Supplementary data

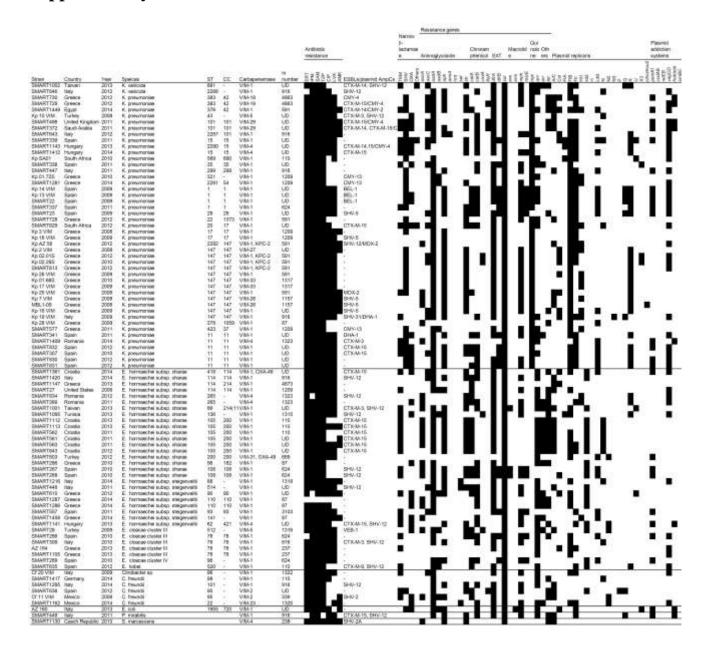


Figure S1. Resistance genes, antibiotic susceptibilities, plasmid replicons, and plasmid addictions systems. The order of strains is the same as that in each phylogenetic tree (Figs. 2, 3, 4). Abbreviations: ertapenem, ETP; imipenem, IPM; ampicillin/sulbactam, SAM; piperacillin/tazobactam, TZP; ciprofloxacin, CIP; levofloxacin, LVX; amikacin, AMK; trimethoprim/sulfamethoxazole, SXT. Non-susceptibility to antibiotics or the presence of genes were shown in black.

Table S1. Promoter types of class 1 integrons with bla_{VIM} .

Promoter type	No. of integron types (%)	No. of isolates (%)		
PcS	9 (60%)	18 (60%)		
PcS _{TGN-10}	0	0		
PcH2	2 (13%)	7 (23%)		
PcH2 _{TGN-10}	0	0		
PcW_{TGN-10}	2 (13%)	2 (7%)		
PcW-P2	1 (7%)	1 (3%)		
PcH1	0	0		
PcH1 _{TTN-10}	1 (7%)	2 (7%)		
No. of types/isolates determined	15	30		
Total no. of types/isolates	21	59		

The denominators of percentages are calculated using numbers of types/isolates determined.

Promoter types were presented in order of promoter strength.

Table S2. Downstream of gene cassettes of class 1 integrons with blavim.

	No. of integron types	No. of	
Immediate downstream	(%)	isolates (%)	
3'-CS-like			
3'-CS (<i>qacEΔ1-sul1-orf5</i>)-IS <i>1326-ΔtniB-tniA</i> -IRt (type-A)	1 (6%)	1 (3%)	
IS1326 deletion or ISCR1 insertion variants of type-A	2 (13%)	3 (8%)	
(type-B)			
IS26 insertion variants of type-B	8 (50%)	17 (44%)	
3'CS (qacE∆1-sul1-orf5-orf6)-IS6100°	4 (25%)	5 (13%)	
3'CS (qacE∆1-sul1)-ISCR1	1 (6%)	2 (5%)	
3'CS (ΔqacEΔ1)-IS10	1 (6%)	1 (3%)	
Non-3'-CS			
IS1R or ISPa21-like ^b	4 (25%)	10 (26%)	
No. of types/isolates determined	16	39	
Total no. of types/isolates	21	59	

CS, conserved segment; IRt, inverted repeat of Tn402-like transposon.

The denominators of percentages are calculated using numbers of types/isolates determined.

^a *chrA-padR* was inserted between a part of 3'-CS ($qacE\Delta 1$ -sul1- $\Delta orf5$) and IS6100 in 1 integron type (2 isolates). A part of 3'-CS (orf6) was deleted in 1 integron type (1 isolates).

^b 3'-CS-like segment were present downstream of IS*Pa21*-like sequence in 2 integron types (2 isolates).

Table S3. Average nucleotide identity (ANI) of a *Citrobacter* isolate that does not belong to any known species.

		Reference strain				
		<i>C</i> .	freundii	C.	braakii	C. werkmanii CIP
Isolate		CAV132	1	CIP10455	54	104555
Cf 20 VIM		94.33%		92.30%		90.54%
SMART1417 ^a	(<i>C</i> .	98.39%		92.30%		90.50%
freundii)						

ANI was calculated by BLAST (referred as ANIb in JSpecies).

^a This isolate, identified as *C. freundii* based on the phylogenetic tree (Fig. 4), was presented to show validity of the ANI analysis. The isolate has >95% identity against *C. freundii* CAV1321 and <95% identity against *C. braakii* CIP104554 and *C. werkmanii* CIP104555.