

Correction

MICROBIOLOGY

Correction for “A comparative genomics approach identifies contact-dependent growth inhibition as a virulence determinant,” by Jonathan P. Allen, Egon A. Ozer, George Minasov, Ludmilla Shuvalova, Olga Kiryukhina, Karla J. F. Satchell, and Alan R. Hauser, which was first published March 10, 2020; 10.1073/

pnas.1919198117 (*Proc. Natl. Acad. Sci. U.S.A.* **117**, 6811–6821).

The authors note that, due to a printer’s error, Table 1 is missing the rows for AGEv14 and AGEv15. The corrected table appears below.

Table 1. Summary of investigated AGEs

AGE	Isolates*	Features	Context [†]	Mutant background [‡]	Dose [§]	n	P level [#]
AGEv							
AGEv1	14	Glucan synthesis, fatty acid metabolism	GI	PABL012 PABL057	6.5 6.2	10 10	<0.0001 0.0010
AGEv2	16	Phage-related, hypothetical	Phage	PABL026 PABL049	7.0 6.7	10 10	<0.0001 <0.0001
AGEv3	8	Transposon, hypothetical	Tn	PABL016	6.6	15	0.5755
AGEv4	5	Restriction modification	Tn	PABL007	7.0	10	0.0017
AGEv5	15	Substrate transport & metabolism		PABL049 PABL070	6.6 6.8	10 10	0.0002 0.0002
AGEv6	9	Phage-related, hypothetical	Phage	PABL012 PABL049	6.6 6.5	20 10	<0.0001 0.0085
AGEv7	49	Phage-related, hypothetical	Phage	PABL012 PABL049	6.5 6.9	15 10	<0.0001 <0.0001
AGEv8	3	RHS-containing gene	PMT	PABL016	6.6	15	0.0008
AGEv9	10	Phage-related	Phage	PABL012 PABL049	6.6 6.7	15 10	0.0164 0.0139
AGEv10	4	RND family heavy metal efflux proteins		PABL016 PABL068	6.8 5.8	15 10	0.4811 0.3933
AGEv11	2	Phage-related	Phage	PABL012	6.5	30	0.0001
AGEv12	82	ICE proteins	GI	PABL012 PABL049	6.6 6.7	15 10	0.0008 <0.0001
AGEv13	18	Autotransporter protein		PABL083 PABL107	6.5 6.5	20 30	0.5694 0.0526
AGEv14	10	DnaB, DnaC (phage replication)	Phage	PABL012 PABL013	6.6 6.5	10 15	<0.0001 0.2061
AGEv15	10	Contact-dependent growth inhibition	PMT	PABL017	6.8	20	0.0041
AGEx							
AGEx1	14	Phage related	Phage	PABL012	6.5	10	0.6789
AGEx2	69	Helicase, hypothetical	Phage	PABL012	6.5	10	0.2059
AGEx3	48	Peptide synthase, hypothetical		PABL016	6.7	10	0.2247
AGEx4	35	Hypothetical		PABL012	6.5	10	0.4328
AGEx5	32	Hypothetical		PABL049	6.7	10	0.2402

*Number of isolates in which the AGE was observed.

[†]Genomic context in which the AGE was observed. Abbreviations include pKLC102-like genomic island (GI), transposon (Tn), polymorphic toxin (PMT), or predicted prophage (Phage).

[‡]PABL isolate in which the AGE mutation was constructed.

[§]Dose for mouse bacteremia infection (log₁₀ CFU).

^{||}Number of mice infected.

[#]Log-rank test.

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