

UNVEILING THE EMERGING PATTERNS OF ANTIBIOTIC RESISTANCE IN CLINICAL PATHOGENS

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Abstract A major health issue facing modern medicine is antimicrobial resistance. Millions of people are affected annually due to improper participation and misuse of antibiotics. The WHO categorized the AMR as one of the top ten worldwide health issues. However, there is limited recent surveillance and resistance data. This study aims to identify the emerging resistance trends in clinical isolates that are contributing to better antibiotic management and infection control techniques. A cross-sectional study is conducted at the microbiology lab at COMSATS University Islamabad. Clinical specimens were collected from different patients within healthcare institutes and labs with suspected bacterial infections. A total of 458 clinical samples is obtained, including blood (88) (19.2%), urine (178) (38.9%), wound swabs (138) (30.1%), and body fluid (54) (11.1%). These samples were cultured on MacConkey agar, blood agar, and nutrient agar for the growth and isolation of microorganisms. Standard biochemical testing was used for confirmation of bacterial species, and the Kirby-Bauer disk diffusion method was used for antibiotic susceptibility. 358 (78.2%) samples show the growth of microorganisms the most frequently. Escherichia coli (104) (28.1) %, Klebsiella pneumonia (96) (26%), Pseudomonas aeruginosa (54) (14.6%) Staphylococcus aureus (42) (11.3%), Serratia marcescens (17) (4.6%), Salmonella typhi (16) (4.3%), Acinetobacter baumannii (16) (4.3%), and Burkholderia cepacia (13) (3.5%) and drug testing on 358 clinical specimens show different sensitivity and resistance patterns. Twenty different types of drugs that are tested in 358 clinical specimens show different sensitivity and resistance patterns among these drugs. Amoxi Clavulanic AMC (35.2% S) (61.2% R) (3.6% I) (S = sensitive, R = resistant, I = intermediate sensitive) Ampicillin (26.5%S) (70.1%R) (3.4%I) I) Ceftazidime. Avibactam CZA (28.2% S) (67.3% R) (4.2% I) Cefexime (27.4%S) (64.5%R) (8.1% I) CefepimeFEP (35.5% S) (52.0% R) (12.6%I) Ceftazidime CAZ (38.3% S)(55.0% R)(6.7% I), Ceftriaxone CRO (40.2% S)(1.4% R,) (8.1% I) Ciprofloxacin CIP (42.2%S)(53.4%R)(4.2%I) Co. Trimoxazole SXT (45.8%S)(48.3%R)(5.6%I) Colistin (49.7% S) (43.3% R) (6.4% I) Doxycycline DC (50.6% S) (48.9% R) (0.3% I), Ertapenem (53.1% S) (43.9% R) (2.8% I) Imipenem IPM (52.0% S)(47.2% R)(0.3% I) Levofloxacin LEV (55.9%S), , (42.2%R), (1.4%I)



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Meropenem MEM (57.0%S)(40.2%R)(2.5%I) Minocycline (57.0%S) (39.9%R) (2.9%I), Pip Tazobactam TZP (58.7%S) (38.8%R) (2.2%I), and Tigecycline (59.2%S) (39.1%R) (1.4%I). The results highlight the critical need for alternate treatment approaches and antimicrobial stewardship initiatives to counteract the rise in resistance.

INTRODUCTION

A major problem facing modern medicine and public health is antimicrobial resistance. Microbes are continually evolving making them resistant to most of the antibiotics used for treatment. (Oliveira et al. 2024). The WHO categorized antimicrobial resistance as one of the top ten worldwide public health issues faced by humanity. In 2019 about 4.95 million deaths were reported globally due to antimicrobial resistance with low and middle-income countries mostly affected by the AMR burden. (Walsh et al. 2023). Many factors contribute to antibiotic resistance but antibiotic misuse plays a major role. The usage of antibiotics increased by 65% from 2001 to 2015 (Klein et al. 2019). Bacteria are very complicated organisms that can receive and transfer DNA at alarming frequency also the mobile genetic elements can transfer the AMR genes. (Orlek et al. 2023)Antimicrobial resistance is a critical public health concern spared from humans, domestic and wild animals from environment soil water. Inadequate water and sanitation at health care setups also transfer the AMR. (Russell et al. 2023) Antimicrobial resistance is referring as a silent pandemic issue that requires urgent attention and management. It is predictive that if preventive measures are not taken against microbial resistance it become the leading cause of death by 2050 (Founou et al. 2021). Low and middle-income countries have limited resources and a high burden of infectious diseases and there is limited data on the prevalence and burden of antimicrobial resistance. (Iskandar et al. 2021)Many studies around the world report Increasing resistance among pathogens such as Pseudomonas aeruginosa, Klebsiella pneumoniae, and Acinetobacter baumannii. (Gajic et al. 2022)However, there is limited recent surveillance and resistance data. This study aims to identify the emerging resistance trends in clinical isolates that are contributing to better antibiotic management and infection control techniques.

Methodology

Study Design and setting

This cross-sectional study was conducted at the microbiology lab of COMSATS University Islamabad. The clinical specimen was collected from different patients in health care institutes and labs with suspected bacterial infections.

Sample collection and processing

A total (of 458) clinical samples is obtained including, Blood (88) (19.2%), Urine (178) (38.9%), Wound swab, (138) (30.1%) Boady Fluid, (54) (11.1%). These samples were cultured on MacConkey agar, Blood agar, and nutrient agar for the growth and isolation of microorganisms. Standard Biochemical testing was used for confirmation of bacterial species.

Antibiotic Susceptibility testing

Antibiotic susceptibility testing was performed by using the Kirby-Bauer disk diffusion method following clinical and laboratory standard institute (CLSI).(Gajic et al. 2022) The following classes were tested Beta lactam (Penicillin, Cephalosporin, and Carbapenems)QUINOLONES(Ciprofloxacin,

Levofloxacin,)Sulfonamides(Trimethoprim,

Sulfamethoxazole)TETRACYCLINES (Minocycline, Tigecycline, Doxycycline) and the drugs include PENCILLINS (Ampicillin, Amoxil Clavul.acid AMC, Pip. Tazobactam TZP) TETRACYCLINES (Minocycline, Tigecycline, Doxycycline,) CARBAPENEMS (Imipenem, Meropenem, Ertapenem) SULFONAMIDES (Co. Trimoxazole SXT),) QUINOLONES (Levofloxacin, Ciprofloxacin) **CEPHELOSPORINS** (Cefixime, Cefepime, Ceftazidime, Ceftriaxone CRO Cefixime CFM Ceftazidime. Avibactam)

Data Analysis

Data were analyzed by using Microsoft excel. Descriptive statics were used to calculate the frequency and percentage of resistance isolates.



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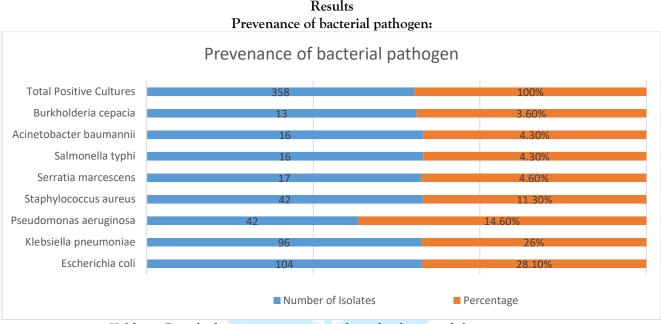


 Table 1: Detail of microorganisms, number of isolates, and their percentage.

Out 458 Clinical samples 358 (78.2%) sample show the growth of microorganism the most frequently Escherichia coli (104) (28.1) %, Klebsiella pneumonia (96) (26%), Pseudomonas aeruginosa (54) (14.6%) Staphylococcus aures (42) (11.3%), Serratia marcescens (17) (4.6%) (Salmonella typhi (16) (4.3%), Acinetobacter baumannii (16) (4.3%), Burkholderia cepacia (13) (3.5%) as shown in table number 2. Sensitive, MDR, XDR percentage of different species which is isolated from 358. Is mostly cases were MDR while Serratia marcescens have (64.7%) Escherichia coli (22.1%), Klebsiella pneumoniae (34.3%), Pseudomonas aeruginosa (24.07%) XDR cases as shown in table number 3.

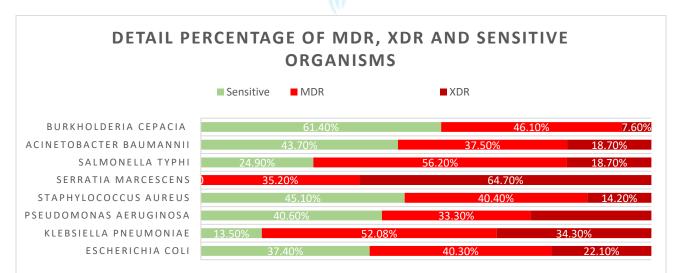


Table :2 Detail percentage of MDR, XDR, and Sensitive organismsS .as shown in table number 2.

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Overall, all percentages of different drug sensitivity patterns were tested on 358 isolated species of

microbes most of the drugs are resistant to different species as shown Table in number.



Table:3 Detail pattern of drugs which is tested on 358 clinical isolates

Twenty different types of drugs which are tested in 358 clinical species show different Sensitivity and Resistance patterns among these drugs Amoxi Clavulanic AMC (35.2% S) (61.2% R) (3.6%I) (S sensitive, R resistance, I intermediate sensitive) Ampicillin (26.5%S) (70.1%R) (3.4%I), Ceftazidime. Avibactam CZA(28.2%S)(67.3%R)(4.2%I) Cefexime (27.4%S)(64.5%R)(8.1%I)Cefepime CFM FEP (35.5%S)(52.0%R)(12.6%I)Ceftazidime CAZ (38.3% S)(55.0% R)(6.7%I), Ceftriaxone CRO (40.2% S)(1.4%R,)(8.1%I)CiprofloxacinCIP (42.2%S)(53.4%R)(4.2%I) Co. Trimoxazole SXT (45.8%S)(48.3%R)(5.6%I)(Colistin (49.7%S)(43.3%R)(6.4%I)DoxycyclineDC(50.6%S)(4 8.9%R)(0.3%I),Ertapenem (53.1%S),(43.9%R)(2.8I)Imipenem IPM (52.0%S)(47.2%R)(0.3%I) Levofloxacin LEV (55.9%S),(42.2%R)(1.4%I)Meropenem MEM (57.0%)(40.2%R)(2.5%I) Minocycline (57.0%S), (39.9%R)(2.9%I)PipTazobactam TZP (58.7%S)(38.8%R)(2.2%) and Tigecycline (59.2%S) (39.1%R)(1.4%I)

Discussion

The finding of this study shows the significant variation of antimicrobial susceptibility multiresistance (MDR) and extensive drug-resistant (XDR) Profiles among clinically relevant bacterial pathogens. Our study demonstrated that the Salmonella typhi 56.2% and Klebsiella pneumoniae have 52.08% MDR cases show the increasing trend of MDR among these species (Talukder et al. 2023)(Muraya et al. 2022) The XDR cases of Klebsiella pneumoniae 34.30% and Serratia marcescens 64.70% indicating the serious public health (WHO-2022) the Serratia marcescens high extensive drug resistance pattern indicate the limited therapeutic option and increasingly documented ICU related infection (Findlay et al. 2021) .E.coli shows the substantial resistance (40.30%%) MDR and (22.10%) XDR cases align well with the surveillance data of low middle income countries where ESBL producing strains are pandemic (Cassini et al. 2019) while in contrast the Burkholderia cepacia have lowest XDR (7.60%) possible due to intrinsic mechanism rather than acquired resistance (de Mesquita Souza Saraiva et al. 2022) The relatively high MDR rates reported for Pseudomonas (33.30%)aeruginosa and

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Acinetobacter baumannii (37.50%) reveal their significance in hospital outbreaks, most notably associated with ventilators Here, however, no sensitive Serratia marcescens isolates (Nil) were evidenced which are more difficult to find in older studies but also establishes evidence for rapid resistance development due to antibiotic over uses (Laxminarayan et al. 2020) The presents study highlight the emerging trend of antimicrobial resistance in clinical isolates the high resistance rate was observed in Ampicillin 70%Amoxicillin-Clavulanic Acid (61.2%) indicate the wide spread of beta lactam antibiotic which align well the global report of increasing resistance to first line of antibiotic by (WHO 2022) .Similarly resistance to Ceftazidime-Avibactam (67.3%) and Cefepime (52%) shows the emerging resistance in newer combination of beta lactam antibiotic due to wide use of be ESBL inhibitors (Bush and Bradford 2020). Carbapenem consider the last option for treatment also shows the resistance Imipenem 47.2% and Meropenem 40.2% this is alarming and critical public health threat(Flynn and Guarner 2023). However, tigecycline (39.1%) resistance) and piperacillin-tazobactam (38.8%) resistance) have the batter efficacy consider effective against the pathogen. High resistance was shown by fluoroquinolones (Ciprofloxacin: 53.4% resistance, Levofloxacin: 42.2% resistance), which is in line with research that links their abuse to plasmid-mediated resistance.(Hooper and Jacoby 2016) Due to their limited clinical use, minocycline (39.9% resistance) and colistin (43.3% resistance) shown moderate effectiveness. The significant levels of resistance to Doxycycline (48.9%) and Co-Trimoxazole (48.3%) indicate that these medications have limited use in empirical therapy(Laxminarayan et al. 2020). This study is conducted at local level and resistance level may varies regionally further molecular studied is needed to identify the resistance gene and under laying mechanism

Conclusion

The results highlight the critical need for alternate treatment approaches and antimicrobial stewardship initiatives to counteract the rise in resistance.



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REFERENCES

- Bush, Karen, and Patricia A. Bradford. 2020. "Epidemiology of β-Lactamase-Producing Pathogens." *Clinical Microbiology Reviews* 33(2). doi:10.1128/CMR.00047-19.
- Cassini, Alessandro, Liselotte Diaz Högberg, Diamantis Plachouras, Annalisa Quattrocchi, Ana Hoxha, Gunnar Skov Simonsen, Mélanie Colomb-Cotinat, et al. 2019. "Attributable Deaths and Disability-Adjusted Life-Years Caused by Infections with Antibiotic-Resistant Bacteria in the EU and the European Economic Area in 2015: A Population-Level Modelling Analysis." The Lancet Infectious Diseases 19(1): 56–66. doi:10.1016/S1473-3099(18)30605-4.
- Findlay, Jacqueline, Laurent Poirel, Mario Juhas, and Patrice Nordmann. 2021. "KPC-Mediated Resistance to Ceftazidime-Avibactam and Collateral Effects in Klebsiella Pneumoniae." Antimicrobial Agents and Chemotherapy 65(9). doi:10.1128/AAC.00890-21.
- Flynn, Cynthia E., and Jeannette Guarner. 2023. "Emerging Antimicrobial Resistance." *Modern Pathology* 36(9): 100249. doi:10.1016/j.modpat.2023.100249.
- Founou, Raspail C, Ariel J Blocker, Michel Noubom, Cedrice Tsayem, Siméon P Choukem, Maarten Van Dongen, and Luria L Founou. 2021. "The COVID-19 Pandemic: A Threat to Antimicrobial Resistance Containment." *Future Science* OA 7(8). doi:10.2144/fsoa-2021-0012.
- From:, World Health Organization. Antimicrobial Resistance (2021). Available, Https://www.who.int/news-room/factsheets/detail/antimicrobial-resistance, and 2023). (Accessed March 21. "No Title."
- Gajic, Ina, Jovana Kabic, Dusan Kekic, Milos Jovicevic, Marina Milenkovic, Dragana Mitic Culafic, Anika Trudic, Lazar Ranin, and Natasa Opavski. 2022. "Antimicrobial Susceptibility Testing: A Comprehensive Review of Currently Used Methods." Antibiotics 11(4): 427. doi:10.3390/antibiotics11040427.
- Hooper, David C., and George A. Jacoby. 2016. "Topoisomerase Inhibitors: Fluoroquinolone Mechanisms of Action and Resistance." Cold Spring Harbor Perspectives in Medicine 6(9):

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a025320. doi:10.1101/cshperspect.a025320.

- Iskandar, Katia, Laurent Molinier, Souheil Hallit, Massimo Sartelli, Timothy Craig Hardcastle, Mainul Haque, Halyna Lugova, et al. 2021. "Surveillance of Antimicrobial Resistance in Low- and Middle-Income Countries: A Scattered Picture." Antimicrobial Resistance & Infection Control 10(1): 63. doi:10.1186/s13756-021-00931-w.
- Klein, Eili Y., Katie K. Tseng, Suraj Pant, and Ramanan Laxminarayan. 2019. "Tracking Global Trends in the Effectiveness of Antibiotic Therapy Using the Drug Resistance Index." BMJ Global Health 4(2): 1–7. doi:10.1136/bmjgh-2018-001315.
- Laxminarayan, Ramanan, Thomas Van Boeckel, Isabel Frost, Samuel Kariuki, Ejaz Ahmed Khan, Direk Limmathurotsakul, D G Joakim Larsson, et al. 2020. "The Lancet Infectious Diseases Commission on Antimicrobial Resistance: 6 Years Later." *The Lancet Infectious Diseases* 20(4): e51–60. doi:10.1016/S1473-3099(20)30003-7.
- de Mesquita Souza Saraiva, Mauro, Kelvin Lim, Daniel Farias Marinho do Monte, Patrícia Emília Naves Givisiez, Lucas Bocchini Rodrigues Alves, Oliveiro Caetano de Freitas Neto. Samuel Kariuki, et al. 2022. "Antimicrobial Resistance in the Globalized Food Chain: A One Health Perspective Applied to the Poultry Industry." Brazilian Journal of Microbiology 53(1): 465-86. doi:10.1007/s42770-021-00635-8.
- Muraya, Angela, Cecilia Kyany'a, Shahiid Kiyaga, Hunter J. Smith, Caleb Kibet, Melissa J. Martin, Josephine Kimani, and Lillian Musila. 2022. "Antimicrobial Resistance and Virulence Characteristics of Klebsiella Pneumoniae Isolates in Kenva by Whole-Genome Sequencing." Pathogens 11(5): 545. doi:10.3390/pathogens11050545.
- Oliveira, Manuela, Wilson Antunes, Salete Mota, Áurea Madureira-Carvalho, Ricardo Jorge Dinis-Oliveira, and Diana Dias da Silva. 2024. "An Overview of the Recent Advances in Antimicrobial Resistance." *Microorganisms* 12(9): 1920. doi:10.3390/microorganisms12091920.

ISSN: (e) 3007-1607 (p) 3007-1593

- Orlek, Alex, Muna F. Anjum, Alison E. Mather, Nicole Stoesser, and A. Sarah Walker. 2023. "Factors Associated with Plasmid Antibiotic Resistance Gene Carriage Revealed Using Large-Scale Multivariable Analysis." *Scientific Reports* 13(1): 2500. doi:10.1038/s41598-023-29530-y.
- Russell, Neal J., Wolfgang Stöhr, Nishad Plakkal, Aislinn Cook, James A. Berkley, Bethou Adhisivam, Ramesh Agarwal, et al. 2023. "Patterns of Antibiotic Use, Pathogens, and Prediction of Mortality in Hospitalized Neonates and Young Infants with Sepsis: A Global Neonatal Sepsis Observational Cohort Study (NeoOBS)." *PLOS Medicine* 20(6): e1004179.

doi:10.1371/journal.pmed.1004179.

- Talukder, Himel, Shamsul Alam Roky, Konad Debnath, Binayok Sharma, Juned Ahmed, and "Prevalence Sawrab Rov. 2023. and Antimicrobial Resistance Profile of Salmonella Isolated from Human. Animal and Environment Samples in South Asia: A 10-Year Meta-Analysis." Journal of Epidemiology and Global Health 13(4): 637-52. doi:10.1007/s44197-023-00160-x.
- Walsh, Timothy R., Ana C. Gales, Ramanan Laxminarayan, and Philippa C. Dodd. 2023. "Antimicrobial Resistance: Addressing a Global Threat to Humanity." *PLOS Medicine* 20(7): e1004264.

doi:10.1371/journal.pmed.1004264.

World Health Organization. (2022). Global antimicrobial resistance and use surveillance system (GLASS) report 2022. World Health Organization