

1 **Whole-genome Sequencing for Tracing the Transmission Link between Two ARD**
2 **Outbreaks Caused by a Novel HAdV Serotype 7 Variant, China**

3 Shaofu Qiu,^{1*} Peng Li,^{1*} Hongbo Liu,^{1*} Yong Wang,^{1*} Nan Liu,^{1*} Chengyi Li,¹ Shenlong Li,¹
4 Ming Li,² Zhengjie Jiang,³ Huandong Sun,³ Ying Li,² Jing Xie,¹ Chaojie Yang,¹ Jian Wang,¹ Hao
5 Li,¹ Shengjie Yi,¹ Zhihao Wu,¹ Leili Jia,¹ Ligui Wang,¹ Rongzhang Hao,¹ Yansong Sun,¹ Liuyu
6 Huang,¹ Hui Ma,⁴ Zhengquan Yuan,¹ and Hongbin Song¹

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1 **Supplemental materials**

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15 **Figure S1. Geographic distribution of the two HAdV-7 outbreaks in China.** A and B
16 represent the Xiangyang and Jingmen training base, respectively. The affiliated Xiangyang
17 hospital was located in the Fancheng district, Xiangyang City, Hubei Province of China.

18 This figure was generated using ESRI ArcGIS for Desktop v10.1
19 (ESRI Inc., <http://www.esri.com>).

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21 **Figure S2. The incidence rates of HAdV-7 infections among the outbreak patients, close**
22 **contacts and local patients with ARD.** The HAdV-7 strains were confirmed by real-time PCR,
23 PCR sequencing and viral culture.

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1 **Table S1. Primers used in this study for amplification and sequencing of possible pathogen**
 2 **target genes.**

| Primer | Target gene | Sequence (5'-3') | Amplicon (bp) | Reference |
|-----------|-------------|--------------------------|---------------|------------|
| adv-F | Hexon | ACATGCACATCGCCGG | 145 | 1 |
| adv-R | | CGRTCSGTGGTCACATC | | |
| adv-P | | FAM-CGGGTCTGGTGCAGT-BHQ1 | | |
| adv-BL | Hexon | TTGACTTGCAGGACAGAAA | 597 | 2 |
| adv-BR | | CTTGTATGTGGAAAGGCAC | | |
| adv-FiBL | Fiber | TACCCCTATGAAGATGAAAGCA | 1000 | 2 |
| adv-FiBR | | GGAGGCAAAATAACTACTCG | | |
| adv-VA-F2 | VA RNA | TACTGGCACTCCCGTCTCG | 465 | This study |
| adv-VA-R2 | | CCTCGCCCTCTTCCAATC | | |
| rRNA-F | 16S rRNA | GTGCCAGCMGCCGCGGTAA | 877 | This study |
| rRNA-R | | GACGGGCGGTGWGTRCA | | |

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1 **Table S2. The HAdV strains used in this study.**

| Isolate | Genotype | Serotype | Accession ID |
|--|----------|-----------------|--------------|
| HAdV isolate XY6 from Index case B of the Xiangyang outbreak | B | 7 | KJ019879 |
| HAdV isolate XY1 from Index case A of the Xiangyang outbreak | B | 7 | KJ019880 |
| HAdV isolate L34 from a quarantined patient of the Xiangyang outbreak | B | 7 | KJ019881 |
| HAdV isolate K57 from from a quarantined patient of the Jingmen outbreak | B | 7 | KJ019882 |
| HAdV isolate K22 from a quarantined patient of the Jingmen outbreak | B | 7 | KJ019883 |
| HAdV isolate CDC228 from a sporadic patient in the local | B | 7 | KJ019884 |
| HAdV isolate H12 from the Index case C from the Jingmen outbreak | B | 7 | KJ019885 |
| HAdV isolate H18 from a hospitalized patient with severe pneumonia from the Jingmen outbreak | B | 7 | KJ019886 |
| HAdV isolate JM11 from a quarantined patient of the Jingmen outbreak | B | 7 | KJ019887 |
| HAdV isolate L14 from a hospitalized patient of the Xiangyang outbreak | B | 7 | KJ019888 |
| HAdV type 3 strain GB | B | 3 | AY599834 |
| HAdV B strain Guangzhou01 | B | 3 | DQ099432 |
| HAdV B strain Guangzhou02 | B | 3 | DQ105654 |
| HAdV B strain human/CHN/Ad4/2007/NEW [P3H3F7] | B | NEW [P3H3F7] | KF268311 |
| HAdV type 7 | B | 7 | AC_000018 |
| HAdV type 7 vaccine strain | B | 7 | AY495969 |
| HAdV type 7 strain Gomen | B | 7 | AY594255 |
| HAdV type 7 vaccine strain | B | 7 | AY594256 |
| HAdV type 7 strain NHRC 1315 | B | 7 | AY601634 |
| HAdV 7 VA RNA region, strain hAdVi/Caen.FRA/11.07(5043) | B | 7 | FR718945 |
| HAdV 7 strain GZ08 | B | 7 | GQ478341 |
| HAdV 7 strain gz07 | B | 7 | HQ659699 |
| HAdV 7 strain 0901HZ/ShX/CHN/2009 | B | 7 | JF800905 |
| HAdV 7d2 strain FS2154 | B | 7 | JN860677 |

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|--|---|----|----------|
| HAdV B strain human/USA/ak35_AdV7d2/2006/7[P7H7F7] | B | 7 | JX423383 |
| HAdV B strain human/ARG/ak38_AdV7h/2003/7[P7H7F7], | B | 7 | JX423386 |
| HAdV B strain human/USA/ak39_AdV7d2/1997/7[P7H7F7] | B | 7 | JX423387 |
| HAdV B strain human/USA/ak40_AdV7b/1997/7[P7H7F7] | B | 7 | JX423388 |
| HAdV 7 isolate CQ1198 | B | 7 | JX625134 |
| Human adenovirus 7 strain human/CHN/DG01/2011/7[P7H7F7] | B | 7 | KC440171 |
| HAdV B strain human/USA/UFL_Adv7d2-2/unknown/7[P7H7F7], | B | 7 | KF268117 |
| HAdV B strain human/USA/CL_44/1988/7[P7H7F7] | B | 7 | KF268125 |
| HAdV B strain human/USA/UFL_Adv7h/2005/66[P7H7F3] | B | 7 | KF268126 |
| HAdV B strain human/USA/CL_43/1988/7[P7H7F7] | B | 7 | KF268134 |
| HAdV B strain human/USA/UFL_Adv7d2-3/unknown/7[P7H7F7] | B | 7 | KF268135 |
| HAdV B strain human/CHN/DG/2011/7[P7H7F7] | B | 7 | KF268314 |
| HAdV B strain human/CHN/a238/2011/7[P7H7F7] | B | 7 | KF268316 |
| HAdV type 11 strain Ad11p Slobitski | B | 11 | AY163756 |
| HAdV 14 strain HAdV14-BJ430/CHN2010 | B | 14 | JN032132 |
| HAdV 14 isolate CHN 2012 | B | 14 | JX892927 |
| HAdV type 16 strain ch. 79 | B | 16 | AY601636 |
| HAdV type 21 strain AV-1645 | B | 21 | AY601633 |
| HAdV type 34 strain Compton | B | 34 | AY737797 |
| HAdV type 35 strain Holden | B | 35 | AY128640 |
| HAdV type 50 strain Wan | B | 50 | AY737798 |
| HAdV 55 strain QS-DLL | B | 55 | FJ643676 |
| HAdV B isolate Human/CHN/BJ01/2011/55/P14H11F14 | B | 55 | JX491639 |

1 **Table S3. Primers used in this study for gap closure of the genomes from the HAdV-7**
 2 **outbreak strains.**

| Primer | Sequence (5'-3') | replicon (bp) |
|-----------|----------------------|---------------|
| CDC228_1F | GGAGAACCTGCACTACACCT | 145 |
| CDC228_1R | TTTAAGGGTGGTGTGCAGGA | |
| CDC228_2F | CAGGGTACTCTGCGAAACG | 209 |
| CDC228_2R | GGTAGGAGAGGTAGTTGGCC | |
| XY1_1F | ACCACACTACCTCCTATGCA | 263 |
| XY1_1R | ATACAGTCTGGGCTTGCAGT | |
| XY1_2F | CCTTCAACCCTGTCTACCCC | 245 |
| XY1_2R | AGTCTTAACGAGTGGTGTGG | |
| L34_1F | AATTAATCGCCAGGGTTGCC | 219 |
| L34_1R | TTTGTGGCTGTCGTTGTAGC | |
| H12_1F | CAGGGTACTCTGCGAAACG | 209 |
| H12_1R | GGTAGGAGAGGTAGTTGGCC | |
| JM11_1F | ACCACACTACCTCCTATGCA | 263 |
| JM11_1R | ATACAGTCTGGGCTTGCAGT | |

1 **Table S4. General characteristics of sequenced reads of the samples.**

| Sample | No. of raw reads | No. of viral reads | Expected coverage |
|---------------|-------------------------|---------------------------|--------------------------|
| CDC228 | 121,882 | 109,743 | 158 |
| H12 | 159,250 | 138,165 | 137 |
| H18 | 123,492 | 64,031 | 57 |
| JM11 | 123,298 | 82,930 | 114 |
| K22 | 122,774 | 76,930 | 61 |
| K57 | 136,722 | 106,110 | 62 |
| L14 | 142,878 | 39,820 | 23 |
| L34 | 123,808 | 75,176 | 63 |
| XY1 | 127,836 | 109,492 | 124 |
| XY6 | 106,966 | 103,586 | 65 |

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1 **Table S5. Demographic and epidemiologic characteristics of the patients from the two**
 2 **HAdV-7 outbreaks.**

| Characteristic | Value | |
|-----------------------------------|----------------------------|-------------------------|
| | Xiangyang outbreak (n=858) | Jingmen outbreak (n=88) |
| Age, mean, yr | 19.7±1.9 | 20.1±1.9 |
| Male sex — no. (%) | 773 (90.1) | 88 (100) |
| Incidence rate, no./total no. (%) | 858/1290 (66.5) | 88/865 (10.2) |
| Smoking status — no. (%) | | |
| Current smoker | 65 (7.6) | 8 (9.1) |
| No history of smoking | 747 (87.1) | 77 (87.5) |
| Unknown/missing | 46 (5.4) | 3 (3.4) |
| Underlying condition — no. (%) | | |
| Any | 82 (9.6) | 15 (17.0) |
| Allergy to antibiotics | 52 (6.1) | 7 (8.0) |
| Excimer laser eye surgery | 10 (1.2) | 2 (2.3) |
| Tonsillectomy | 4 (0.5) | 2 (2.3) |
| Pneumonia | 5 (0.6) | 0 |
| Chronic gastritis | 3 (0.3) | 1 (1.1) |
| Chronic rhinitis | 2 (0.2) | 1 (1.1) |
| Appendicitis | 2 (0.2) | 0 |
| Hernia surgery | 0 | 1 (1.1) |
| Hepatitis B infection | 0 | 1 (1.1) |
| Hyperthyroidism | 1 (0.1) | 0 |
| Hydrocele surgery | 1 (0.1) | 0 |
| Otitis media | 1 (0.1) | 0 |
| Hemorrhoid surgery | 1 (0.1) | 0 |
| No underlying conditions | 730 (85.1) | 70 (79.5) |
| Unknown/missing | 46 (5.4) | 3 (3.4) |

1 **References**

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3 analysis of the entire spectrum of human adenoviruses by a two-reaction real-time PCR
4 assay. *J Clin Microbiol* 43 (7), 3049-3053 (2005).

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