**Supplementary Material**

1. **Sequences for the primers and probes used in the amplification and sequencing of the outbreak specimens.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Assay Name** | **Primer/Probe Name** | **Sequence** | **Probe type** | **Final Concentration (nM)** |
| Pan-HRV TaqMan RT-PCR | Pan-HRV-F1Pan-HRV-F2Pan-HRV-F3 | GCCYGCGTGGCTGCCGCCYGCGTGGTGCCCGCCTGCGTGGCGGCC | N/A | 200200100 |
| Pan-HRV-R | GAAACACGGACACCCAAAGTAGT | N/A | 400 |
| Pan-HRV-P | FAM-TCCGGCCCCTGAATGYGGCTAA-TAMRA | TaqMan-FAM/TAMRA | 120 |
| HRV Genotyping RT-PCR | HRV-seqFU(also as sequencing primer) | ACTACTTTGGGTGTCCGTGTTTC | N/A | 200 |
| HRV-seqRL | TCNGGHARYTTCCAVCACCA | N/A | 800 |

1. **Additional details on viral nucleic acid amplification, sequencing and phylogenetic analysis.**

RNA was extracted directly from 200 μl of clinical sample with the MagNA Pure LC total nucleic acid isolation kit (Roche Molecular System, Laval, Quebec, Canada). Reverse transcription and PCR amplification of a 540-nucleotide fragment of the HRV VP4/VP2 capsid genes were performed with the One-Step RT-PCR Kit (QIAGEN, Mississauga, Ontario, Canada). VP4/VP2 amplicons were sequenced using an ABI3730xl DNA Analyzer (Applied Biosystems, Foster City, CA, USA). Relatedness of outbreak and community strains (GenBank accession nos. MH603569–MH603590), as well as prototypical HRV species A, B and C strains obtained from GenBank (Figure 1), was assessed by phylogenetic analyses conducted in the MEGA7 software (v. 7.0.21). The evolutionary history was computed by the Neighbor-Joining method, the evolutionary distances by the Maximum Composite Likelihood method and the topology accuracy by 1000 bootstrap replicates.

1. **Supplementary Table 1.**

**Table 1.** Epidemiologic data and clinical manifestations of the rhinovirus infections for each outbreak case.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Patient**  | **Birth weight (g)** | **GA at birth** **(weeks + days)** | **Day of outbreak on which symptoms were first present** | **Age at diagnosis (days)** | **Significant underlying cardiorespiratory comorbidities** | **Respiratory symptoms** | **Other symptoms** | **Fever****(peak temp.; °C)** | **Type of baseline resp. support** | **Escalation of respiratory support (Yes/No)** | **Death** |
| 1 | 2490 | 40 + 1 | 1 | 42 | Hypertrophic cardiomyopathy | Apnea, cough/sneeze, thick secretions | - | Yes(38.6) | None | Yes | Yes |
| 2 | 760 | 27 + 0 | 2 | 465 | BPD, Laryngomalacia | Cough/sneeze, thick secretions | - | No(36.8) | HME (day), HHTC (night) | No | No |
| 3 | 890 | 24 + 3 | 4 | 74 | BPD, Ventricular septal defect | Apnea, thick secretions | Irritability, Abdominal distension | No(37.4) | CPAP | No | No |
| 4 | 1110 | 28 + 6 | 5 | 81 | BPD, Laryngomalacia | - | Irritability, vomiting | No(37.5) | LFNC | No | No |
| 5 | 680 | 25 + 1 | 7 | 122 | BPD, Pulmonary hypertension | Apnea | Vomiting | No(36.8) | LFNC | No | No |
| 6 | 710 | 24 + 3 | 12 | 121 | BPD | Apnea, cough/sneeze, thick secretions | Irritability | No(37.2) | LFNC | No | No |
| 7 | 820 | 24 + 3 | 14 | 123 | BPD, Left Pneumatocele | Apnea, thick secretions | Abdominal distension | No(37.3) | LFNC | No | No |

*GA: Gestational Age; BPD: bronchopulmonary dysplasia; CPAP: Continuous positive airway pressure; HHTC: Highly humidified tracheal collar; HME: Heat and Moisture Exchanger; LFNC: Low flow nasal cannula; RDS: Respiratory distress syndrome.*

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **EXIT****Waiting Rm****Washroom** | **Patient Room** | **Patient Room** | **Patient Room** | **Transport Zone** | **Patient Room** | **Patient Room** | **Patient Room** | **Patient Room** |  | **Patient Room** |
|  |
| **Nurse Station** |  | **Employee Washroom** | **Patient Room** |  | **Patient Room** | **Patient Room** |  | **Patient Room** | **Nurse Station** |  | **Patient Room** |
| **Medication Room** | **Patient Room** | **Patient Room** | **Patient Room** | **Patient Room** | **Patient Room** | **Patient Room** | **Patient Room** |
| **6****(12)** | **Patient Room** | **Patient Room** | **Patient Room** | **4****(5)** | **Patient Room** |  | **Patient Room** |
| **Patient Bed** | **Patient Room** | **Patient Bed** |
| **7****(14)** | **Patient Room** | **Patient Room** | **Patient Room** | **Patient Bed** | **Patient Room** | **Patient Room** |
| **Developmental Care Room** | **Clean Utility Room** | **Medication Room** | **Patient Room** | **Patient Room** | **Medication Room** | **Patient Room** |
| **Patient Room** | **Patient Room** | **Nurse Station** | **Patient Room** | **Patient Room** | **Patient Room** | **Patient Room** | **Electrical Room** |
|  |
| **Family Room****Toilet** | **Simulation****Room** | **1****(1)** | **3****(4)** | **2****(2)** | **Patient Room** | **Patient Room** | **Patient Room** | **Patient Room** | **5****(7)** | **Patient Room** | **Family Room****Toilet** |

**Supplementary Figure 1**

**Supplementary Figure 1 Legend:**

Architectural plan of the Montreal Children’s Hospital Neonatal Intensive Care Unit. Each room is designated by a two-digit number. The rooms in color represent the location of the cases, with each of the four clades represented by a distinct color: clade 1 in red; clade 2 in green; clade 3 in blue; clade 4 in yellow. The day of outbreak on which symptoms of HRV infection started are written for each patient in brackets under the room numbers.