Clinical characteristics and molecular epidemiology of human metapneumovirus in children with acute lower respiratory tract infections in China, 2017 to 2019: a multicentre prospective observational study

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Table S1 Temporal, geographical and molecular characteristics of 27 complete HMPV genomes obtained in this study.

| No. | HMPV isolate | City      | Year | Subtype | GenBank accession number |
|-----|--------------|-----------|------|---------|-------------------------|
| 1   | BCH19067     | Beijing   | 2019 | A2c     | OM262393                |
| 2   | WZ17192      | Wenzhou   | 2018 | A2c     | OM262394                |
| 3   | WZ17369      | Wenzhou   | 2019 | A2c     | OM262395                |
| 4   | WZ17372      | Wenzhou   | 2019 | A2c     | OM262396                |
| 5   | WZ17391      | Wenzhou   | 2019 | A2c     | OM262397                |
| 6   | GZFE17003    | Guangzhou | 2017 | A2c     | OM262398                |
| 7   | GZFE17006    | Guangzhou | 2017 | A2c     | OM262399                |
| 8   | WZ17126      | Wenzhou   | 2018 | A2c     | OM262400                |
| 9   | GZFE17009    | Guangzhou | 2017 | A2c     | OM262401                |
| 10  | BCH18026     | Beijing   | 2018 | A2c     | OM262402                |
| 11  | BCH18060     | Beijing   | 2018 | A2c     | OM262403                |
| 12  | BCH18063     | Beijing   | 2018 | A2c     | OM262404                |
| 13  | GY17001      | Guiyang   | 2017 | A2c     | OM262405                |
| 14  | GY18083      | Guiyang   | 2018 | A2c     | OM262406                |
| 15  | GY18166      | Guiyang   | 2018 | A2c     | OM262407                |
| 16  | GZFE17101    | Guangzhou | 2017 | A2c     | OM262408                |
| 17  | GZFE17150    | Guangzhou | 2017 | A2c     | OM262409                |
| 18  | WZ17133      | Wenzhou   | 2018 | A2c     | OM262410                |
| 19  | WZ17152      | Wenzhou   | 2018 | A2c     | OM262411                |
| 20  | WZ17170      | Wenzhou   | 2018 | A2c     | OM262412                |
| 21  | WZ17335      | Wenzhou   | 2019 | A2c     | OM262413                |
| 22  | WZ17336      | Wenzhou   | 2019 | A2c     | OM262414                |
| 23  | WZ17341      | Wenzhou   | 2019 | A2c     | OM262415                |
| 24  | WZ17350      | Wenzhou   | 2019 | A2c     | OM262416                |
| 25  | YC18077      | Yinchuan  | 2018 | A2c     | OM262417                |
| 26  | GZ19199      | Guangzhou | 2019 | B2      | OM262418                |
| 27  | GZFE19009    | Guangzhou | 2019 | B1      | OK644703                |
Figure S1. Phylogenetic tree constructed based on (A) F gene, (B) SHI gene and (C) G gene. The phylogenetic tree was generated using the neighbour-joining method based on the Kimura two-parameter model with 1000 replicates. The strains isolated in different years are marked by ● with different colours: strains from 2017 are marked with blue, strains from 2018 are marked with green, and strains from 2019 are marked with purple. For (C), 111 nt-dup variants isolated in different years are marked by ▲ with different colours: strains from 2017, 2018 and 2019 are marked with blue, green and purple respectively. Sequences were named with abbreviations of cities they were collected. BCH, WZ, GZFE, GY and YC were abbreviation of samples from Beijing Children’s Hospital, the 2nd Affiliated Hospital and Yuying Children’s Hospital of Wenzhou Medical University, Guangzhou Women and Children’s Medical Center, Guiyang Women and Children Healthcare Hospital and Yinchuan Maternal and Child Health Hospital respectively.
Figure S1(B)
Figure S1(C)