

Antimicrobial Multidrug Resistance Profiles in Uropathogenic Bacteria: Prevalence, Patterns, and Implications for Therapy

Niveditha Thomas*

Department of Neurosurgery, University of Florida, Gainesville, FL, USA

Abstract

Antimicrobial multidrug resistance (MDR) in uropathogenic bacteria poses a significant challenge to the successful treatment of urinary tract infections (UTIs). This article provides an overview of the prevalence, patterns, and implications of MDR profiles in uropathogenic bacteria and discusses their impact on therapy.

A quarter of the bacteria were MDR and the most common MDR profile, including resistance to penicillins, quinolones, and sulfonamides (antibiotics with different mechanisms of action, all mainly recommended by the European Association of Urology for empirical therapy of uncomplicated UTI), was observed, alone or in association with resistance to other antimicrobial classes, in the main bacteria implicated in UTI. The penicillin class was included in all the frequent MDR profiles observed in the ten main bacteria and was the antibiotic with the highest prescription during the study period.

Keywords: Antimicrobial multidrug resistance; Uropathogenic bacteria; Urinary tract infections

Introduction

Urinary tract infections are among the most common bacterial infections, affecting millions of individuals worldwide each year. Uropathogenic bacteria have developed various mechanisms to resist the action of antimicrobial agents, leading to the emergence of multidrug-resistant strains. Understanding the prevalence and patterns of antimicrobial MDR in uropathogenic bacteria is crucial for effective treatment and infection control strategies [1].

Multidrug resistant (MDR) bacteria are more usually associated with nosocomial infections. However, their emergence at the community level has increased, making the infections treatment more difficult, namely, the most common ones, such as the urinary tract infection (UTI) [2]. Uncomplicated cystitis in women is the most common UTI and according to the European Association of Urology is defined as the growth of a single pathogen of $>10^3$ colony-forming units mL⁻¹ from properly collected midstream urine. Some studies performed at community level showed that MDR bacterial percentage observed among the most prevalent bacteria involved in the community-acquired UTI, *Escherichia coli*, varied between 38 and 54%.

Resistance to antibiotics occurs classically as a result of drug modification, target alteration, and reduced accumulation owing to decreased permeability and/or increased efflux. It may be an innate feature of a microorganism or may result from mutation or acquisition of exogenous resistance genes [3]. The acquisition of resistant genes has been well described in the literature and it is particularly important because acquisition regularly might confer cross- or coresistance which may turn bacteria MDR to specific antibiotics even when these antibiotics are not frequently prescribed or had even been abolished.

Prevalence of antimicrobial multidrug resistance

Recent studies have reported an alarming increase in the prevalence of antimicrobial MDR among uropathogenic bacteria. These resistant strains exhibit resistance to multiple classes of antimicrobial agents, severely limiting treatment options [4]. The prevalence of MDR varies geographically and is influenced by factors such as antibiotic usage, healthcare settings, and patient demographics.

Patterns of antimicrobial multidrug resistance

Uropathogenic bacteria demonstrate diverse resistance patterns, with certain pathogens exhibiting higher resistance rates compared to others. The most common MDR profiles include resistance to beta-lactams, fluoroquinolones, aminoglycosides, and sulfonamides. The emergence of extended-spectrum beta-lactamases (ESBLs) and carbapenemases has further complicated the treatment landscape [5].

Implications for therapy

The presence of antimicrobial MDR in uropathogenic bacteria significantly impacts therapy decisions. Empirical treatment guidelines must consider local resistance patterns to ensure appropriate antibiotic selection. In cases where MDR strains are identified, alternative treatment options such as combination therapy or newer agents may be necessary. Antimicrobial stewardship programs play a crucial role in optimizing therapy, preventing further resistance development, and preserving the effectiveness of available antimicrobial agents [6].

Infection control and prevention strategies

The rising prevalence of antimicrobial MDR in uropathogenic bacteria highlights the need for robust infection control measures. Stringent adherence to hand hygiene, proper catheter management, and judicious use of antibiotics are essential in preventing the spread of resistant strains. Surveillance programs and molecular typing techniques facilitate the identification of outbreaks and the tracking of resistant clones [7].

*Corresponding author: Niveditha Thomas, Department of Neurosurgery, University of Florida, Gainesville, FL, USA, E-mail: Thomasnivi553@edu.org

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Discussion Multidrug resistance was observed among the most prevalent bacteria involved in the community-acquired UTI, a quarter of these bacteria being resistant to three or more antimicrobials of distinct classes, and the most incident MDR profile includes resistance to "PQS." The most common MDR profile was found in five of the main ten bacteria implicated in UTI but was also observed in the other five bacteria implicated in UTI which present simultaneously resistance to other antibiotic classes. As sulfonamides are not used for *P. aeruginosa* this MDR profile was not observed for this bacterium. Moreover, this MDR profile includes antibiotics with three different mechanisms of action which limits the therapeutic options available to treat UTI.

The penicillins class was included in the most frequent MDR profile and also in the other 5 MDR profiles more frequently among the ten main bacteria. The high administration of penicillins in Portugal at community level between 2000 and 2009 and the ESBL-production among the main bacteria involved in UTI may explain the low efficacy of penicillins in the treatment of these infections [8]. The quinolones, although included in the most common MDR profile, were the antimicrobial class less frequent in the 6 MDR profiles observed in the main ten bacteria implicated in UTI but were yet present in 50% of the 6 MDR profiles. Portugal continues to be the third country among the European countries with the highest quinolones consumption which may explain the presence of this antimicrobial class in the most common MDR profile.

The presence of quinolones in 50% of the most common MDR profiles and the high resistance among the main bacteria implicated in community-acquired UTI may be explained by the high consumption levels. Studies performed at community level showed that a huge decrease of quinolones prescription may contribute to diminishing the prevalence of resistance to this antimicrobial class since bacteria pay a high fitness cost on the transmissibility of quinolone resistance [9]. Although only a slight increase in the incidence of the six most common MDR profiles was observed during the study period, the MDR profiles that include simultaneously resistance to quinolones and cephalosporins showed a higher increase. The increase of resistance to cephalosporins may be related with a possible increase of ESBL-production among Enterobacteriaceae that also confers resistance to other betalactams antibiotics, including third- and fourth-generation cephalosporins.

Future directions

Further research is required to gain a deeper understanding

of the molecular mechanisms underlying antimicrobial MDR in uropathogenic bacteria [10]. The development of novel antimicrobial agents, diagnostic tools for rapid identification of resistance markers, and alternative therapeutic approaches such as phage therapy hold promise in combating antimicrobial MDR.

Conclusion

Antimicrobial multidrug resistance in uropathogenic bacteria is a global health concern with significant implications for therapy. Understanding the prevalence and patterns of resistance is crucial in guiding treatment decisions and implementing effective infection control strategies. Continued surveillance, antimicrobial stewardship, and research efforts are essential in addressing this growing public health threat and preserving the effectiveness of antimicrobial agents for the management of urinary tract infections.

References

1. Kobo O, Nikola S, Geffen Y, Paul M (2017) The pyogenic potential of the different *Streptococcus anginosus* group bacterial species: retrospective cohort study. *Epidemiol Infect* 145:3065-3069.
2. Noguchi S, Yatera K, Kawanami T, Yamasaki K, Naito K, et al. (2015) The clinical features of respiratory infections caused by the *Streptococcus anginosus* group. *BMC Pulm Med* 26:115:133.
3. Yamasaki K, Kawanami T, Yatera K, Fukuda K, Noguchi S, et al. (2013) Significance of anaerobes and oral bacteria in community-acquired pneumonia. *PLoS One* 8:e63103.
4. Junckerstorff RK, Robinson JO, Murray RJ (2014) Invasive *Streptococcus anginosus* group infection-does the species predict the outcome? *Int J Infect Dis* 18:38-40.
5. Okada F, Ono A, Ando Y, Nakayama T, Ishii H, et al. (2013) High-resolution CT findings in *Streptococcus milleri* pulmonary infection. *Clin Radiol* 68:e331-337.
6. Gogineni VK, Modrykamien A (2011) Lung abscesses in 2 patients with Lancefield group F streptococci (*Streptococcus milleri* group). *Respir Care* 56:1966-1969.
7. Kobashi Y, Mouri K, Yagi S, Obase Y, Oka M (2008) Clinical analysis of cases of empyema due to *Streptococcus milleri* group. *Jpn J Infect Dis* 61:484-486.
8. Shinzato T, Saito A (1994) A mechanism of pathogenicity of "*Streptococcus milleri* group" in pulmonary infection: synergy with an anaerobe. *J Med Microbiol* 40:118-123.
9. Zhang Z, Xiao B, Liang Z (2020) Successful treatment of pyopneumothorax secondary to *Streptococcus constellatus* infection with linezolid: a case report and review of the literature. *J Med Case Rep* 14:180.
10. Che Rahim MJ, Mohammad N, Wan Ghazali WS (2016) Pyopneumothorax secondary to *Streptococcus milleri* infection. *BMJ Case Rep* bcr 2016217537.