**Virologica Sinica**

**Supplementary Data**

**RNA viromes of*****Dermacentor nuttalli* ticks reveal a novel uukuvirusin** **Qīnghǎi Province, China**

Yaohui Fang a, b, Jun Wang a, Jianqing Sun c, Zhengyuan Su a, Shengyao Chen a, b, Jian Xiao a, b, Jun Ni a, b, Zhihong Hu a, Yubang He c, Shu Shen a, d, \*, Fei Deng a, \*

a Key Laboratory of Special Pathogens and Biosafety and National Virus Resource Center, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan 430071, China

b University of Chinese Academy of Sciences, Beijing 101408, China

c Qinghai lake national nature reserve administration, Xining 810000, China

d Hubei Jiangxia Laboratory, Wuhan 430200, China

\* Corresponding authors.

Email addresses: [shenshu@wh.iov.cn](mailto:shenshu@wh.iov.cn) (S. Shen), [df@wh.iov.cn](mailto:df@wh.iov.cn) (F. Deng).

ORCID: 0000-0002-0013-5365 (S. Shen), 0000-0002-5385-083X (F. Deng)

**Supplementary figures and tables**

**Figure. S**1. The phylogenetic tree constructed by using the *ITS2* genes of different tick

species, including those collected from Qīnghǎi Lake (in red).

**Figure. S2.** A heatmap showing the abundance of viruses identified from 5 pools in

2016 and 2017.

**Figure. S3.** Genome organizations of XJTAV1, QHLV1, and QHLV2. Black lines

represent contigs, yellow arrows represent ORFs, and purple regions represent

conserved domains.

**Figure. S4.** Pairwise comparison of viral protein sequence identities of RdRp, GP, and

NP among phenuiviruses.

**Table S1.** The sampling information of ticks each year and the six tick pools prepared for metagenomic sequencing.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Year** | **No. individuals** | **No. groups** | **Library** | **No. mixed groups(ticks)** | **No. Raw Reads** | **No. Viral related reads** |
| 2015 | 1384 | 31 | 2015-1 | 3(190) | 21,959,458 | 11,003 |
| 2016 | 854 | 29 | 2016-1 | 3(315) | 70,256,126 | 4,984 |
|  |  |  | 2016-2 | 2(17) | 77,080,126 | 10 |
| 2017 | 924 | 37 | 2017-1 | 3(336) | 97,269,152 | 4,043 |
|  |  |  | 2017-2 | 3(336) | 122,540,082 | 3,881 |
|  |  |  | 2017-3 | 3(38) | 104,613,136 | 846 |
| Total | 3162 | 97 |  | 17(1232) | 493,718,080 | 24,767 |

**Table S2.** Sequence of primers for detection of XJTAV1, QHLV1, QHLV2, and QHLV3.

|  |  |
| --- | --- |
| **Primers** | **Sequences** |
| XJTAV1-F(499) | 5’-TTCAGGCTTTCGTTTCTTTGC-3’ |
| XJTAV1-R(499) | 5’-GCTGTTACAACCGCCATCTCC-3’ |
| XJTAV1-Fn(124) | 5’-CCGATTCCGTCAATGTCCTGG-3’ |
| XJTAV1-Rn(124) | 5’-AGCCAAATAGCCGCTTCATCT-3’ |
| QHLV1-F(460) | 5’-CTGCCAAAGCTTGGTGGTTC-3’ |
| QHLV1-R(460) | 5’-CTGCCAGTCGACGCTATCAT-3’ |
| QHLV1-Fn(405) | 5’-ACACCGGTAACAACCGAGTC-3’ |
| QHLV1-Rn(405) | 5’-GCCAGTCGACGCTATCATCA-3’ |
| QHLV2-F(373) | 5’-TCTGGTAATCCTGCCCGTCCTT-3’ |
| QHLV2-R(373) | 5’-ATGGGTATCAACATCCTCCTCC-3’ |
| QHLV2-Rn(233) | 5’-CACCTCTTTCTCGGCTTCGTTG-3’ |
| QHLV3-L-F(413) | 5’- AATCGGCAAGTACACTGTAGCAT-3’ |
| QHLV3-L-R(413) | 5’-CGAACTGGTGGTCTTTCTTTAGG-3’ |
| QHLV3-L-Fn(197) | 5’-CGACTGTTCAGGGCTCTAATGTG-3’ |
| QHLV3-L-Rn(197) | 5’-CTGGTGGTCTTTCTTTAGGTCTTCA-3’ |
| QHLV3-M-F(338) | 5’-ATTCTTGCCTTTGCCATTACC-3’ |
| QHLV3-M-R(338) | 5’-CCTTCGCCTATCCCTCTTTCC-3’ |
| QHLV3-M-Fn(232) | 5’-TCTTGCCTTTGCCATTACCAT-3’ |
| QHLV3-M-Rn(232) | 5’-TGCGAGTGAATCCGAAGTGTT-3’ |
| QHLV3-S-F(464) | 5’-GGAATCCCTCACATCCACAACT-3’ |
| QHLV3-S-R(464) | 5’-GCGGCAAAGCAAAGAACCAGTC-3’ |
| QHLV3-S-Fn(254) | 5’-GGAATCCCTCACATCCACAACT-3’ |
| QHLV3-S-Rn(254) | 5’-TGACCTACCCAGCCATCACAAT-3’ |

**Table S3.** The L, M, and S segments of Qīnghǎi Lake virus 3 identified in 5 pools compared with Chāngpíng tick virus 1.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Library** | **Segment of QHLV3** | **Length, nt** | **Viral protein identity compared with Chāngpíng tick virus 1** | **TPM values** |
| 2015-1 | L | 303−2427 & | 77.40%−91.68% | 31.01−42.27 |
|  | M | 3339 | N/A | 32.64 |
|  | S | 1166 | 77.13% | 17.54 |
| 2016-1 | L | 2247−3949 & | 85.06%−89.31% | 15.72−21.19 |
|  | M | 388−655 & | N/A | 1.44−2.46 |
|  | S | 1045 | 83.40% | 7.89 |
| 2017-1 | L | 6655 | 83.43% | 3.36 |
|  | M | 3397 | N/A | 3.30 |
|  | S | 1894 | 77.13% | 1.60 |
| 2017-2 | L | 6655 | 83.43% | 2.03 |
|  | M | 3351 | N/A | 0.77 |
|  | S | 1302 | 77.13% | 1.08 |
| 2017-3 | L | 252−1106 & | 72.15%−91.67% | 0.17−0.40 |
|  | M | 3396 | N/A | 3.20 |
|  | S | 372−480 & | 65%−97% | 0.19−0.46 |

& Several contigs related to the L or S segment were obtained but could not be assembled in to the full-length sequence of the respective segment. Therefore, a range of the length as for those contigs are listed.

N/A, not applicable.