Supplementary data for article:

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## Supplementary Tables for Nastasijevic et al.

Seasonal prevalence and characterization of Shiga toxin-producing *Escherichia coli* on pork carcasses at three steps of the harvest process at two commercial processing plants in the US

- TABLE S1. Characterization of STEC O121(n=229) isolated from pork processing.
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										STEC	C O121								
	$n^{\mathrm{b}}$	2 (sp)	1	1	2	1	2	6	163	1 (f)	2 (p)	20	1	2 (p)	17	1	1	2	4 (sp)
with ar	hin season 1d plant <sup>c</sup>						+	+			+	+		+	+				
xin <sup>d</sup>	stx <sub>1a</sub>	+																	
<u>ga to</u>	stx <sub>2e</sub>	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+			
<u>Shig</u>	$stx_{2x}$																+	+	+
	katP		+	+	+	+											+		
57e	espP		+																
<u>p01</u>	etpD		+	+															
	cnf1/2																		
	eastA I	+				+	+	+	+	+	+							+	
	eastA II	+	+		+	+	+	+	+			+	+				+	+	
	chuA		+	+			+												
	iha		+					+		+			+	+		+			
	saa		+													+			

TABLE S1. Characterization of STEC O121(n=229)<sup>a</sup> isolated from pork processing

<sup>a</sup>Shiga toxin-producing *E. coli* serogroup O121, lacking intimin (*eae*) gene, not all isolates were available for characterization. <sup>b</sup>All isolates recovered from skin of stunned exsanguinated pigs sampled along belly midline, unless indicated by letter(s) in parenthesis: s=skin, p=post-scald pre-evisceration pig carcasses, f=chilled finished pig carcasses.

<sup>c</sup>When more than one similar strain was identified, "+" indicates whether the strains were all recovered during the same sample collection period and at the same plant.

<sup>d</sup>Shiga toxin gene subtypes. " $stx_{2x}$ " indicates that the  $stx_2$  subtype could not be definitively identified.

<sup>e</sup>Genes common to the large virulence plasmid of *E. coli* O157:H7.

	O Group	O2	05		08				0	20		O32		055	5	O74	O86		O91						
	n <sup>c</sup>	1	1	17 (sp)	3	2 1	1	1	6	1	1	1	1	5	1	1	1	1 (p )	1 (p)	11	7 (sp )	1	1	1	1
within season and plant <sup>d</sup>					+									+											
<u>Shiga toxin<sup>e</sup></u>	stx <sub>1a</sub>											+	+								+				
	stx <sub>2a</sub>					+																			
	$stx_{2c}$																								
	$stx_{2e}$	+	+	+	+	+	+	+	+	+	+			+	+	+	+	+	+	+		+	+	- +	
	$stx_{2x}$					+							+												+
f	hlyA											+	+								+				+
157	katP							+				+									+				+
Od	espP							+																	
	etpD							+																	
	cnf1/2						+											+							
	eastA I									+														+	-
	eastA II	+			+				+		+				+			+	+		+		+	- +	-
	<i>chuA</i>						+	+										+							
	iha							+			+	+				+					+	+			+

TABLE S2. Characterization of STEC<sup>a</sup> O2, O5, O8, O20, O32, O55, O74, O86 and O91 isolated from pork processing.

<sup>a</sup>Shiga toxin-producing *E. coli* of serogroups indicated, lacking intimin (eae) gene.

<sup>b</sup>ONT = serogroup was not typable using limited antisera sets available.

<sup>c</sup>All isolates recovered from skin of stunned exsanguinated pigs sampled along belly midline, unless indicated by letter(s) in parenthesis: s=skin, p=post-scald pre-evisceration pig carcasses, f=chilled finished pig carcasses.

parentnesis: s=skin, p=post-scald pre-evisceration pig carcasses, i=chilled finished pig carcasses.

<sup>d</sup>When more than one similar strain was identified, "+" indicates whether the strains were all recovered during the same sample collection period and at the same plant.

<sup>e</sup>Shiga toxin gene subtypes. " $stx_{2x}$ " indicates that the  $stx_2$  subtype could not be definitively identified.

<sup>f</sup>Genes common to the large virulence plasmid of *E. coli* O157:H7 (*hlyA, katP, espP, etpD*).

	O Group	O103	O110	0112		O139 O			O141	0	146	ONT <sup>b</sup>															
	n <sup>c</sup>	1	1	1	8	5	1	1	3	2	1	2	1	8	1	1	1	1 3	5	1	2	1	1	1	1	1	1
witl ar	nin season 1d plant <sup>d</sup>									+																	
	$stx_{1a}$		+	+									+		+	+	+	+				+				+	
<u>Shiga toxin</u> <sup>e</sup>	$stx_{2a}$																										
	$stx_{2c}$																						+				
	stx <sub>2e</sub>	+			+	+	+	+	+	+	+			+					+	+	+			+	+	+	+
	$stx_{2x}$											+			+	+							+				
	hlyA															+											
57 <sup>f</sup>	katP		+					+					+		+			+							+	+	+
p01	espP																										
	etpD																										+
	cnf1/2																										
	eastA I	+																						+			+
	eastA II	+			+			+			+						+	+	+		+	+	+	+			+
	chuA						+	+														+		+	+	+	
	iha																+			+	+	+	+		+	+	

TABLE S3. Characterization of STEC<sup>a</sup> O103, O110, O112, O139, O141, O146 and O not typable isolated from pork processing

<sup>a</sup>Shiga toxin-producing *E. coli* of serogroups indicated, lacking intimin (*eae*) gene.

<sup>b</sup>ONT = serogroup was not typable using limited antisera sets available.

<sup>c</sup>All isolates recovered from skin of stunned exsanguinated pigs sampled along belly midline, unless indicated by letter(s) in parenthesis: s=skin, p=post-scaldpre-evisceration pig carcasses, f=chilled finished pig carcasses.

<sup>d</sup>When more than one similar strain was identified, "+" indicates whether the strains were all recovered during the same sample collection period and at the same plant.

"eShiga toxin gene subtypes. " $stx_{2x}$ " indicates that the  $stx_2$  subtype could not be definitively identified.

<sup>f</sup>Genes common to the large virulence plasmid of *E. coli* O157:H7 (*hlyA, katP, espP, etpD*).

	n <sup>b</sup>	1	1	1	1	4	12	1(p)	2	1	1	3	1
wit aı	hin season nd plant <sup>c</sup>					-	-		-			+	
<u>xin<sup>d</sup></u>	stx <sub>1a</sub>	+	+	+	+	+	+	+	+	+	+	+	+
ta to	stx <sub>2a</sub>	+	+	+	+	+	+	+	+	+	+	+	+
Shig	stx <sub>2e</sub>								+				+
	nleA				+	+	+	+	+	+	+	+	+
	nleB	+	+	+	+	+	+	+	+	+	+	+	+
	nleC	+	+	+	+	+	+	+	+	+	+	+	+
	nleD	+	+	+	+	+	+	+	+	+	+	+	+
	nleE	+	+	+	+	+	+	+	+	+	+	+	+
	nleF	+	+	+	+	+	+	+	+	+	+	+	+
enes	nleG	+	+	+	+	+	+	+	+	+	+	+	+
ılege	G2-1	+	+	+	+	+	+	+	+	+	+	+	+
T	G2-3									+	+	+	+
	G5-2	+	+	+	+	+	+	+	+	+	+	+	+
	G6-2	+	+	+	+	+	+	+	+	+	+	+	+
	<i>G</i> 9		+	+	+	+	+	+	+	+	+	+	+
	H1												
	ent	+	+	+	+	+	+	+	+	+	+	+	+
	hlyA	+	+	+	+	+	+	+	+	+	+	+	+
57 <sup>f</sup>	katP	+	+	+	+	+	+	+	+	+	+	+	+
p01	espP	+	+	+	+	+	+	+	+	+	+	+	+
	etpD	+	+	+	+	+	+	+	+	+	+	+	+
	cnf1/2		+					+			+		
	eastA I	+			+		+	+	+			+	+
	eastA II	+	+	+		+	+	+	+	+	+	+	+
	chuA	+	+	+	+	+	+	+	+	+	+	+	+
	iha	+	+	+	+	+	+	+	+	+	+	+	+

TABLE S4. Characterization of EHEC O157:H7 isolates<sup>a</sup>

**TABLE S4.** Characterization of EHEC O157:H7 isolates<sup>a</sup> (continued).

<sup>a</sup>Isolates wereconfirmed to be serotype O157:H7 and all possessed intimin (*eae*) genesubtype gamma.

<sup>b</sup>All isolates recovered from skin of stunned exsanguinated pigs sampled along belly midline, unless indicated by letter(s) in parenthesis: s=skin, p=post-scald pre-evisceration pig carcasses, f=chilled finished pig carcasses.

<sup>c</sup>When more than one similar strain was identified, "+" indicates whether the strains were all recovered during the same sample collection period and at the same plant.

<sup>d</sup>Shiga toxin gene subtypes. " $stx_{2x}$ " indicates that the  $stx_2$  subtype could not be definitively identified.

<sup>e</sup>Non-locus of enterocyte effacement (LEE) genes located in O-Islands:36, 57, 71, and122 associated with more severe disease causing EHEC pathoserotypes.

<sup>f</sup>Genes common to the large virulence plasmid of *E. coli* O157:H7 (*hlyA, katP, espP, etpD*)

	O group	08	(	D26	01	103		(	0121				0	NT <sup>b</sup>		
	n <sup>c</sup>	1	1	2(f)	1	1	2	1	1	1	1	1	l(p)	1	1	1
with	nin season			+			+									
an	nd plant <sup>d</sup>															
cin <sup>e</sup>	stx <sub>1a</sub>	+	+	+			+	+	+		+	+	+			
tox	stx <sub>2a</sub>		+		+	+	+	+	+			+				
iiga	$stx_{2c}$															+
SI	stx <sub>2e</sub>	+					+		+	+	+				+	
	universal	+	+	+	+	+	+	+	+	+	+	+	+	+	+	+
nin <sup>f</sup>	gamma											+				
ntin	beta 1		+	+										+	+	
•=	epsilon				+	+	+	+	+							
	nleA		+	+			+	+	+			+	+			+
gg	nleB	+	+	+	+	+	+	+	+	+	+	+	+	+	+	
	nleC		+		+	+	+	+	+	+		+			+	
	nleD		+				+	+	+	+		+				
	nleE		+	+			+	+	+				+			+
	nleF		+	+	+	+	+	+	+		+	+	+	+		+
snes	nleG		+	+			+	+	+		+	+	+			+
lege	G2-1		+				+	+	+	+		+				
n	G2-3			+								+	+			+
	G5-2		+	+			+	+	+	+		+	+			+
	G6-2		+	+			+	+	+		+	+	+			+
	<i>G</i> 9		+				+	+	+			+				+
	nleH1			+										+		
	ent		+	+			+	+	+	+	+	+				
-	hlyA	+	+	+		+	+	+	+	+	+	+	+	+		+
57	katP	+	+	+	+	+	+	+	+	+		+	+	+		+
p01	espP		+	+			+	+	+			+				
	etpD		+		+	+	+	+	+			+		+		+
	lifA			+												
	cnf 1/2								+	+		+				
	eastA I		+				+	+	+	+						
	eastA II	+	+				+	+	+			+				+
	chuA	+	+				+	+	+	+		+		+		
	iha	+	+	+	+		+	+	+			+				+

TABLE S5. Characterization of non-O157 EHEC<sup>a</sup> isolates

**TABLE S5.** Characterization of non-O157 EHEC<sup>a</sup> isolates (continued).

<sup>a</sup>EHEC are enterohemorrhagic*E*. *coli* possessing Shiga toxin (*stx*) and intimin (*eae*) genes belonging to the O-serogroup indicated.

<sup>b</sup>ONT=serogroup was not typable using limited antisera sets available

<sup>c</sup>All isolates recovered from skin of stunned exsanguinated pigs sampled along belly midline, unless indicated by letter(s) in parenthesis: s=skin, p= post-scald pre-evisceration pig carcasses, f=chilled finished pig carcasses.

<sup>d</sup>When more than one similar strain was identified, "+" indicates whether the strains were all recovered during the same sample collection period and at the same plant.

<sup>e</sup>Shiga toxin gene subtypes. " $stx_{2x}$ " indicates that the  $stx_2$  subtype could not be definitively identified.

<sup>f</sup>Intimin (*eae*) genes were determined to be present in each isolate using universal oligonucleotide primers. Then only specific subtypes gamma, beta 1 or epsilon were identified. Some isolates possess a non-identified subtype.

<sup>g</sup>Non-locus of enterocyte effacement (LEE) genes located in O-Islands:36, 57, 71, and122 associated with more severe disease causing EHEC pathoserotypes.

<sup>h</sup>Genes common to the large virulence plasmid of *E. coli* O157:H7 (*hlyA, katP, espP, etpD*)