leftover medication, showing how easily antibiotics can be accessed outside proper medical channels. Treatment adherence was also inconsistent: only about onequarter of respondents completed their full antibiotic course, while most stopped early or took them irregularly. These behaviors selfmedication, misuse, and incomplete treatment create ideal conditions for resistant bacteria to develop and spread. Overall, the findings make it clear that Sri Lanka is at a critical point in its fight against antimicrobial resistance. Awareness alone is not enough; people need accurate knowledge, responsible access to antibiotics, and stronger guidance on how to use them correctly. Improving public education, regulating antibiotic sales more effectively, and promoting responsible healthseeking behavior are essential steps to protect the effectiveness of antibiotics for future generations. Without these efforts, AMR will continue to rise, threatening the country's health system and the wellbeing of its communities.

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Amine Errati

Scientific supervisor: PhD, Associate Professor A. A. Litvin

Educational Establishment
"Gomel State Medical University"
Gomel, Republic of Belarus

AI SYSTEM FOR ANTIMICROBIAL RESISTANCE ANALYSIS

Introduction

Antimicrobial resistance poses a serious threat to patients in the world and the Gomel region too. Rapid identification of resistant pathogens is crucial for effective treatment and antimicrobial stewardship. This study analyzes resistance patterns among clinical isolates obtained from the Gomel Regional Center for Hygiene, Epidemiology, and Public Health to guide empirical antibiotic selection and local stewardship efforts [1, 2].

Traditional culture-based susceptibility testing can take 24–72 hours, delaying optimal therapy [3]. Whole-genome sequencing (WGS) combined with machine learning (ML) offers a faster alternative by predicting resistance from genomic markers [4]. However, implementing ML models typically requires programming skills and computational infrastructure, limiting their adoption in clinical and educational settings.

Recent efforts have produced accessible tutorials that guide beginners through ML-based AMR prediction. Notably, a tutorial published in PLOS Computational Biology (2024) provides step-by-step instructions and Google Colab notebooks for building and evaluating ML models on a real Escherichia coli dataset [5]. The dataset comprises 1,936 isolates with gene presence-absence profiles and susceptibility results for 12 antibiotics, making it an ideal resource for hands-on learning.

Goal

To characterize antimicrobial resistance patterns among clinically significant bacterial isolates from patients in the Gomel region, with particular focus on multidrugresistant organisms and their susceptibility profiles.

Material and methods of research

A retrospective analysis was conducted on clinical microbiological study results from the Gomel Regional Center for Hygiene, Epidemiology, and Public Health. Bacterial isolates were identified using standard microbiological techniques, and antimicrobial susceptibility testing was performed using disk diffusion methods according to EUCAST guidelines. Results were interpreted as sensitive or resistant based on standardized zone diameter breakpoints. Data were extracted from laboratory records for isolates obtained during routine clinical diagnostics between March 2023 and March 2026. A total of 59 records across three organism types were analyzed for resistance patterns, all bearing Document No. 4141, suggesting they were part of a standardized surveillance protocol.

The results of the research and their discussion

Analysis of clinical isolates from the Gomel Regional Center for Hygiene, Epidemiology, and Public Health revealed distinct and clinically significant resistance patterns among three Gram-negative pathogens. Table 1 presents the complete antimicrobial susceptibility profiles of Acinetobacter baumannii, Proteus mirabilis, and Enterobacter cloacae isolated from patients in the Gomel region between March 2023 and March 2026 (Table 1)

Table 1 – Antimicrobial susceptibility profiles of clinical isolates

Organism	Isolation date	Susceptible antibiotics	Susceptible antibiotics
Acinetobacter baumannii	March 5, 2026	Polymyxin B, Amikacin	Imipenem, Meropenem, Ciprofloxacin, Gentamicin, Tobramycin, Tetracycline, Doxycycline, Cefoperazone/ Sulbactam, Piperacillin/Tazobactam
Proteus mirabilis	March 5, 2023	Ceftazidime, Meropenem, Imipenem	Gentamicin, Ceftriaxone, Amoxicillin/Clavulanate, Ciprofloxacin, Nitroxoline, Chloramphenicol, Polymyxin B
Enterobacter cloacae	March 1, 2025	Polymyxin B	Cefotaxime, Ceftriaxone, Chloramphenicol, Cefoperazone, Amoxicillin/Clavulanate, Imipenem, Meropenem, Ampicillin, Ciprofloxacin, Gentamicin, Tetracycline

The Acinetobacter baumannii isolate demonstrated an extensively drug-resistant phenotype with susceptibility limited to polymyxin B and amikacin. Complete resistance to carbapenems (imipenem, meropenem), fluoroquinolones (ciprofloxacin), aminoglycosides (gentamicin, tobramycin), tetracyclines, and beta-lactam combinations severely limits therapeutic options. Such resistance patterns pose significant challenges in intensive care settings where A. Baumannii causes ventilator-associated pneumonia and bloodstream infections. The preserved susceptibility to polymyxin B and amikacin is clinically valuable, though both agents require therapeutic monitoring due to nephrotoxicity risk.

The Proteus mirabilis isolate remained susceptible to ceftazidime and carbapenems, providing reliable treatment options. However, resistance to aminoglycosides, ceftriaxone, amoxicillin/ clavulanate, ciprofloxacin, and polymyxin B was observed. Polymyxin B resistance is consistent with intrinsic resistance in Proteus species, highlighting the importance of species-specific knowledge when selecting empirical therapy.

The Enterobacter cloacae isolate exhibited the most concerning profile with susceptibility only to polymyxin B and resistance to eleven other antibiotics including all beta-lactams, carbapenems, aminoglycosides, fluoroquinolones, tetracyclines, and phenicols. Carbapenem resistance is particularly alarming as these agents are last-line drugs for serious Enterobacteriaceae

infections. This pattern strongly suggests carbapenemase production (e.g., KPC, NDM), which can horizontally transfer to other species via mobile genetic elements.

All isolates bore Document No. 4141, suggesting standardized surveillance protocol participation. The temporal distribution from 2023 to 2026 indicates ongoing circulation of resistant organisms, emphasizing need for sustained infection prevention efforts. These findings underscore that susceptibility testing must guide therapy rather than empirical regimens, and infection control measures including contact precautions and environmental cleaning are essential to prevent transmission.

Study limitations include small sample size, lack of clinical outcome data, and absence of molecular resistance mechanism characterization. Future studies should incorporate molecular typing to elucidate resistance genes and transmission dynamics.

Conclusion

Clinical isolates from Gomel Regional Center demonstrate concerning multidrug resistance patterns across three Gram-negative pathogens. The Acinetobacter baumannii isolate showed susceptibility only to polymyxin B and amikacin, with resistance to carbapenems, fluoroquinolones, and aminoglycosides, while the Enterobacter cloacae isolate exhibited the most limited therapeutic options with susceptibility only to polymyxin B and resistance to carbapenems and all tested beta-lactams. In contrast, the Proteus mirabilis isolate retained susceptibility to carbapenems and ceftazidime but demonstrated resistance to multiple other antibiotic classes. These species-specific resistance patterns highlight the critical importance of accurate susceptibility testing for guiding appropriate antibiotic therapy, and the limited therapeutic options underscore the urgent need for robust antimicrobial stewardship programs and continued surveillance of local resistance patterns.

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K. Kavya

Scientific supervisor: Ph.D., Associate Professor E. I. Kozorez

Educational Establishment
"Gomel State Medical University"
Gomel, Republic of Belarus

KNOWLEDGE AND AWARENESS OF LISTERIOSIS IN PREGNANCY: A CROSS-SECTIONAL STUDY

Introduction

Listeriosis is a serious foodborne infection caused by Listeria monocytogenes. In pregnancy, it can lead to miscarriage, stillbirth, preterm labor, and neonatal sepsis, with mortality rates of 20–50% [1]. Pregnant women are 10–100 times more susceptible due to immunological changes