Supplementary Material

Figure S1. Organization of GTA structural genes in *Citromicrobium* genomes. A, GTA in strains JL31, JL354, JL477, JL1351, JL2201, RCC1878, RCC1885 and RCC1897; B, GTA in strain WPS32. Yellow, conversed upstream and downstream genes (from 1 to 7) of the GTA structural gene cluster in *Citromicrobium* genomes; red, a putative transposase; pink, functions known in GTA genes; white, hypothetical genes; gray, conserved hypothetical genes belonging to GTA.
Figure S2. Structure and organization of prophage in *Citromicrobium*. Pink, early expression genes; orange, heads; yellow, tails; red, transposase; green, lysozyme genes; light gray, putative proteins.

Table S2. Average Nucleotide Identity by pairwise genome comparison



Figure S1

Figure S2



	JL31	JL354	JL477	JL1351	JL2201	RCC1878	RCC1885	RCC1897	WPS32
JL31	*	99.86	99.88	100	100	96.32	96.32	96.32	96.29
		[96.54]	[96.55]	[99.63]	[99.67]	[91.00]	[90.99]	[90.99]	[90.41]
JL354	99.71	*	100	99.71	99.63	96.04	96.04	96.04	96.19
	[93.86]		[98.73]	[93.88]	[94.85]	[88.79]	[88.78]	[88.78]	[87.26]
JL477	99.72	99.98	*	99.73	99.64	95.96	95.96	95.96	96.15
	[93.70]	[98.69]		[93.75]	[94.87]	[88.84]	[88.84]	[88.84]	[87.09]
JL1351	100	99.83	99.84	*	100	96.34	96.34	96.34	96.31
	[99.59]	[96.58]	[96.63]		[99.66]	[91.01]	[91.00]	[91.03]	[90.60]
JL2201	100	99.57	99.57	100	* 96.17 * [90.06	96.17	96.17	96.17	96.34
	[96.25]	[94.63]	[94.83]	[96.28]		[90.06]	[90.06]	[90.06]	[87.43]
RCC1878	96.47	96.26	96.22	96.47	96.46	*	100	100	96.45
	[87.37]	[87.53]	[87.49]	[87.43]	[88.33]		[99.62]	[99.62]	[87.04]
RCC1885	96.47	96.27	96.24	96.47	96.45	100 [99.65]	*	100	96.47
	[87.40]	[87.47]	[87.42]	[87.44]	[88.32]			[99.65]	[86.97]
RCC1897	96.40	96.22	96.16	96.40	96.39	99.98 [99.64]	99.98	*	96.48
	[87.35]	[87.31]	[87.42]	[87.37]	[88.21]		[99.64]		[86.65]
WPS32	96.39	96.44	96.41	96.39	96.39	96.51	96.51 96.51 [89.98] [89.98]	96.51	÷
	[89.91]	[89.07]	[88.84]	[89.95]	[89.90]	[89.98]		*	

 Table S2. Average Nucleotide Identity by pairwise genome comparison