**SUPPLEMENTARY MATERIAL**

**Supplementary Table 1.** Norovirus genotypes in outbreaks reported to the National Outbreak Reporting System (NORS) and CaliciNet, 2009–2016 (n=3,747)

|  |  |  |
| --- | --- | --- |
|  | n | % |
| **GII.4 genotypes** | **2,353** | **62.8** |
| Sydney | 1,521 | 40.6 |
| New Orleans | 739 | 19.7 |
| Den Haag | 82 | 2.2 |
| Other GII.4a | 11 | 0.3 |
| **Other GII (non GII.4)** | **839** | **22.4** |
| GII.6 | 214 | 5.7 |
| GII.2 | 172 | 4.6 |
| GII.1 | 129 | 3.4 |
| GII.7 | 81 | 2.2 |
| GII.12 | 61 | 1.6 |
| GII.3 | 56 | 1.5 |
| GII.13 | 52 | 1.4 |
| GII.17 | 42 | 1.1 |
| Other GIIa | 32 | 0.9 |
| **GI genotypes** | **553** | **14.8** |
| GI.3 | 229 | 6.1 |
| GI.6 | 143 | 3.8 |
| GI.5 | 61 | 1.6 |
| GI.2 | 57 | 1.5 |
| GI.4 | 37 | 1.0 |
| Other GIa | 26 | 0.7 |

aOther genotypes reported in <1% of outbreaks: GII.14 (15), GI.7 (15), GII.5 (12), GII.4 Osaka (10), GI.1 (9), GI.9 (2), GII.16 (2), GII.4 untypeable (1), GII.15 (1), GII.25 (1), GII.8 (1). 2 GIV genotypes also reported. Virus genotyping was based on VP1 region.

**Supplementary Table 2.** Selected characteristics of genotype GII.4 and non-GII.4 norovirus outbreaks reported to the National Outbreak Reporting System (NORS) and CaliciNet, 2009–2016

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | **GII.4 outbreaks**  **(n=2,353)** | | **Non-GII.4 outbreaks**  **(n=1,394)** | | **p-value** |
|  | *Median* | *Interquartile Range* | *Median* | *Interquartile Range* |  |
| **Sex of ill persons**a |  |  |  |  |  |
| Female (%) | 73 | 57 – 82 | 54 | 50 – 79 | <0.0001 |
| Male (%) | 28 | 18 – 43 | 38 | 37 – 40 | <0.0001 |
| **Age of ill persons** (years)b |  |  |  |  |  |
| 0 to 74 (%) | 40 | 18 – 94 | 91 | 31 – 100 | <0.0001 |
| 75+ (%) | 60 | 6 – 82 | 9 | 0 – 69 | <0.0001 |
| **Symptoms**c |  |  |  |  |  |
| Fever (%) | 18 | 7 – 38 | 24 | 8 – 50 | 0.0065 |
| Vomiting (%) | 69 | 55 – 90 | 79 | 61 – 100 | 0.0002 |

aOutbreaks reporting any sex information: GII.4 = 1,506, non-GII.4 = 927

bOutbreaks reporting any age information: GII.4 = 1,609, non-GII.4 = 1,003

cOutbreaks reporting any symptom information: GII.4 = 2,003, non-GII.4 = 1,216

**Supplementary Table 3.** Association of transmission mode with GII.4 versus non-GII.4 norovirus genotypes, stratified by setting, in outbreaks reported to the National Outbreak Reporting System (NORS) and CaliciNet, 2009–2016a

|  | **Non-Healthcare Setting (N = 1326)** | | | | **Healthcare Setting (N = 2383)** | | | | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Transmission Mode** | **No. of Outbreaks** | **Odds Ratio for GII.4** | **95% CI** | **P value** |  | **No. of Outbreaks** | **Odds Ratio for GII.4** | **95% CI** | **P value** |
|  |  | | | | | | | | |
| Non-Foodborne | 725 | 1.00 | – | – |  | 2389 | 1.00 | – | – |
| Foodborne | 621 | 1.95 | (1.49, 2.55) | < 0.0001 |  | 54 | 0.97 | (0.49, 2.02) | 0.94 |

aMultivariable models of genotype as a function of transmission mode, adjusted for case demographics, reported symptoms, and seasonality.