

	percent	Annotation
Metaplasmidome (PLCs)		
	3.01 %	putative transposase (K07497)
	1.67 %	transposase (K07486)
	1.36 %	site-specific DNA recombinase (K06400)
	1.16 %	transposase (K07483)
	1.06 %	putative tricarboxylic transport membrane protein (K07795)
	0.94 %	integrase (K14059)
	0.76 %	putative transposase (K07493)
	0.74 %	transposase (K07484)
	0.72 %	REP-associated tyrosine transposase (K07491)
	0.70 %	putative transposase (K07496)
NCBI database		
	4.95 %	putative transposase (K07497)
	3.77 %	putative transposase (K07498)
	2.97 %	transposase (K07483)
	2.58 %	transposase, IS6 family (K18320)
	2.07 %	putative DNA-invertase from lambdoid prophage Rac (K14060)
	2.01 %	insertion element IS1 protein InsB (K07480)
	1.71 %	transposase (K07486)
	1.56 %	transposase (K07484)
	1.04 %	transposase, IS30 family (K07482)
	1.04 %	transposase, IS5 family (K07481)

Supplementary Tab. 1: KEGG annotation harboured by PLCs and by plamids in the RefSeq database (NCBI)

Metaplasmidome (PLCs)		RefSeq database (NCBI)	
ABC Transporter	33.75 %	ABC Transporter	34.25 %
Glycopeptide Resistance	32.56 %	Glycopeptide Resistance	20.04 %
Gene Modulating Resistance	6.75 %	RND Antibiotic Efflux	8.51 %
RND Antibiotic Efflux	5.73 %	Beta-Lactamase	6.95 %
Beta-Lactamase	5.58 %	Aminoglycoside Modifying Enzyme	6.73 %
MFS Transporter	4.79 %	Gene Modulating Resistance	6.64 %
Chloramphenicol Resistance	2.10 %	MFS Transporter	5.21 %
Quinolone Resistance	2.00 %	Chloramphenicol Resistance	3.61 %
rRNA Methyltransferase	1.97 %	Tetracycline MFS Efflux	2.38 %
Aminoglycoside Modifying Enzyme	1.51 %	Other Efflux	2.29 %
Tetracycline MFS Efflux	1.32 %	Quinolone Resistance	1.12 %
Tetracycline Inactivation	0.98 %	rRNA Methyltransferase	0.78 %
Other Efflux	0.50 %	Tetracycline Ribosomal Protection	0.64 %
Other	0.24 %	Tetracycline Inactivation	0.63 %
Tetracycline Ribosomal Protection	0.12 %	Other	0.12 %
Aminoglycoside Resistance	0.09 %	Aminoglycoside Resistance	0.06 %

Supplementary Tab. 2: Annotation of ARGs harboured by PLCs and by plamids in the RefSeq database (NCBI)

9.62%	hypothetical protein
2.49%	msbA: ATP-binding cassette (ABC) antibiotic efflux pump [ARO:3000460]
1.64%	VanS: transcriptional regulator of van glycopeptide resistance genes [ARO:3000071]
1.2%	Multidrug export protein MepA
1.04%	macB: subunit of efflux pump conferring antibiotic resistance [ARO:3000535]
0.58%	major facilitator superfamily (MFS) antibiotic efflux pump [ARO:0010002]
0.46%	Uncharacterized signaling protein PA1727
0.4%	Chromosome partition protein Smc
0.38%	VanR: transcriptional activator regulating VanA%2C VanH and VanX" [ARO:3000574]
0.36%	PF00209 Sodium:neurotransmitter symporter family

Supplementary Tab. 4 : Recent gene transfers (100 % identity) between keyPLCs and MAGs inferred from the relationships within the bipartite network