



# The Open Microbiology Journal

Content list available at: <https://openmicrobiologyjournal.com>

## Supplementary Material



## EDL933 Strains of *Escherichia coli* O157 can Demonstrate Genetic Diversity and Differential Adherence to Bovine Recto-Anal Junction Squamous Epithelial Cells

Raegan S. Hoefler<sup>1,2,#</sup> and Indira T. Kudva<sup>1,\*</sup>

<sup>1</sup>U.S. Department of Agriculture, Food Safety and Enteric Pathogens Research Unit, National Animal Disease Center, Agricultural Research Service, Ames, Iowa

<sup>2</sup>College of Agriculture and Life Sciences, Iowa State University, Ames, Iowa

### Article History

Received: January 11, 2021

Revised: July 01, 2021

Accepted: July 12, 2021

**Table S1. Quantitation of RSE cells with adherent EDL933 strains and isogenic mutants.**

Bacteria Tested	Bacterial Adherence Pattern	Eukaryotic cells (n=80) <sup>1</sup> with adherent bacteria, in the ranges shown, for two different trials <sup>2</sup> (MOI <sup>3</sup> = 10 <sup>6</sup> bacteria:10 <sup>5</sup> cells)				Percent Mean +/- standard error of mean, of eukaryotic cells with adherent bacteria in the ranges shown <sup>6</sup>	
		Trial I		Trial II		>10	1-10
		>10	1-10 <sup>4</sup>	>10	1-10		
EDL933WT <sup>5</sup> ATCC 43895	Aggregative, Moderate	24	56	12	68	23± 8	78± 8
<b>Source A:</b>							
EDL933-T	Diffuse, Moderate	23	56	10	70	21± 8	80± 10
TUV 933-1	Aggregative, Strong	79	1	77	3	98± 2	3± 1
TUV 933-2	Aggregative, Strong	64	16	71	9	85± 5	16± 5
TUV 933-2c	Aggregative, Strong	80	0	80	0	100± 0	0
<b>Source B:</b>							
EDL933-R	Aggregative, Strong	80	0	76	4	98± 3	3± 3
EDL933-R $\Delta$ stx1	Aggregative, Strong	80	0	80	0	100± 0	0
EDL933-R $\Delta$ stx2	Aggregative, Strong	80	0	80	0	100± 0	0
EDL933-R $\Delta$ stx1, $\Delta$ stx2	Aggregative, Strong	80	0	80	0	100± 0	0
<b>Source C:</b>							
EDL933-E	Aggregative, Strong	45	35	54	26	62± 6	38± 6
EDL933-E strR1	Aggregative, Strong	54	26	64	16	74± 6	26± 6
EDL933-E strR2	Aggregative, Strong	74	6	71	9	91± 2	9± 2
EDL933-E strR3	Aggregative, Strong	53	27	65	15	74± 8	27± 8

<sup>1</sup>Total number of cells evaluated in each trial.

<sup>2</sup>Each trial had one slide per bacterial group. Each slide in turn had 4 technical replicates spotted on it; 20 well-dispersed cells were evaluated per spot.

<sup>3</sup>MOI, multiplicity of infection.

<sup>4</sup>Number of bacteria adhering to each cell is shown as a range of >10, and 1-10. Number of cells without bacteria is not shown.

<sup>5</sup>WT, wild type

<sup>6</sup>Percent means for ranges used to determine "moderate or strong" adherence are in bold.

Table S2. Quantitation of HEp-2 cells with adherent EDL933 strains and isogenic mutants.

Bacteria Tested	Bacterial Adherence Pattern	Eukaryotic cells (n=80) <sup>1</sup> with adherent bacteria, in the ranges shown, for two different trials <sup>2</sup> (MOI <sup>(3)</sup> = 10 <sup>6</sup> bacteria:10 <sup>5</sup> cells)				Percent Mean +/- standard error of mean, of eukaryotic cells with adherent bacteria in the ranges shown <sup>6</sup>	
		Trial I		Trial II		>10	1-10
		>10	1-10 <sup>(4)</sup>	>10	1-10		
EDL933WT <sup>5</sup> ATCC 43895	Diffuse, Moderate	0	40	0	41	0	51± 0.7
<b>Source A:</b>							
EDL933- T	Diffuse, Moderate	0	47	0	57	0	65± 9
TUV 933-1	Diffuse, Moderate	0	47	3	57	2± 2	65± 9
TUV 933-2	Diffuse, Moderate	2	40	0	64	1.5± 1.5	65± 15
TUV 933-2c	Diffuse, Moderate	0	45	0	68	0	71± 15
<b>Source B:</b>							
EDL933-R	Diffuse, Moderate	1	32	2	48	2± 1	50± 10
EDL933-R $\Delta$ stx1	Diffuse, Moderate	0	39	0	40	0	50± 1
EDL933-R $\Delta$ stx2	Diffuse, Moderate	1	49	1	53	1± 0	64± 3
EDL933-R $\Delta$ stx1, $\Delta$ stx2	Diffuse, Moderate	0	37	0	48	0	53± 7
<b>Source C:</b>							
EDL933-E	Diffuse, Moderate	0	49	1	55	0.5± 0.5	65± 4
EDL933-E Str 1	Diffuse, Moderate	0	50	0	35	0	54± 10
EDL933-E Str 2	Diffuse, Moderate	4	37	0	48	2.5± 2.5	53± 7
EDL933-E Str 3	Diffuse, Moderate	0	36	2	48	1.5± 1.5	53± 8

<sup>1</sup>Total number of cells evaluated in each trial.<sup>2</sup>Each trial had one slide per bacterial group. Each slide in turn had 4 chambers (technical replicate) on it; 10-20 well-dispersed cells were evaluated per chamber.<sup>3</sup>MOI, multiplicity of infection.<sup>4</sup>Number of bacteria adhering to each cell is shown as a range of >10, and 1-10. Number of cells without bacteria is not shown.<sup>5</sup>WT, wild type<sup>6</sup>Percent means for ranges used to determine "moderate or non-adherent" adherence are in bold.

© 2021 Hoefler and Kudva

This is an open access article distributed under the terms of the Creative Commons Attribution 4.0 International Public License (CC-BY 4.0), a copy of which is available at: <https://creativecommons.org/licenses/by/4.0/legalcode>. This license permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.