**Epidemiology & Infection**

**A Large Outbreak of Acute Gastroenteritis in Shippensburg, Pennsylvania, 1972 Revisited: Evidence for Common Source Exposure to a Recombinant GII.Pg/GII.3 Norovirus**

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**Supplementary Material**

**Supplemental Table S1 – Symptoms in cases at Shippensburg College and town**

|  |  |  |
| --- | --- | --- |
| **Symptom** | **% College** | **% Towns** |
| **Nausea** | 91.0 | 73.0 |
| **Vomiting** | 75.8 | 50.7 |
| **Diarrhoea** | 79.1 | 66.9 |
| **Stomach cramps** | 76.4 | 64.0 |
| **Fever or feverish feeling** | 77.4 | 28.6 |
| **Chills** | 74.2 | 41.8 |
| **Muscle aches** | 60.4 | 31.4 |
| **Headache** | 72.4 | 48.7 |
| **Dizziness** | 65.9 | 29.3 |
| **Sore throat** | 24.3 | 18.9 |
| **Cough** | 12.7 | 16.9 |
| **Runny nose** | 18.4 | 17.7 |

Table adapted from the initial CDC outbreak report. Symptoms were similar for both the college and town, with 91.0% of the college cases experiencing nausea compared to 73.0% of the town cases. The percentage experiencing a particular symptom was higher in the college except for cough.

**Supplemental Table S2 – Next generation sequencing coverage**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Sample | Median sequencing depth | Interquartile range | Mean sequencing depth | Standard deviation |
| B24 | 3367.5 | 2642-4537 | 3651.9 | 1435.8 |
| C1 | 8702 | 7111-10798 | 9064.5 | 2937.4 |
| C2 | 15041 | 11683-19302 | 15754.6 | 5710.8 |
| PB | 9142.5 | 6572-11888 | 9968.3 | 4731.6 |

Median and mean sequencing depth with appropriate measures of dispersion for each sample are provided.

**Supplemental Figure S1 – Predicted ORF1 features and underlying variation in the viral genome.**

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**B**

**A**

A) Predicted ORF1 features are illustrated based on norovirus GII genome [1]. Protein size and amino acid cleavage sites are noted above the map, with nucleotide boundaries noted below. B) Underlying amino acid variation in the four cases is indicated in the nonstructural polyprotein, VP1, and VP2. Nucleotide boundaries of the ORFs are noted above the graph. Blue lines signify amino acids with >10% of the read population differing from consensus. The red line in VP1 is amino acid 68 in case C2 that differed from the other consensus sequences.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Accession Number | Polymerase genotype | Capsid genotype | Year isolated | Strain Name |
| KY442319 | GII.Pg | GII.3 | 1972 | ShippB24 |
| KM198484, KM198493, KM198496, KM198500, KM198505, KM198509, KM198511, KM198528, KM198529, KM198547, KM198553, KM198561, KM198563, KM198572, KM198573, KM198583, KM198586, KM198590 | GII.P21 | GII.3 | 2009-2011 | 30212, 30468, 20419, C2H-20, 20460, 20479, C2H-24, C2H-25, C2H-27, C2H-47, 30381, 30303, C2365, 20370, C2H-45, 20493, 30400, C2H-39 |
| KM198492, KM198503 | GII.Pg | GII.12 | 2010 | 30448, C2033 |
| KC464496, KC464497, KC464498, KC464499, KC464500 | GII.Pg | GII.12 | 2010 | CGMH38, CGMH39, CGMH40, CGMH41, CGMH42 |
| EU921389 | GII.P21 | GII.3 | 2007 | Pune/PC52 |
| AB365435 | GII.P21 | GII.3 | 2004 | TCH04-577 |
| LN854569 | GII.P21 | GII.3 | 2014 | Groningen |
| LN854570 | GII.Pg | GII.1 | 2014 | Groningen |
| GU980585 | GII.P12 | GII.3 | 2006 | CBNU1 |
| GU991355 | GII.P12 | GII.3 | 2009 | SH312 |
| KF306213 | GII.P12 | GII.3 | 2013 | Jingzhou/2013402 |
| JX846924 | GII.Pg | GII.3 | 1978 | HK71 |
| HQ449728, HQ664990 | GII.Pg | GII.12 | 2010 | HS210, HS206 |
| JQ613568, JQ613569 | GII.Pg | GII.12 | 2009-2010 | Wahroonga/NSW004P, Gunnedah/NSW895P |
| GQ845370 | GII.Pg | GII.12 | 2008 | StGeorge/NSW199U |
| KF895841, KF944110, KF944111 | GII.P16 | GII.3 | 2011-2012 | Smolensk/S12-31, Novosibirsk/Nsk-N1659, Novosibirsk/Nsk-N1648 |
| U02030 | GII.P3 | GII.3 | 1993 | Toronto/TV24 |
| DQ379713 | GII.PX | GII.3 | 1983 | Goulburn Valley/G5175A |
| DQ379714 | GII.Pg | GII.13 | 1983 | Goulburn Valley/G5175B |
| KC962457 | GII.P21 | GII.3 | 2010 | 6108 |
| KC962458 | GII.PX | GII.3 | 2010 | Bushbuckridge6387 |
| KC962459 | GII.Pg | GII.1 | 2011 | 6799 |
| KJ710246 | GII.Pg | GII.12 | 2012 | Bushbuckridge9306 |
| KR904231 | GII.Pg | GII.10 | 2013 | Johannesburg12243 |
| KR904232 | GII.Pg | GII.2 | 2013 | Bushbuckridge12257 |

**Supplemental Table S3 – Genbank strains used for phylogenetic analysis of Shippensburg strain**

Accession numbers for GenBank strains used in phylogenetic analyses are provided. Strain names and years are abstracted from GenBank names. Polymerase and capsid genotypes were identified using the norovirus typing tool [2].

**References**

1. **Belliot G, *et al.*** In vitro proteolytic processing of the MD145 norovirus ORF1 nonstructural polyprotein yields stable precursors and products similar to those detected in calicivirus-infected cells. *Journal of Virology* 2003; **77**(20): 10957–10974.

2. **Kroneman A, *et al.*** An automated genotyping tool for enteroviruses and noroviruses. *Journal of Clinical Virology* 2011; **51**(2): 121–125.