

Norovirus Genotype Profiles Associated with Foodborne Transmission, 1999–2012

Technical Appendix

Technical Appendix Table. Proportion of foodborne outbreaks per genotype as estimated based on norovirus surveillance data in Noronet, ESR-EpiSurv, CaliciNet and an updated systematic review of scientific literature

Profile	FBVE/Noronet 1999-2012				ESR-EpiSurv 2008-2012				CaliciNet 2009-2012		Systematic literature review			
	P-type (n=4580)		C-type (n=2196)		P-type (n=685)		C-type (n=813)		C-type (n=3094)		P-type (n=107)		C-type (n=127)	
Group Type	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)
GI	315	0.36 (0.29-0.42)	169	0.53 (0.43-0.62)	56	0.28 (0.17-0.40)	66	0.28 (0.18-0.39)	322	0.30 (0.24-0.36)	15	0.71 (0.46-0.91)	14	0.91 (0.69-1.00)
I.1	12	0.17 (0.01-0.52)	10	0.57 (0.23-0.88)	0		0		4	0.25 (0.01-0.71)	0		0	
I.2	20	0.57 (0.32-0.81)	12	0.75 (0.43-0.96)	4	0.20 (0.01-0.61)	6	0.29 (0.05-0.65)	10	0.44 (0.15-0.75)	0		1	0.66 (0.15-0.99)
I.3	99	0.27 (0.18-0.38)	50	0.41 (0.26-0.58)	13	0.29 (0.09-0.54)	15	0.31 (0.12-0.55)	77	0.29 (0.18-0.41)	8	0.63 (0.29-0.90)	2	0.67 (0.15-0.99)
I.4	85	0.37 (0.25-0.50)	52	0.50 (0.35-0.66)	20	0.38 (0.19-0.59)	21	0.36 (0.18-0.57)	38	0.26 (0.11-0.45)	3	0.75 (0.28-0.99)	2	0.67 (0.16-0.99)
I.5	4	0.50 (0.10-0.90)	5	0.80 (0.39-0.99)	1	0.33 (0.01-0.84)	1	0.33 (0.01-0.85)	17	0.22 (0.07-0.43)	1	0.66 (0.15-0.99)	0	
I.6	0		32	0.56 (0.37-0.73)	14	0.27 (0.08-0.51)	21	0.23 (0.08-0.42)	150	0.29 (0.21-0.38)	1	0.33(0.01-0.84)	0	
I.7	12	0.50 (0.18-0.81)	7	0.57 (0.22-0.88)	0		0		24	0.60 (0.35-0.82)	0		0	
I.8	2	0.33 (0.01-0.84)	0		2	0.50 (0.09-0.91)	2	0.50 (0.09-0.91)	1	0.67 (0.16-0.99)	0		2	0.67 (0.17-0.99)
I.9	0		0		0		0		1	0.33 (0.01-0.84)	0		0	
I.14	0		0		0		0		0		0		3	0.67 (0.15-0.99)
I.a	2	0.75 (0.30-0.99)	n.a.		0		n.a.		n.a.		0		n.a.	
I.b	72	0.38 (0.26-0.50)	n.a.		2	0.25 (0.01-0.70)	n.a.		n.a.		0		n.a.	
I.d	4	0.60 (0.19-0.93)	n.a.		0		n.a.		n.a.		0		n.a.	
I.e	2	0.50 (0.09-0.90)	n.a.		0		n.a.		n.a.		0		n.a.	
I.f	1	0.67 (0.05-1.00)	n.a.		0		n.a.		n.a.		0		n.a.	
GII non4	656	0.28 (0.24-0.32)	467	0.44 (0.39-0.49)	71	0.31 (0.21-0.43)	190	0.28 (0.22-0.35)	602	0.25 (0.21-0.29)	23	0.56 (0.33-0.77)	46	0.82 (0.64-0.94)
II.1	17	0.57 (0.32-0.80)	50	0.52 (0.38-0.67)	0		3	0.40 (0.07-0.80)	208	0.18 (0.13-0.24)	2	0.26 (0.01-0.71)	3	0.33 (0.01-0.84)
II.2	72	0.25 (0.14-0.38)	39	0.56 (0.39-0.72)	7	0.33 (0.09-0.65)	22	0.37 (0.16-0.53)	47	0.18 (0.07-0.32)	7	0.50 (0.15-0.85)	5	0.80 (0.39-0.99)

Profile	FBVE/Noronet 1999-2012				ESR-EpiSurv 2008-2012				CaliciNet 2009-2012		Systematic literature review			
	P-type (n=4580)		C- type (n=2196)		P-type (n=685)		C-type (n=813)		C-type (n=3094)		P-type (n=107)		C-type (n=127)	
	Group Type	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N	Proportion FB (95%CI)	N
II.3	5	0.33 (0.05-0.72)	142	0.21 (0.13-0.30)	0		48	0.22 (0.11-0.35)	22	0.31 (0.13-0.54)	10	0.62 (0.29-0.90)	11	0.80 (0.39-0.99)
II.5	5	0.20 (0.01-0.60)	3	0.80 (0.40-0.99)	1	0.67 (0.16-0.99)	2	0.50 (0.09-0.91)	4	0.80 (0.40-0.99)	2	0.50 (0.10-0.91)	3	n.a.
II.6*	2	0.25 (0.01-0.71)	93	0.53 (0.41-0.65)	1	0.66 (0.15-0.99)	59	0.20 (0.10-0.31)	128	0.28 (0.20-0.37)	0		7	0.67 (0.29-0.95)
II.7	195	0.27 (0.19-0.35)	71	0.64 (0.48-0.78)	3	0.50 (0.09-0.91)	27	0.41 (0.23-0.60)	66	0.29 (0.17-0.42)	1	0.33 (0.01-0.95)	7	0.86 (0.55-1.00)
II.8	9	0.50 (0.21-0.78)	4	0.80 (0.40-0.99)	0		0		0		0		2	0.67 (0.15-0.99)
II.10	0		1	0.33 (0.01-0.84)	0		0		0		0		1	0.67 (0.16-0.99)
II.12	14	0.46 (0.18-0.74)	30	0.46 (0.26-0.66)	16	0.31 (0.12-0.56)	17	0.53 (0.30-0.75)	98	0.42 (0.30-0.55)	1	0.67 (0.17-0.99)	0	
II.13	0		14	0.54 (0.28-0.79)	0		7	0.22 (0.03-0.54)	19	0.07 (0.00-0.25)	0		0	
II.14	0		9	0.38 (0.10-0.71)	0		1	0.67 (0.16-0.99)	3	0.50 (0.10-0.91)	0		1	n.a.
II.15	5	0.25 (0.01-0.71)	0		0		0		0		0		1	0.67 (0.16-0.99)
II.16	3	0.75 (0.29-0.99)	2	0.33 (0.01-0.84)	8	0.30 (0.07-0.60)	0		3	0.50 (0.10-0.90)	0		0	
II.17	8	0.50 (0.21-0.79)	2	0.25 (0.01-0.71)	0		0		3	n.a.	0		0	
II.20	4	0.33 (0.29-0.84)	6	0.38 (0.10-0.71)	4	0.34 (0.05-0.71)	4	0.34 (0.05-0.71)	0		0		0	
II.21	0		0		0		0		1	0.16 (0.05-0.32)	0		0	
II.22	2	0.75 (0.29-0.99)	0		1	0.33 (0.01-0.84)	0		0		0		0	
II.b	213	0.24 (0.18-0.30)	n.a.		14	0.13 (0.02-0.34)	0	n.a.	0		0		n.a.	
II.c	0		n.a.		14	0.57 (0.32-0.81)	0	n.a.	0		0		n.a.	
II.g	100	0.30 (0.21-0.40)	n.a.		3	0.40 (0.07-0.81)	0	n.a.	0		0		n.a.	
II.m	1	0.67 (0.15-0.99)	n.a.		0		0	n.a.	0		0		n.a.	
nonGII.4	971	0.30 (0.27-0.34)	636	0.46 (0.41-0.51)	127	0.29 (0.22-0.38)	256	0.29 (0.22-0.38)	924	0.26 (0.23-0.30)	38	0.63 (0.46-0.80)	60	0.87 (0.74-0.96)
GII.4***	3595	0.08 (0.07-0.09)	1528	0.19 (0.16-0.21)	547	0.09 (0.07-0.12)	546	0.09 (0.07-0.12)	2139	0.12 (0.10-0.14)	59	0.31 (0.18-0.45)	45	0.75 (0.52-0.92)
Mixed outbreak	14	0.71 (0.46-0.91)	31	0.81 (0.64-0.93)	11	0.46 (0.21-0.72)	11	0.46 (0.22-0.72)	31	0.16 (0.05-0.33)	10	0.63 (0.29-0.90)	22	0.88 (0.68-0.98)

* Region B does not well distinguish between the polymerase of GII.6/7/8.

** Estimates in green fonts do not statistically differ, i.e. 95% confidence intervals overlap, with FBVE/Noronet polymerase proportions as a reference; estimates given in red fonts do statistically differ.

***II.e is seen with the new variant II.4-Sydney capsid and thereby it is unclear whether this polymerase-based genotype should be considered a II.4 or II-non-4 genotype. This II.e polymerase genotype was included in the II.4 group in the polymerase profile, since it statistically showed most correspondence to the II-4 group.

Systematic Literature Review Update

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