Supplementary file 1.

**Laboratory methodology and statistical analysis**

***HCV antibody testing***

The presence of HCV antibody in patients’ sera were tested with the ARCHITECT Anti-HCV chemiluminescence immunoassay (Abbott Laboratories, Wiesbaden, Germany) in the Architect i2000SR system (Abbott Diagnostics, Abbott Park, IL) according to manufacturer’s instructions.

***HCV viral load quantitation***

HCV RNA measurements were performed by Abbott RealTi*me* HCV assay (Abbott Molecular, Des Plaines, IL) using the mSample Preparation System reagents, m2000sp and m2000rt instruments (Abbott Molecular, Des Plaines, IL). Briefly, 700μl of plasma was isolated from the patient’s EDTA blood and processed according to the manufacturer instructions.1 One low-positive, one high-positive and a negative control were included in each batch of sample run. The assay has a lower limit of detection (LOD) at 12 IU/ml and a linear range of quantitation from 1.08 to 8.0 log IU/ml.

***HCV genotyping***

The HCV genotypes were determined using the Abbott RealTi*me* HCV Genotype II assay (Abbott Molecular, Des Plaines, IL). The assay targets the 5’ untranslated region (UTR) of the HCV genome and the NS5b region of HCV genotype 1a and 1b. The assay could differentiate HCV genotype 1, 1a, 1b, 2, 3, 4, 5 and 6. All samples were processed according to manufacturer instructions. Briefly, RNA was extracted from 700μl plasma using the Abbott m2000sp instrument followed by RT-PCR using the Abbott m2000rt instrument. Positive and negative controls were included in each batch of sample run. The assay has a LOD at 500 IU/ml. For the specimens with indeterminate genotyping result using Abbott-RT-HCV assay, genotyping was performed by sequencing of HCV partial NS5B gene using forward primer (5’-TTAACCACATCMRCTCCGTGTG-3’) and reverse primer (5’-GTACCTGGTCATAGCYTCCGTRAA-3’).2,3 Briefly, RT-PCR was performed using SuperScript III One-Step RT-PCR System (Invitrogen, Carlsbad, CA). The mixtures were incubated at 55°C for 30 min and 94°C for 2 min, followed by 40 cycles of 94°C for 30 s, 56°C for 40 s, and 68°C for 1 min and a final extension at 68°C for 5 min. The PCR products were purified and sequenced with an ABI 3130xl DNA Analyzer (Applied Biosystems, Foster City, CA) using the PCR primers described above.

***Phylogenetic analysis of the HCV strains***

The phylogenetic relationships among the HCV strains were further determined by analyzing the hypervariable region of the partial HCV envelope E1-E2 region. The first round of RT-PCR targeting the HCV partial envelope E1-E2 region was performed using the SuperScript III One-Step RT-PCR System (Invitrogen, Carlsbad, CA) with forward primer F1 (5’-ATGGCNTGGGAYATGATGATGA-3’) and reverse primer R3 (5’-GCACGTCCACDATRTTYTGRTG-3’). The mixtures were incubated at 55°C for 30 min and 94°C for 2 min, followed by 40 cycles of 94°C for 15 s, 55°C for 30 s, and 68°C for 1 min and a final extension at 68°C for 5 min. This was followed by a semi-nested PCR using AmpliTaq Gold DNA polymerase (Applied Biosystems, Foster City, CA) with the forward primer F1, reverse primer R2 (5’-CGGAAGCARTCNGTRGGRCA-3’) and 1μl of the 1st-round PCR product. The mixtures were incubated at 95°C for 10 min, followed by 40 cycles of 94°C for 1 min, 55°C for 1 min, and 72°C for 1 min and a final extension at 72°C for 10 min. The products were then purified and sequenced by using the F1 and R2 primers by using the ABI 3130xl Genetic Analyzer (Applied Biosystems, Foster City, CA). The sequences were checked manually and trimmed for the construction of phylogenetic tree using the neighbor-joining method with ClustalX version 2.0 as we previously described.4

***Statistical analysis***

Venous pressure before and after release of tourniquet for all maneuvers were compared using one-tailed paired sample t test, with p value of < 0.05 considered as statistical significant. SPSS version 23 (SPSS, Chicago, IL) was used to perform the statistical analyses.

References

**1.** Abbott. Abbott RealTIme HCV 2011. <https://www.molecular.abbott/sal/en-us/staticAssets/realtime-hcv-package-insert.pdf>. Accessed 23rd April, 2018, 2018.

**2.** Sridhar S, Yip CCY, Chan JFW, To KKW, Cheng VCC, Yuen KY. Impact of inter-genotypic recombination and probe cross-reactivity on the performance of the Abbott RealTime HCV Genotype II assay for hepatitis C genotyping. *Diagn Microbiol Infect Dis* 2018;91:34-37.

**3.** Tong YQ, Liu B, Liu H, et al. Accurate genotyping of hepatitis C virus through nucleotide sequencing and identification of new HCV subtypes in China population. *Clin Microbiol Infect* 2015;21:874 e879-874 e821.

**4.** Larkin MA, Blackshields G, Brown NP, et al. Clustal W and Clustal X version 2.0. *Bioinformatics* 2007;23:2947-2948.