Supplementary Files

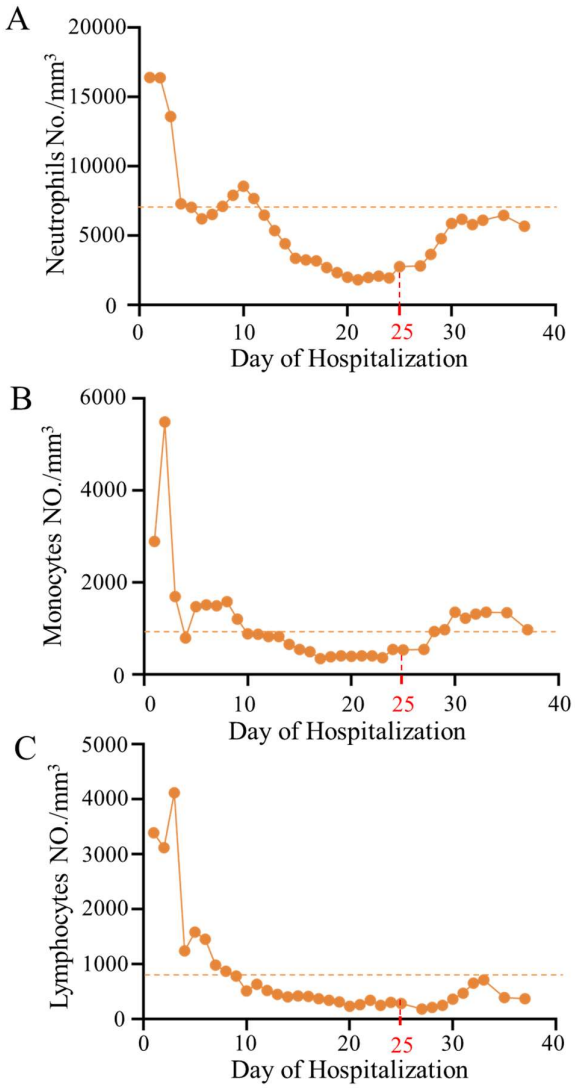

Figure S1. Absolute values for the three declined white-cell types of the patient. Panel A, B, C show the absolute values of the neutrophils, monocytes, and lymphocytes count for the patient during the hospitalization, respectively. The dashed lines indicate the lowest normal values.

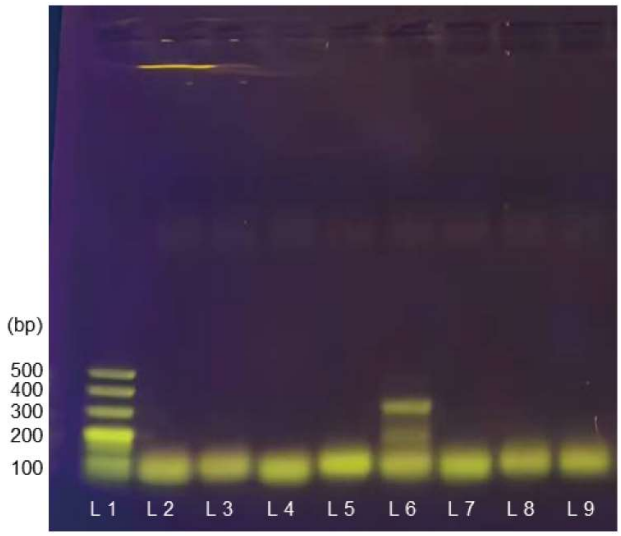

Figure S2. Detection of Hantaviruses and Human Parvovirus B19 (PV B19) using semi-nested PCR. L1, DNA Marker; L2, Hantaan virus; L3, Seoul virus; L4, Amur virus; L5, PV B19 negative control; L6, PV B19; L7, Hantaan virus negative control; L8, Seoul virus negative control; L9, Amur virus negative control.

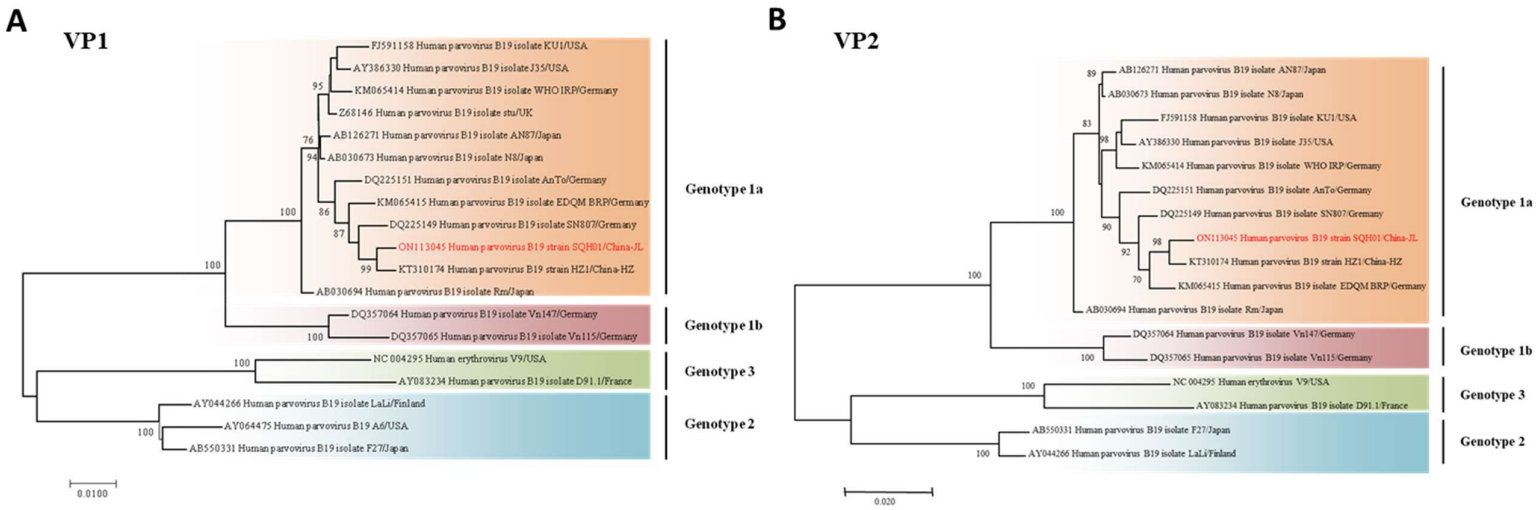

Figure S3. Phylogenetic analyses of Human Parvovirus B19 (PV B19). (A) Phylogenetic analysis of VP1 nucleotide sequences based on PV B19; (B) Phylogenetic analysis of VP2 nucleotide sequences based on PV B19. The construction of the trees is based on the maximum likelihood method, using the MEGA 7.0 presets. A bootstrap analysis was conducted on 1000 replicates and a bootstrap value >70% was considered significant and shown in the figure.

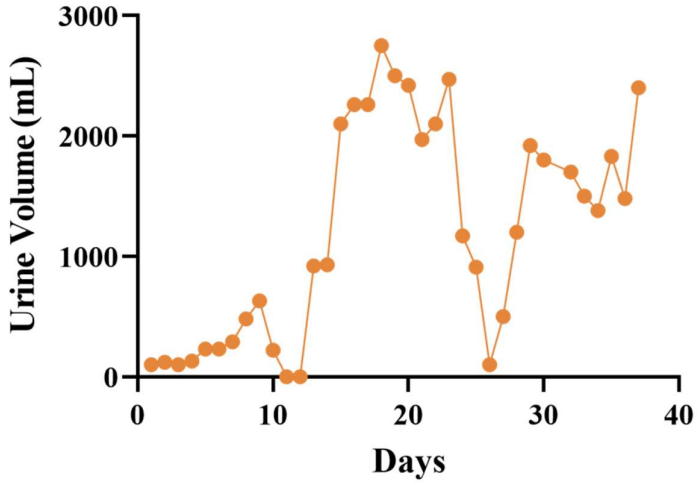

Figure S4. Urine volume of the patient collected during the hospitalization.

Table S1. The co-infection reports in the Hemorrhagic fever with renal syndrome patients.

Infection type	Pathogen	Region	References
Bacteria	Orientia tsutsugamushi	China	[1]
	Human granulocytic anaplasmosis	Korea	[2]
	Acinetobacter baumannii	Korea	[3]
	Leptospira	Croatia	[4]
	Methicillin-resistant Staphylococcus aureus	Korea	[3]
Virus	Dengue virus	Barbados、Malaysia	[5, 6]
	Lymphocytic choriomeningitis virus	Finland	[7]
	Ljungan virus	Finland	[7]
	Orthopoxviruses	Finland	[7]
	Hepatitis B virus	*Croatia*	[8]
Fungi	Mucor	Korea	[3]
	Aspergillus	Korea	[3]
Parasite	Plasmodium	China	[9]

Table S2. The primers used for the detection of Human Parvovirus B19 and Hantaviruses.

Primer	Position (bp)*	Sequence (5'→3')	Polarity	Amplicon (bp)
Human parvovirus B19				
B19 F	664	AGGCTATCATATTCATGTGGT	+	334
B19 R2	998	TAGACTCCCCAGCATCACT	-	
B19 R1	1053	TTATGCTAGCCTTAGTTCCCT	-	
Seoul virus				
SEOV F1	416	ATCTGACATCATTCGTGGT	+	288
SEOV F2	485	CTTCAAAGGACAACAAGGGG	+	
SEOV R	773	GACTCTGCCATGAACTTGC	-	
Amur virus				
AMRV F1	413	CTTTGTRGTTCCRATACTRCTY	+	239
AMRV F2	432	CTYAAAGCCCTCTACATGC	+	
AMRV R	671	CTCATRACTGGGCTWACCATC	-	
Hantaan virus				
HTNV F	1262	TRGCACAGAGCCTGATTGATG	+	183
HTNV Rl	1468	CCCACAACGGATTAAMTGAYC	-	
HTNV R2	1445	ACCCTCTGAGTAATRATTCCCA	-	

Table S3. The primers designed for the complete genome amplification of Human Parvovirus B19.

Primer	Position (bp)*	Sequence (5'→3')	Polarity	Amplicon (bp)
1 B19 F	1	TTGCTTGATCTTAGTGGCACG	+	300
1 B19 R2	301	TATATACTGTAGTCCCCGC	-	
1 B19 R1	532	AGTATGAGTTAGTGGTTCC	-	
2 B19 F	208	TTTTCCCGCCTTATGCAAA	+	800
2 B19 R2	1008	CCTGTGCTGCTAGACTCCC	-	
2 B19 R1	1053	TTATGCTAGCCTTAGTTCCCT	-	
3 B19 F1	958	CAAGAAACCCCGCATGACCA	+	829
3 B19 F2	1062	AGGCTAGCATAAAGTTTCAGAC	+	
3 B19 R	1891	AGGGCATCTGCATTAATTCCA	-	
4 B19 F1	1590	TTTTAGGCGGGCAACCTACCA	+	850
4 B19 R2	2402	CAATCCAGACAGGTAAGCACA	-	
4 B19 R1	2440	CCATTTGCCACTTTCTTTACTCA	-	
5 B19 F1	2049	GCTCTAGTACGCCCATCCC	+	917
5 B19 F2	2079	CAAGAGAATCATCTGTCGGAA	+	
5 B19 R	2996	ACTACTTGTGCTTGAAACCCA	-	
6 B19 F2	2709	CCCCATGCCTTATCATCCAG	+	812
6 B19 R	2795	GCAAGTTAGCGTACAACTACCC	-	
6 B19 R	3607	AAGTATCCTGACCTTGCCCTA	-	
7 B19 F1	3594	TACCCATATGTGTTAGGGCAA	+	933
7 B19 F2	3623	TACTTTAGCCCCAGAACTTCC	+	
7 B19 R	4556	ATAATTCCCACGGCATACTGA	-	
8 B19 F1	4563	GCCGTGGGAATTATGACAGT	+	542
8 B19 F2	4627	GGAATCCTCAACCTGGAGT	+	
8 B19 R	5169	CTGCGGTGAGCCAACCCTAATTC	-	

Table S4. Information of Human Parvovirus B19 strains used in this study.

Genotype	Accession number	Strain	Country
1a	Z68146	stu	UK
	FJ591158	KU1	USA
	AY386330	J35	USA
	AB030694	Rm	Japan
	AB126271	AN87	Japan
	AB030673	N8	Japan
	ON113045	SQH01	China-JL
	KT310174	HZ1	China-HZ
	KM065414	WHO IRP	Germany
	KM065415	EDQM BRP	Germany
	DQ225149	SN807	Germany
	DQ225151	AnTo	Germany
1b	DQ357064	Vn147	Germany
	DQ357065	Vn115	Germany
2	AY064475	A6	USA
	AB550331	F27	Japan
	AY044266	LaLi	Finland
3	NC_004295	V9	USA
	AY083234	D91.1	France

Table S5. The sequence identities of Human Parvovirus B19 VP1 at the nucleotide (upper right) and amino acid (lower left) levels. Orange, red, green, and blue colors represent the virus strains in subtype 1a, 1b, 2, and 3, respectively.

Strain	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Z68146/UK		0.991	0.993	0.99	0.993	0.994	0.98	0.979	0.993	0.985	0.984	0.986	0.954	0.946	0.884	0.88	0.904	0.911	0.911
FJ591158/USA	0.998		0.99	0.982	0.987	0.988	0.975	0.974	0.988	0.981	0.977	0.98	0.948	0.94	0.885	0.88	0.904	0.911	0.912
AY386330/USA	0.998	0.997		0.986	0.99	0.991	0.976	0.976	0.991	0.983	0.981	0.983	0.95	0.942	0.881	0.876	0.903	0.909	0.91
AB030694/Japan	0.993	0.992	0.992		0.991	0.992	0.978	0.977	0.986	0.983	0.983	0.984	0.956	0.949	0.885	0.879	0.904	0.912	0.912
AB126271/Japan	0.997	0.996	0.996	0.993		0.997	0.981	0.981	0.99	0.986	0.985	0.988	0.953	0.945	0.881	0.878	0.905	0.911	0.912
AB030673/Japan	0.997	0.996	0.996	0.993	0.997		0.982	0.982	0.991	0.987	0.986	0.989	0.954	0.946	0.882	0.879	0.905	0.912	0.912
ON113045/China-JL	0.993	0.994	0.992	0.989	0.993	0.993		0.991	0.979	0.985	0.985	0.982	0.952	0.942	0.88	0.877	0.899	0.907	0.907
KT310174/China-HZ	0.991	0.992	0.989	0.987	0.991	0.991	0.997		0.978	0.986	0.985	0.982	0.95	0.941	0.88	0.876	0.898	0.905	0.905
KM065414/Germany	1	0.998	0.998	0.993	0.997	0.997	0.993	0.991		0.983	0.981	0.984	0.951	0.943	0.881	0.877	0.901	0.907	0.908
KM065415/Germany	0.996	0.997	0.994	0.992	0.996	0.996	0.994	0.992	0.996		0.986	0.985	0.954	0.945	0.881	0.878	0.899	0.906	0.905

DQ225149/Germany	0.987	0.985	0.985	0.983	0.987	0.987	0.988	0.985	0.987	0.985		0.986	0.95	0.942	0.877	0.874	0.897	0.905	0.904
DQ225151/Germany	0.991	0.989	0.989	0.987	0.991	0.991	0.987	0.984	0.991	0.989	0.983		0.95	0.942	0.881	0.877	0.901	0.91	0.91
DQ357064/Germany	0.971	0.97	0.97	0.97	0.971	0.971	0.967	0.965	0.971	0.97	0.961	0.965		0.982	0.883	0.88	0.899	0.906	0.906
DQ357065/Germany	0.964	0.962	0.962	0.965	0.964	0.964	0.96	0.957	0.964	0.962	0.953	0.957	0.978		0.878	0.875	0.893	0.901	0.899
NC_004295/USA	0.969	0.967	0.967	0.969	0.969	0.969	0.969	0.966	0.969	0.969	0.962	0.962	0.955	0.951		0.946	0.901	0.905	0.905
AY083234/France	0.964	0.962	0.964	0.964	0.964	0.964	0.962	0.96	0.964	0.964	0.956	0.957	0.95	0.946	0.984		0.897	0.901	0.901
AY064475/USA	0.97	0.969	0.969	0.966	0.967	0.967	0.964	0.961	0.97	0.966	0.957	0.962	0.948	0.943	0.964	0.962		0.982	0.979
AB550331/Japan	0.975	0.974	0.974	0.974	0.975	0.975	0.971	0.969	0.975	0.974	0.965	0.969	0.956	0.951	0.97	0.967	0.983		0.987
AY044266/Finland	0.979	0.978	0.978	0.978	0.979	0.979	0.975	0.973	0.979	0.978	0.969	0.973	0.959	0.953	0.973	0.97	0.985	0.993	

Table S6. Sequence identities of Human Parvovirus B19 VP2 at the nucleotide (upper right) and amino acid (lower left) levels. Orange, red, green, and blue colors represent the virus strains in subtype 1a, 1b, 2, and 3, respectively.

Strain	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
FJ591158/USA		0.988	0.979	0.984	0.986	0.971	0.97	0.985	0.976	0.975	0.977	0.939	0.935	0.874	0.871	0.894	0.896
AY386330/USA	0.998		0.984	0.989	0.991	0.972	0.973	0.99	0.979	0.981	0.981	0.941	0.936	0.869	0.866	0.893	0.893
AB030694/Japan	0.994	0.996		0.988	0.99	0.973	0.974	0.983	0.978	0.983	0.98	0.95	0.947	0.875	0.87	0.896	0.895
AB126271/Japan	0.996	0.998	0.994		0.996	0.977	0.977	0.987	0.982	0.985	0.985	0.944	0.939	0.869	0.868	0.894	0.894
AB030673/Japan	0.998	1	0.996	0.998		0.978	0.979	0.989	0.984	0.987	0.987	0.946	0.942	0.87	0.869	0.894	0.894
ON113045/China-JL	0.998	0.996	0.992	0.994	0.996		0.99	0.974	0.984	0.984	0.978	0.944	0.936	0.866	0.866	0.888	0.887
KT310174/China-HZ	0.996	0.994	0.99	0.992	0.994	0.998		0.975	0.986	0.986	0.978	0.943	0.937	0.866	0.865	0.887	0.887
KM065414/Germany	0.998	1	0.996	0.998	1	0.996	0.994		0.978	0.98	0.98	0.942	0.938	0.869	0.867	0.89	0.89
KM065415/Germany	1	0.998	0.994	0.996	0.998	0.998	0.996	0.998		0.987	0.982	0.945	0.939	0.867	0.866	0.887	0.886
DQ225149/Germany	0.994	0.996	0.992	0.994	0.996	0.992	0.99	0.996	0.994		0.985	0.945	0.939	0.866	0.866	0.889	0.888

DQ225151/Germany	0.989	0.99	0.987	0.989	0.99	0.987	0.985	0.99	0.989	0.987		0.942	0.938	0.868	0.868	0.893	0.893
DQ357064/Germany	0.967	0.969	0.969	0.967	0.969	0.965	0.963	0.969	0.967	0.965	0.96		0.984	0.87	0.867	0.889	0.887
DQ357065/Germany	0.969	0.971	0.974	0.969	0.971	0.967	0.965	0.971	0.969	0.967	0.962	0.981		0.869	0.866	0.887	0.884
NC_004295/USA	0.983	0.985	0.987	0.983	0.985	0.981	0.98	0.985	0.983	0.981	0.976	0.965	0.969		0.939	0.899	0.9
AY083234/France	0.981	0.983	0.985	0.981	0.983	0.98	0.978	0.983	0.981	0.98	0.974	0.963	0.967	0.992		0.895	0.894
AB550331/Japan	0.987	0.989	0.989	0.987	0.989	0.985	0.983	0.989	0.987	0.985	0.98	0.965	0.967	0.987	0.987		0.987
AY044266/Finland	0.987	0.989	0.989	0.987	0.989	0.985	0.983	0.989	0.987	0.985	0.98	0.965	0.967	0.987	0.987	1	

Table S7. Sequence identities of Human Parvovirus B19 NS1 at the nucleotide (upper right) and amino acid (lower left) levels. Orange, red, green, and blue colors represent the virus strains in subtype 1a, 1b, 2, and 3, respectively.

Strain	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
Z68146/UK		0.995	0.995	0.991	0.995	0.996	0.983	0.988	0.998	0.990	0.986	0.994	0.943	0.944	0.866	0.873	0.871	0.869	0.869
FJ591158/USA	0.998		0.992	0.987	0.990	0.992	0.979	0.984	0.993	0.988	0.981	0.990	0.940	0.941	0.866	0.872	0.870	0.868	0.868
AY386330/USA	0.994	0.992		0.989	0.994	0.995	0.981	0.988	0.996	0.988	0.985	0.993	0.941	0.942	0.864	0.871	0.870	0.868	0.868
AB030694/Japan	0.991	0.992	0.988		0.989	0.990	0.978	0.984	0.992	0.985	0.982	0.990	0.947	0.947	0.866	0.873	0.874	0.873	0.872
AB126271/Japan	0.991	0.989	0.988	0.986		0.995	0.981	0.987	0.996	0.987	0.985	0.992	0.942	0.943	0.865	0.871	0.871	0.869	0.868
AB030673/Japan	0.997	0.995	0.994	0.991	0.994		0.981	0.988	0.997	0.989	0.985	0.994	0.942	0.943	0.866	0.873	0.873	0.871	0.870
ON113045/China-JL	0.989	0.988	0.983	0.980	0.980	0.986		0.987	0.983	0.981	0.982	0.980	0.939	0.942	0.858	0.867	0.866	0.863	0.864
KT310174/China-HZ	0.994	0.992	0.991	0.988	0.988	0.994	0.989		0.989	0.988	0.988	0.987	0.943	0.945	0.863	0.871	0.872	0.870	0.871
KM065414/Germany	0.998	0.997	0.995	0.992	0.992	0.998	0.988	0.995		0.990	0.987	0.995	0.945	0.946	0.866	0.873	0.873	0.871	0.871
KM065415/Germany	0.994	0.992	0.991	0.988	0.988	0.994	0.986	0.994	0.995		0.987	0.989	0.942	0.944	0.864	0.870	0.871	0.869	0.870
DQ225149/Gremany	0.985	0.983	0.982	0.979	0.979	0.985	0.980	0.988	0.986	0.985		0.987	0.943	0.945	0.860	0.867	0.869	0.868	0.868
DQ225151/Germany	0.995	0.994	0.992	0.989	0.989	0.995	0.985	0.992	0.997	0.992	0.983		0.943	0.944	0.865	0.872	0.873	0.872	0.872
DQ357064/Germany	0.952	0.953	0.949	0.955	0.946	0.952	0.947	0.953	0.953	0.952	0.949	0.950		0.991	0.851	0.849	0.859	0.858	0.858
DQ357065/Germany	0.959	0.961	0.956	0.959	0.953	0.959	0.955	0.961	0.961	0.959	0.956	0.958	0.979		0.853	0.852	0.862	0.860	0.860
NC_004295/USA	0.941	0.940	0.938	0.941	0.941	0.944	0.932	0.938	0.943	0.940	0.932	0.940	0.916	0.919		0.954	0.925	0.925	0.924
AY083234/France	0.947	0.946	0.944	0.949	0.944	0.947	0.938	0.944	0.949	0.946	0.938	0.946	0.919	0.923	0.988		0.925	0.930	0.928
AY064475/USA	0.940	0.938	0.937	0.938	0.937	0.940	0.931	0.937	0.941	0.938	0.929	0.938	0.916	0.919	0.971	0.973		0.983	0.983
AB550331/Japan	0.940	0.938	0.937	0.940	0.937	0.940	0.931	0.937	0.941	0.938	0.929	0.938	0.915	0.919	0.973	0.974	0.994		0.991
AY044266/Finland	0.940	0.938	0.937	0.940	0.937	0.940	0.934	0.940	0.941	0.941	0.932	0.938	0.918	0.922	0.970	0.973	0.991	0.994	

References for Table S1

[1] X. L. Gu, R. Qi, W. Q. Li, Y. J. Jiao, H. Yu, X. J. Yu, Misdiagnosis of scrub typhus as hemorrhagic fever with renal syndrome and potential co-infection of both diseases in patients in Shandong Province, China, 2013-2014, PLoS Negl. Trop. Dis. 15 (2021) e0009270, https://doi: 10.1371/journal.pntd.0009270.

[2] D. H. Heo, J. H. Hwang, S. H. Choi, M. Jeon, J. H. Lee, S. D. Hwang, K. A. Lee, S. H. Lee, C. S. Lee, Recent increase of human granulocytic anaplasmosis and co-infection with scrub typhus or korean hemorrhagic fever with renal syndrome in Korea. J. Korean Med. Sci. 34 (2019) e87, https://doi: 10.3346/jkms.2019.34.e87.

[3] D. Zhang, X. Wang, J. Lv, Y. Dong, Treatment of a patient with severe hemorrhagic fever accompanied by infection with methicillinresistant *Staphylococcus aureus*, *Acinetobacter baumannii*, *aspergillus* and mucor: a case report, Int. J. Clin. Pharmacol. Ther. 53 (2015) 1028-1034. https://doi: 10.5414/CP202395

[4] D. Golubić, A. Markotić, Leptospirosis and hemorrhagic fever with renal syndrome in northwestern Croatia, Acta Med. Croatica. 57 (2003) 369-372.

[5] K. O. Douglas, T. A. Samuels, M. Gittens-St Hilaire, Serum LPS associated with hantavirus and Dengue disease severity in Barbados, Viruses 11 (2019) 838, https://doi: 10.3390/v11090838.

[6] S. S. Sam, S. F. Omar, B. T. Teoh, J. Abd-Jamil, S. AbuBakar, Review of Dengue hemorrhagic fever fatal cases seen among adults: a retrospective study. PLoS Negl. Trop. Dis. 7 (2013) e2194. https://doi: 10.1371/journal.pntd.0002194.

[7] C. Fevola, K. M. Forbes, S. Mäkelä, N. Putkuri, H. C. Hauffe, H. Kallio-Kokko, et al. Lymphocytic choriomeningitis, Ljungan and orthopoxvirus seroconversions in patients hospitalized due to acute Puumala hantavirus infection. J. Clin. Virol. 84 (2016) 48–52. https://doi: 10.1016/j.jcv.2016.10.002.

[8] M. Miletić-Medved, A. Markotić, I. Kuzman, Z. Marić, T. Avsic-Zupanc, An epidemic of hemorrhagic fever with renal syndrome at the therapeutic community for treatment of psychoactive drug dependence in Ivanovac. Acta Med. Croatica. 57 (2003) 361-364.

[9] H. D. Zhao, H. B. Qian, Z. K. Wang, R. K. Ren, T. B. Yu, H. L. Liu, Patient with suspected co-infection of hemorrhagic fever with renal syndrome and malaria: a case report, Front. Med. 11 (2024) 1341015, https://doi: 10.3389/fmed.2024.1341015.