



Corrigendum: Composition and Diversity of CRISPR-Cas13a Systems in the Genus *Leptotrichia*

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A Corrigendum on

Composition and Diversity of CRISPR-Cas13a Systems in the Genus *Leptotrichia*

by Watanabe, S., Cui, B., Kiga, K., Aiba, Y., Tan, X.-E., Sato'o, Y., et al. (2019). *Front. Microbiol.* 10:2838. doi: 10.3389/fmicb.2019.02838

In the original article, there was a mistake in **Table 1** as published. “GC% of *L. wadei* JMUB3933, JMUB3934, JCM16777, *Leptotrichia* sp.-1 JMUB3936, *L. shahii* JCM16776, *L. hofstadii* JCM16775, *L. trevisanii* JMUB3870, JMUB4039, JMUB3935 and *L. buccalis* C-1013-b, *Leptotrichia* sp.-3 F0260, *Leptotrichia* sp. F0590, *L. goodfellowi* JCM16774 and *Leptotrichia* sp.-6 W10393, and chromosome length of *L. wadei* JCM16777” were incorrect. The corrected **Table 1** appears below.

In the original article, there was an error. GC% of genome-sequenced strains was incorrect.

A correction has been made to Results and Discussion, Comparative Analysis of *Leptotrichia* Genome, line 373-375:

As shown in **Table 1**, the chromosome size of the genus *Leptotrichia* varies from 2,142,946 to 2,829,322 bp with GC contents of 29.5% to 31.7%.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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TABLE 1 | Genome and CRISPR-Cas system information of genus *Leptotrichia*.

Species	Strain	Genome information				CRISPR/Cas class							Number of spacer ^c	
		Genome sequencing type ^b	Chromosome length (bp)	GC%	GenBank accession no.	Number of plasmid	Number of prophage/genomic island	I	II	III	IV	V		VI
<i>L. wadei</i>	KA00185	Draft genome	n/a ^a	n/a	GCA_001553045.1	n/a	n/a	-	-	-	-	-	-	5
<i>L. wadei</i>	JMUB3933	Complete genome	2361227	29.6%	AP019834	0	2	I-B	-	-	-	-	VI-A1, VI-A2	47
<i>L. wadei</i>	JMUB3934	Complete genome	2414633	29.6%	AP019835	4	2	-	-	-	-	-	VI-A	1
<i>L. wadei</i>	F0279	Draft genome	n/a	n/a	GCA_000469405.1	n/a	n/a	-	-	-	-	-	VI-A	7
<i>L. wadei</i>	JCM16777	Complete genome	2305216	29.5%	AP019829	1	0	-	-	-	-	-	-	3
<i>L. wadei</i>	DSM 19758	Draft genome	n/a	n/a	GCA_000373345.1	n/a	n/a	-	-	-	-	-	-	3
<i>Leptotrichia</i> sp.-1	JMUB3936	Complete genome	2335974	30.1%	AP019841	3	1	-	-	III-A1, III-A2	-	-	-	22
<i>L. shahii</i>	DSM 19757	Draft genome	n/a	n/a	GCA_000373045.1	n/a	n/a	I-B	-	III-A	-	-	VI-A	51
<i>L. shahii</i>	JCM16776	Complete genome	2142946	29.7%	AP019827	1	1	I-B	-	III-A	-	-	VI-A	63
<i>Leptotrichia</i> sp.-2	F0557	Draft genome	n/a	n/a	GCA_000469385.1	n/a	n/a	-	-	-	-	-	VI-A	6
<i>L. hongkongensis</i>	JMUB5056	Complete genome	2261073	29.9%	AP019846	1	1	-	-	-	-	-	-	11
<i>L. massiliensis</i>	P3007	Draft genome	n/a	n/a	GCA_900104625.1	n/a	n/a	-	-	-	-	-	VI-A1, VI-A2	21
<i>L. massiliensis</i>	F0581	Draft genome	n/a	n/a	GCA_000469525.1	n/a	n/a	-	-	-	-	-	VI-A	10
<i>L. hofstadii</i>	JCM16775	Complete genome	2548198	30.6%	AP019823	3	1	-	-	III-A	-	-	-	10
<i>L. hofstadii</i>	DSM 21651	Draft genome	n/a	n/a	GCA_000428965.1	n/a	n/a	-	-	III-A	-	-	-	6
<i>L. hofstadii</i>	F0254	Draft genome	n/a	n/a	GCA_000162955.1	n/a	n/a	-	-	-	-	-	-	0
<i>L. trevisanii</i>	DSM 22070	Draft genome	n/a	n/a	GCA_000482505.1	n/a	n/a	I-B	-	III-D	-	-	-	17
<i>L. trevisanii</i>	JMUB3870	Complete genome	2829322	30.6%	AP019831	2	1	I-B	-	III-D	-	-	-	78
<i>L. trevisanii</i>	JMUB4039	Complete genome	2685755	30.8%	AP019845	0	1	I-B	-	III-D	-	-	VI-A	56
<i>L. trevisanii</i>	JMUB3935	Complete genome	2729392	30.6%	AP019840	0	2	-	-	III-D	-	-	-	14
<i>L. buccalis</i>	C-1013-b	Complete genome	2465610	29.6%	GCA_000023905.1	0	0	I-B	-	III-D	-	-	VI-A	102
<i>Leptotrichia</i> sp.-3	F0260	Complete genome	2194935	29.8%	GCA_001553645.1	0	2	-	-	-	-	-	-	1
<i>Leptotrichia</i> sp.-4	bin_23	Draft genome	n/a	n/a	GCA_003638725.1	n/a	n/a	-	-	-	-	-	-	0
<i>Leptotrichia</i> sp.-4	F0590	Complete genome	2152181	29.6%	GCA_002240055.1	0	1	-	-	III-D	-	-	-	37
<i>L. goodfellowii</i>	F0264	Draft genome	n/a	n/a	GCA_000176335.1	n/a	n/a	-	-	-	-	-	-	11
<i>L. goodfellowii</i>	JCM16774	Complete genome	2290729	31.7%	AP019822	0	1	I-B	-	III-like	-	-	-	38
<i>L. goodfellowii</i>	DSM 19756	Draft genome	n/a	n/a	GCA_000516535.1	n/a	n/a	I-B	-	III-like	-	-	-	39
<i>Leptotrichia</i> sp.-5	W9775	Draft genome	n/a	n/a	GCA_000469505.1	n/a	n/a	-	II-C	-	-	-	-	19
<i>Leptotrichia</i> sp.-6	W10393	Complete genome	2444904	31.4%	GCA_001274535.1	0	0	I-B	-	III-like	-	-	-	201

^an/a indicates not applicable; ^bBold font indicates that genome sequences were determined in this study; ^cTotal number of spacer carried by all types of CRISPR-Cas systems.