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THE CONTRIBUTION OF VIRUSES TO THE STRUCTURE OF ACUTE RESPIRATORY DISEASES IN THE POPULATION OF YAKUTSK IN 2019-2020

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The aim of the study was to identify the viral etiology of acute respiratory diseases in patients hospitalized to the infectious hospitals in Yakutsk. **Methods:** nasal and pharyngeal swabs were obtained from the examined patients. The presence of the genetic material of the respiratory viruses was determined by real-time PCR. **Results:** During the study, 178 patients admitted to the infectious hospitals in Yakutsk from November 2019 to April 2020 were selected according to the inclusion criteria. 99/178 (55.6%) samples were positive for at least one of the studied viruses, 79/178 (44.4%) samples were negative. Respiratory syncytial virus; rhinoviruses; metapneumovirus; parainfluenza viruses of types 1, 2, 3 and 4; coronaviruses NL-63, 229E, HKU-1 and OC-43; adenoviruses groups B, C and E; bokavirus, as well as influenza A and influenza B viruses were identified. The results of the study are necessary to improve and optimize diagnostic tactics, for control and prevention of respiratory viral infections.

Keywords: human viruses, acute respiratory viral infections, influenza, respiratory syncytial virus, rhinovirus, bronchiolitis, fever.

Introduction. Acute respiratory viral infections (ARVI) occupy a leading place in infectious pathology, accounting for about 90% in the structure of infectious diseases, which is associated with high contagiousness and rapid spread of infections by airborne transmission, while the most susceptible to infection is the child population and the elderly [14,15]. In addition, cases of severe course of the disease are more often observed in young children, the risk of complications and deaths is higher[10]. The diverse etiological structure of ARVI is characterized by heterogeneity and variability of pathogens not only in time, but also in space [2,5]. In the distribution of ARVI diseases among the population, the territory of his residence is of great importance. The presence of territorial differences in the circulation of pathogens and the incidence of respiratory diseases (in particular, pneumonia, chronic bronchitis, bronchial asthma, etc.) have been studied by various authors. It has been shown that the severity of these diseases is due to the climatic and socio-demographic features of the habitat [1].

Materials and methods. The study was organized on the basis of infectious

diseases hospitals in Yakutsk. The study was approved by the Committee on Biomedical Ethics at FITZ FTM (Protocol No. 4-2019).

The study included hospitalized patients of all age groups in the acute stage of respiratory disease (no later than 7 days after the onset of symptoms).

Taking samples. In all patients participating in the study, sterile probe swabs were taken from the nose and throat and placed in a test tube with a transport medium. Test tubes with samples were stored in a Dewar vessel with liquid nitrogen before the study.

Real-time polymerase chain reaction. All the samples obtained were used to identify the genetic material of the influenza virus and other respiratory viruses (respiratory syncytial virus; rhinoviruses; metapneumovirus; parainfluenza viruses of types 1, 2, 3 and 4; seasonal coronaviruses(NL-63, 229E, HKU-1 and OC-43); adenoviruses of groups B, C and E; bokavirus) using polymerase chain reaction (PCR) in real time using kits of reagents "Amplification of influenza virus A/B-FL", " Influenza A/H1-swine-FZ virus Amplification", "Influenza A-type-FZ virus amplification", "ARVI-screen-FL b Amplification" (InterLabService, Russia) in accordance with the manufacturer's instructions.

Statistical analysis. Statistical analysis was pperformed using Statistics 10.0 software. The reliability of differences between groups was evaluated using the Chi-square criterion.

Results and discussion. Selection of patients in accordance with the criteria for inclusion in the study.

During the study, doctors of infectious diseases hospitals in Yakutsk for the period from November 2019 to March 2020 selected 178 patients who met the criteria for inclusion of patients in the study. Each patient received written informed consent to participate in the study, after which samples of clinical material were taken. A total of 123/178 (69.1%) children aged 0-17 years and 55/178 (30.9%) adults aged 18-70 years were included in the study. At the same time, in children 56/123 (45.5%) samples were obtained from boys and 67/123 (54.5%) samples were obtained from girls; in adults, 20/55 (36.4%) samples were obtained from men and 35/55 (63.6%) samples were obtained from women. Among the children included in the study, 36.5% (65/178) were aged 0 - 2 years. The smallest number of samples were obtained from children aged 15-17 years (10 samples, which was 5.6% (10/178) of all samples received from children) and from elderly people aged over 65 years (5 samples, which was 9.1% (5/55) of samples received from adult patients), which was associated with a low level of hospital admissions of patients of these age groups. The gender and age structure of the sample is shown in Figure 1.

Detection of the genetic material of the influenza virus and other respiratory viruses by PCR in real time. 99/178 (55.6%) samples were positive for at least one of the studied viruses, 79/178 (44.4%) samples were negative. These data are consistent with previous studies in Pittsburgh (59.7%), in Vitoria in southeastern Brazil (54.3%), in Huzhou in China (57.7%), while in our earlier study in Novosibirsk, the detection rate of respiratory viruses was significantly higher (72,3%) [10,7-9,18]. Such differences in the level of virus detection may be related to differences in the design of studies (in particular, the age structure of the included patients), different geographical territories, climatic conditions, population density [6,7]. The level of virus detection in children was significantly higher (64.2%) than in adults (36.4%), which is probably due to the peculiarities of the immune status in children and their higher susceptibility to viruses than in adults [16,13]. The detection of the influenza virus was 8.4% (15/178). Influenza B virus infection was detected in only two of all analyzed cases (13.3% of all positive flu samples). Among the influenza A virus, A (H1N1) pdm09 prevailed, which was detected in 80% (12/15) of all influenza cases. Influenza A (H3N2) virus was detected in 6.7% (1/15) of cases. Thus, in studies conducted in China, the detection rate of the virus among hospitalized children with ARVI was 8.9% in Beijing and Shanghai [19], and according to estimates presented in a systematic review of 100 studies, the influenza virus accounted for 5% of hospitalizations with acute lower respiratory tract infection [17]. These data are consistent with our results, although direct comparison is impractical due to differences in the structure of the study and differences in influenza activity in different seasons, in different regions and population groups [6]. Among other respiratory viruses, the most common were bokavirus - 17.4% (31/178), parainfluenza viruses - 14.6% (26/178), rhinovirus - 10.6% (19/178), seasonal coronaviruses (NL-63, 229E, HKU-1, OC-43) - 6.7% (12/178) and adenovirus - 6.2% (11/178). The remaining respiratory viruses were detected in less than 5% of cases. Viral co-infection was observed in 20/123 (16.2%) children, 1/55 (1.8%) cases of co-infection were detected among adults (Figure 2). According to the results of previous studies, the level of co-infection in children can reach 30% [9,16], which is associated with the immaturity of the immune system and, consequently, greater susceptibility to infections [8].

Age and sex differences in the level of detection of influenza virus and other respiratory viruses. When comparing the level of virus detection in different age groups, it was shown that the proportion of influenza virus increased with age with the highest frequency of occurrence in the adult population (80%). The remaining respiratory viruses were significantly more common in children than in adults. At the same time, bokavirus was found only among children, and the detection rate among children was significantly higher in the age group of 0 - 2 years compared with children older than 3

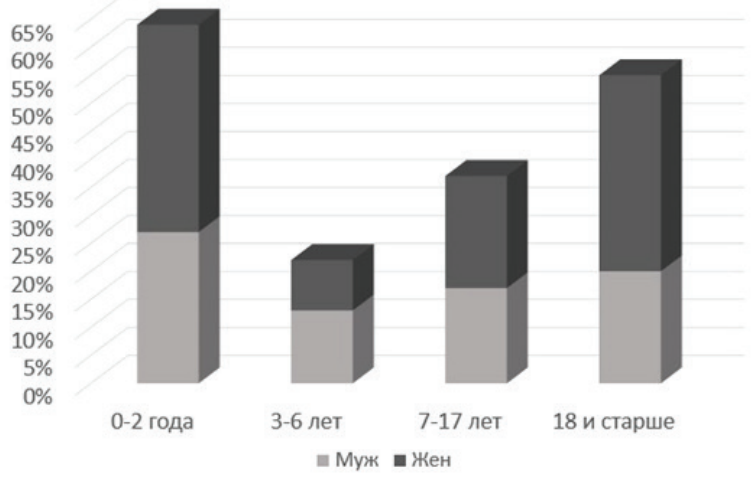

Fig. 1. Age and sex composition of the sample of patients included in the study

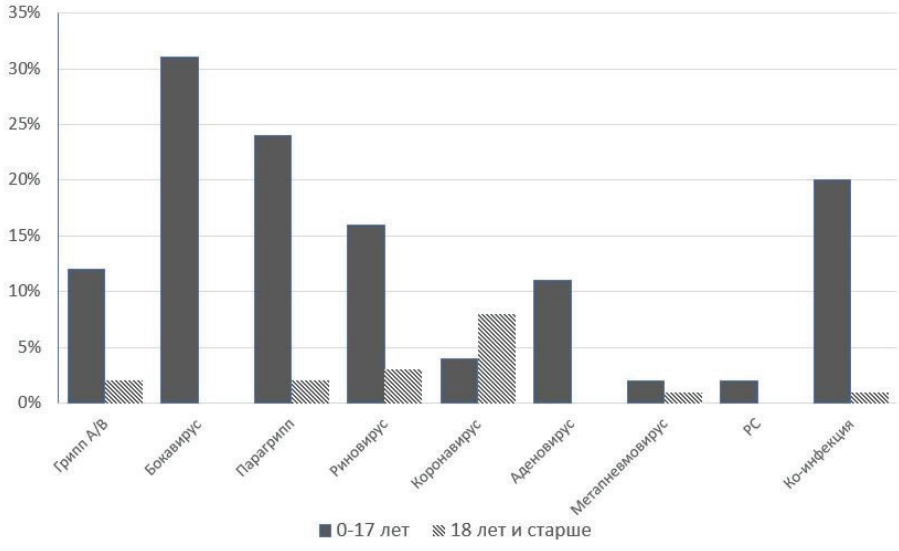

Fig. 2. The level of detection of respiratory viruses in patients as a percentage of the total number of examined patients in each group

years (67.7% and 32.3%, respectively, -2 = 27.79 and -2 = 48.03). For other respiratory viruses, no significant differences were found in different age groups. There were no sexual differences in the frequency of occurrence. In the study conducted by A.A. Sominina et al., there were also no sex differences in the frequency of occurrence of respiratory viruses [3].

The influence of bad habits and background diseases on the level of detection of influenza viruses and other respiratory viruses. Among 99 patients in whom influenza viruses and other acute respiratory infections were detected by PCR, 73 patients have never smoked, 2 patients have smoked before and 24 patients are currently smoking (for patients under the age of 14, the smoking habit of one of the parents was taken into account). At the same time, the detection rate of influenza virus and other respiratory viruses in smoking patients was 13.7 times higher than in non-smokers. Among the patients included in the study, concomitant chronic pathology was observed in 21 (11.8% of the total number of examined) people in the following age groups: 0-17 years - in 5 patients, 18 years and older - in 16 patients. Of the chronic pathology, neuromuscular disease was noted in 5 people, cardiovascular diseases in 3 people, chronic obstructive pulmonary disease and bronchial asthma - 1 patient each, other background diseases were noted in 10 people. When comparing the frequency of detection of respiratory viruses and influenza virus in the presence of background pathology and without it, no significant differences were found. Similar data were obtained earlier by A.A. Sominina et al. [3].

Etiology of diseases in patients admitted to the intensive care unit. A total of 5 patients aged 0 to 14 years (2.8% of the total number included in the study) were hospitalized in the intensive care unit (ICU) during the follow–up, of which 2 (40%) patients were children of the age group 0 - 2 years. Not a single patient over the age of 15 required hospitalization in the ICU. In 4 patients hospitalized in the ICU, any respiratory virus (bokavirus, type 1 parainfluenza virus) was detected, the influenza virus was not detected in this group.

Clinical diagnoses at discharge from the hospital. The most frequent (44.7%) diagnosis upon discharge to the hospital was "Pneumonia without specifying the causative agent", of which 61.8% had a viral infection. Bokavirus was detected in 27.6% of the examined, parainfluenza virus and rhinovirus - in 23.7% and 9.2% of patients with this diagnosis, respectively.

"Acute upper respiratory tract infection" was the second most common diagnosis at discharge - 22.3%. Among these patients, the viral etiology of the disease was confirmed in 39.4% of cases, seasonal coronavirus (NL-63, 229E, OC-43, HCU-1) was detected most often in this group of patients - 33.3%.

15.8% of patients were hospitalized with a diagnosis of Acute bronchitis, of which 81.5% of patients had respiratory viruses, and the most frequently detected were bokavirus and rhinovirus - in 25.9% and 22.2%, respectively.

Conclusion. Early and rapid detection of respiratory viruses by molecular methods is important for the prevention and control of emerging viral diseases [4]. The study demonstrates the contribution of viral infections to the structure of acute respiratory pathology of the upper and lower respiratory tract in hospitalized patients in Yakutsk. The results of the study are necessary to improve and optimize diagnostic and therapeutic tactics, control and prevention of respiratory viral infections.

In addition, knowledge of the viral etiology of respiratory infections is also important for differentiating bacterial and viral infections [11], since the use of antibiotics in viral infections does not improve clinical results, but exacerbates problems associated with antimicrobial resistance. Informing doctors about making decisions about the rational administration of antibiotics, taking into account the viral etiology, not only improves the clinical outcomes of the disease, but will also contribute to reducing antibiotic resistance [12].

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TOPICAL ISSUE

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PREDICTORS OF THE DEVELOPMENT OF HYPERTENSION IN YOUNG PEOPLE WITH HIGH NORMAL BLOOD PRESSURE

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Aim: to identify predictors of the development of arterial hypertension (AH) in young people with high normal blood pressure (HNP) based on the study of risk factors, hemodynamic parameters, structural and functional parameters of target organs. 155 patients under 45 years of age were included, mean age 35.1±3.2 years. Taking into account the indicators of office and ambulatory blood pressure (BP), the distribution into groups of HNP (68 patients) and AH (87 patients) was carried out. Conducted general clinical, laboratory, functional examination. Daily BP monitoring was performed for 24 hours using the BpLAB device (LLC Petr Telegin) with the integrated Vasotens® system, which makes it possible to evaluate central BP along with BP in the brachial artery. A complex of factors that increase the risk of developing hypertension in young people with HNP has been identified. Among them are hemodynamic, a number of risk factors (increased very low density lipoprotein cholesterol, triglycerides, total cholesterol, low density lipoprotein cholesterol, smoking experience, body mass index and waist circumference, age), intima-media thickness of brachiocephalic vessels, LA dimensions.

Keywords: arterial hypertension, high normal blood pressure, developmental predictors, young age.

Introduction. Numerous studies demonstrate that high normal blood pressure (HNP) is an independent risk factor (RF) for the development of cardiovascular disease (CVD). Patients with HNP have a higher risk of developing arterial hypertension (AH) than patients with optimal blood pressure (BP) [4]. The data obtained in the epidemiological study Framingham Heart Study revealed the formation of hypertension in HNP and normotensive profile in 54.2% and 23.6% in men and in 60.6% and 36.2% (respectively in HNP and normal blood pressure) in women . Thus, the risk of AH in baseline HNP increased by 2.25 times ($p<0.0001$) in men and by 1.89 times in the female population ($p<0.0001$) [8]. According to Y. Ishikawa et al. in a prospective cohort study conducted in Japan, it was shown that after 11 years, 26.1% of persons with prehypertension developed AH, the risk of developing AH in persons with VNP was 3.57 times higher than in persons with normotension [5].

The combination of several RFs contributes to the earlier progression of VNP to AH. Thus, the results of an American study involving more than 30,000 patients showed that in individuals with VNP and three RFs, the appearance of stable AH was noted for 4 years [1]. In a Korean cohort study that included patients with a normotensive status and prehypertension, the main predictors of the transformation of HNP into AH were: hypercholesterolemia, hyperglycemia, hyperuricemia, smoking, age, and an early family history of hypertension [7]. In another study, ethnicity, older age, higher body mass index (BMI), and the presence of diabetes or chronic kidney disease were independently and positively associated with the development of hypertension [11]. It should be noted that the studies included either adolescents or patients of older age groups; there are no data on predictors of hypertension in patients under 45 years of age. In addition, a complex of factors possibly associated with the development of AH has not been previously studied: hemodynamic, behavioral, structural and functional.

The aim of the study was to identify predictors of the development of arterial hypertension in young people with high normal blood pressure based on the study of risk factors, hemodynamic parameters, structural and functional parameters of target organs.

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