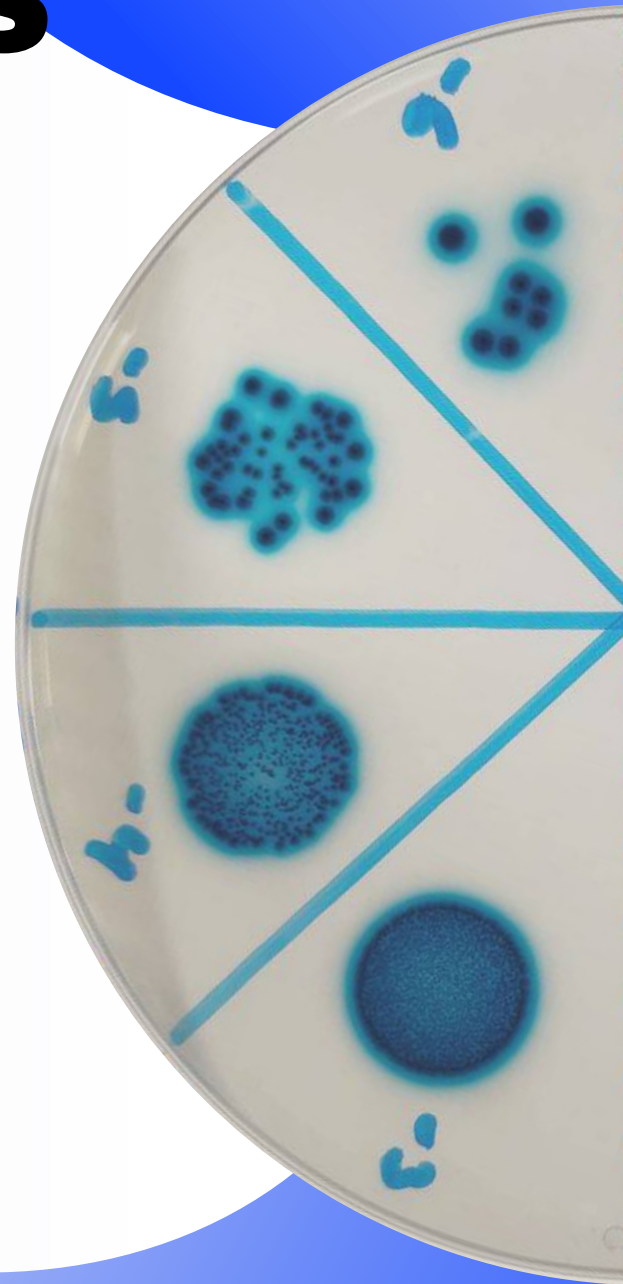

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**"MODERN ASPECTS OF
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November 15-16, 2023

Kyiv, Ukraine



D.K. Zabolotny Institute of Microbiology and Virology
of the National Academy of Sciences of Ukraine

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ANALYSIS OF THE SPECIES COMPOSITION AND SENSITIVITY TO ANTIBIOTICS OF OPPORTUNISTIC MICROORGANISMS IN BRONCHITIS

KOVALENKO N.I.¹, VOVK O.O.¹, NOVIKOVA I.V.², KRASNIKOVA L.V.¹

¹Kharkiv National Medical University, Kharkiv, Ukraine,

²Communal non-profit enterprise of the Kharkiv Regional Council "Regional Clinical Hospital",
Kharkiv, Ukraine
yatiger@ukr.net

Influenza, parainfluenza, respiratory syncytial viruses, as well as chlamydia, mycoplasma, streptococci, staphylococci bacteria play a leading role in the etiology of bronchitis [1, 2]. However, bacteria inhabiting the upper respiratory tract, in case of a decrease in the body's resistance, can colonize the bronchi and cause inflammatory processes [3]. Active reproduction of certain species of microbiocenosis can disrupt the qualitative and quantitative balance of microbiota, provoking the development of the pathological process.

Antibiotics are prescribed to treat bronchitis when the bacterial etiology of the disease is confirmed and to prevent complications [4, 5]. However, abuse of antibiotics, especially broad-spectrum antibiotics, can play a role in the selection and spread of resistance among potentially pathogenic microorganisms [6]. The development of microorganism resistance to antimicrobial drugs remains one of the key problems of health care [7].

The following antibiotics are recommended for bacterial etiology of acute bronchitis: amoxicillin, azithromycin, clarithromycin, alternative antibiotics - respiratory fluoroquinolones, protected penicillins (amoxicillin/clavulanic acid), cephalosporins of the III generation [8, 9]. Regional data on the resistance of microorganisms to antimicrobial drugs are of significant importance when choosing a scheme of empiric therapy [10].

The aim was to study the microflora's species composition isolated from patients with bronchitis and to determine the frequency of resistant isolates in cases of acute bronchitis.

Research materials and methods. The results of bacteriological studies of the clinical material of 50 patients with diagnosed bronchitis were used in this study. Bronchial lavage and sputum were taken as clinical material.

Microbiological research of pathogens was carried out in accordance with regulatory documents [11], and sensitivity to antibiotics was determined in accordance with [12].

Results and their discussion. Sixty-six strains of microorganisms belonging to 18 species of bacteria and fungi *Candida albicans* were isolated. Most isolated microorganisms were representatives of Gram-positive bacteria (54.6 %). The Gram-negative bacteria and *C. albicans* fungi were isolated in 30.3% and 15.1 % of cases, respectively. The most common were *Staphylococcus aureus* (19.7 %), *Klebsiella pneumoniae* (15.1 %), and *C. albicans* (15.1 %). Among Gram-positive bacteria, *Streptococcus anginosus* (7.6 %), *S. mitis* (7.6 %), *S. viridans* (4.6 %)

dominated. *Pseudomonas aeruginosa* (6 %) and *Acinetobacter baumannii* (6 %) also prevailed in the case of Gram-negative bacteria. A small amount (1,5 %) of *Streptococcus mutans*, *S. salivarius*, *S. anhaemolyticus*, *S. pyogenes*, *Serratia marcescens*, *S. haemolyticus*, *Enterococcus faecalis*, *Enterobacter cloacae*, *Klebsiella ozaena*, *Proteus vulgaris* and *P. mirabilis* were isolated. Microorganisms were found both in monoculture and as part of associations. A significant part of the strains (74 %) was represented in monoculture. The spread of two-component associations was 20 %, and three-component associations – 6 %. Some microorganisms belonged to associations more often than others, namely *K. pneumoniae* (40 % in two-component and 20 % in three-component associations), *S. aureus* (40 % in two-component and 30 % in three-component associations) and *C. albicans* (30 % in two-component and 50 % in three-component associations).

Regarding antibiotic resistance, the largest number of resistant strains is registered for *K. pneumoniae*. This type of bacteria was insensitive to amoxiclav in 89 % of cases, cefepime - in 83.9 %, cefotaxime - in 71.4 %, ceftazidime - in 66.7 %, cefoperazone - in 66.7 %, ceftriaxone - in 64 %, levofloxacin - in 63.6 %, gentamicin - in 25 %, imipenem - in 58.3 %, meropenem - in 45.4 %, amikacin - in 30 %.

S. aureus was resistant to amoxicillin (50 %), lincomycin (25 %), penicillin (20 %), azithromycin (14.3 %). Staphylococci had sensitivity to cefazolin, cefotaxime, ceftriaxone, levofloxacin, norfloxacin, and vancomycin.

S. anginosus was characterized by resistance to amoxicillin, oxacillin, azithromycin, and levofloxacin in 30 % of cases, to clindamycin in 50 %, but it was sensitive to cefazolin, cefotaxime, ceftriaxone, lincomycin, and penicillin.

Isolated *P. aeruginosa* strains were resistant to ceftazidime, cefoperazone, cefepime, levofloxacin, gentamicin, amikacin, imipenem, meronem. This species had absolute sensitivity only to cefotaxim.

Conclusions.

1. In the clinical material of patients with bronchitis, an expanded spectrum of opportunistic microorganisms belonging to both permanent and transient microbiota of the upper respiratory tract was revealed. *S. aureus*, *K. pneumoniae*, and *C. albicans* predominated both in monoculture and associative form.

2. The studied strains of *K. pneumoniae* and *P. aeruginosa* were characterized by multiple resistance to beta-lactam antibiotics, fluoroquinolones, and aminoglycosides.

3. The frequency of *S. aureus* isolates resistant to amoxicillin, azithromycin, lincomycin, and penicillin ranged from 14.3 % to 50 %.

4. *S. anginosus* as a representative of the permanent microbiota of the oral cavity was resistant to amoxicillin, oxacillin, azithromycin, levofloxacin in 30 % of cases and to clindamycin in 50 % of cases, which may be a factor of selection and spread of antibiotic resistance among potential pathogens of respiratory tract infections.

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**MICROBIOTA OF THE RHIZOSPHERE ZONE OF *COLOBANTHUS QUITENSIS* (Kunth) Bartl.
(KING GEORGE ISLAND, MARITIME ANTARCTICA)**

VRONSKA I., ZINCHUK D., KOMPLIKEVYCH S., MASLOVSKA O., HNATUSH S.

Ivan Franko National University of Lviv, Lviv, Ukraine

iruna.vronska@gmail.com

Topicality. Antarctica is a continent with unfavorable conditions. Bacteria, algae, fungi, and viruses form the majority of the biomass and biodiversity of terrestrial and aquatic ecosystems of Antarctica. The microbiota of different parts of the continent differs, but a high level of endemism characterizes some groups of microorganisms despite the anthropogenic impact [3]. The rhizosphere contains diverse groups of microorganisms that affect plant growth [6]. Rhizobacteria directly affect plant development by nitrogen fixation, phosphorus solubilization, production of siderophores and phytohormones, in particular, indole-3-acetic acid (IAA), gibberellic acid, and disaminases, which are involved in the regulation of ethylene biosynthesis [8]. Siderophores improve plant growth by increasing the availability of iron in the rhizosphere [7]. IAA belongs to the auxins synthesized by plants. IAA promotes root length, which helps absorb nutrients from the environment. IAA is synthesized by plants and microorganisms in various pathways, including the tryptophan-dependent pathway [1].

The objective of the study was to study the number of different groups of microorganisms in the rhizosphere zone of *Colobanthus quitensis* (Kunth) Bartl. and to characterize the properties of some isolates.

Materials and Methods. In this work, *C. quitensis* samples obtained during Ukrainian Antarctic expeditions in 2021-2022 were studied. To determine the enumeration of groups of microorganisms in the rhizosphere of *C. quitensis*, 1 g of soil from the rhizosphere zone was added to 9 ml of 0.9 % NaCl solution. The resulting suspension was mixed thoroughly and incubated for