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**Supplementary Data**

**Analysis of severe human adenovirus infection outbreak in Guangdong Province, southern China in 2019**

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**Supplementary Table S1** Primers and probes for identification of various human adenovirus types.

|  |  |  |
| --- | --- | --- |
| **HAdV Type** | **Primer and probe** | **Sequence (5**′**–3**′**)** |
| HAdV21 | AD21F | GGGCTTGTTAATGGCTACGTATCT |
|  | AD21R | TGCTGACTTTTGTGTGAACATTTG |
|  | AD21Probe | FAM-AGTTGGTGTATCAGACACT-MGB |
| HAdV3 | AD3F | CGAGACCTCCTACCCATGAACTAA |
|  | AD3R | GACTGTATTGCTGATTTCAAGTAAGTGTCT |
|  | AD3Probe | FAM- TCATTGCCCCTACCTTACCCAATCCAA-BHQ1 |
| HAdV7 | AD7F | CAGGAGAAGAAAGAGCAGTAACTACCA |
|  | AD7R | TGCAGTAATGTCTTTCCCAATTTCTA |
|  | AD7Probe | FAM-CAAACACATTTGGCATTGCTTCCATGAA-BHQ1 |
| HAdV14 | AD14F | GTGAAAGGCGGACAGGCAAA |
|  | AD14R | CAAAAAAGTTCATGTCAATGTCATATTCAA |
|  | AD14Probe | FAM-TGAAAACAGAAGAAGGCAACAA-BHQ1 |
| HAdV55 | AD55F | AAGGCGGTCAGGCAAAACC |
|  | AD55R | CCATGTCAATATCATATTCGACTTTCTGA |
|  | AD55Probe | FAM-AAAACAACGGAGCAGCCA-BHQ1 |
| HAdV5 | ADV5F | ACGATGACAACGAAGACGAAGTAG |
|  | ADV5R | GGCGCCTGCCCAAATAC |
|  | ADV5Probe | FAM-CGAGCAAGCTGAGCAGCAAAAAACTCA-BHQ1 |
| HAdV4 | AD4F | GCAAGCTACTGCTCTTCCGAC |
|  | AD4R | GTGTGATGGCAGGGTCCCGAG |
|  | AD4Probe | FAM- CTTCCTACCAGGGATCTATCAGTGCGTC-BHQ1 |

**Supplementary Table S2** Primer sequences for analyses of structural capsid genes (hexon, penton base, and fiber) in human adenovirus type 7.

|  |  |  |
| --- | --- | --- |
| **Gene** | **Primer** | **Sequence (5**′**–3**′**)** |
| Hexon: 18372**–**21176 | 15AD-18094F | TGTTCCCAAACCTGTCGCTAC |
|  | 15AD-19504R | TCCACAGCCTGATTCCACATG |
|  | 16AD-19400F | AGTGGTTGACTTGCAGGACAGAA |
|  | 16AD-20806R | CAACACAACAACTCTGGCTTTGTAGG |
|  | 17AD-20702F | CAGAAACTTCCAGCCTATGAGCA |
|  | 17AD-22127R | GTGATTTCAAGATCTCTGCTCCTGA |
| Penton base: 13855**–**15489 | 11AD-12875F | GCAGTTTGGAAGCCACCCT |
|  | 11AD-14297R | ATCACCCTCGCCTTGAACTTG |
|  | 12AD-14180F | AGACCATCAACTTTGACGAGCG |
|  | 12AD-15575R | GCGCCTCCATACATCTTGGT |
| Fiber: 31233**–**32210 | 24AD-29870F | TATGATTAGTCGTCCCCATATGGC |
|  | 24AD-31299R | AGGTGCTTTCATCTTCATASGGGTA |
|  | 25AD-31209F | CAATCTTCATKTCTTTMTYCCCAGAT |
|  | 25AD-32606R | ATAAACAGCAGTCGCACGGAG |

M = A/C; Y = C/T; K = G/T.

**Supplementary Table S3** Comparative genomics analysis of human adenovirus isolates with the reference strain CQ1198.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Region** | **Gene** | **Position (nt)** | **Isolate** | | | | |
| **GZ04090** | **GZ04160** | **GZ06091** | **GZ06173** | **GZ07010** |
| E2B | 19 kDa protein | 6609 | – | – | C→T ( G→E) | C→T ( G→E) | C→T ( G→E) |
|  | 12.6 kDa protein | 8464 | C→G (V→V) | C→G (V→V) | C→G (V→V) | C→G (V→V) | C→G (V→V) |
|  | DNA-binding protein | 9689 | G→A (L→L) | – | – | – | – |
|  | NCR | 10808 | ▲T | ▼TT | ▲T | ▲T | ▲T |
| L2 | NCR | 15518 | ▼AA | ▼A | ▼AA | ▼A | ▼A |
| L3 | 23 kDa protein | 21805 | C→T (H→Y) | – | C→T (H→Y) | C→T (H→Y) | C→T (H→Y) |
| L4 | 100 kDa protein | 24292 | T→C (A→A) | T→C (A→A) | T→C (A→A) | T→C (A→A) | T→C (A→A) |
| E3 | 19 kDa MHC class I antigen-binding glycoprotein | 28142 | – | C→T (F→F) | – | – | – |
|  | NCR | 29940 | ▲T | – | ▲T | – | – |
| E4 | 32 kDa protein | 32926 | G→A (Y→Y) | – | G→A (Y→Y) | G→A (Y→Y) | G→A (Y→Y) |
|  |  | 33149 | T→G (Q→P) | T→G (Q→P) | T→G (Q→P) | T→G (Q→P) | T→G (Q→P) |
|  | NCR | 35131 | A→C | – | – | – | – |
|  | NCR | 35137 | T→C | – | – | – | – |
|  | NCR | 35144 | A→C | – | – | – | – |
|  | NCR | 35153 | ▼C | – | – | – | – |

Differences in nucleic acid and amino acid sequences are shown as DNA (AA) along with their genomic locations. The reference genome is HAdV-7 strain CQ1198 (accession no. JX625134). NCR, non-coding region; ▼, insertion; ▲, deletion; –, no change or not applicable.