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Corrigendum: Physiology of Highly Radioresistant *Escherichia coli* After Experimental Evolution for 100 Cycles of Selection.

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Publication Date

2020

DOI

10.3389/fmicb.2020.617806

Peer reviewed



Corrigendum: Physiology of Highly Radioresistant *Escherichia coli* After Experimental Evolution for 100 Cycles of Selection

OPEN ACCESS

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Specialty section:

This article was submitted to
Evolutionary and Genomic
Microbiology,
a section of the journal
Frontiers in Microbiology

Received: 15 October 2020

Accepted: 05 November 2020

Published: 11 December 2020

Citation:

Bruckbauer ST, Martin J, Minkoff BB,
Veling MT, Lancaster I, Liu J,
Trimarco JD, Bushnell B, Lipzen A,
Wood EA, Sussman MR,
Pennacchio C and Cox MM (2020)
Corrigendum: Physiology of Highly
Radioresistant *Escherichia coli* After
Experimental Evolution for 100 Cycles
of Selection.
Front. Microbiol. 11:617806.
doi: 10.3389/fmicb.2020.617806

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Keywords: ionizing radiation, experimental evolution, reactive oxygen species, double-strand breaks, DNA Repair, *Escherichia coli*, *Deinococcus radiodurans*

A Corrigendum on

Physiology of Highly Radioresistant *Escherichia coli* After Experimental Evolution for 100 Cycles of Selection

by Bruckbauer, S. T., Martin, J., Minkoff, B. B., Veling, M. T., Lancaster, I., Liu, J., et al. (2020) *Front. Microbiol.* 11:582590. doi: 10.3389/fmicb.2020.582590

In the original article, there was a mistake in **Table 1** as published. Three rows in **Table 1** were inadvertently labeled incorrectly. The rows are in the “Transversions” category as follows: GC to TA, AT to TA, and GC to CG. We have re-labeled these rows so that these data under each population heading now reflects the correct number of each mutation type (in order, these rows are now AT to TA, GC to CG, and GC to TA). The corrected **Table 1** appears below.

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 | Number and types of mutations in evolved populations after 100 cycles of selection.

	Parent bp	Mutant bp	IR9-100	IR10-100	IR11-100	IR12-100
Transitions	AT	GC	275	257	109	170
	GC	AT	445	376	244	484
Transversions	AT	CG	63	48	26	55
	AT	TA	196	139	79	186
	GC	CG	75	78	42	91
	GC	TA	350	267	173	348
Totals	Total		1404	1165	673	1334
	Transitions		720	633	353	654
	Transversions		684	532	320	680
Coding	Ts:Tv		1.05	1.19	1.10	0.96
	Synonymous		356	311	171	317
	Non-synonymous		822	669	383	813
	Stop gained		52	36	24	46
	Stop lost		3	2	1	1
	Start lost		3	2	0	2
	Insertions	+1	3	5	3	3
		+2	1	0	0	0
		+6	0	0	1	0
		+12	0	0	1	0
	Deletions	-1	137	79	32	65
		-2	4	1	2	3
		-3	1	0	0	2
		-11	0	1	0	0
		-29	1	0	0	0
-39		0	0	1	0	
Total		1383	1106	619	1252	
Non-coding	SNPs		189	158	100	169
	Insertions	+1	0	0	0	1
	Deletions	-1	15	11	5	12
		-2	0	0	0	1
Allele frequencies	Total		204	169	105	183
	Fixed (>99%)		332	95	164	306
	>50%		516	279	336	336
	>10%		1087	850	543	933
	>2%		1668	1260	732	1469