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TOWARD THE STUDY OF ETIOLOGIC AND EPIDEMIOLOGIC CHARACTERISTICS OF A NEW CORONAVIRUS INFECTION (COVID-19) IN THE WORLD

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Abstract:

To date, more than two hundred viruses causing respiratory infections in humans have been discovered and studied. At the same time, the emergence of pathogens is, firstly, a natural process that reflects the natural course of biological evolution, and, secondly, the result of active development of molecular diagnostic methods. Most newly discovered pathogens are represented by viruses [1, 2, 3, 16]. The etiologic spectrum of acute respiratory viral infections has been expanded due to the "newest" viruses discovered at the beginning of the 21st century. Such pathogens include the new coronavirus [3,4,6].

Keywords: coronavirus infection, pandemic, etiologic structure of the virus.

The COVID - 19 ("coronavirus disease 2019") epidemic has already made history as an international emergency. To date, the number of infected people in the world has exceeded 80 million, the World Health Organization has declared a state of "pandemic".

Coronavirus infection is an acute viral disease with predominant upper respiratory tract involvement caused by an RNA-containing virus of the genus Betacoronavirus of the family Coronaviridae. Coronaviruses (Coronaviridae) is a family including, as of January 2020, 40 species of RNA-containing, complexly organized viruses with a supercapsid. Combined into two subfamilies that affect humans and animals. The name is related to the structure of the virus: large mace-like spikes protruding from the supercapsid, which resemble a crown [8].

Virions are 80-220 nm in size. The nucleocapsid is a flexible helix consisting of genomic plus-strand RNA and many nucleoprotein N molecules. It has the largest genome among RNA-genomic viruses. Its structure is characterized by a supercapsid that contains a glycoprotein trimeric shield glycoprotein (peplomer), a membrane glycoprotein, a small envelope glycoprotein, and a hemagglutinin esterase. Corona assignment in coronaviruses is associated with a specific mechanism of penetration through the cell membrane by mimicking molecules to which cell transmembrane receptors respond [8, 9].

Currently, four coronaviruses (HCoV-229E, -OC43, -NL63, -HKU1) are known to circulate in the population, which are present year-round in the structure of acute respiratory infections and, as a rule, cause mild to moderate upper respiratory tract infections [3,6].

Based on the results of serologic and phylogenetic analysis, coronaviruses are divided into four genera: Alphacoronavirus, Betacoronavirus, Gammacoronavirus, and Deltacoronavirus. The natural hosts of most of the currently known coronaviruses are mammals.

Until 2002, coronaviruses were agents causing non- serious upper respiratory tract disease (with very rare fatalities). In late 2002, coronavirus (SARS-CoV), the causative agent of SARS, emerged and caused severe acute respiratory syndrome (SARS) in humans. The causative agent of SARS (SARS-related human coronavirus Urbani virus - SARS-Cov) belongs to the genus Betacoronavirus. The disease, which first emerged in November 2002 in Guangdong Province of China, was described by an Italian physician C. Urbani, who became infected and died while treating patients. The prototype strain of the isolated virus was named in his honor. [12, 13, 15]. The source of human infection was probably Himalayan civets Paguma larrata [13], as well as raccoon dogs Nyctereutes procyonoides, Burmese ferret badgers Melogale personata and others.

[15,16]. However, further studies have shown that natural foci of SARS-CoV, as well as many other coronaviruses, are associated with members of the order Chiroptera, primarily bats. SARS-CoV-like viruses have been isolated from bats, mainly from Rhinolophus horseshoe bats, as well as from species belonging to other genera in Asia (primarily China), Africa, Australia, Europe, and America [1, 9, 16, 19]. Population transit of SARS-CoV- like coronaviruses occurs from bats (natural foci) to small mammals that eat them (ecologically related) with further spread to humans, mainly by respiratory route, less frequently - alimentary.

According to the World Health Organization (WHO), by the end of August 2003, 8,098 cases of SARS had been reported with a 4-11% mortality rate. The largest numbers of cases were found in the People's Republic of China (PRC), Singapore, and Canada. The virus spread from Southeast Asia via international airlines due to the short incubation period (2-3 days). [1, 9]. The spread of the disease occurred mainly in hospital settings. One patient infected three or four contacts on average.

According to data [1, 2, 9], 60% of all fatal cases occurred among health care workers. In severe forms with pneumonia, diffuse lesions of alveoli develop due to disruption of the integrity of their walls, increased capillary membrane permeability with subsequent pulmonary edema, hypoxia, arterial hypoxemia, respiratory acidosis and alkalosis.

In 2012, a new coronavirus MERS-CoV or Middle East Respiratory Syndrome - MERS, which causes a more severe disease with high mortality, was already discovered in Saudi Arabia. [11, 13, 15]. The first human cases of BVRS, were reported in eastern Saudi Arabia in September 2012. Infections have been detected in other Middle Eastern countries (Jordan, Qatar, United Arab Emirates), North Africa (Tunisia), Europe (France, Germany, UK, Italy) and America (USA, Canada) [17, 18, 19]. Epizootic cases have also been reported in Saudi Arabia. As of December 2019, 2,484 cases have been confirmed, of which 857 (34.5%) were fatal.

According to several authors, infection occurs through the products of bats, which are the natural reservoir of the virus, and possibly also through intermediate hosts, such as camels [6, 15]. Direct transmission has been established among humans, especially to health care workers in close contact with patients. The clinical picture of BVRS is not fundamentally different from SARS. The causative agent of BVRS (MERS-CoV virus) also belongs to the genus Betacoronavirus.

It should be borne in mind that several species of Chiroptera, like birds, make annual seasonal migrations, wintering also within the range of natural foci of the BVRS virus [1, 6, 15, 19].

According to the authors, the virus, in addition to export with infected humans, can also enter the CIS countries with bats. It is not accidental that all epidemic outbreaks occurred in the fall, during the migration period of bats. The same situation is characteristic of outbreaks of new variants of avian influenza, which occur during or after mass migration, when there is a high concentration of animals in wintering grounds and mixing of populations.

An outbreak of novel coronavirus 2019-nCov (COVID-19) was reported in December 2019 in Wuhan, Hubei Province, PRC, although the first cases were reported in November 2019. The outbreak tends to spread to other 30 cities in the PRC, including Beijing and Shanghai [1, 6, 10]. Infected patients have been identified in at least 40 countries in Asia, America, Europe, and Australia. Two cases have been identified in the Russian Federation. In the PRC and several other countries, more than 80 thousand cases with 2% mortality have been registered by 01.03. 2020. Quarantine was declared in Wuhan and 17 other cities, additional 4000 medical personnel including 450 military doctors were sent there, two modern boxed hospitals for 1000 beds each were built within 2 weeks. The PRC has taken swift and tough measures to limit the spread of infection and minimize the consequences.

The primary source of infection at the first stage of research was considered to be seafood at the food market, where many other animal products, in particular snakes, are sold (the second hypothesis of the primary source). However, analysis of data on the phylogenetics of the isolated strains shows that the primary natural reservoir, similar to SARS-CoV and MERS - CoV viruses, is bat species gravitating to human habitation [1, 2, 6, 10, 11]. Horseshoe bats (Rhinilophidae, Rhinolophus), including the greater horseshoe bat R ferrumeguinum), are of major importance. The range of the great horseshoe includes Europe, Crimea, Caucasus, Central Asia, North Africa, North India, China, Korea, and Japan. Other vertebrates with direct ecological links to bats (civets, bat-eating snakes, etc.) serve as intermediate hosts. If they are used for food purposes, they may become sources of human infestation [18, 19].

On February 11, 2020, the International Committee on Taxonomy of Viruses assigned its own name to the COVID-19 infectious agent, SARS-CoV- 2. The new coronavirus SARS-CoV-2 is a single-stranded RNA-containing virus and belongs to the family

Coronaviridae, Beta-CoV B. The virus is assigned to pathogenicity group II, as well as other representatives of this family (SARS- CoV and MERS-CoV).

The SARS-CoV-2 coronavirus is presumably a recombinant virus between a bat coronavirus and a coronavirus of unknown origin. The genetic sequence of SARS-CoV-2 is at least 79% similar to that of SARA-Cov [1, 6, 10, 15].

Phylogenetic studies of isolated strains have shown that the genomic sequences of viruses found in bats are 99 percent identical to those isolated from COVID-19 patients [10, 11, 13].

Currently, the main source of infection is an infected person, including those at the end of the incubation, prodromal period (the beginning of virus release from target cells) and during clinical manifestations.

Mechanism of transmission - aspiration, Routes of transmission: airborne (release of the virus by coughing, sneezing, talking) by close contact.

The household contact route of infection is realized through transmission factors: water, food, and objects (door handles, smartphone screens) contaminated with the pathogen [5, 6, 9, 10]. The risk of virus transfer from hands to the mucous membranes of the eyes, nasal and oral cavity and disease is proven. A fecal-oral mechanism is possible (the pathogen was detected in fecal samples from patients infected with SARS-CoV-2). [6, 10, 17]. The nucleocapsid protein COVID-19 was detected in the cytoplasm of epithelial cells of salivary glands, stomach, duodenum and rectum, and urinary tract. The fact of realization of the artificial mechanism of transmission of SARS CoV-2 has been established. In the PRC, more than 1700 confirmed cases of COVID-19 have been reported in health care workers providing care to COVID-19 patients [1, 6, 10]. Susceptibility to the pathogen is high in all population groups. Risk groups for severe course of the disease and risk of lethal outcome include people over 60 years of age, patients with chronic diseases (respiratory diseases, cardiovascular diseases, diabetes mellitus, oncologic diseases), lethality varies from 2 to 4%. [10, 15, 17].

The entry gate of the pathogen is the epithelium of the upper respiratory tract and epitheliocytes of the stomach and intestine. The initial stage of infection is the penetration of SARS-Cov-2 into target cells with angiotensin- converting enzyme type II (ACE2) receptors. ACE2 receptors are present on cells of the respiratory tract, kidney, esophagus, esophagus, bladder, ileum, heart, and CNS. However, type II alveolar cells (AT2) of the lung are the main and rapidly attainable target, which determines the development of pneumonia. The role of CD147 in the invasion of SARS - CoV-2 cells has also been discussed [6, 11, 13].

It has been established that dissemination of SARS-CoV-2 from the systemic bloodstream or through the lamina cribrosa can lead to brain damage. Changes in the sense of smell (hyposmia) in patients at an early stage of the disease may indicate both CNS damage and edema of the nasopharyngeal mucosa [10,19].

The first symptoms of COVID-19 include fever (90%), dry or sputum- filled cough (80%), dyspnea (55%), myalgia and fatigue (44%), chest tightness (20%), and headache (8%), hemoptysis (5%), diarrhea and nausea (3%). These symptoms at the onset of infection may also be observed in the absence of fever (11, 19).

Many aspects of the pathogenesis and clinic of coronavirus infection need further comprehensive study.

The emergence of COVID-19 has posed challenges for health care professionals related to the rapid diagnosis and provision of medical care to patients. Currently, there is limited information on the epidemiology, clinical features, prevention and treatment of this disease worldwide. It is known that the most common clinical manifestation of a new variant of coronavirus infection is bilateral pneumonia, and the development of acute respiratory distress syndrome (ARDS) has been registered in 3-4% of patients. [11,12,13].

To date, the only means of preventing further spread of the virus among the population is specific prophylaxis (vaccination). It should be noted that the measures taken in many countries of the world to prevent the introduction of the virus are undoubtedly important. However, they cannot completely prevent the introduction of the virus by infected people, during the incubation period, or those who have erased and inapparent forms of the disease. The task is further complicated by the fact that events are unfolding against the background of a seasonal influenza epidemic as well as 8 other respiratory viruses, including seasonal coronavirus (Alphacoronavirus). It is obvious that similar situations will continue to arise in the foreseeable future The COVID-19 epidemic is not the last threat in the 21st century [1, 3, 6, 10, 16, 18].

Thus, all countries under the auspices of the UN should be ready for coordinated action to prevent the emergence and spread of infections, to diagnose them in a timely manner, to develop treatment and prevention methods, and to create vaccines. This requires united international action for the integrated development of plans by specialists (epidemiologists, ecologists, virologists, clinicians, health care organizers) to minimize the consequences of emerging and re-emerging infections.

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