World Bulletin of Public Health (WBPH)
Available Online at: https://www.scholarexpress.net
Volume-8, March 2022
ISSN: 2749-3644

CLINICAL DESCRIPTION OF TREATMENT OF PEOPLE WITH CRIMEAN-CONGO HEMORRHAGIC FEVER AS A LITERATURE REVIEW

Hamidova Saodat Khikmatovna
Associate Professor of the Department of "Microbiology",Bukhara State Medical Institute

Article history:

Received: January 4th 2022
Accepted: February 4th 2022
Published: March 12th 2022

Abstract:

Crimean-Congo hemorrhagic fever virus (CCHF) is a tick-borne virus whose RNA consists of S, L and M segments. The virus can migrate through ticks with animals and migratory birds, and therefore it is possible to study the geographical distribution through genetic analysis [1]. Temporal and spatial analysis of the diversity of virus strains can serve as a key factor for a better understanding of the relationship between seropositivity and mortality [1]. The clinical spectrum of CCHF ranges from mild infections to severe to fatal. According to recent data, in severe cases of CCHF, hemorrhagic manifestations may develop with a mortality rate of 4 to 20%, depending on the geographical region and the quality of medical care [2].

Keywords: Crimean-Congo, virus

Crimean-Congo hemorrhagic fever virus (CCHF) is a tick-borne virus whose RNA consists of S, L and M segments. The virus can migrate through ticks with animals and migratory birds, and therefore it is possible to study the geographical distribution through genetic analysis [1]. Temporal and spatial analysis of the diversity of virus strains can serve as a key factor for a better understanding of the relationship between seropositivity and mortality [1]. The clinical spectrum of CCHF ranges from mild infections to severe to fatal. According to recent data, in severe cases of CCHF, hemorrhagic manifestations may develop with a mortality rate of 4 to 20%, depending on the geographical region and the quality of medical care [2].

MATERIALS AND METHODS.

A search was made for sources in the electronic databases of PubMed, The Cochrane Library, Scopus. The search depth was 10 years from 2012 to 2022. Inclusion criteria: reports of randomized and cohort studies, meta-analyses and systematic reviews; articles in English and Russian. Exclusion criteria: materials that do not have an evidence base, newspaper articles.

RESULTS AND DISCUSSION.

At present, the geographical range of the CCHF virus prevalence is extensive and includes more than 30 states (Asia, Europe, the Middle East, Africa) [3]. The phylogenetic analysis carried out by foreign researchers shows that the CCHF virus has 7 genetic groups: 3 African (Africa-1, Africa-2, Africa-3), 2 Asian (Asia-1, Asia-2), 2 European (Europe-1, Europe-2) correlated with geographic location [4,5]. On average, the annual mortality rate from CCHF is approximately one tenth of the total number of cases of CCHF in the population. Thus, the mortality rate from CCHF in Europe is 33.8%, in Asia 33.5%, in Africa 22.0%, respectively [6]. At the same time, the highest mortality is observed in 28.9% of agricultural workers, 19.2% of medical workers, 16.7% of slaughterhouse workers and 13.9% of farmers [6]. The RNA virus genome of CCHF consists of three segments: a small segment (S) is approximately 1.7 Kb long, encoding a nucleoprotein, a medium segment (M) is about 5.3 Kb long, encoding a single open reading frame that cleaves into two envelope glycoproteins and a hypervariable a protein of approximately 250 amino acids known as the mucin-like domain and a large segment (L) of approximately 12.1 kb in length encoding a single protein containing the polymerase domain. These segments contain short 5' and 3' untranslated regions of 55-170 bases [7]. According to a literature review, the CCHF virus has several different clones, called genotypes, with their own predominant geographical areas of distribution [7]. Due to the rearrangement of the segments, there are differences in the structure of clones in different segments of the genome, while five to seven genotypes are traditionally denoted by Roman numerals. An alternative designation for the same pedigrees refers to the main geographic location [7]. The most ancient lineages (branching close to the tree root in phylogenetic reconstructions) are found in Africa, with the exception of the Ap92 strain, which was isolated in Greece [7]. Most European strains belong to GtV and are much more conserved than CCHF genotypes circulating in other regions [7]. Strains with affinity for Ap92 (GtVI) can also be found in Europe [7].According to the results of phylogenetic analysis by researchers of

World Bulletin of Public Health (WBPH)
Available Online at: https://www.scholarexpress.net
Volume-8, March 2022
ISSN: 2749-3644

all three segments of the genome, it is shown that the CCHF virus originated in Africa several thousand years ago and is considered the most ancient of all representatives of the CCHF genotypes [7]. Previous phylogenetic analysis of S-segment strains subdivided strains into 6-7 groups depending on geographic location, so West Africa belongs to group I, Central Africa (Uganda and the Democratic Republic of the Congo (DRC)) - to group II, South Africa and West Africa is in group III, the Middle East and Asia (Asia-1 and Asia-2) are in group IV, Europe and Turkey are in group V, and Greece is in group VI [8]. Previous 60 years of CCHF outbreak Phylogenetic analyzes have shown that CCHF genotype II has been identified exclusively in the Democratic Republic of the Congo and Uganda, while different lineages of the CCHF pathogen have been identified in neighboring northern countries [8]. In European countries, especially in Spain, according to the results of the study, 2 genetic lines of the CCHF virus are circulating. A death from genotype III CCHF virus has been described, the S-segment is closely related to genotype IV sequences and has the highest identity with strains BT 958 (92.62%) from the Central African Republic and IbAn7620 (92.58%) from Nigeria [9]. The results of the performed sequence analyzes described by the investigators confirm that genotype III (Africa-3) circulates in southwestern Europe. This strain circulating in Spain caused 2 cases resulting in the death of the first patient and serious illness in the second case, indicating its high pathogenicity. Although, according to the authors, the risk of infection in Spain is considered low, it is indicated that human infection caused by the bite of an infected tick occurred 6 years after the virus was detected in ticks [9,10,11,12]. In recent years, the country has also noted the circulation of a new European genotype V of the CCHF virus, which served as the cause of a febrile illness of unknown origin. The new virus strain was probably imported from Eastern Europe [10,11,12]. A recent study in Greece showed that 2 out of 106 selected ticks from goats and sheep in the counties of Corinth and Phocis by PCR (Dermacentor marginatus and Haemaphysalis parva) were positive for CCHF virus, because the S-segment sequences (GenBank accession numbers KU365757 and KU365758) were 99% identical between them at the level of nucleotides and amino acids. In addition, these sequences showed 98% and 99-100% identity at the level of nucleotides and amino acids, respectively, with the strain CCHF AP92 (DQ211638). Then, to confirm the identity of the amplified and sequenced PCR products, a proteomic analysis was performed using the tissues of infected and control uninfected ticks [13]. Virus peptides corresponding to the L segment containing the putative RNA-dependent RNA polymerase and unique to the virus were identified in infected ticks marginatus and H. parva. The results confirmed CCHF infection in these ticks using an alternative method and a region of the genome different from the region of the genome (L segment) targeted by PCR (S segment). At the same time, the sequences of the L-segment peptides were 100% identical to the corresponding sequence of the prototype strain AP92 (ABB30012) [13]. The results of the study demonstrated that the CCHF virus identified in the present study in ticks is a genetic variant of the AP92 strain, but closer to the old AP92 strain (98% nucleotide sequence identity) than to the new AP92-like strain (91% nucleotide sequence identity) [13]. Thus, Greece is one of the Mediterranean countries where only one case of CCHF has been reported so far. It is assumed that the AP92 strain is not pathogenic to humans.While, in addition to the prototype strain AP92, there is a new AP92-like strain (KF146306) recently discovered in Greece in R. bursa collected from sheep in an area with a 6% prevalence of the CCHF virus and is pathogenic [13]. Currently, two cases of AP92-like strain of CCHF virus are reported, one of which was a case of the disease in a person with mild symptoms in Turkey, and the other death was recently reported in Iran [13]. Authors from Kosovo state that different variants of the CCHF genotype V virus are circulating, with Turkey being a possible source of CCHF outbreaks in southern Europe, including in their country [14,15]. Currently, the dominant number of cases of CCHF is indeed registered in Turkey, but it is indicated that the mortality rate in the country is lower than in other regions and averages 5% [2]. Other investigators from Turkey argue otherwise, as the partial sequences obtained were reported to be related to the European strain, with strains closely related to Turkey-Kelkit06, Turkey 200310849 viruses and viruses from Russia and Kosovo. So, when comparing with previously analyzed isolates from GenBank, the sequence similarity was found to be 95% -99%. This is proved by the fact that the increase in the number of cases of CCHF in the country does not come from local isolates, but is associated with circulating strains imported from countries neighboring Turkey [16]. Researchers from Turkey also studied the relationship between the D32 mutation of the chemokine receptor 5 (CCR5) D32 gene and the pathogenicity, severity, and mortality of CCHF. The results of the study suggest that the CCR5 gene and its product may play a role in the pathogenesis of CCHF disease [17]. Other authors write that the NF-KB1-94W/D and NF-KBIA 3 UTR A G polymorphisms may be valuable predictors of the clinical course of

World Bulletin of Public Health (WBPH)
Available Online at: https://www.scholarexpress.net
Volume-8, March 2022
ISSN: 2749-3644

CCHF [18]. The presence of single nucleotide gene polymorphisms (SNPs) in cytokines can cause sensitivity or resistance to viral agents and a variable clinical course. Pakistan is also considered a CCHF endemic country with numerous outbreaks and sporadic cases reported over the past two decades, most in Balochistan province with subsequent transmission to non-endemic areas. Thus, the results presented by the researchers confirm the existence of the Asia-1 genotype [19,20] Samaya in the Chakwal region (24.13%), followed by Mianwali (23.68%), Rawalpindi (23.07%), Attok (20 .0%), Rajanpur (10.52%) and Lahore (8.33%). In positive tick pools, the highest prevalence of CCHF virus antigen was found in H. antolicum (39.6%), followed by H. marginatum (30.18%), H. rufipes (13.2%), H. impressum(3.77%), H. dromedarii. (1.88%), R. microplus (5.66%) and R. sanguineus (5.66%) [19,20]. Phylogenetic analysis also showed that all the studied viruses, periodically detected in Pakistan in the period 1976-2002, belonged to the Asia-1 genotype and had the greatest similarity (99-100%) with previously registered strains from Afghanistan, Iran, the United Arab Emirates and Iraq [21].However, in recent decades, the country has increasingly registered the Asia-2 genotype, which is distributed mainly in China and Central Asian countries such as Uzbekistan, Tajikistan and Kazakhstan, despite the fact that the Asia-1 genotype of the CCHF virus remains endemic in Pakistan [21,22]. The Asia-1 genotype is also endemic in Iran, although a case of CCHF caused by a virus belonging to the Asia-2 genotype has been reported on Qeshm Island in the south of the country [23]. Outbreaks of CCHF disease are also recorded in India, for example, the phylogenetic tree revealed that, along with the previously described strains of the CCHF pathogen belonging to the Asia-2 group, cases of disease caused by pathogens belonging to the Asia-1 group, which have the maximum identity, began to be registered in the country. to strains from Pakistan, Afghanistan and Iran [24,25,26,27]. In China, the first case of CCHF was reported in 1965 in Xinjiang Province, with sporadic outbreaks in the region in subsequent years. So far, only one genome-wide sequence of the Chinese CCHF isolate (C-68031) has been reported [28]. The authors report that there are genome-wide sequences of two new isolates, 79121M18 and YL04057, both from Xinjiang, China. Strain 79121M18 was isolated from rodents (Euchoreutesnaso) in 1979, and YL04057 from ticks (Hyalommaasiaticum) in 2004, while 79121M18 and YL04057 form a cluster together with other Chinese isolates and are combined into the Asia-2 group [28]. While two new strains (FK16116 and WJQ16206) and another strain from the city of Fukang (Fub90009) belonged to the Asia-1 genotype [29]. In recent years, researchers have identified and isolated a new strain of CCHF from Hyalommaasiaticum ticks collected north of the Tarim Basin in Xinjiang, China [30]. In the Russian Federation, there is a Russian line of the European genotype V (commonly referred to as GtVa), which differs from the GtV isolates from Turkey and the Balkan countries [31]. There are data on the circulation of the Europe-1 genotype (second line VLG/ROS) in the Stavropol region of Russia, in addition to the previously known line STV-ROS [32]. In the Crimean Federal District, when conducting an epidemiological study, an imported case of CCHF from the Crimea was investigated in 2016, according to the results of molecular genetic analysis, it was revealed that the CCHF virus belongs to a new genetic subtype Crimea (Vd), belonging to the Europe-1 genotype [33]. Tajikistan is also a CCHF endemic region, as a recent phylogenetic analysis has shown that Asia-1 and Asia-2 CCHF virus genotypes circulate in the country [34]. In Kazakhstan, a study was conducted to identify the seroprevalence of CCHF virus in endemic (Kyzylorda) and non-endemic (Almaty) regions of Kazakhstan. Phylogenetic analysis of partial segments L and S showed the CCHF Asia-2 genotype and a possible reassortment between the Asia-1 and Asia-2 genotypes [35].

CONCLUSIONS:

Thus, there is a wide variety of genotypes of Crimean-Congo hemorrhagic fever viruses in the world, which is the cause of various clinical outcomes of the disease. We consider it necessary to perform genotyping of the virus using genetic analysis methods to establish the prognosis of the disease and coordinate successful anti-epidemic and preventive measures in regions that are unfavorable for Crimean Congo hemorrhagic fever.

REFERENCES

1. Khikmatovna, Hamidova Saodat. "Drinking water quality source of life." *Web of Scientist: International Scientific Research Journal* 2.10 (2021): 35-40.
2. Саломова Н. К. Особенности течения и клинико-патогенетическая характеристика первичных и повторных инсультов //central asian journalof medical and natural sciences. – 2021. – С. 249-253.
3. Atayeva M. A., Jarylkasynova G. J., Baratova M. S. Assesment of heart rhythm disorders at left atrial stanning at early stages of left ventricular modeling //Journal of Critical Reviews JCR. –

World Bulletin of Public Health (WBPH)
Available Online at: https://www.scholarexpress.net
Volume-8, March 2022
ISSN: 2749-3644

2020. – Т. 7. – №. 4. – С. 1695-1699.
4. Atayeva M. A. Cardiomyopathy as a Manifestation of Complications of Chronic Viral Hepatitis //American Journal of Medicine and Medical Sciences. – 2020. – Т. 10. – №. 4. – С. 258-261.
5. Baratova M. S., Ataeva M. A. Modern Ultrasound Methods for Assessing Indicators of The Latent Diastolic Function of The Left Ventricle //International Journal of Pharmaceutical Research. – 2021. – Т. 13. – №. 1.
6. Baratova M. S. Algorithm and ultrasonic indicators of stanning of the left atrial in diastolic dysfunction of the left ventricular. – 2021.
7. Баратова М. С., Атаева М. А. Оценка ранней дисфункции миокарда у больных с пороговой артериальной гипертензий и артериальной гипертензией I-степени //Международный журнал прикладных и фундаментальных исследований. – 2015. – №. 8-2. – С. 232-233.
8. Akhmedov A. T. et al. Congenital heart defects in children and comorbidity //E-Conference Globe. – 2021. – С. 102-102.
9. Sh, Navruzova, and A. T. Akhmedov. "Autoimplantation Of Thymus In Surgical Correction Of Congenital Heart Defects." *Central Asian Journal Of Medical And Natural Sciences* 2.3 (2021): 88-98.
10. Khasanovna, Mansurova Malika, and Tosheva Dilnoza Rahmatovna. "Helicobacter Pylori and the Risk of Coronary Heart Disease (Literature Review)." *International Journal of Innovative Analyses and Emerging Technology* 1.4 (2021): 147-150.
11. Khikmatovna, Hamidova Saodat. "Establishing the systematic position of fungi of the genus trichoderma, isolated from soils of the bukhara region." International Engineering Journal For Research & Development 5.7 (2020): 6-6.
12. Хамидова, Саодат Хикматовна. "Создание таксономического положения грибов, относящихся к типу триходермий, выделенных из почвы." *Интернаука* 2-1 (2021): 19-20.