DOI 10.25789/YMJ.2025.90.05

UDC 616-022.7

A.F. Potapov, S.Kh. Shamaeva, U.S. Portnyagina, S.S. Kampeev, A.A. Ivanova, L.A. Vinokurova

THE ANTIBIOTIC RESISTANCE OF *KLEBSIELLA PNEUMONIA* AND *ESCHERICHIA COLI* ISOLATES AND THE SPREAD OF CARBAPENEMASES IN A MULTIDISCIPLINARY IMPATIENT FACILITY

POTAPOV Aleksandr Filippovich – Dr. Sci. (Medicine), Professor, Department of Anesthesiology, Resuscitation and Intensive Care with a course of Emergency Medicine, Faculty of Postgraduate Training of Doctors, Institute of Medicine, M.K. Ammosov North-Eastern Federal University, ORCID: 0000-0003-2087-543X, Web of Science Researcher ID: AAG-6758-2019, Author ID (Scopus): 7201761921; SPIN: 3615-7735; e-mail: potapov-paf@mail.ru; **SHAMAEVA Stepanida Kharitonovna** – Cand. Sci. (Biology), head of the Laboratory of Clinical Microbiology (Bacteriology), Republic Hospital No. 2 – Center for Emergency Medical Aid; Associate Professor, Department of Health Organization and Preventive Medicine, Institute of Medicine, M. K. Ammosov North-Eastern Federal University; ORCID 0000-0001-9172-4327, SPIN: 2176-9610, AuthorID: 848478, e-mail: stevas@mail.ru; **PORTNYAGINA Uliana Semyonovna** – Cand. Sci. (Medicine), Associate Professor, Department of Internal Diseases and General Medical Practice (Family Medicine), Faculty of Postgraduate Training of Doctors, Institute of Medicine, M. K. Ammosov North-Eastern Federal University, ORCID: 0000-0003-2791-9933, e-mail: ulyana-nsk@mail.ru; **KAMPEEV Stanislav Stanislavovich** – Head of the Department of Clinical Pharmacology, Republic Hospital No. 2 – Center for Emergency Medical Aid; Chief External Expert on clinical pharmacology, Ministry of Health of the Sakha Republic (Yakutia). e-mail: kampeev@mail.ru; **IVANOVA Albina Ammosovna** – Dr. Sci. (Medicine), Docent, head of the Department of Anesthesiology, Resuscitation and Intensive Care with a course of Emergency Medicine, Faculty of Postgraduate Training of Doctors, Institute of Medicine, M. K. Ammosov North-Eastern Federal University, ORCID: 0000-0002-3782-6867, Web of Science Researcher ID AAO-2223-2020, Author ID (Scopus) 55611584600, SPIN: 8998-3793, e-mail: iaa_60@mail.ru; **VINOKUROVA Lidia Alekseevna** – assistant lecturer, Department of Anesthesiology, Resuscitation and Intensive Care with a course of Emergency Medicine, Faculty of Postgraduate Training of Doctors, Institute of Medicine, M. K. Ammosov North-Eastern Federal University, e-mail: lid.vi@mail.ru.

Aim of the Research. A study of antimicrobial resistance of *Klebsiella pneumonia* and *Escherichia coli* isolates and the spread of carbapenemase genes in a multidisciplinary emergency inpatient facility in the Sakha Republic (Yakutia).

Materials and Methods. There was conducted a retrospective observational study of the results of microbiological tests of patients treated in the period 2021–2023 in a multidisciplinary emergency inpatient facility with surgical and therapeutic departments in the Sakha Republic (Yakutia). The spread and identification of carbapenemase genes was performed in *K. pneumonia* and *E. coli* isolates isolated in biological media from 254 patients.

Results and Discussion. The structure of the isolated microorganisms was dominated by pathogens of the *Enterobacterales* genus: *K. pneumonia* was isolated in 29.9% (n=3,314) and *E. coli* – in 20.8% (n=2,306) of the samples. The proportion of meropenem-resistant *K. pneumonia* strains was 47.5% of the isolates, *E. coli* – 13%. As a result of the study, a total of eight carbapenemase genes were isolated. The most common genes for the *K. pneumonia* and *E. coli* isolates by detection frequency were *OXA48* (24.9%), *ctxM-1* (24.0%), *SHV* (21.8%), *TEM* (12.9%), and *NDM* (10.8%). As a rule, there were combinations of three to five gene types: three types were isolated in 86 (33.9%) strains, four types – in 56 (22.0%), and five types – in 54 (21.3%). The presence of one gene type was detected in 33 (13.0%) strains, two types – in 16 (6.3%), six types in 3 (1.2%), and seven types in 6 (2.4%).

Conclusion. Microbiological monitoring, control of local resistance to antibiotics in inpatient facilities and the study of resistance mechanisms can improve the effectiveness of antimicrobial therapy and also serve as an effective method of combating the spread of antibiotic-resistant strains of microorganisms.

Keywords*:* nosocomial infection, *Klebsiella pneumonia, Escherichia coli*, antimicrobial resistance, carbapenemases, carbapenemase genes.

For citation: Potapov A.F., Shamaeva S.Kh., Portnyagina U.S., Kampeev S.S., Ivanova A.A., Vinokurova L.A. The antibiotic resistance of *Klebsiella pneumonia* and *Escherichia coli* isolates and the spread of carbapenemases in a multidisciplinary impatient facility. Yakut Medical Journal. 2025; 90(2): 22-26. https://doi.org/10.25789/YMJ.2025.90.05

Introduction. The rapid spread of bacteria with multiple or total resistance to antimicrobial drugs worldwide is a global health problem. According to the World Health Organization (WHO), high rates of microbial resistance to antibiotics and a decrease in the effectiveness of antimicrobial drugs are observed worldwide. The past decade witnessed an extremely negative trend: an increased number of nosocomial strains resistant to carbapenems, which had been considered a reliable and backup class of antibiotics. [9]

Studies on antibiotic resistance indicate that the most common pathogens of nosocomial infections are representatives of enterobacteria, and an increased level of resistance to carbapenems is due to the production of carbapenemases. [2,3,12,13] Thus, the Russian long-term multicenter epidemiological study "MARATHON", conducted since 2011, has revealed that enterobacteria make up 48.2% of all isolated nosocomial bacterial pathogens, with *K. pneumonia* (47.2%) and *E. coli* (30.0%) being the most frequent species. At the same time, there is a clear trend towards increasing resistance to carbapenems – Imipenem, Meropenem and Ertapenem: 6.9%, 6.5% and 23.6% of enterobacteria isolates are resistant to them, respectively. [3] The next stage of this study confirmed that clinical isolates of *K. pneumoniae* are becoming increasingly resistant to carbapenems due to the spread of carbapenemases, which are characterized by diversity and the simultaneous existence

of several genes for their production. The most common carbapenemases are of three main groups: *OXA-48*, *NDM* and *KPC*. [2]

Recent studies abroad also indicate the relevance of the problem with *K. pneumoniae* and *E. coli* and their resistance to antimicrobial drugs. The prospective multicenter cohort study CRACKLE-2, having covered 49 hospitals in the USA to study the molecular and clinical epidemiology of carbapenem-resistant enterobacteria, showed that they accounted for 59%, with *K. pneumoniae* being the most common carbapenemase-producing pathogen. [13] Another large-scale study, INVIFAR (INnvestigación y VIigilancia de la FArmacorResistencia), aimed at analyzing carbapenemase genotypes of clinical isolates collected from 41 medical centers in Mexico, revealed high carbapenem resistance in *E. coli* in the group of patients aged 0–17 years, and in *K. pneumoniae* in the group of 18–59 years of age. The highest resistance to carbapenems was observed in clinical isolates from patients in intensive care units ($p < 0.035$). [12]

The strategy for combating antimicrobial resistance includes the monitoring of antibiotic resistance and collecting information on resistance mechanisms. Here, recording, analysis and systematization of information should be carried out at all levels: globally, within individual countries and regions, as well as in each individual medical organization. [4] Therefore, phenotypic detection of carbapenemase genes (*OXA*, *TEM*, *SHV*, *KPC*, *VIM*, *ctxM-1*, *NDM*, etc.) should be considered one of the conditions for monitoring and combating antibiotic resistance. From this perspective, the analysis of the spread of carbapenem-resistant isolates of *K. pneumonia* and *E. Coli*, as well as the genes responsible for producing carbapenemases in a multidisciplinary inpatient facility, is relevant, has scientific interest and practical significance.

The aim of the study was to examine the resistance of *K. pneumonia* and *E. coli* isolates to antibiotics and the spread of carbapenemase genes in a multidisciplinary emergency inpatient facility in the Sakha Republic (Yakutia).

Materials and Methods. We conducted a retrospective observational study of the results of microbiological tests of patients treated in the period 2021–2023 in a multidisciplinary emergency inpatient facility with surgical and therapeutic departments in the Sakha Republic (Yakutia).

For the period 2021–2023, there was studied the etiological structure of the pathogens isolated in biological media of the patients (tracheobronchial aspirate (TBA), blood, urine, wound drainage, peritoneal and pleural exudate, bile), and the resistance of *K. pneumonia* and *E. coli* isolates to screening antibiotics was determined. The microbiological studies in the patients were performed every 7–10 days. A repeated isolation of the pathogen during the study in a patient was considered as one agent.

The spread and detection of carbapenemase genes were performed in *K. pneumonia* and *E. coli* isolates obtained in the bio-media of 254 patients from the surgical and therapeutic profiles (127 (50%) patients of each profile). The patients' age ranged from 18 to 97 years (median age 66 [50–75] years), including 141 (55.5%) men and 113 (44.5%) women. The length of staying in the intensive care unit was 8 [2–16] days; the total number of patient days in the hospital was 25.5 [17–40.7] days. The mortality rate of the patients was 30.3% (77 patients).

All the patients gave informed consent for the processing and use of personal data upon admission to the hospital.

Data processing and antibiotic resistance analysis were performed on the AMRcloud online platform (version: Beta, 30.01.2023). [10]

Species identification and determination of susceptibility to antibacterial drugs were performed on an automatic analyzer VITEK-2 Compact (bioMerieux, France), as well as by the disk diffusion method on Mueller-Hinton agar using antimicrobial disks (BioRad, USA).

Determination of susceptibility to antibiotics was carried out in accordance with the guidelines of the European Committee on Antimicrobial Susceptibility Testing (EUCAST) and the guidelines of the Interregional Association for Clinical Microbiology and Antimicrobial Chemotherapy (IACMAC) for determining the susceptibility of microorganisms to antimicrobial drugs. [5]

The genes of acquired carbapenemases of the main groups were identified using NG-Test CARBA5 (NG Biotech Z.A., France) and the molecular genetic method (real-time PCR) using the BakRezista GLA kits (DNA-Technology).

The collection, storage and systematization of the database, construction of diagrams were carried out in Microsoft Office Excel 2016 spreadsheets. The statistical processing of quantitative data (age, duration of treatment) was performed using the Jamovi-2.6.44 statistical software and included an assessment of the normality of the sample distribution using the asymmetry and kurtosis testing method, which revealed an abnormal distribution; due to that, the median (Me),

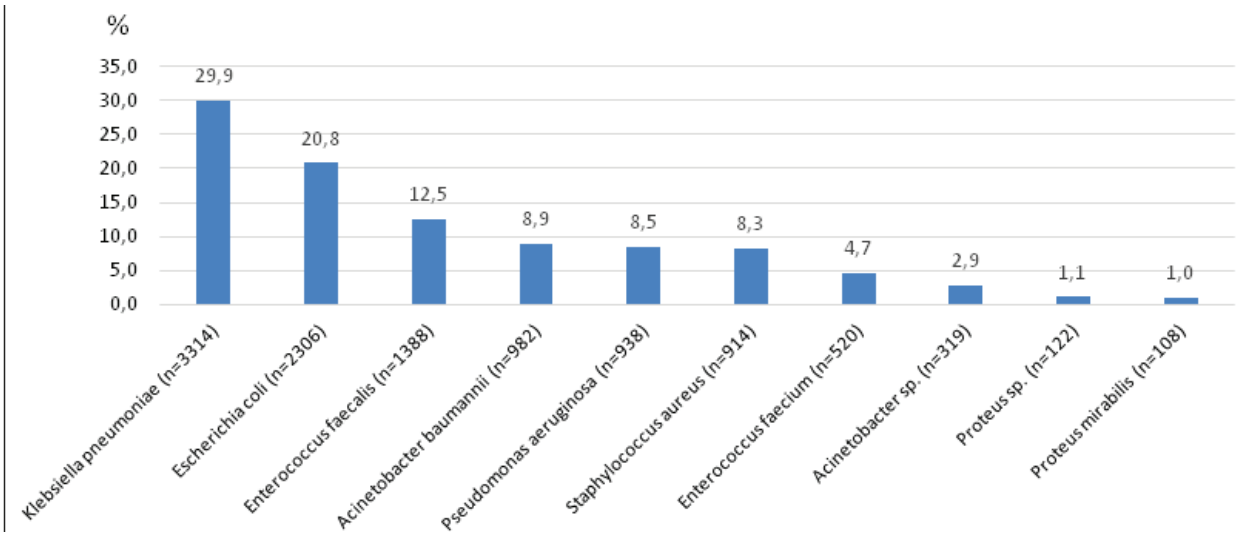

Fig. 1. The structure of the isolated pathogens in the inpatient facility in 2021–2023

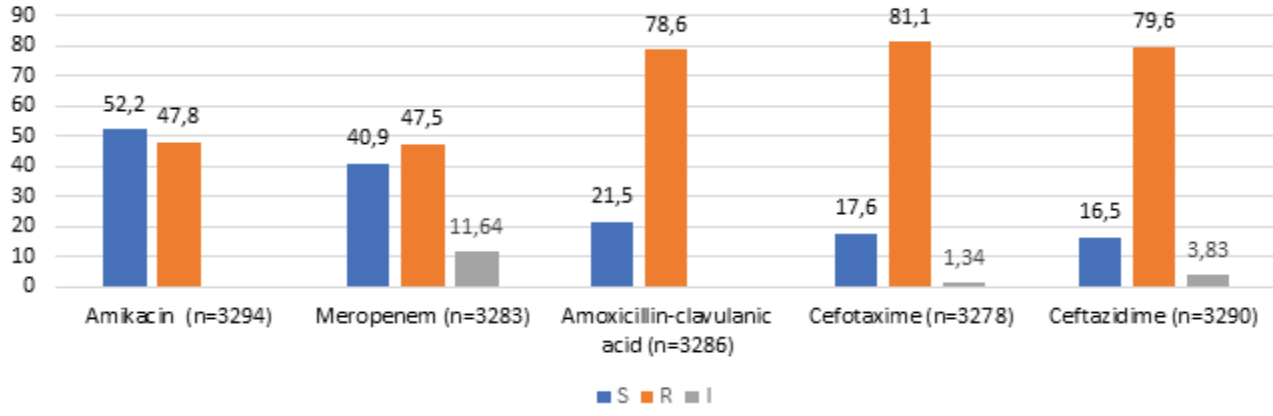

Fig. 2. *Klebsiella pneumonia* resistance to antibacterial drugs

lower and upper quartiles [Q1–Q3] were determined.

Results and Discussion. At the initial stage of our study, we carried out an analysis of the general structure of microorganisms isolated in the inpatient facility in the period 2021–2023, showing the dominance the genus *Enterobacterales* pathogens: *K. pneumonia* and *E. coli*, which were detected in 29.9% (n=3,314) and 20.8% (n=2,306) of the samples, respectively. The proportion of other clinically significant pathogens was as follows: *Enterococcus faecalis* – 12.5% (n=1,388), *Acinetobacter baumannii* – 8.9% (n=982), *Pseudomonas aeruginosa* – 8.5% (n=938), *Staphylococcus aureus* – 8.3% (n=914). Other representatives of the microbial flora were isolated in less than 5% of the tests (Figure 1).

The study of the susceptibility of *K. pneumonia* to antibacterial drugs indicated its susceptibility to aminoglycosides (Amikacin) in 52.2% and to carbapenems (Meropenem) in 40.9% of the isolates. At the same time, they demonstrated low susceptibility to penicillinase-resistant penicillins (Amoxiclav) and third-generation cephalosporins (Cefotaxime, Ceftazidime) (Figure 2).

The susceptibility of *E.coli* to the used antibacterial drugs was significantly higher and was at the level of 92% to Nitrofurantoin, 81.7% to Meropenem, 71.4% to Amikacin, and 65.5% to Amoxiclav. The exception was low susceptibility to Ceftazidime: 35.4% of the isolated strains were sensitive and 10.8% were moderately sensitive (Figure 3).

The next stage of the study was to investigate the prevalence of carbapenemase production genes. For this purpose, microbiological studies of bio-media were conducted in 254 patients of surgical and therapeutic profiles. Among the patients of the surgical profile, the majority were patients of surgical departments No. 1 (17.7%), No. 2 (11.4%) and the proctology department (6.3%). The patients of the therapeutic profile were mainly represented by patients from the neurological department for patients with acute cerebrovascular accident (ACVA) – 66 patients (25.9%) and the emergency department – 38 (15.0%). The anesthesiology, resuscitation and intensive care department (ICU) treated 98 (77.2%) surgical patients and 66 (51.9%) therapeutic patients.

In the studied patients, *K. pneumonia* was isolated in 238 (84.7%) and *E. coli* – in 43 (15.3%) tests. Figure 4 demonstrates the distribution of carbapenemase genes in these isolates.

As a result of the study, a total of eight carbapenemase genes were isolated. The most common genes by detection frequency for *K. pneumonia* and *E. coli* isolates were *OXA48* (24.9%), *ctxM-1* (24.0%), *SHV* (21.8%), *TEM* (12.9%) and *NDM* (10.8%). In most cases, there were combinations of three to five gene types: three types were isolated in 86 (33.9%) strains, four types – in 56 (22.0%) and five types – in 54 (21.3%). The presence of one gene type was found in 33 (13.0%) strains, two types – in 16 (6.3%), six types – in 3 (1.2%) and seven types – in 6 (2.4%).

Thus, as our study showed, the structure of isolated microorganisms in a multidisciplinary inpatient facility in the period 2021–2023 was dominated by *K. pneumonia* and *E. coli*. The share of meropen-

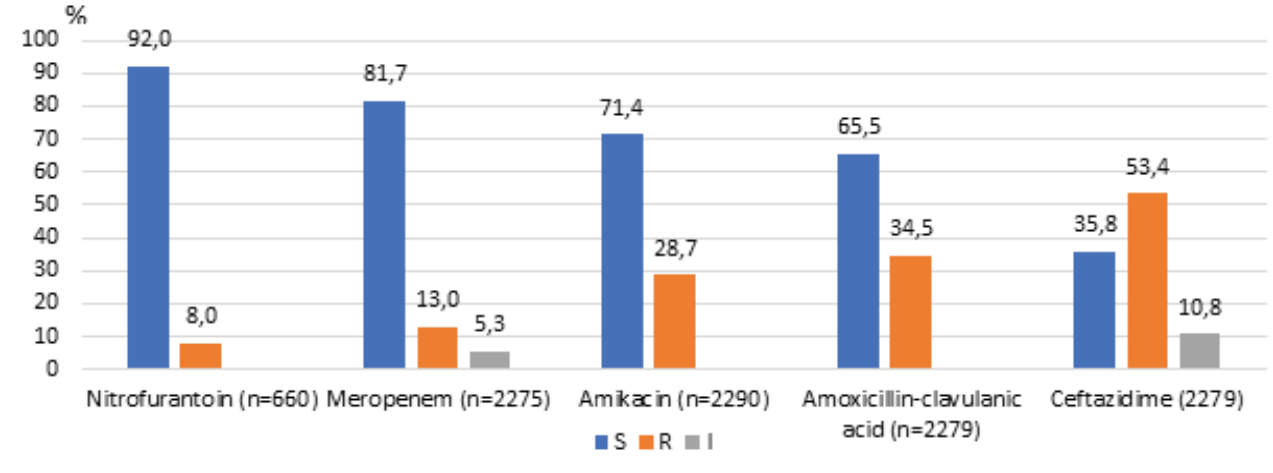

Fig. 3. *Escherichia coli* resistance to antibacterial drugs

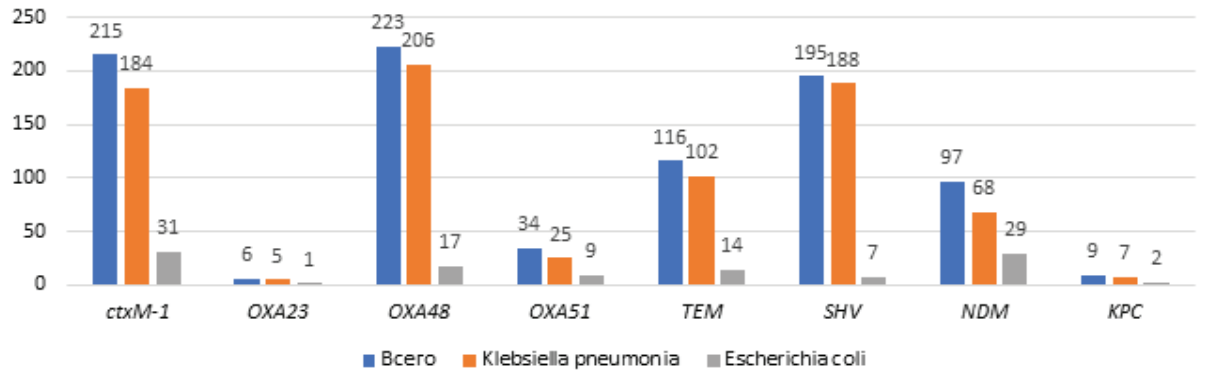

Fig. 4. *Klebsiella pneumonia* and *Escherichia coli* carbapenemase genes

em-resistant *K. pneumonia* strains was 47.5% of the isolates, *E. coli* – 13%. The presented results confirm our previously obtained data on the increased share of meropenem-resistant *K. pneumonia* strains in this inpatient facility, which grew over the period 2016–2022 from 26.7% (95% CI: 16.47–25.61) to 44.1% (95% CI: 40.56–47.8); *E. coli* strains – from 9.5% (95% CI: 6.87–13.21) to 18% (95% CI: 14.98–21.54). [9]

The predominance of *K. pneumonia* and *E. coli* with multiple resistance to antimicrobial drugs in the microbial spectrum is typical of many inpatient facilities and intensive care units in Russia and worldwide [1,2,3,8,12,13,14]. For instance, according to Belotserkovsky et al., the leading pathogens of infection in surgical intensive care units were *K. pneumoniae* (18.5%), whose resistance to meropenem was 83.0%. [1] Jeong et al. (2022) indicate that *K. pneumoniae* account for 81.8% in the group of carbapenem-resistant enterobacteria. [11]

Our results on carbapenemase genes do not contradict, in general, the data of other studies, as well. As in other studies, gene diversity is common; isolates often contain various combinations of them, the number of which can reach seven. In our study, *OXA48* (24.9%), *ctxM-1* (24.0%), *SHV* (21.8%), *TEM* (12.9%) and *NDM* (10.8%) were most frequently observed in *K. pneumonia* and *E. coli* strains. A similar high resistance of *K. pneumoniae* to carbapenems mainly due to the spread of *OXA-48* and *NDM* carbapenemases is presented in the studies by the Kommunarka Moscow Multidisciplinary Clinical Center [6] and in the Russian multicenter study "MARATHON". [3] However, it should be noted that in the above-mentioned works, among the genes encoding carbapenemase, the *KPC* gene was often observed, which was not detected in our study. In the INVIFAR study, the carriage of the *KPC* gene was also observed quite often – in 40% of *K. pneumoniae* strains, and the resistance of *E. coli* to Meronem was represented by the *NDM* gene in 59.2%. [12]

The similarity of carbapenemase phenotypes indicates the resistance of microorganisms to the same carbapenems; conversely, their differences indicate local features of resistance, which should be taken into account when choosing an antibiotic.

Conclusion. The results of this study indicate the relevance of the problem of resistance to carbapenems in the conditions of a multidisciplinary emergency inpatient facility in the Sakha Republic (Yakutia). A crucial and clinically significant factor is the high level of carbapenemase producers in *K. pneumonia* strains, which should be taken into account when choosing antimicrobial therapy.

The need for further study of the mechanisms of resistance to antimicrobial drugs is beyond doubt. Microbiological monitoring, control of local resistance to antibiotics in an inpatient facility and the study of resistance mechanisms can increase the effectiveness of antimicrobial therapy, and also serve as an effective method of combating the spread of resistant strains of microorganisms.

The authors declare no conflict of interest in the submitted article.

References

1. Bykov A.O., et al. Analiz struktury bakteriemii i chuvstvitel'nosti k antibiotikam mikroorganizmov, vydelennykh v otdeleniiakh reanimatsii i intensivnoi terapii v skoropomoshchnom statsionare v period s 2003 po 2021 g.: retrospektivnoe nabliudatel'noe issledovanie [Analysis of the structure of bacteremia and sensitivity to antibiotics of microorganisms isolated in intensive care units in an emergency hospital in the period from 2003 to 2021: a retrospective observational study]. Vestnik intensivnoi terapii imeni A.I. Saltanova [Annals of Critical Care. 2023; 2:55–65 (In Russ.).] DOI:10.21320/1818-474X-2023-2-55-65

2. Edelstein M.V., et al. Antibiotikorezistentnost' klinicheskikh izoliatov Klebsiella pneumoniae i Escherichia coli v statsionarakh Rossii: rezul'taty mnogotsentrovogo epidemiologicheskogo issledovaniia [Antimicrobial resistance of clinical isolates of *Klebsiella pneumoniae* and *Escherichia coli* in Russian hospitals: results of a multicenter epidemiological study]. Klinicheskaia mikrobiologiia i antimikrobnaia khimioterapiia [Clinical microbiology and antimicrobial chemotherapy. 2024; 26(1): 67–78. (In Russ.).] DOI: 10.36488/cmac.2024.1.67–78

3. Sukhorukova M.V., et al. Antibiotikorezistentnost' nozokomial'nykh shtammov Enterobacterales v statsionarakh Rossii: rezul'taty mnogotsentrovogo epidemiologicheskogo issledovaniia "Marafon 2015-2016" [Antimicrobial resistance of nosocomial Enterobacterales isolates in Russia: results of multicenter epidemiological study "MARATHON 2015–2016"]. Klinicheskaia mikrobiologiia i antimikrobnaia khimioterapiia [Clinical microbiology and antimicrobial chemotherapy. 2019; 21(2): 143–155. (In Russ.).] DOI: 10.36488/cmac.2019.2.147-159

4. Kozlov R.S., Golub A.V. Ostanovit' tempy rosta antibiotikorezistentnosti mikroorganizmov segodnia – dat' shans na vyzhivanie chelovechestva zavtra [To stop the progress of antimicrobial resistance today means to give a chance of mankind surviving tomorrow]. Klinicheskaia mikrobiologiia i antimikrobnaia khimioterapiia [Clinical microbiology and antimicrobial chemotherapy. 2019; 21(4): 310–315. (In Russ.).] DOI: 10.36488/cmac.2019.4.310-315

5. Shamaeva S.Kh., et al. Monitoring karbapenemrezistentnykh Escherichia coli i Kkebsiella pneumonia v usloviiakh mnogoprofil'nogo statsionara. Tezisy XXV mezhdunarodnogo kongressa MAKMAKh po antimikrobnoi terapii i klinicheskoi mikrobiologii. 24–26 maia 2023, Moskva [Monitoring of carbapenem-resistant Escherichia coli and Klebsiella pneumoniae in a multidisciplinary hospital. Abstracts of the 25th International MACMACH Congress on Antimicrobial Therapy and Clinical Microbiology, May 24–26, 2023, Moscow]. Klinicheskaia mikrobiologiia i antimikrobnaia khimioterapiia [Clinical Microbiology and antimicrobial chemotherapy. 2023; 25, Appendix 1: 64–65 (In Russ.).]

6. Ni O.G., et al. Rasprostranennost' nositel'stva genov, kodiruiushchikh karbapenemazy, sredi patsientov, gospitalizirovannykh v mnogoprofil'nyi statsionar g. Moskvy [Prevalence of carbapenemase-encoding genes carriage in patients admitted to multidisciplinary hospital in Moscow]. Klinicheskaia mikrobiologiia i antimikrobnaia khimioterapiia [Clinical Microbiology and antimicrobial chemotherapy. 2024; 26(3): 345–355. (In Russ).]. DOI: *10.36488/cmac.2024.3.345-355*

7. Rossiiskie rekomendatsii. Opredelenie chuvstvitel'nosti mikroorganizmov k antimikrobnym preparatam. Versiia 2024-02. God utverzhdeniia (chastota peresmotra) [Russian recommenda-

tions. Determination of the sensitivity of microorganisms to antimicrobial drugs. Version 2024-02. Year of approval (frequency of revision): 2024; MAKMAKH, SSMU]. Smolensk: 192. https://www.antibiotic.ru/minzdrav/category/clinical-recommendations/ (In Russ).

8. Belotserkovskiy B.Z., et al. Etiologicheskaia struktura infektsii u patsientov otdeleniia khirurgicheskoi reanimatsii i intensivnoi terapii v postkovidnuiu epokhu [Etiological structure of infections in patients of the surgical intensive care unit in the post-covid era]. Klinicheskaia mikrobiologiia i antimikrobnaia khimioterapiia [Clinical Microbiology and antimicrobial chemotherapy. *2024; 26(2): 124–140.* (In Russ).]. DOI:*10.36488/cmac.2024.2.124-140*

9. Antimicrobial-resistance. https://www.who.int/ru/news-room/fact-sheets/detail/antimicrobial-resistance.

10. AntiMicrobial Resistance Cloud – online platform. https://amrcloud.net/ru/

11. Jeong I.S., Song J.Y. Epidemiological Characteristics of Carbapenemase Producing Carbapenem-Resistant Enterobacteriaceae Colonization. Asian Nurs Res (Korean Soc Nurs Sci). 2022; 16(3):134–139. DOI: 10.1016/j.anr.2022.05.002

12. Colín-Castro C.A., et al. The ongoing antibiotic resistance and carbapenemase encoding genotypes surveillance. The first quarter report of the INVIFAR network for 2024. PLoS One. 2025; 20(4). DOI: 10.1371/journal.pone.0319441

13. Van Duin D., et al. Resistant Organism Network Investigators. Molecular and clinical epidemiology of carbapenem-resistant Enterobacterales in the USA (CRACKLE-2): a prospective cohort study. Lancet Infect Dis. 2020; 20(6):731–741. DOI: 10.1016/S1473-3099(19)30755-8

14. Zaragoza R., Vidal-Cortés P., Aguilar G. Update of the treatment of nosocomial pneumonia in the ICU. Crit Care. 2020; 24(1):383. DOI: 10.1186/s13054-020-03091-2

F.M. Teryutin, T.V. Borisova, A.M. Cherdonova, G.P. Romanov, V.G. Pshennikova, A.V. Solovyov, S.A. Fedorova, N.A. Barashkov

DOI 10.25789/YMJ.2025.90.06

UDC 575.174

ATYPICAL CASES OF HEARING LOSS IN PATIENTS WITH A MITOCHONDRIAL VARIANT m.1555A>G OF THE *MT-RNR1* GENE IN THE REPUBLIC OF BURYATIA

Yakut Science Center of Complex Medical Problems (YSC CMP): **TERYUTIN Fedor Mikhailovich** – PhD, researcher of the Laboratory of Molecular Genetics, e-mail: rest26@mail.ru, ORCID: 0000-0002-8659-0886; **PSHENNIKOVA Vera Gennadievna** – PhD in Biology, visiting research fellow, Laboratory of Molecular Genetics, e-mail: psennikovavera@mail.ru, ORCID: 0000-0001-6866-9462; **BARASHKOV Nikolay Alekseevich** – PhD in Biology, visiting research fellow, head of the Laboratory of Molecular Genetics, e-mail: barashkov2004@mail.ru, ORCID: 0000-0002-6984-7934; M.K. Ammosov North-Eastern Federal University (M.K. Ammosov NEFU): **BORISOVA Tuyara Valeryevna** – junior researcher of the research laboratory of molecular biology, Institute of Natural Sciences, e-mail: borisovatv96@gmail.com ORCID: 0000-0002-5019-067; **CHERDONOVA Alexandra Matveevna** – junior researcher of the research laboratory of molecular biology of IEN e-mail: cherdonovasasha96@gmail.com ORCID: 0000-0002-4168-9516; **ROMANOV Georgiy Prokopievich** – PhD in Biology, Research Fellow of the Research Laboratory of Molecular Biology, Institute of Natural Sciences, e-mail: gpromanov@gmail.com, ORCID: 0000-0002-2936-5818; **SOLOVYOV Aisen Vasilyevich** – PhD in Biology, Senior Researcher of the Research Laboratory of Molecular Biology, Institute of Natural Sciences, e-mail: nelloann@mail.ru, ORCID: 0000-0003-0914-3609; **FEDOROVA Sardana Arkadievna** – Doctor of Biology, head of the Research Laboratory of Molecular Biology, Institute of Natural Sciences, e-mail: sardaanafedorova@mail.ru, ORCID: 0000-0002-6952-3868.

In a previous study, we found a high prevalence of the m.1555A>G variant of the *MT-RNR1* gene, which causes mitochondrial hearing loss (OMIM 561000) among deaf patients living in the Baikal Lake region. In this regard, in the present study, a genotype-phenotypic analysis of the hearing function in individuals with the m.1555A>G variant was carried out in the discovered Siberian region. Clinical and audiological analysis was performed in 48 people with this mitochondrial variant, whose average age was 51.3±15.5 years. The obtained genotype-phenotypic data are consistent with previously conducted studies of the features of the auditory function in individuals with m.1555A>G, which note incomplete penetrance of the manifestation of the pathological phenotype. Of particular interest in our cohort are three cases of mixed hearing loss, including both sensorineural (inner ear defect) and conductive (middle ear defect) components. The detected conductive component, which is atypical for this mitochondrial form of the disease, may be associated with idiopathic non-infectious foci of the pathological process in the middle ear. We do not exclude the possibility that the detected clinical signs may be a consequence of systemic damage to the hearing organ in this mitochondrial variant. On the other hand, the detected cases may be related to a cross-pathological effect caused by another form of a less common or rare disease. The obtained results require further genotype-phenotypic studies.

Keywords: mitochondrial hearing loss, m.1555A>G variant, *MT-RNR1* gene, genotype-phenotypic analysis, Buryatia

For citation: Teryutin F.M., Borisova T.V., Cherdonova A.M., Romanov G.P., Pshennikova V.G., Solovyov A.V., Fedorova S.A., Barashkov N.A. Atypical cases of hearing loss in patients with a mitochondrial variant m.1555A>G of the *MT-RNR1* gene in the Republic Buryatia. 2025; 90(2): 26-30. https://doi.org/10.25789/YMJ.2025.90.06

Introduction. Mitochondria are intracellular organelles responsible for the production of adenosine triphosphate (ATP) through a process called oxidative phosphorylation [20]. In this process, energy is released by breaking down glucose and fatty acids via the mitochondrial respiratory chain [31]. Mutations in mitochondrial DNA have been described primarily in various rare syndromes, but are also found in more common diseases such as sensorineural hearing loss. One such mitochondrial mutation leading to isolated hearing loss is m.1555A>G in the *MT-RNR1* gene (OMIM 561000). There are several hypotheses regarding the pathogenetic mechanism of m.1555A>G in the *MT-RNR1* gene. In general, researchers believe that the m.1555A>G variant of the *MT-RNR1* gene is one of the “mild” ones compared to other pathogenic variants in mitochondrial DNA, since it does not lead to systemic disorders and does not always lead to hearing loss, and the manifestation of the pathogenic effect of