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National Surveillance of Antimicrobial Susceptibility of Bacteremic Gram-Negative Bacteria with Emphasis on Community-Acquired Resistant Isolates: Report from the 2019 Surveillance of Multicenter Antimicrobial Resistance in Taiwan (SMART)

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ABSTRACT A multicenter collection of bacteremic isolates of *Escherichia coli* (n = 423), *Klebsiella pneumoniae* (n = 372), *Pseudomonas aeruginosa* (n = 300), and *Acinetobacter baumannii* complex (n = 199) was analyzed for susceptibility. Xpert Carba-R assay and sequencing for *mcr* genes were performed for carbapenem- or colistin-resistant isolates. Nineteen (67.8%) carbapenem-resistant *K. pneumoniae* (n = 28) and one (20%) carbapenem-resistant *E. coli* (n = 5) isolate harbored bla_{KPC} (n = 17), bla_{OXA-48} (n = 2), and bla_{VIM} (n = 1) genes.

KEYWORDS *Enterobacteriaceae*, KPC, carbapenemases, colistin, *mcr-1*

The increase in antimicrobial-resistant infections is a concern worldwide (1). The World Health Organization has published a list of antibiotic-resistant bacteria that pose a substantial threat to human health (2). *Acinetobacter baumannii* complex, *Pseudomonas aeruginosa*, and *Enterobacteriaceae* isolates are at the top of the list.

In Taiwan, the increase in antimicrobial-resistant Gram-negative bacteria has caused a significant increase in infections, and an association with poorer patient outcomes has been observed (3). Generally, antimicrobial resistance focuses on nosocomial infections; however, there are increasing concerns regarding community-acquired antimicrobial-resistant microorganisms (4). A community may act as a reservoir and breeding ground for the transmission of microorganisms (5). The growing numbers of senior and long-term-care facilities further complicate the transmission dynamics of antimicrobial-resistant bacteria between the community and hospital (6, 7). The increasing interchange between patients and microorganisms as they move back and forth between hospitals and communities may blur the distinction between community-acquired and hospital-acquired pathogens (8).

The Surveillance of Multicenter Antimicrobial Resistance in Taiwan (SMART) is an ongoing surveillance study conducted by the Taiwan Centers for Disease Control. SMART has been monitoring the *in vitro* resistance of clinically important bacteria obtained from hospitals throughout Taiwan since 2017 (9, 10). In this study, we analyzed data on antimicrobial susceptibility and major resistance mechanisms, especially for carbapenem and colistin resistance, of clinically important Gram-negative bacteria from 18 hospitals in Taiwan in 2019, with emphasis on isolates from community-acquired infections.

Escherichia coli, *Klebsiella pneumoniae*, *P. aeruginosa*, and *A. baumannii* complex isolates obtained from patients with bloodstream infections were included in this study. When multiple isolates of the same species were obtained from the same patient, only the first isolate was included. The identification of isolates was confirmed using the Phoenix PMIC/ID-30 identification system (Becton, Dickinson, Sparks, MD). Community-acquired isolates were defined as isolates obtained within 48 h after admission to a hospital with symptoms and signs of infection on admission, in the absence of recent hospitalization or residence in a skilled-nursing facility, and with no history of antibiotic therapy within the last 3 months. Hospital-acquired isolates were defined as those obtained $>$48 h after admission from patients who initially did not have symptoms or signs of infection. The study was approved by the research ethics committees or institutional review boards of the participating hospitals.

For all antibiotics tested, except for colistin, MICs were determined using the Vitek 2 antimicrobial susceptibility system (AST-NB card; bioMérieux, Marcy-l'Étoile, France) (10). The MICs for colistin were determined using the broth microdilution method as recommended by CLSI (11). *E. coli* ATCC 25922 and *P. aeruginosa* ATCC 27853 were used as quality control strains. According to the MIC breakpoints recommended by CLSI for colistin, an MIC of $\leq$2 μg/ml was considered intermediate and an MIC of $\geq$4 μg/ml was considered resistant for *Enterobacteriaceae*, *P. aeruginosa*, and *A. baumannii* complex isolates (11).

Carbapenem-nonsusceptible *Enterobacteriaceae*, *P. aeruginosa*, and *A. baumannii* complex isolates were tested for genes encoding bla_{KPC}, bla_{NDM}, bla_{IMP}, bla_{VIM}, and

bla_{OXA-48} using the Xpert Carba-R assay (Cepheid, Sunnyvale, CA). The sequence types (STs) were determined using multilocus sequence typing (MLST) for isolates harboring the carbapenemase gene. Screening for *mcr-1* to *mcr-5* genes was performed for colistin-resistant *Enterobacteriaceae*, *P. aeruginosa*, and *A. baumannii* complex isolates (12).

During the study period, 1,294 bloodstream isolates (only 1 per patient was included), including *E. coli* ($n = 423$), *K. pneumoniae* ($n = 372$), *P. aeruginosa* ($n = 300$), and *A. baumannii* complex ($n = 199$), were collected consecutively. Of the 1,294 isolates studied, 772 (59.6%) were community acquired and 522 (40.3%) were hospital acquired. The *in vitro* activities of the antimicrobial agents tested are shown in Table 1. There were no significant differences ($P > 0.05$) in the percentage of resistance to ampicillin-sulbactam, ciprofloxacin, levofloxacin, and trimethoprim-sulfamethoxazole between hospital-acquired and community-acquired *E. coli* isolates. Carbapenems, amikacin, and colistin were the most-active agents tested against *E. coli*. The community-acquired isolates showed significantly higher ($P < 0.001$) rates of susceptibility to cefazolin (65.3% versus 41.0%), cefmetazole (92.1% versus 72.3%), cefotaxime (72.4% versus 42.2%), ceftazidime (83.8% versus 57.8%), and cefepime (92.1% versus 92.1%).

Hospital-acquired *K. pneumoniae* isolates were less susceptible than community-acquired *K. pneumoniae* isolates (Table 1). Both community-acquired and hospital-acquired isolates demonstrated the highest rates of susceptibility to amikacin (97.9% and 96.6%, respectively) and colistin (94.0% and 93.9%, respectively). The rates of susceptibility to third-generation cephalosporins (cefotaxime and ceftazidime) were >84% for community-acquired *K. pneumoniae* isolates but <60% for hospital-acquired isolates. Compared with community-acquired isolates, hospital-acquired *K. pneumoniae* isolates exhibited a significantly lower susceptibility to ciprofloxacin (54.9% versus 79.5%) and levofloxacin (46.6% versus 76.2%).

The rates of susceptibility of *P. aeruginosa* isolates to ciprofloxacin and levofloxacin were <80%, with nonsignificant differences between community-acquired and hospital-acquired isolates. The rates of susceptibility to agents against *A. baumannii* isolates were <65% except for amikacin (80.9%) and colistin (91.5%); the rates were similar in community-acquired and hospital-acquired isolates.

The carbapenem resistance rates were 1.2% (5/423) in *E. coli*, 7.5% (28/372) in *K. pneumoniae*, 14.3% (43/300) in *P. aeruginosa*, and 42.7% (85/199) in *A. baumannii* complex isolates. The rate of community-acquired isolates in colistin-resistant isolates was 40% (2/5) for *P. aeruginosa* and 13.3% (2/17) for *A. baumannii* complex. Approximately 77.7% (7/9) of *E. coli* and 50% (8/16) of *K. pneumoniae* that were resistant to colistin were community-acquired isolates.

Carbapenem-resistant *E. coli* ($n = 5$), *K. pneumoniae* ($n = 28$), *P. aeruginosa* ($n = 43$), and *A. baumannii* complex ($n = 85$) isolates were screened for carbapenemase genes (Table 2). Carbapenemase genes were detected mostly in *K. pneumoniae* isolates (67.8%, 19/28). Among the carbapenem-resistant *K. pneumoniae* isolates, 57.1% (16/28) harbored bla_{KPC}. Twenty-one percent (4/19) of carbapenemase-producing *K. pneumoniae* isolates were community acquired. All of the community-acquired carbapenemase-producing *K. pneumoniae* strains belonged to ST11. Of the carbapenemase-producing *Enterobacteriaceae*, 75% (15/20) were isolated from samples collected in central Taiwan, including all community-acquired carbapenemase-producing *K. pneumoniae* isolates (Fig. 1).

In this study, we demonstrated that the susceptibility rates of Gram-negative clinically important pathogens to several medically important antibiotics were similarly low in community-acquired and hospital-acquired isolates. Previously published surveillance studies in Taiwan reported that Gram-negative bacilli generally demonstrated higher rates of antimicrobial resistance in Taiwan than in Western countries (10, 13).

The extensive spread of resistance in *E. coli* isolates seen in this study was consistent with a previous study (14). We found a higher prevalence of third-generation cephalosporin resistance in *E. coli* isolates in this study than reported in Western countries, i.e., ~10% (15, 16). Prevalence rates similar to those from our findings have been reported

TABLE 1 *In vitro* susceptibility to tested antimicrobial agents among bloodstream isolates of *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* complex obtained from patients at 18 participating hospitals in Taiwan in 2019 and their *in vitro* susceptibility among community-acquired and hospital-acquired isolates

Bacterial species (n^a) and antimicrobial agent	MIC (μg/ml)			No. (%) of isolates with indicated susceptibility[b]			No. (%) of isolates with susceptibility category:		
	Range	50%	90%	S	I	R	Community acquired	Hospital acquired	*P* value
E. coli (423/340/83)									
Ampicillin-sulbactam	≤2 to ≥32	16	≥32	156 (36.9)	76 (18.0)	191 (45.2)	133 (39.1)	23 (27.7)	0.058
Cefazolin	≤4 to ≥64	≤4	≥64	256 (60.5)		167 (39.5)	222 (65.3)	34 (41.0)	<0.001
Cefmetazole	≤1 to ≥64	≤1	8	373 (88.2)	26 (6.1)	24 (5.7)	313 (92.1)	60 (72.3)	<0.001
Cefotaxime	≤1 to ≥64	≤1	≥64	281 (66.4)	3 (0.7)	139 (32.9)	246 (72.4)	35 (42.2)	<0.001
Ceftazidime	≤1 to ≥64	≤1	16	333 (78.7)	3 (0.7)	87 (20.6)	285 (83.8)	48 (57.8)	<0.001
Cefepime	≤1 to ≥64	≤1	2	377 (89.1)	19 (4.5)	27 (6.4)	313 (92.1)	64 (77.1)	<0.001
Piperacillin-tazobactam	≤4 to ≥128	≤4	8	387 (91.5)	21 (5.0)	15 (3.5)	316 (92.9)	71 (85.5)	0.046
Ertapenem	≤0.5 to 4	≤0.5	≤0.5	417 (98.6)	1 (0.2)	5 (1.2)	337 (99.1)	80 (96.4)	0.093
Imipenem	≤0.25 to 1	≤0.25	≤0.25	422 (99.8)	0 (0)	1 (0.2)	340 (100)	81 (97.6)	0.038
Meropenem	≤0.25	≤0.25	≤0.25	422 (99.8)	0 (0)	1 (0.2)	340 (100)	82 (98.8)	0.196
Ciprofloxacin	≤0.25 to ≥4	≤0.25	≥4	232 (54.8)	36 (8.5)	155 (36.6)	192 (56.5)	40 (48.2)	0.179
Levofloxacin	≤0.12 to ≥8	1	≥8	201 (47.5)	80 (18.9)	142 (33.6)	165 (48.5)	36 (43.4)	0.462
Gentamicin	≤1 to ≥16	≤1	≥16	334 (79.0)	0 (0)	89 (21.0)	266 (78.2)	68 (81.9)	0.549
Amikacin	≤2 to 16	≤2	4	422 (99.8)	0 (0)	1 (0.2)	340 (100)	82 (98.8)	0.196
TMP-SMX[c]	≤1 to ≥16	≤1	≥16	242 (57.2)		181 (42.8)	201 (59.1)	41 (49.4)	0.137
Tigecycline	≤0.5 to 4	≤0.5	≤0.5	NA	NA	NA	NA	NA	
Colistin	≤0.5 to ≥16	≤0.5	≤0.5		414 (97.9)	9 (2.1)	333 (97.9)[d]	81 (97.6)[d]	0.691
K. pneumoniae (372/239/133)									
Ampicillin-sulbactam	≤2 to ≥32	8	≥32	246 (66.1)	8 (2.2)	118 (31.7)	185 (77.4)	61 (45.9)	<0.001
Cefazolin	≤4 to ≥64	≤4	≥64	262 (70.4)		110 (29.6)	198 (82.8)	64 (48.1)	<0.001
Cefmetazole	≤1 to ≥64	≤1	≥64	299 (80.4)	22 (5.9)	51 (13.7)	210 (87.9)	89 (66.9)	<0.001
Cefotaxime	≤1 to ≥64	≤1	≥64	279 (75)	17 (4.6)	76 (20.4)	203 (84.9)	76 (57.1)	<0.001
Ceftazidime	≤1 to ≥64	≤1	≥64	285 (76.6)	15 (4.0)	72 (19.4)	207 (86.6)	78 (58.6)	<0.001
Cefepime	≤1 to ≥64	≤1	32	325 (87.4)	7 (1.9)	40 (10.8)	225 (94.1)	100 (75.2)	<0.001
Piperacillin-tazobactam	≤4 to ≥128	≤4	≥128	298 (80.1)	14 (3.8)	60 (16.1)	216 (90.4)	82 (61.7)	<0.001
Ertapenem	≤0.5 to ≥8	≤0.5	≤0.5	335 (90.1)	9 (2.4)	28 (7.5)	227 (95.0)	108 (81.2)	<0.001
Imipenem	≤0.25–≥16	≤0.25	1	343 (92.2)	12 (3.2)	17 (4.6)	228 (95.4)	115 (86.5)	0.004
Meropenem	≤0.25–≥16	≤0.25	≤0.25	349 (93.8)	1 (0.3)	22 (5.9)	233 (97.5)	116 (87.2)	<0.001
Ciprofloxacin	≤0.25 to ≥4	≤0.25	≥4	263 (70.7)	17 (4.6)	92 (24.7)	190 (79.5)	73 (54.9)	<0.001
Levofloxacin	≤0.12 to ≥8	≤0.12	≥8	244 (65.6)	55 (14.8)	73 (19.6)	182 (76.2)	62 (46.6)	<0.001
Gentamicin	≤1 to ≥16	≤1	≥16	300 (80.6)	11 (3.0)	61 (16.4)	214 (89.5)	86 (64.7)	<0.001
Amikacin	≤2 to ≥64	≤2	≤2	359 (96.5)	0 (0)	13 (3.5)	234 (97.9)	125 (94.0)	0.073
TMP-SMX	≤1 to ≥16	≤1	≥16	267 (71.8)		105 (28.2)	195 (81.6)	72 (54.1)	<0.001
Tigecycline	≤0.5 to ≥8	≤0.5	2	NA	NA	NA	NA	NA	
Colistin	≤0.5 to ≥16	≤0.5	≤0.5	NA	356 (95.7)	16 (4.3)	231 (96.6)[d]	125 (93.9)[d]	0.286
P. aeruginosa (300/146/154)									
Ceftazidime	≤1 to ≥64	4	16	257 (85.7)	19 (6.3)	24 (8)	136 (93.2)	121 (78.6)	<0.001
Cefepime	≤1 to ≥64	2	8	272 (90.7)	13 (4.3)	15 (5)	141 (96.6)	131 (85.1)	0.001
Piperacillin-tazobactam	≤4 to ≥128	8	≥128	238 (79.3)	24 (8)	38 (12.7)	128 (87.7)	110 (71.4)	0.001
Imipenem	≤0.25 to ≥16	2	≥16	257 (85.7)	0 (0)	43 (14.3)	135 (92.5)	122 (79.2)	0.002
Meropenem	≤0.25 to ≥16	≤0.25	4	260 (86.7)	12 (4)	28 (9.3)	139 (95.2)	121 (78.6)	<0.001
Ciprofloxacin	≤0.25 to ≥4	≤0.25	1	257 (85.7)	13 (4.3)	30 (10)	127 (87.0)	130 (84.4)	0.622
Levofloxacin	≤0.12 to ≥8	0.5	4	252 (84)	7 (2.3)	41 (13.7)	127 (87.0)	125 (81.2)	0.208
Gentamicin	≤1 to ≥16	≤1	2	282 (94)	2 (0.7)	16 (5.3)	136 (93.2)	146 (94.8)	0.63
Amikacin	≤2 to ≥64	≤2	4	296 (98.7)	1 (0.3)	3 (1)	146 (100)	150 (97.4)	0.123
Colistin	≤0.5 to ≥16	≤0.5	≤0.5	NA	295 (98.3)	5 (1.7)	144 (98.6)[d]	151 (98.4)[d]	0.999
A. baumannii complex (199/47/152)									
Ampicillin-sulbactam	≤2 to ≥32	≤2	≥32	122 (61.3)	16 (8.0)	61 (30.7)	32 (68.1)	90 (59.2)	0.307
Ceftazidime	≤1 to ≥64	16	≥64	96 (48.2)	25 (12.6)	78 (39.2)	24 (51.1)	72 (47.4)	0.739
Cefepime	≤1 to ≥64	8	≥64	105 (52.8)	8 (4.0)	86 (43.2)	26 (55.3)	79 (52.0)	0.74
Piperacillin-tazobactam	≤4 to ≥128	32	≥128	98 (49.2)	7 (3.5)	94 (47.2)	25 (53.2)	73 (48.0)	0.617
Imipenem	≤0.25 to ≥16	≤0.25	≥16	115 (57.8)	0 (0)	84 (42.2)	32 (68.1)	83 (54.6)	0.128
Meropenem	≤0.25 to ≥16	0.5	≥16	112 (56.3)	2 (1.0)	85 (42.7)	32 (68.1)	80 (52.6)	0.067
Ciprofloxacin	≤0.25 to ≥4	0.5	≥4	110 (55.3)	1 (0.5)	88 (44.2)	27 (57.4)	83 (54.6)	0.867
Levofloxacin	≤0.12 to ≥8	≤0.12	≥8	111 (55.8)	30 (15.1)	58 (29.1)	27 (57.4)	84 (55.3)	0.867

(Continued on next page)

TABLE 1 (Continued)

Bacterial species (n^a) and antimicrobial agent	MIC (μg/ml)			No. (%) of isolates with indicated susceptibility[b]			No. (%) of isolates with susceptibility category:		
	Range	50%	90%	S	I	R	Community acquired	Hospital acquired	*P* value
Gentamicin	≤1 to ≥16	≤1	≥16	119 (59.8)	7 (3.5)	73 (36.7)	31 (66.0)	88 (57.9)	0.395
Amikacin	≤2 to ≥64	≤2	≥64	161 (80.9)	5 (2.5)	33 (16.6)	39 (83.0)	122 (80.3)	0.832
TMP-SMX	≤1 to ≥16	≤1	≥16	113 (56.8)		86 (43.2)	32 (68.1)	81 (53.3)	0.092
Tigecycline	≤0.5 to ≥8	≤0.5	4	NA	NA	NA	NA	NA	
Colistin	≤0.5 to 2	≤0.5	≤0.5		182 (91.5)	17 (8.5)	45 (95.7)[d]	137 (90.1)[d]	0.370

[a]Number of total tested/community-acquired/hospital-acquired isolates.
[b]S, susceptible; I, intermediate; R, resistant; NA, not available.
[c]TMP-SMX, trimethoprim-sulfamethoxazole.
[d]Isolates with intermediate resistance to colistin.

in Africa, where third-generation cephalosporin resistance was found to be 10% to 30% (17). Subgroup analysis in our study revealed that 27.1% of community-acquired *E. coli* isolates were resistant to cefotaxime. In Taiwan, the proportion of third-generation cephalosporin-resistant *E. coli* isolates causing community-onset bacteremia was 0.5% from 2001 to 2002 (18) and 19.7% in 2015 (4). Moreover, the activity of antibiotics in an oral formulation, such as ampicillin-sulbactam, fluoroquinolones, and trimethoprim-sulfamethoxazole (TMP-SMX), in community-acquired *E. coli* infection was low. These findings have been observed in other studies (19–21). Controlling the spread of drug-resistant *E. coli* isolates in the community may be a challenge because of their broad distribution in the ecosystem (22).

In our study, 67.8% of carbapenem-nonsusceptible *K. pneumoniae* and 20% of carbapenem-nonsusceptible *E. coli* isolates carried the carbapenemase genes. ST11 KPC-2-producing *K. pneumoniae* isolates are endemic in Taiwan and China (23, 24), as demonstrated in our study. Moreover, the incidence of fluoroquinolone-resistant community-acquired carbapenemase-producing *K. pneumoniae* infection exceeded that of hospital-acquired *K. pneumoniae* infection. The incidence of fluoroquinolone-resistant *Enterobacteriaceae* correlated with fluoroquinolone usage (25, 26). Continued surveillance of carbapenem-resistant *Enterobacteriaceae* in the community is needed to reveal its nature (27).

TABLE 2 Characteristics of 20 *Enterobacteriaceae* isolates with carbapenemase-mediated genes

Carbapenemase gene	Species	ST[a]	MIC (μg/ml)					Site of acquisition[b]
			Ertapenem	Imipenem	Meropenem	Ciprofloxacin	Colistin	
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	>32	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{OXA-48}	*K. pneumoniae*	307	≥8	1	1	≥4	2	HA
bla_{OXA-48}	*K. pneumoniae*	11	≥8	8	4	≥4	2	CA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	16	CA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	16	CA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	1	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	CA
bla_{VIM}	*K. pneumoniae*	NA	≤0.5	2	≥16	0.5	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{KPC}	*K. pneumoniae*	2640	4	≥16	≥16	≥4	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	16	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{KPC}	*K. pneumoniae*	11	≥8	≥16	≥16	≥4	1	HA
bla_{KPC}	*E. coli*	3492	≥8	≥16	≥16	≥4	1	HA

[a]ST, type was not present in the MLST database. NA, not available.
[b]CA, community acquired; HA, hospital acquired.

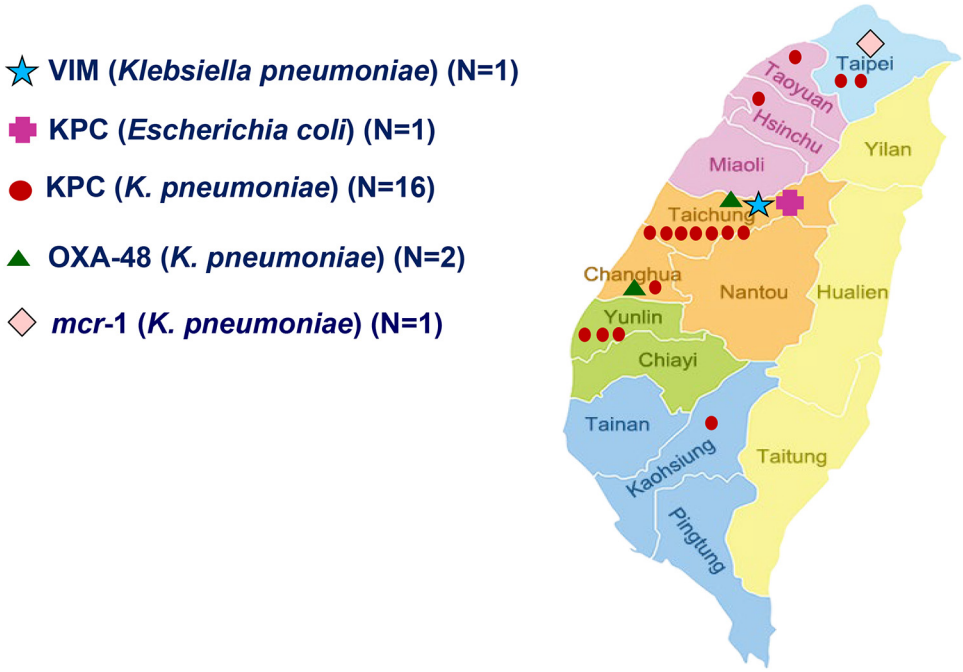

FIG 1 Geographical distribution of *E. coli* and *K. pneumoniae* isolates carrying bla_{KPC}, bla_{OXA-48}, bla_{VIM}, and *mcr-1*, identified by 2019 Surveillance of Multicenter Antimicrobial Resistance in Taiwan (SMART) program. KPC, *K. pneumoniae* carbapenemase; OXA-48, oxacillinase-48 carbapenem-hydrolyzing class D β-lactamase; *mcr-1*, mobilized colistin resistance-1; VIM, Verona integron-encoded metallo-β-lactamase.

The resistance pattern of *P. aeruginosa* isolates found in our study is consistent with other reports in Asia (28). Our data reveal that the rates of susceptibility to fluoroquinolones are similar in community-acquired and hospital-acquired *P. aeruginosa* isolates. Community-acquired *P. aeruginosa* infections had markedly high mortality rates in other studies (29). It has been demonstrated that the avoidance of fluoroquinolone-based empirical regimens for *P. aeruginosa* infections in settings with high rates of fluoroquinolone resistance improves patient outcomes and future susceptibility (30). Further studies are needed to assess the clinical impact of antimicrobial stewardships aimed at curbing the inappropriate use of fluoroquinolones.

Our results showed high resistance in *A. baumannii* complex isolates, which is consistent with previous studies (31). We further demonstrated that susceptibility to carbapenem is equally low in community-acquired and hospital-acquired *A. baumannii* complex isolates. A study in Taiwan revealed that the mortality rates were comparable between community-acquired and hospital-acquired *A. baumannii* bacteremia, and unfavorable outcomes were associated with carbapenem resistance (32). The spread of *A. baumannii* infection may be the result of patient migration between homes, hospitals, and long-term-care facilities (33).

This study has a number of limitations. The SMART project was an observational study. The prevalence of resistance among key pathogens may be influenced by several clinical parameters, but these data were not reported, and thus subgroup analysis based on these factors was not possible. Moreover, the role of environmental contamination is underreported in current studies. Several studies have demonstrated the importance of environmental surveillance in the investigation of antimicrobial resistance (34, 35).

In conclusion, we demonstrated the extent of antimicrobial resistance in clinically important Gram-negative bacteria in Taiwan. Because a community may act as a breeding ground for emerging resistance, the importance of antimicrobial resistance surveillance in communities cannot be overemphasized.

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