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**Supplementary Data**

**Identification and genetic characterization of Bovine Hepacivirus in China: A large scale epidemiological study**

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**Table S1 Primers used for genomic sequencing of CQ/166.**

|  |  |  |
| --- | --- | --- |
| Primer name | Primer sequences (5′→3′) | Product size (bp) |
| BovHepV-59F a | GCCCCTAGTAGGAGGCG | 1025 |
| BovHepV-1059R b | ATTAAGGGTAAGATGAGTAGGTAGA |
| BovHepV-800F a | ATTGTTGTCAAGATGATGATGTCCT | 760 |
| BovHepV-1537R b | AGGCCAGGAAGGTAAGGCAGCCG |
| BovHepV-1512F a | CGACGGCAAAAATGTGTCCTTAG | 1644 |
| BovHepV-3133R b | TCATCAAACACCACAGGTGGGAG |
| BovHepV-3003F a | ACTTTGGGAGGGCAATATTTTCA | 1594 |
| BovHepV-4574R b | CCACGTAAAGGAAGTGGAATGTA |
| BovHepV-4320F a | GGGAGCTCCTGGTGTGTACTATT | 1264 |
| BovHepV-5559R b | AGGAGAGATGACATTGGATTTAGCA |
| BovHepV-5444F a | TAAATTGTGCCTTTGCCCCGG | 1498 |
| BovHepV-6919R b | GCAAGATGGGCTACATAAGGGAG |
| BovHepV-68541F a | AAGATTCCCTTTCCGCTTTGG | 1441 |
| BovHepV-8271R b | AATCCGTCGTTTCCATGCATG |
| BovHepV-8025F a | TTTTTTCTTGACGCGTGACCC | 610 |
| BovHepV-8610R b | TCAGTGTTTGAGGAGGAAAAACAGT |

a Forward; b Reverse.

Primers are designed based on the genomic sequence of BovHepV\_209/Ger/2014 (KP641124).

**Table S2 Detailed information on 49 field BovHepV strains determined in the present study.**

|  |  |  |  |
| --- | --- | --- | --- |
| Strain name | Sampling time | Sampling province | Accession number |
| CQ/5 | 2018 | Chongqing | MW830328 |
| CQ/8 | 2018 | Chongqing | MW830329 |
| CQ/16 | 2018 | Chongqing | MW830330 |
| CQ/18 | 2018 | Chongqing | MW830331 |
| CQ/20 | 2018 | Chongqing | MW830332 |
| CQ/24 | 2018 | Chongqing | MW830333 |
| CQ/27 | 2018 | Chongqing | MW830334 |
| CQ/34 | 2018 | Chongqing | MW830335 |
| CQ/35 | 2018 | Chongqing | MW830336 |
| CQ/39 | 2018 | Chongqing | MW830337 |
| CQ/40 | 2018 | Chongqing | MW830338 |
| CQ/55 | 2018 | Chongqing | MW830339 |
| CQ/68 | 2018 | Chongqing | MW830340 |
| CQ/72 | 2018 | Chongqing | MW830341 |
| CQ/80 | 2018 | Chongqing | MW830342 |
| CQ/89 | 2018 | Chongqing | MW830343 |
| CQ/94 | 2018 | Chongqing | MW830344 |
| CQ/153 | 2018 | Chongqing | MW830345 |
| CQ/161 | 2018 | Chongqing | MW830346 |
| CQ/163 | 2018 | Chongqing | MW830347 |
| CQ/164 | 2018 | Chongqing | MW830348 |
| CQ/166 | 2018 | Chongqing | MW830376 |
| HLJ/174 | 2018 | Heilongjiang | MW830349 |
| HLJ/176 | 2018 | Heilongjiang | MW830350 |
| HLJ/177 | 2018 | Heilongjiang | MW830351 |
| HLJ/244 | 2018 | Heilongjiang | MW830352 |
| HLJ/247 | 2018 | Heilongjiang | MW830353 |
| HLJ/249 | 2018 | Heilongjiang | MW830354 |
| HLJ/262 | 2018 | Heilongjiang | MW830355 |
| HLJ/268 | 2018 | Heilongjiang | MW830356 |
| HLJ/275 | 2018 | Heilongjiang | MW830357 |
| GD/371 | 2020 | Guangdong | MW830358 |
| GD/380 | 2020 | Guangdong | MW830359 |
| GD/387 | 2020 | Guangdong | MW830360 |
| GD/389 | 2020 | Guangdong | MW830361 |
| GD/396 | 2020 | Guangdong | MW830362 |
| GD/404 | 2020 | Guangdong | MW830363 |
| GD/407 | 2020 | Guangdong | MW830364 |
| SC/422 | 2018 | Sichuan | MW830365 |
| SC/423 | 2018 | Sichuan | MW830366 |
| SC/429 | 2018 | Sichuan | MW830367 |
| SC/430 | 2018 | Sichuan | MW830368 |
| IM/490 | 2019 | Inner Mongolia | MW830369 |
| HN/511 | 2019 | Henan | MW830370 |
| HN/512 | 2019 | Henan | MW830371 |
| SD/581 | 2020 | Shandong | MW830372 |
| SD/589 | 2020 | Shandong | MW830373 |
| SD/590 | 2020 | Shandong | MW830374 |
| SD/592 | 2020 | Shandong | MW830375 |

**Table S3 Detailed information on 33 previously reported BovHepV strains in China, Ghana, Germany, Brazil, and Italy.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Accession number** | **Strain name** | **Genotype** | **Country** | **Nucleotide similarity (%)** |
| KP641123 | BovHepV B1/Ger/2013 | A | Germany | 97.6–99.4 |
| MN939661 | 912/17-858 | A | Italy | 96.3–98.2 |
| NC\_038432 | BovHepV 463/Ger/2014 | A | Germany | 97.0–98.8 |
| KP641125 | BovHepV\_379/Ger/2014 | A | Germany | 97.0–98.8 |
| KP641126 | BovHepV\_438/Ger/2014 | A | Germany | 97.0–98.8 |
| KP641124 | BovHepV\_209/Ger/2014 | A | Germany | 97.0–98.8 |
| MN939660 | 850/14-SP12 | A | Italy | 97.0–98.8 |
| MN939657 | 912/17-139 | A | Italy | 97.0–98.8 |
| MN939662 | 933/17- B8 | A | Italy | 97.0–98.8 |
| MN939658 | 368/19-52 | A | Italy | 97.0–98.8 |
| MN939659 | 368/19-54 | A | Italy | 97.0–98.8 |
| MH027953 | BH204/16-6 | A | Germany | 97.6–99.4 |
| MN939652 | 786/14-SP1 | B | Italy | 94.5–96.3 |
| MN939653 | 786/14-SP2 | B | Italy | 95.1–97.0 |
| MN939654 | 786/14-SP13 | B | Italy | 95.1–97.0 |
| MN939663 | 933/17- E12 | B | Italy | 95.1–97.0 |
| MN939655 | 786/14-SP14 | B | Italy | 95.7–97.6 |
| NC\_026797 | GHC25 | B | Ghana | 95.1–97.0 |
| MN939656 | 292/19-39 | C | Italy | 93.9–95.7 |
| KP265946 | GHC52 | C | Ghana | 94.5–96.3 |
| MG781019 | BR\_RN034B019 | D | Brazil | 95.7–97.6 |
| MG257793 | BovHepV/GD/01 | E | China | 95.7–97.6 |
| MG257794 | BovHepV/GD/02 | E | China | 95.7–97.6 |
| MH027948 | BH181/16-20 | F | Germany | 94.5–96.3 |
| MN939651 | 292/19-35 | F | Italy | 94.5–96.3 |
| MN939650 | 80/15-175 | F | Italy | 94.5–96.3 |
| MN939648 | 770/13-10 531 | F | Italy | 93.9–95.7 |
| MN939646 | 770/13-11 520 | F | Italy | 93.9–95.7 |
| MN939649 | 770/13-5 572 | F | Italy | 95.1–97.0 |
| MN939647 | 770/13-14 527 | F | Italy | 95.1–97.0 |
| MN266283 | BovHepV/JS/02 | G | China | 98.2–100 |
| MN266284 | BovHepV/JS/05 | G | China | 97.6–99.4 |
| MN266285 | BovHepV/JS/06 | G | China | 97.6–99.4 |

The 5′ UTR sequences of 33 previously reported BovHepV strains in China, Ghana, Germany, Brazil, and Italy were aligned with that of 49 field BovHepV strains determined in the present study. The nucleotide similarity between the 49 field BovHepV strains and each of the 33 previously reported BovHepV strains was indicated.