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Organization of a system for microbiological monitoring and antimicrobial resistance in a multidisciplinary hospital

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ABSTRACT. Healthcare-associated infections (HAI) are one of the most pressing problems facing modern medicine. One of the elements of organization of control of HAI in hospital is microbiological monitoring and assessment of antimicrobial resistance of strains isolated from patients. Of particular concern is the high prevalence of Klebsiella pneumoniae strains. These strains frequently cause urinary tract infections, pneumonia and have multiple resistance to antibacterial drugs. In this regard, the aim of the study is to evaluate the organization of the microbiological monitoring system to improve the internal system of epidemiological safety and control of UTIs in hospitals. In this article, a retrospective analysis of the results of microbiological monitoring of two hospitals in the city of St. Petersburg, carried out in the period from May to October 2024, is carried out. The results of the study confirm the high epidemiologic significance of the group of ESCAPE-pathogens, in particular Klebsiella pneumoniae, and demonstrate their pronounced resistance to antibiotics compared to other relevant strains. The necessity of regular microbiological monitoring for timely correction of empirical therapy protocols, early prescription of rational antibiotic therapy and prevention of the spread of antibiotic-resistant strains in medical institutions was substantiated.

KEYWORDS: healthcare-associated infections (HAI), microbiologic monitoring, strain, *Klebsiella pneumoniae*, beta-lactamases, antibiotic resistance, empirical and rational antibiotic therapy, digital technologies

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Организация системы микробиологического мониторинга и антимикробной резистентности в многопрофильном стационаре

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РЕЗЮМЕ. Инфекции, связанные с оказанием медицинской помощи (ИСМП), являются одной из актуальных проблем, с которой сталкивается современная медицина. Одним из элементов организации контроля за ИСМП в стационаре является микробиологический мониторинг и оценка антимикробной резистентности штаммов, выделенных от пациентов. Особую озабоченность вызывает широкое распространение штаммов *Klebsiella pneumoniae*. Данные штаммы часто вызывают инфекционные заболевания мочевыводящих путей, пневмонию и обладают множественной устойчивостью к антибактериальным препаратам. В этой связи целью исследования является проведение оценки организации системы микробиологического мониторинга для совершенствования внутренней системы эпидемиологической безопасности и контроля за ИСМП в стационарах. В статье проведен ретроспективный анализ результатов микробиологического мониторинга двух стационаров города Санкт-Петербурга, выполненный в период с мая по октябрь 2024 года. Результаты исследования подтверждают высокую эпидемиологическую значимость группы ESCAPE-патогенов, в частности *Klebsiella pneumoniae*, и демонстрируют их выраженную устойчивость к антибиотикам по сравнению с другими актуальными штаммами. Обоснована необходимость регулярного микробиологического мониторинга для своевременной коррекции протоколов эмпирической терапии, раннего назначения рациональной антибиотикотерапии и предотвращения распространения антибиотикорезистентных штаммов в медицинских учреждениях.

КЛЮЧЕВЫЕ СЛОВА: инфекции, связанные с оказанием медицинской помощи (ИСМП), микробиологический мониторинг, штамм, *Klebsiella pneumoniae*, бета-лактамазы, антибиотикорезистентность, эмпирическая и рациональная антибиотикотерапия, цифровые технологии

INTRODUCTION

Organisation of the internal control for healthcare-associated infections (HAI) plays a key role in providing microbiological monitoring and allows to characterize the etiological structure of HAI [1–3]. According to data of microbiological monitoring, the main causative agent of HAI is *Klebsiella pneumoniae.* Resistant strains of this species have actively spread in hospitals in St. Petersburg in the post-COVID period [4]. Infections caused by *Klebsiella pneumoniae* strains often lead to death in patients, especially those with the weakened immune system, such as cancer patients, patients with endocrine diseases, patients in intensive care units and those who have recently undergone surgery. Clinical pictures of infections caused by *Klebsiella pneumoniae* are extremely diverse and can range from mild urinary tract infections to severe ones such as pneumonia and sepsis [1, 5].

Of particular concern are strains of *Klebsiella pneumoniae* that produce enzymes that are resistant to antibacterial drugs, such as carbapenemases, in particular NDM (New Delhi Metallo-beta-lactamase), which cause a high level of resistance of this microorganism to antibiotics [6, 7].

Klebsiella pneumoniae strains containing the NDM gene were first identified in 2008 in India [8]. Since then, they have spread globally, leading to significant changes in the epidemiological situation and an increase in the frequency of infections caused by these strains.

The main risk factors for spread of these strains are associated with an increase in the number of invasive procedures, the use of broad-spectrum antibiotics, and poor control methods for infections associated with healthcare. Limiting the spread of *Klebsiella pneumoniae* strains that are not resistant to antimicrobial drugs in healthcare facilities through compliance with anti-epidemic measures is an important link in the fight against HAI.

AIM

To evaluate the organization of the microbiological monitoring system to improve the internal system of epidemiological safety and control of HAI in hospitals.

MATERIALS AND METHODS

At the first stage of the study, a retrospective analysis of the results of microbiological monitoring of the multidisciplinary hospital in St. Petersburg with 1000 beds, working under the compulsory medical insurance system, was carried out. The study period was from May to October 2024, during which 4,760 strains isolated from patients (Hospital No. 1) were analyzed. Then, an analysis of the microbiological monitoring data of the new multidisciplinary hospital serving the population of St. Petersburg and the Leningrad Region under compulsory medical insurance, voluntary medical insurance and for cash was performed. The number of beds was 230, 465 isolates were identified (Hospital No. 2). The obtained data were processed using the computer analytical program WHONET and the online platform AMRCloud. Statistical analysis was performed using parametric and non-parametric methods. The reliability of the research results was ensured by the representativeness of the sample and a sufficient volume of empirical data. The level of evidence was accepted as $p > 0.05$. To analyze the reliability of differences in the distribution of the frequencies of *Klebsiella pneumonia* strains isolation between hospitals, the leading pathogens in the etiological structure of Hospitals No. 1 and No. 2 were identified. The analysis of differences in the levels of resistance of *Klebsiella pneumoniae* to antimicrobial drugs was carried out using calculation of the median method.

RESULTS AND DISCUSSION

During the microbiological monitoring in studied hospitals, results of bacteriological examination of 5225 samples were used: 4760 from Hospital No. 1 and 465 from Hospital No. 2. In the etiological structure of Hospital No. 1, the leading pathogens are the following microorganisms (Fig. 1): *Klebsiella pneumoniae* — 27.52% (n=1310), *Escherichia coli* — 19.79% (n=942), *Staphylococcus epidermidis* — 10.09% (n=480), *Staphylococcus aureus* — 8.89% (n=420), *Acinetobacter baumannii* — 7.35% (n=350). A total of 18 microorganisms were isolated.

In the etiological structure of Hospital No. 2, 71 types of microorganisms were identified (Fig. 2), including the following: *Escherichia coli* — 22.63% (n=105), *Klebsiella pneumo-*

niae — 11.21% (n=52), *Staphylococcus aureus* — 10.78% (n=50), *Enterococcus faecalis* — 7.76% (n=36), *Candida albicans* — 5.60% (n=26).

The number of isolated microorganism species in Hospital No. 1 is statistically significantly lower than in Hospital No. 2 (p <0.05). These differences are explained by the fact that Hospital No. 2 uses more modern laboratory diagnostic methods and also provides medical care to patients who require in-depth examination and treatment.

Despite the differences in the species composition of isolates in the hospitals we are consi-

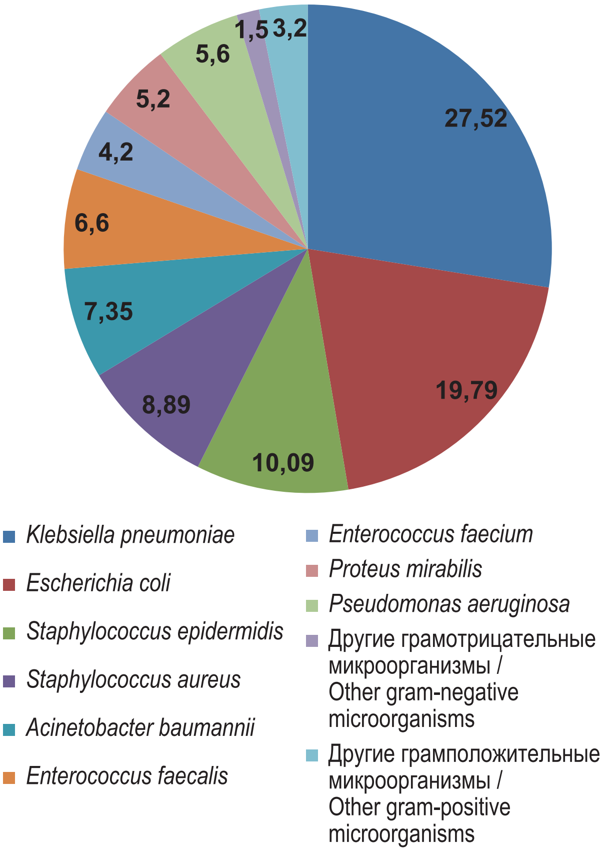

Fig. 1. Etiological structure of isolates in hospital No. 1

Рис. 1. Этиологическая структура изолятов в стационаре № 1

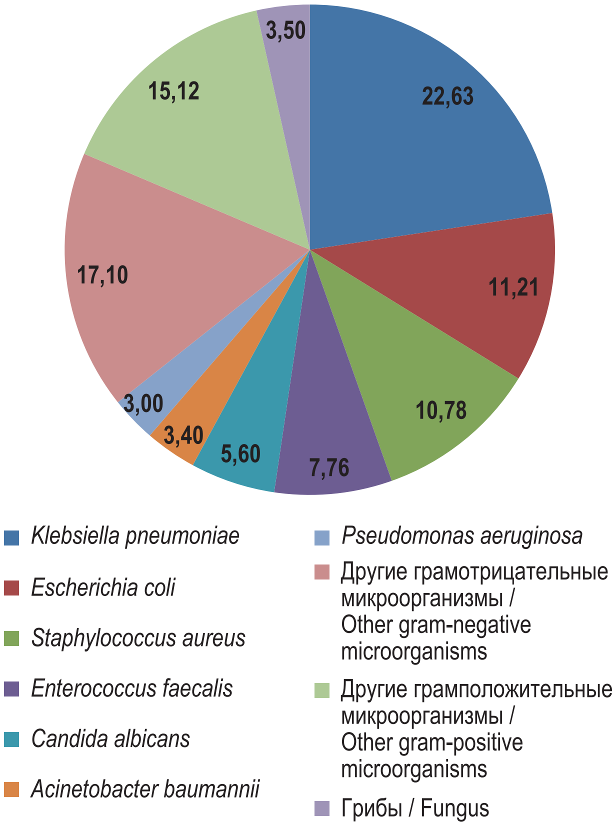

Fig. 2. Etiological structure of isolates in hospital No. 2

Рис. 2. Этиологическая структура изолятов в стационаре № 2

Table 1

Distribution of isolates depending on the location of infection

Таблица 1

Распределение изолятов в зависимости от локализации инфекции

№	Стационар № 1 / Hospital No. 1		Стационар № 2 / Hospital No. 2	
	Биологический субстрат / Biological substrate	**Процент / Абсолютное количество / Percentage / Absolute count**	**Биологический субстрат / Biological substrate**	**Процент / Абсолютное количество / Percentage / Absolute count**
1	Моча / Urine	38,8 / 1858	Моча / Urine	29,7 / 138
2	Мокрота / Sputum	26,9 / 1289	Мокрота / Sputum	12,7 / 59
3	Рана / Wound	17,2 / 824	Кровь / Blood	6,9 / 32
4	Кровь / Blood	7,5 / 362	Бронхоальвеолярный лаваж / Bronchoalveolar lavage	5,6 / 29
5	Прочее / Other	9,6 / 427	Прочее / Other	45,1 / 206

dering, the leading place in the etiological structure of HAI is occupied by microorganisms of the ESCAPE pathogen group, which includes microorganisms with high resistance to antibiotics — *Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa* and *Enterobacter* spp.

These microorganisms are the most common pathogens of HAI [9]. One of the leading positions belongs to *Klebsiella pneumoniae.*

During the analysis of microbiological study of clinically significant loci obtained from patients of Hospital No. 1, it was established that the maximum frequency of isolation of microorganisms from biological material falls on: urine (38.8%), sputum (26.9%), wounds (17.2%), blood (7.5%). In Hospital No. 2, significant biological substrates were also urine (29.7%), sputum (12.7%), blood (6.9%), bronchoalveolar lavage (5.6%) (Table 1).

In the process of epidemic surveillance, determining of risk groups is very important. When analyzing the data, greatest amount of isolates in Hospital No. 1 fell on the following departments: intensive care (24.8%), intensive care for neurological diseases (13.1%), neurology (8.7%), hepatobiliary surgery 5.5%, urology (5.2%). In Hospital No. 2, such departments were: therapy (22.2%), intensive care (18.9%), surgery (18.9%), urology (14.4%) and the Center for Specialized Medicine (11.8%) (Table 2). The data obtained show the need to take into account the specifics of the department when organizing measures to prevent HAI.

Of particular concern is the identification and spread of beta-lactamase-producing *K. pneumoniae* strains due to the severe condition of patients and the difficulty of selecting antibacterial drugs for their treatment [3, 5, 6]. The data analysis showed, that in Hospital No. 1 amount of beta-lactamase-producing *K. pneumoniae* strains among all found *K. pneumoniae* isolates, the percentage was 6.2% (82 isolates). The main biological substrate from which beta-lactamase-producing *K. pneumoniae* strains were obtained is urine (Fig. 3).

In the Hospital No.2, the amount of *K. pneumonia* strains was 38.4% (20 isolates) among all detected isolates of *K. pneumonia* (Fig. 4).

The next step was to analyze the antibiotic resistance of the isolated *Klebsiella pneumoniae* strains to various classes of antimicrobial drugs using the AMRcloud online platform. Also, a comparative analysis of sensitivity of beta-lactamase-producing *Klebsiella pneumoniae* strains to the same antibiotics was performed. When assessing sensitivity based on the results of laboratory studies, it was found that strains producing beta-lactamases exhibit greater resistance to antimicrobial drugs (Tables 3, 4).

Table 2

Distribution of isolated isolates by main hospital departments

Таблица 2

Распределение выделенных изолятов по основным отделениям стационаров

№	**Стационар № 1 / Hospital No. 1**		**Стационар № 2 / Hospital No. 2**	
	Отделение / Department	**Процент / Абсолютное количество / Percentage / Absolute count**	**Отделение / Department**	**Процент / Абсолютное количество / Percentage / Absolute count**
1	Реанимация / Resuscitation	24,8 / 1190	Терапия / Therapy	22,2 / 103
2	Нейрореанимация / Neuroreanimation	13,1 / 627	Реанимация / Resuscitation	18,9 / 88
3	Неврология / Neurology	8,7 / 419	Хирургия / Surgery	18,9 / 88
4	Гепатохирургия / Hepatobiliary surgery	5,3 / 256	Урология / Urology	14,4 / 67
5	Урология / Urology	5,2 / 251	Центр профильной медицины / Center for Specialized Medicine	11,8 / 55
6	Прочее / Other	42,9 / 2017	Прочее / Other	13,8 / 64

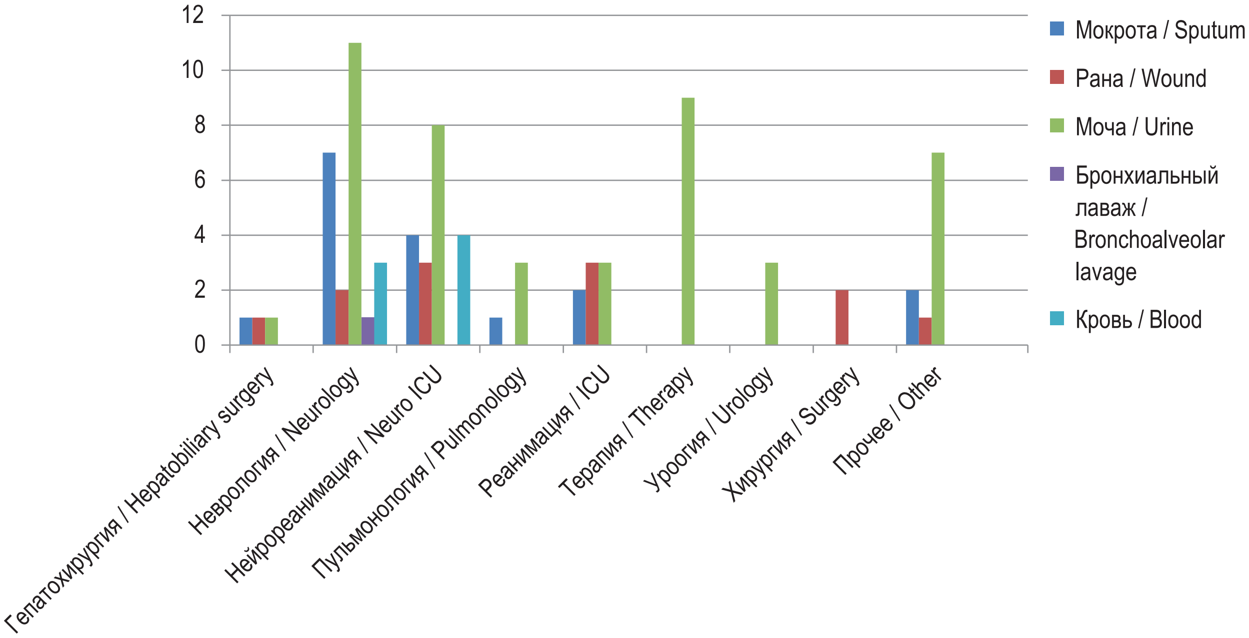

Fig. 3. Distribution of *K. pneumoniae* strains by departments and biological substrate in hospital No. 1

Рис. 3. Распределение штаммов *K. pneumoniae* по отделениям и биологическому субстрату в стационаре № 1

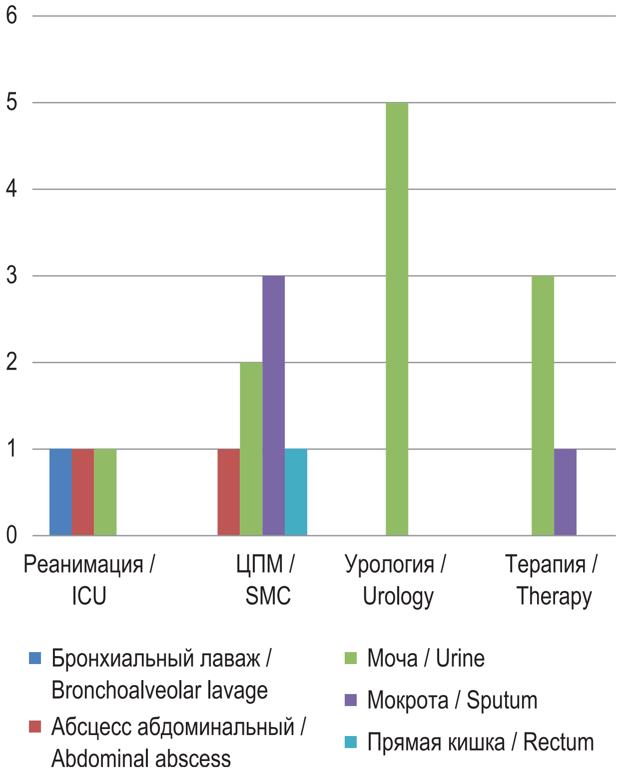

Fig. 4. Distribution of *K. pneumoniae* strains by departments and biological substrate in hospital No. 2

Рис. 4. Распределение штаммов *K. pneumoniae* по отделениям и биологическому субстрату в стационаре № 2

To analyze differences in *Klebsiella pneumoniae* resistance to antimicrobial drugs in two hospitals, the median was calculated.

Hospital No.1: Sorted data: 56, 59.7, 83, 84, 85, 85.

$$Median = \frac{83 + 84}{2} = 83{,}5\,.$$

Hospital No. 2: Sorted data: 40, 56,8, 68,7, 69,4, 71,7, 71,7.

$$Median = \frac{68{,}7 + 69{,}4}{2} = 69{,}05\,.$$

The median resistance of *K. pneumoniae* to antimicrobial drugs in Hospital No. 1 is higher (83.5%) compared to the median in Hospital No. 2 (69.05%).

Beta-lactamase-producing *Klebsiella pneumoniae* strains are widespread and can be found in various conditions and locations in the human body (for example, in the respiratory system (development of pneumonia, especially in immunocompromised patients), urogenital tract, and bloodstream) and the environment [1, 5].

Mortality associated with infections caused by NDM-producing *Klebsiella pneumoniae*

Table 3

Sensitivity of *K. pneumoniae* to antibacterial drugs in hospital No. 1

Таблица 3

Чувствительность *K. pneumoniae* к антибактериальным препаратам в стационаре № 1

Антибиотик / Antibiotic	**Доля резистентных штаммов / Proportion of resistant strains (n=1310), %**	**Доля резистентных штаммов, продуцирующих бета-лактамазы / Proportion of resistant strains producing beta-lactamases (n=82), %**
Амикацин / Amikacin	59,7	30,4
Меропенем / Meropenem	56,0	0,0
Цефтазидим / Ceftazidime	85,0	96,3
Цефепим / Cefepime	84,0	97,5
Цефотаксим / Cefotaxime	85,0	100,0
Ципрофлоксацин / Ciprofloxacin	83,0	84,1

Table 4

Sensitivity of *K. pneumoniae* to antibacterial drugs in hospital No. 2

Таблица 4

Чувствительность *K. pneumoniae* к антибактериальным препаратам в стационаре № 2

Антибиотик / Antibiotic	**Доля резистентных штаммов / Proportion of resistant strains (n=52), %**	**Доля резистентных штаммов, продуцирующих бета-лактамазы / Proportion of resistant strains producing beta-lactamases (n=20), %**
Амикацин / Amikacin	40,0	66,6
Меропенем / Meropenem	56,8	100,0
Цефтазидим / Ceftazidime	71,7	100,0
Цефепим / Cefepime	68,7	100,0
Цефотаксим / Cefotaxime	69,4	100,0
Ципрофлоксацин / Ciprofloxacin	71,7	100,0

strains varies depending on different factors, including severity of a disease, patient's condition, comorbidity, and effectiveness of treatment [1, 2, 10]. Among both critically ill patients treated in intensive care unit and patients with immune pathology, mortality rate reaches 50%. In patients with sepsis caused by NDM-producing Klebsiella pneumoniae strains, lethal outcomes occur in 40–60% of cases. The similar situation is observed in patients with pneumonia, particularly in patients with chronic diseases of lungs. However, mortality rate varies significantly by region: countries with high levels of antibiotic resistance and insufficient control measures have higher rates of HAI than countries with more developed healthcare systems.

Diagnosis of infections caused by NDM-producing *Klebsiella pneumoniae* strains is associated with other problems. Standard identification methods may not detect strains with high levels of resistance. Therefore, the use of molecular methods such as PCR for rapid identification of resistant bacteria is required, which will be the second stage of our study [11].

CONCLUSION

The problem of antibiotic resistance is currently particularly relevant for modern healthcare. In hospitals, of particular importance is the problem of increasing resistance of *Klebsiella pneumoniae* strains. One of the ways to control antibiotic resistance is to constantly conducted microbiological monitoring in a medical institution, since the microbial landscape of each institution, depending on its profile and characteristics of incoming patients, acquires its own "uniqueness".

However, despite this fact, there are also general patterns. Microbiological monitoring data indicate the prevalence of microorganisms from the ESCAPE pathogen group in the etiological structure of the two hospitals, with one of the leading positions belonging to *Klebsiella pneumoniae* (in Hospital No. 1 — 27.52%, in Hospital No. 2 — 11.21%). The priority departments where biological material for our analysis was obtained were intensive care unit, surgery, therapy, and urology departments, which is due to the fact that these departments receive the most severe comorbid patients with reduced immunity. The main biological materials were urine, sputum, wound, and blood. It is obvious that invasive interventions are more often associated with these loci increasing the risk of developing HAI, which confirms the literature data on the most frequent localization of the pathogen [1, 12, 13].

The study results show that when comparing two medical institutions, in hospital No. 1 the proportion of *K. pneumoniae* strains resistant to various antibacterial drugs is statistically significantly higher than in hospital No. 2. The differences identified can be explained by the fact that hospital No. 1 has been operating for over 50 years, its capacity significantly exceeds that of the recently commissioned hospital No. 2, which may have led to the formation of hospital strains and determines the diversity of surgical pathology. The differences are also influenced by longer stays and the severity of the condition of hospitalized patients in hospital No. 1 compared to hospital No. 2.

Analysis of the laboratory studies results of resistance to antibacterial drugs showed that during the study period, beta-lactamase-producing *K. pneumoniae* strains were isolated, which in most cases are characterized by greater resistance to antimicrobial drugs compared to *K. pneumoniae* without the production of resistance enzymes.

Regular microbiological monitoring allows us to identify changes in the structure of microorganisms and to suspect the precursors of an unfavorable epidemiological situation in time. The analysis of pathogens' resistance to antimicrobial drugs is necessary for timely adjustment of empirical antibiotic therapy and control of the spread of these microorganisms in medical institutions. Such work is associated with the need for rapid analysis of a large array of data, which requires the development of completely new digital technology systems for their implementation in medical information systems (MIS) and laboratory information systems (LIS) of hospitals.

ADDITIONAL INFORMATION

Author contribution. Thereby, all authors made a substantial contribution to the conception of the study, acquisition, analysis, interpretation of data for the work, drafting and revising the article, final approval of the version to be published and agree to be accountable for all aspects of the study.

Competing interests. The authors declare that they have no competing interests.

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Конфликт интересов. Авторы декларируют отсутствие явных и потенциальных конфликтов интересов, связанных с публикацией настоящей статьи.

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REFERENCES

1. Guoying W., Guo Z., Xiaoyu C., Longxiang X., Hongju W. The Characteristic of Virulence, Biofilm and Antibiotic Resistance of *Klebsiella pneumoniae*. Int J Environ Res Public Health. 2020;17(17):6278.
2. Chebotar I.V., Bocharova Iu., Podoprigora I., Shagin D. Why *Klebsiella pneumoniae* is becoming the leading opportunistic pathogen. Clinical Microbiology and Antimicrobial Chemotherapy. 2020;22:4–19. (In Russian).
3. Endimiani A., Depasquale J.M., Forero S. et al. Emergence of blaKPC-containing *Klebsiella pneumoniae* in a long-term acute care hospital: a new challenge to our healthcare system. J Antimicrob Chemother. 2009;64:1102–1110.
4. Clegg S., Murphy CN. Epidemiology and Virulence of *Klebsiella pneumoniae*, Microbiol Spectr. 2016;4(1): 1–17.
5. Paczosa M.K., Mecsas J. *Klebsiella pneumoniae*: Going on the Offense with a Strong Defense. Microbiol Mol Biol Rev. 2016:80(3):629–661.
6. Isler B., Aslan A.T., Akova M., Harris P. & Paterson D.L. Treatment strategies for OXA-48-like and NDM producing *Klebsiella pneumoniae* infections. Clinical Infectious Diseases. 2021;73(8):1389–1400.
7. Bozhkova S.A., Gordina E.M., Schneider O.V., Rukina A.N., Shabanova V.V. Resistance of carbapenemase-producing *Klebsiella pneumoniae* strains isolated from

patients with orthopedic infection. Clinical microbiology and antibacterial chemotherapy. 2020;22(1):47–52. (In Russian).

8. Giske C.G., Fröding I., Hasan C.M., Turlej-Rogacka A., Toleman M., Livermore D., Woodford N. & Walsh T.R. Diverse Sequence Types of *Klebsiella pneumoniae* Contribute to the Dissemination of blaNDM-1 in India, Sweden, and the United Kingdom. J Antimicrob Chemother. 2021;76(8):1934–1942.
9. Denissen J., Reyneke B., Waso-Reyneke M., Havenga B., Barnard T., Khan S., Khan W. Prevalence of ESKAPE pathogens in the environment: Antibiotic resistance status, community-acquired infection and risk to human health. Int J Hyg Environ Health. 2022;244:11400.
10. Lapp Z., Crawford R., Miles-Jay A., Pirani A., Trick W.E., Weinstein R.A., Hayden M.K., Snitkin E.S. & Lin M.Y. Regional Spread of blaNDM-1-Containing *Klebsiella pneumoniae* ST147 in Post-Acute Care Facilities. Clinical Infectious Diseases. 2021;73(8):1431–1438.
11. Hoj R.T., McNeely B., Webber K., Welling E., Pitt G.W., Ford C.L., Robison A.R. A pentaplex real-time PCR assay for rapid identification of major beta-lactamase genes KPC, NDM, CTX, CMY, and OXA-48 directly from bacteria in blood. J Med Microbiol. 2021;70(12):1–10.
12. Gao H., Liu Y., Wang R., Wang Q., Jin L. & Wang H. The transferability and evolution of NDM-1 and KPC-2 co-producing *Klebsiella pneumoniae* from clinical settings. Journal of Global Antimicrobial Resistance. 2021;28:93–99.
13. Xiang T., Chen C., Wen J., Liu Y., Zhang Q., Cheng N., Wu X., & Zhang W. Resistance of *Klebsiella pneumoniae* Strains Carrying blaNDM–1 Gene and the Genetic Environment of blaNDM–1. Microbial Drug Resistance. 2021;27(4):453–462.

ЛИТЕРАТУРА

1. Guoying W., Guo Z., Xiaoyu C., Longxiang X., Hongju W. The Characteristic of Virulence, Biofilm and Antibiotic Resistance of *Klebsiella pneumoniae*. Int J Environ Res Public Health. 2020;17(17):6278.
2. Чеботарь И.В., Бочарова Ю.А., Подопригора И.В., Шагин Д.А. Почему *Klebsiella pneumoniae* становится лидирующим оппортунистическим патогенном. Клиническая микробиология и антибактериальная химиотерапия. 2020;22:4–19.
3. Endimiani A., Depasquale J.M., Forero S. et al. Emergence of blaKPC-containing *Klebsiella pneumoniae* in a long-term acute care hospital: a new challenge to our healthcare system. J Antimicrob Chemother. 2009;64:1102–1110.
4. Clegg S., Murphy CN. Epidemiology and Virulence of *Klebsiella pneumoniae*, Microbiol Spectr. 2016;4(1): 1–17.
5. Paczosa M.K., Mecsas J. *Klebsiella pneumoniae*: Going on the Offense with a Strong Defense. Microbiol Mol Biol Rev. 2016;80(3):629–661.
6. Isler B., Aslan A.T., Akova M., Harris P. & Paterson D.L. Treatment strategies for OXA-48-like and NDM producing *Klebsiella pneumoniae* infections. Clinical Infectious Diseases. 2021;73(8):1389–1400.
7. Божкова С.А., Гордина Е.М., Шнейдер О.В., Рукина А.Н., Шабанова В.В. Резистентность продуцирующих карбапенемазы штаммов *Klebsiella pneumoniae*, выделенных от пациентов с ортопедической инфекцией. Клиническая микробиология и антибактериальная химиотерапия. 2020;22(1):47–52.
8. Giske C.G., Fröding I., Hasan C.M., Turlej-Rogacka A., Toleman M., Livermore D., Woodford N. & Walsh T.R. Diverse Sequence Types of *Klebsiella pneumoniae* Contribute to the Dissemination of blaNDM-1 in India, Sweden, and the United Kingdom. Journal of Antimicrobial Chemotherapy. 2021;76(8):1934–1942.
9. Denissen J., Reyneke B., Waso-Reyneke M., Havenga B., Barnard T., Khan S., Khan W. Prevalence of ESKAPE pathogens in the environment: Antibiotic resistance status, community-acquired infection and risk to human health. Int J Hyg Environ Health. 2022;244:11400.
10. Lapp Z., Crawford R., Miles-Jay A., Pirani A., Trick W.E., Weinstein R.A., Hayden M.K., Snitkin E.S., Lin M.Y. Regional Spread of blaNDM-1-Containing *Klebsiella pneumoniae* ST147 in Post-Acute Care Facilities. Clinical Infectious Diseases. 2021;73(8):1431–1438.
11. Hoj R.T., McNeely B., Webber K., Welling E., G Pitt W., C Ford L., Robison A.R. A pentaplex real-time PCR assay for rapid identification of major beta-lactamase genes KPC, NDM, CTX, CMY, and OXA-48 directly from bacteria in blood. J Med Microbiol. 2021;70(12):1–10.
12. Gao H., Liu Y., Wang R., Wang Q., Jin L., Wang H. The transferability and evolution of NDM-1 and KPC-2 co-producing *Klebsiella pneumoniae* from clinical settings. Journal of Global Antimicrobial Resistance. 2021;28:93–99.
13. Xiang T., Chen C., Wen J., Liu Y., Zhang Q., Cheng N., Wu X., Zhang W. Resistance of *Klebsiella pneumoniae* Strains Carrying blaNDM-1 Gene and the Genetic Environment of blaNDM–1. Microbial Drug Resistance. 2021;27(4):453–462.