



**Table S1. Promoter types of class 1 integrons with *bla*<sub>VIM</sub>.**

Promoter type	No. of integron types (%)	No. of isolates (%)
PcS	9 (60%)	18 (60%)
PcS <sub>TGN-10</sub>	0	0
PcH2	2 (13%)	7 (23%)
PcH2 <sub>TGN-10</sub>	0	0
PcW <sub>TGN-10</sub>	2 (13%)	2 (7%)
PcW-P2	1 (7%)	1 (3%)
PcH1	0	0
PcH1 <sub>TTN-10</sub>	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 *bla*<sub>VIM</sub>.**

	No. of integron types (%)	No. of isolates (%)
Immediate downstream		
<b>3'-CS-like</b>		
3'-CS ( <i>qacEΔ1-sul1-orf5</i> )-IS1326-Δ <i>tniB</i> - <i>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 ( <i>qacEΔ1-sul1-orf5-orf6</i> )-IS6100 <sup>a</sup>	4 (25%)	5 (13%)
3'CS ( <i>qacEΔ1-sul1</i> )-ISCR1	1 (6%)	2 (5%)
3'CS (Δ <i>qacEΔ1</i> )-IS10	1 (6%)	1 (3%)
<b>Non-3'-CS</b>		
IS1R or ISPa21-like <sup>b</sup>	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.

<sup>a</sup> *chrA-padR* was inserted between a part of 3'-CS (*qacEΔ1-sul1-Δorf5*) and IS6100 in 1 integron type (2 isolates). A part of 3'-CS (*orf6*) was deleted in 1 integron type (1 isolates).

<sup>b</sup> 3'-CS-like segment were present downstream of ISPa21-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.**

Isolate	Reference strain		
	<i>C. freundii</i> CAV1321	<i>C. braakii</i> CIP104554	<i>C. werkmanii</i> CIP104555
Cf 20 VIM	94.33%	92.30%	90.54%
SMART1417 <sup>a</sup> ( <i>C. freundii</i> )	98.39%	92.30%	90.50%

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

<sup>a</sup> 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.