3'	232 bp	
	IMP-R: 5' GGTTTAAAYAAAACAACCACC 3'		
OXA-48-Like genes	OXA-48-F: 5'TTGGTGGCATCGATTATCGG 3'	743 bp	[52]
	OXA-48-R: 5'GAGCACTTCTTTTGTGATGGC 3'		
OXA-48- Like (including flanking or pre-gene)	Pre- OXA-48- F: 5' TATATTGCATTAAGCAAGGG 3'	848 bp	[53]
	Pre- OXA-48-R: 5' CACACAAATACGCGCTAACC 3'		
ERIC-2	5' AAGTAAGTACTGGGGTGAGCG 3'	-----	[56]
<i>fimH-1</i>	Virulence Adhesion <i>fimH-1-F5'</i> ATGAACGCCTGGTCCTTTGC 3'	688 bp	[34]
	<i>fimH-1-R5'</i> GCTGAACGCCTATCCCCTGC 3'		
<i>mrkD</i>	Genes <i>mrkD-F:</i> 5' CCACCAACTATTCCTCGAA 3'	240 bp	[62]
	<i>mrkD-R:</i> 5' ATGGAACCCACATCGACATT 3'		