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Case–Control Study of Factors Associated with Hemolytic Uremic Syndrome among Shiga Toxin–Producing *Escherichia coli* Patients, Ireland, 2017–2020

Appendix 2

Appendix 2 Table 1. Microbial genomic factors (individual *stx* genes) associated with hemolytic uremic syndrome development among people notified with Shiga toxin-producing *Escherichia coli* in Ireland, case-control study 2017–2020

		Cases (HUS)		Controls (Non-HUS)						
		n	%	n	%					
Total	Genes	108		416		OR	95% CI			p value*
stx1	None	58	54	116	28	Ref				
	stx1a	48	44	246	59	**0.4**	**0.25**	**-**	**0.61**	**<0.05**
	stx1c	0	0.0	48	12	0.0	NA	-	NA	0.976
	stx1d	0	0.0	3	0.7	0.0	NA	-	NA	0.994
	Missing	2	1.9	3	0.7					
stx2†	None	4	3.7	133	32	Ref				
	stx2a†	97	90	201	48	**16.0**	**6.5**	**-**	**53**	**<0.05**
	stx2b	1	0.9	37	8.9	0.9	0.0	-	6.3	0.925
	stx2c†	4	3.7	32	7.7	4.2	0.9	-	18	0.052
	stx2d	0	0.0	6	1.4	0.0	NA	-	NA	0.989
	stx2e	0	0.0	4	1.0	0.0	NA	-	NA	0.991
	Missing	2	1.9	3	0.7					

*By χ^2 test. Bold text indicates statistical significance.
†One control had both *stx2a* and *stx2c*, and one control had both *stx2c* and *stx2a*: for both controls the second *stx* gene was excluded from the analysis.

Appendix 2 Table 2. Microbial genomic factors from GWAS (n = 26 genes) associated with hemolytic uremic syndrome development among people notified with Shiga toxin-producing *Escherichia coli* in Ireland, case-control study 2017–2020

		Cases (HUS)		Controls (Non-HUS)						
		n	%	n	%					
Total	Gene present	108	-	416	-	OR	95% CI			p value*
stx2B	No	12	11	183	44	Ref				
	Yes	96	89	233	56	**6.3**	**3.5**	**-**	**12**	**<0.05**
ybcQ_1	No	18	17	212	51	Ref				
	Yes	90	83	204	49	**5.2**	**3.1**	**-**	**9.2**	**<0.05**
ydfU_1	No	24	22	227	55	Ref				
	Yes	84	78	189	45	**4.2**	**2.6**	**-**	**7.0**	**<0.05**
group_30198	No	22	20	217	52	Ref				
	Yes	86	80	199	48	**4.3**	**2.6**	**-**	**7.2**	**<0.05**
group_31760	No	22	20	218	52	Ref				
	Yes	86	80	198	48	**4.3**	**2.6**	**-**	**7.3**	**<0.05**
rsxG	No	6	5.6	80	19	Ref				
	Yes	102	94	336	81	**4.1**	**1.9**	**-**	**11**	**<0.05**
sodA	No	32	30	219	53	Ref				
	Yes	76	70	197	47	**2.6**	**1.7**	**-**	**4**	**<0.05**
pfkA	No	32	30	218	52	Ref				
	Yes	76	70	198	48	**2.6**	**1.7**	**-**	**4.2**	**<0.05**

		Cases (HUS)		Controls (Non-HUS)						
		n	%	n	%					
Total	Gene present	108	-	416	-	OR	95% CI			p value*
sbp	No	32	30	210	50	Ref				
	Yes	76	70	206	50	**2.4**	**1.6**	**-**	**3.9**	**<0.05**
cdh	No	32	30	208	50	Ref				
	Yes	76	70	208	50	**2.4**	**1.5**	**-**	**3.8**	**<0.05**
tpiA	No	31	29	209	50	Ref				
	Yes	77	71	207	50	**2.5**	**1.6**	**-**	**4.0**	**<0.05**
group_36684	No	31	29	210	50	Ref				
	Yes	77	71	206	50	**2.5**	**1.6**	**-**	**4.1**	**<0.05**
group_31570	No	31	29	207	50	Ref				
	Yes	77	71	209	50	**2.5**	**1.6**	**-**	**3.9**	**<0.05**
group_33058	No	30	28	208	50	Ref				
	Yes	78	72	208	50	**2.6**	**1.7**	**-**	**4.2**	**<0.05**
uspD	No	31	29	208	50	Ref				
	Yes	77	71	208	50	**2.5**	**1.6**	**-**	**4.0**	**<0.05**
fieF	No	33	31	219	53	Ref				
	Yes	75	69	197	47	**2.5**	**1.6**	**-**	**4.0**	**<0.05**
cpxP	No	31	29	208	50	Ref				
	Yes	77	71	208	50	**2.5**	**1.6**	**-**	**4.0**	**<0.05**
group_34824	No	31	29	208	50	Ref				
	Yes	77	71	208	50	**2.5**	**1.6**	**-**	**4.0**	**<0.05**
cpxA	No	31	29	206	50	Ref				
	Yes	77	71	210	50	**2.4**	**1.6**	**-**	**3.9**	**<0.05**
yiiM	No	31	29	205	49	Ref				
	Yes	77	71	211	51	**2.4**	**1.5**	**-**	**3.9**	**<0.05**
ygiW_2	No	17	16	141	34	Ref				
	Yes	91	84	275	66	**2.7**	**1.6**	**-**	**4.9**	**<0.05**
group_5720	No	32	30	223	54	Ref				
	Yes	76	70	193	46	**2.7**	**1.8**	**-**	**4.4**	**<0.05**
group_30187	No	8	7.4	117	28	Ref				
	Yes	100	93	299	72	**4.9**	**2.5**	**-**	**11**	**<0.05**
group_31748	No	10	9.3	132	32	Ref				
	Yes	98	91	284	68	**4.6**	**2.4**	**-**	**9.6**	**<0.05**
group_20906	No	60	56	313	75	Ref				
	Yes	48	44	103	25	**2.4**	**1.6**	**-**	**3.8**	**<0.05**
yiaU	No	6	5.6	86	21	Ref				
	Yes	102	94	330	79	**4.4**	**2.0**	**-**	**12**	**<0.05**

*By χ^2 test. Bold text indicates statistical significance.