



Copyright © The Author(s) Vol.4, No. 4, January 2024 *e*-ISSN: 2774-4892

The Comprehensive Analysis Of The Urinary Tract Infections In The Patients Admitted At The General Hospital In An-Najaf Province

Ahmed Salim Abed¹*, Eman Hamza Mohammed², Eman Hasani AL-Salami³, And Faten Abed AL-Kadhem Khalaf Aldawmy⁴

^{1,2} Jabir Ibn Hayyan Medical University, Najaf, Iraq.
 ³ Department Of Microbiology, Faculty Of Medicine, University Of Kufa, Iraq.
 ⁴ Faculty Of Pharmacy, University Of Alzahraa, Karbala, Iraq.

*E-mail: a77medsalim2@gmail.com, ahmed.salim@jmu.edu.iq

ABSTRACT

Background: Urinary tract infections (UTIs) are a pressing clinical problem for which relevant to microbial dynamics should be explored in-depth so to have better diagnostics, and treatment strategies for this group of infections. The paper deals complexity of UTI diagnosis containing multiple samples in which microbes were not found, therefore they did not meet the minimum bacterial concentration for diagnosis, thus "traditional" diagnostic paradigms no longer work. The hypothesis posits that this non-growth phenomena may point out the unknown causes instead of the bacterial infections, thus the need of the exploration of more advanced diagnostic protocols. Methods: Among 97 random urine samples of individuals admitted in a general hospital of Najaf city, Iraq, with April 2023 to October 2023 there was UTI. The diagnostic processes comprise of different tiers of clinical pathology tests, culture characteristics assessments and biochemical tests used in the study. Statistical analysis was carried out by using the GraphPad Prism computer software. Results: Microbiome analysis had shown presence of different micro-organismal communities, E. coli being the dominant bacterium for UTI, in conformity with established research propositions. Enlightening is that a three-sized group of samples show no detectable growth of pathogens, indicating the complexity of UTI identification. The plethora of Gram-negative microbes explained by the discovery of fungal isolates including Candida albicans, and the predominance of the less pathogenic strains demonstrate the importance of accuracy in therapeutic effort. Conclusion: This evidence shows the challenges in diagnosis and management of UTI in mouse, humanizing current assumptions. The discovery of "no growth" leads in turn to the need to explore the world of alternative causes for UTI symptoms, not excluding the non-bacterial nature of the

Keywords: Urinary tract infections (UTIs), Microbial dynamics, Cultured urine samples, Escherichia coli (E. coli), Gram-negative bacteria, Fungal UTI.

Article Information

Received: November 25, 2023; Revised: December 30, 2023; Online: January, 2024



INTRODUCTION

In all age categories, females are at a higher risk of UTIs. Escherichia coli (E. coli) – the most frequent cause of it all – can disperse into the bladder either through the urethra or contact with contaminated fluids. [1] However, other conditions including diabetes and an enlarged prostate, can contribute to it, and those men who have a shorter urethra have a high risk of developing it. The pain when urinating, the cloudy urine, the presence of blood in the urine and the increase in frequency of urination, can all be the possible symptoms. [2].

A urinary tract infection (UTI) is a generalized sneeze or accidental spill caused by a bacterial or viral infection in the urinary tract system in human beings. It can be divided into two categories: infectious but also noninfectious too. But one of the main features of asymptomatic UTI is that the patient is not aware of the process going on inside his body and does not present the symptom [3]. We have the contrast with symptomatic UTIs that cause such obvious signs as bright blood in the urine and pain in the bladder just to name a few. The invasion of the urinary tract inflammation at the end of the tube that carries urine outside of the body [4]. Mainly is consists of either the urethra or the bladder. Urinary tract infections may would result if the input is bacteria that is perceived of the urinary system breakdown, for example in menstrual women. [5]. It is most often due to the fact of having unprotected sexual intercourse while being already the carrier of a sexually transmitted disease, such as gonorrhea or chlamydia, and not treating your condition. Recurrence of cystitis, a kind of urinary tract infection, could be the result of the infection. from Language Instagram | Language Blog https://ift.tt/qdcdznC via IFTTT urinary system the insect's epidermis is open to the air as well as to the polluted atmosphere, crises can happen promptly in them. Infections of 2 kinds are more often women's issues rather than men's. At least one woman will experience a minimum of one of these types of violence present in 1 in 5 women throughout their lifetime. [6,8]. Being that the majority of the strains of bacteria isolated from patients diagnosed with either acute or chronic UTIs are

drug resistant, the emergence of antibiotics resistance is a still grave issue.[7]. Therefore, the aim of this study is to evaluate the incidence of UTI in patient during in Najaf City, Iraq.

METHODS:

Total Urine samples Collection and Culturing: .

The sample time spent from April 2023 to October 2023 to collected 97 urine samples, among male and female patients admitted in a general hospital of Najaf City, Iraq, were all with urinary tract infection were conducted. The 5ml of midstream urine samples were incubated with brain heart infusion broth at 48 hr and 37°C temperature. Incubation-48 hours later, the loop of urine was carefully streaked blood agar and MacConky Subsequently, the cultures were left to mature ahead of the next 48 hours at the same temperature. Consequently, the diagnostic processes comprise of different tiers of clinical characteristics pathology tests. culture assessments and biochemical tests [8-9].

Longitudinal Monitoring:

The purpose of the observational study was to understand the spatiotemporal peculiarities of antibiotic resistance; therefore, a cohort of patients was longitudinally monitored to achieve this. Follow-up urine samples were collected regularly with the aim of monitoring, after each interval, the progress of the bacterial barrier and the modification patterns of the antibiotic susceptibility phenomenon. [11] Using a longitudinal approach offered unique

feedback about the consisting or changing nature of resistance in a particular patient over time. These seemed to provide deeper knowledge about the constantly shifting balance between the microbial populations and the employed therapeutic measures. [9]

Quality Control Measures:

The involvement of stringent quality control policies has been unrelenting in the study to ensure the reliability and precision of the obtained results. Such processes involved the cleaning of laboratory equipment and the regular calibration of the equipment as well as the testing of laboratory personnel. [2] Proficiency testing and the inclusion of known antibiotic susceptibility profiles in every analysis batch were also done. Holding up to standardized protocols and rigid quality control schemes establish high significance and reproducibility of the experiments' results. [7]

Statistical Analysis:

The data collected from many urine samples and sensitivity test were analyzed using wellestablished statistical methodologies with GraphPad Prism computer application software version 12. This evaluation helped us make clear statistics and percentages so that we could use them as a basis for comparing all bacterial isolates [10]. The aim of statistical evaluation was to discover trends, patterns, and variations most prominent among data which then can be used as evidence for deeper understanding of microbial landscape antibiotic and susceptibility profiles within that population.

Ethical Considerations:

The research has conducted been in conformance with the Declaration of Helsinki and review protocol by Institutional Review Board (IRB) of the relevant hospital had been obtained. For every participant, prior to the gathering of all information, informed consent was obtained, ensuring their going in into the data gathering as volunteers and their personal information will be treated in confidentiality. The key ethical issues including the ethical aspect of the research were preceded throughout the course of research methodology. However, the research followed the codified medical and scientific ethical standards.

RESULTS:

During the in-depth study of urinary tract infections (UTI) in 97 cultured samples, the investigators went into great details and really observed the presence of microbes. Figure 1,2. The breakdown of identified microorganisms and their respective counts is as follows: The breakdown of identified microorganisms and their respective counts by bacterial Isolates: E. coli (16 samples): In 16 samples, frequency of the presence of Escherichia coli, a bacterium underlying a vast majority of UTI cases, was detected. This also lays emphasis on the wellestablished E. coli recognition as one of the main causes of urinary tract infections. A small step by step approach records the total samples which equals 97. The standout element in the saprophytic profile is the widespread distribution of commonly found pathogens like E. coli, and at the same time, underline the fact that the clinical diagnosis and management of urinary tract infection must take a look at the overall spectrum of bacterial and fungal etiologies (causative agents). In this study, the type of drug formulation needed for therapeutic purposes arises from the fact that various

strains of bacteria are encountered. It may also be a pointer to precision diagnostic methods to unmask the offending strain.

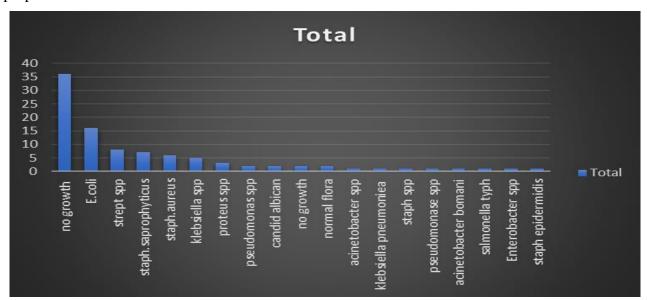


Figure 1: Streptococcus species (8 samples): Eight of the samples carried streptococcal species and therefore revealed that staphylococci are just one of the several key factors responsible for EUTs, being one of the most common such species. Staphylococcus saprophyticus (7 samples) and Staphylococcus aureus (6 samples): S. saprophyticus, from the staphylococcal strain, was observed in 7 samples while S. aureus from the same strain was seen in 6 samples. Such strains further testify of the diverse range of bacterial factors of UTIs implying the complex nature of these infections.

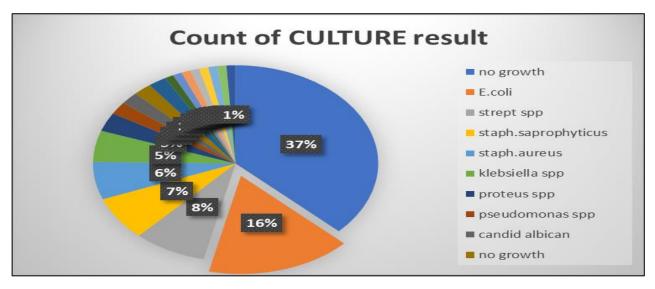


Figure 2: Count of culture result.

The participants were men and the group mean age was approx. 37.74 yrs. Figure 3. The analysis of urine culture ended up showing a plausible positive association between a person's age and the chances of a positive culture result, with an exceptional instance at the age of 70. The detected trend is an accordance with papers that stress the enhanced vulnerability of older people to UTIs. We elucidate the implications in clinical practice which stress the need to take age into account in the evaluation of UTIs among the elderly. At same time, the small sample size the additionally brings about the necessity for the implementation of an extended research that can discover the multifactorial aspects inducing the age-related UTI outcomes. The indicated give relevant guidance for the improvement of the diagnosis and treatment strategies in wide age spectrum of people.

The research of urine cultures results of females had a reference mean age of around 37.85 years. **Figure 4**. The findings showed that the older the individuals in the group, the higher the positive outcomes on the culture. The most remarkable thing was that each of the specified age groups was characterized by distinctive viewpoints, and this made the UTI problem in females look different among different groups. The study suggests that trends could be potential age related which in turn highlights the need for diagnostic and therapeutic approaches that can highlight age

group dynamics for appropriate management. The selected agents from microbes as well as other factors have been identified to be the determinants ofsignificant age-related variations in urinary infections tract occurrences. However, more research is necessary to investigate these specific agents and additional factors further in an attempt to understand the interactions in a better way.

The provided research shows UTI-related data in connection with aging for both men and women, bringing awareness about adjusted patient-related decisions in the clinical settings. It is not removed that with males a male has an intriguing outlier, while in females, a female is influenced with individual ages and a culture result. Acquainting these gender-based nuances brings our knowledge to a different extend influencing the condition toward designing personalized diagnostics and therapy approach.

Population age is widely ranged and covers many ages, More than half of the cases tend to be in a 20 to 40-year age span, while sometimes even younger and older people get affected by this disorder, Most common ages are 23 and 30 with their count being the highest, each at five times. This frequency analysis provides a picture of the age distribution for that dataset putting forward the diversity of the age composition of people with urine culture tests in the region. **Figure 5.**

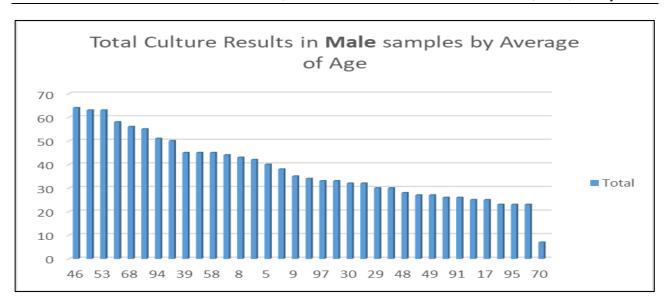


Figure 3: Total culture results in male samples by average of age.

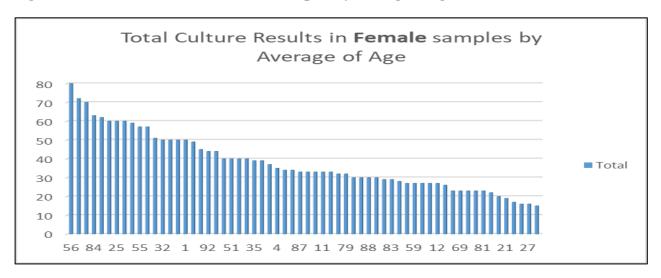


Figure 4: Total culture results in female samples by average of age.

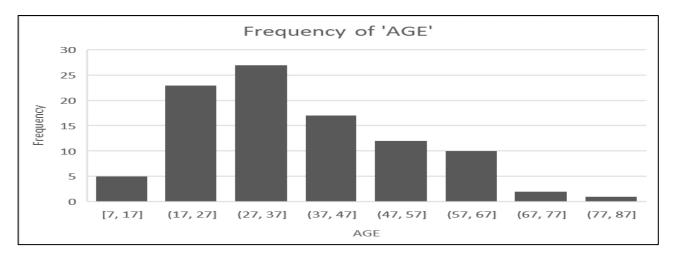


Figure 5: Frequency of 'AGE' Overall Observation.

DISCUSSION:

The investigative assessment of 97 cultured urine samples shows, in summary, the microbial diversity of UTIs (CULTURE result, 2024). Identified microorganism's exhaustion offers a few rallying points.

Prevalence of Pathogens: Common dominance of Exscherichia coli (E. coli) in 16 samples is what allegedly presumed and evidence of its regularity in UTIs cases shows its chief role. To appreciate the gravity of E. coli in this dossier one will have to put an emphasis at diagnostician and therapeutic strategies whose precision is essential. S. saprophyticus, S. aureus, and Streptococcus spp. are no different as they are just part of the tangley trend of the microbial carpet which highlights the complex myriad of UTI-causing microbes. [8] Diversity Among Gram-Negative Bacteria: In addition, bacteria (Gram negatives like Klebsiella, Proteus, Pseudomonas and Acinetobacter) that are highly diversified in UTIs, were detected. We are now aware of the existing bacteria that commonly cause the disease. The diversity of these bacteria requires scientists to provide tailored antibiotic treatments based on the specific strains. As a result, there will be precision in the therapeutic intervention. Seen against this background stands the evidence of less usual perpetrators such as Enterobacter and Salmonella Typhi which stresses the need for a high level of vigilance when it comes to treating such less ordinary infectious diseases. [3] Fungal Involvement: The reference of two samples to Candida albicans will increase the possibility of a mixed infection. This outcome pinpoints the role of fungal etiology in the emergence of UTI, especially a Candida type, and further calls for searching for new antifungal drugs to be included into the list of UTI management therapy. [5] Miscellaneous Findings: Phenomena of presence of pathogen commensals like Staphylococcus epidermidis

prove that the & check the complexity of the problem. These conclusions imply the necessity of better standard to medical reasoning aiming to provide the most effective service to the patients and avoid unnecessary treatments. [19]

Agreed Perspectives: E. coli Prevalence: An investigation done by 2. Alfouzan et al. (2023) has proven a lot of E. coli samples in urine infection to be present and this contributes to its dominance (as found in this research analysis) [2]. Complexities in UTI Diagnosis: In line with the findings of Aljanaby AAJ and Mohammed KJ (2020), even if there is no detectable growth of microbes, it could be possible to diagnose UTIs. This suggests that the diagnostic landscape for UTIs cannot be viewed as a simple scenario, rather as a complex situation [4]. Diversity of Gram-Negative Bacteria: The study of Vaez et al. (2022) that is medical practice has proven like the use of other Gramnegative bacteria, and the reason for special antibiotics treatment in urinary tract infections [18].

Different Perspectives: Alternative Causes of Symptoms: Although broader UTI the knowledge might point to the likelihood that UTI symptoms are caused by bacterial infections, ŞENCAN et al. (2023) in their research sent a signal that factual stand could be different and can be explained by the existence of samples showing no bacterial growth [15]. Less Prevalence of E. coli: It was observed in the study by Jafari et al. (2020) that low circulation of Escherichia coli had been found in the context of urinary tract infections, which contrasts the traditional belief that E. coli is the main culprit behind UTIs and seems to indicate a more diverse microbial world [11].

Limited Fungal Involvement: T contradicting study was provided by Neamati

2020, who offered little suggestive data on the role of fungus Candida albicans in causing UTI, as my present study that highlighted the presence of this fungus [13].

CONCLUSION:

This evidence shows the challenges in diagnosis and management of UTI in mouse, current assumptions. humanizing The discovery of "no growth" leads in turn to the need to explore the world of alternative causes for UTI symptoms, not excluding the nonbacterial nature of the latter. The presence of a diverse microbial cadre necessitates development of precision therapeutic regimens that take into consideration the distinctive pathogens detected. This research provides new data which could help the improvement of UTI diagnostics and treatment schemes to fulfill up the latter objectives with high clinical parameters.

REFERENCES:

- Al Benwan, K., & Jamal, W. (2022). Etiology and Antibiotic Susceptibility Patterns of Urinary Tract Infections in Children in a General Hospital in Kuwait: A 5-Year Retrospective Study. Medical Principles and Practice, 31(6), 562-569.
- 2. Alfouzan, W., Dhar, R., Abdo, N. M., Alali, W. Q., & Rabaan, A. A. (2021). Epidemiology microbiological and profile of common healthcare associated infections among patients in the intensive care unit of a general hospital in Kuwait: a retrospective observational study. Journal epidemiology and global health, 11(3), 302.
- 3. Ali, M. A., & Aljanaby, A. A. J. (2023, July). An Investigation of Bacterial Infections in the Urinary Tract of Babylon City Women in Iraq, a Cross-Sectional Study. In IOP

- Conference Series: Earth and Environmental Science (Vol. 1215, No. 1, p. 012066). IOP Publishing.
- 4. Aljanaby AAJ and Mohammed KJ 2020 Urinary tract infections in Al-Kufa City Iraq and phenotypic detection of antimicrobial sensitivity pattern of bacterial isolates. Int. J. Pharm. Res. 12 pp1454-1458
- Alqani, V. H. A., Meizel, M. M., & ALfuadi, A. H. H. (2023). Problem of antibiotic resistance in urinary tract infection in Al-Diwaniyah city, Iraq. Rawal Medical Journal, 48(1).
- 6. Al-Sa'ady, A. T., Mohammad, G. J., & Hussen, B. M. (2020). Genetic relation and virulence factors of carbapenemase-producing
 Uropathogenic Escherichia coli from urinary tract infections in Iraq. Gene Reports, 21, 100911.
- 7. Al-Terehi, M. N., Jawad, M. A., Kadhim, A. J., & Abed, A. S. (2021). Impact of diabetes mellitus medications in some biomarkers of covid-19 infected patients. International Journal of Pharmaceutical Quality Assurance, 184-186.
- 8. Clinical and Laboratory Standards Institute (CLSI), 2022. Performance Standards for Antimicrobial Susceptibility Testing; 30 ed. Informational Supplement. PA, USA 32(3).
- 9. Harun, A. M., Noor, N. F. M., Zaid, A., Yusoff, M. E., Shaari, R., Affandi, N. D. N., ... & Alam, M. K. (2021). The antimicrobial properties of nanotitania extract and its role in inhibiting the growth of Klebsiella pneumonia and Haemophilus influenza. Antibiotics, 10(8), 961.
- 10. Hayder HT and Aljanaby AAJ 2019 Genotypic characterization of antimicrobial resistance-associated

- genes in citrobacter freundii isolated from patients with urinary tract infection in Al-Najaf GovernorateIraq. Online J. Biol. Sci. 19 pp132-45.
- 11. Jafari, A., Falahatkar, S., Delpasand, K., Sabati, H., & Sedigh Ebrahim-Saraie, H. (2020). Emergence of Escherichia coli ST131 causing urinary tract infection in Western Asia: a systematic review and meta-analysis. Microbial Drug Resistance, 26(11), 1357-1364.
- 12. Naqid, I. A., Hussein, N. R., Balatay, A., Saeed, K. A., & Ahmed, H. A. (2020). Antibiotic susceptibility patterns of uropathogens isolated from female patients with urinary tract infection in Duhok province, Iraq. Jundishapur Journal of Health Sciences, 12(3).
- 13. Neamati, F., Khorshidi, A., Moniri, R., & Hosseini Tafreshi, S. A. (2020). Molecular epidemiology of antimicrobial resistance of uropathogenic Escherichia coli isolates from patients with urinary tract infections in a tertiary teaching hospital in Iran. Microbial Drug Resistance, 26(1), 60-70.
- 14. Salman, H. A., Alsallameh, S. M. S., Muhamad, G., & Taha, Z. (2022). Prevalence of multi-antibiotic resistant bacteria isolated from children with urinary tract infection from Baghdad, Iraq. Microbiology and Biotechnology Letters, 50(1), 147-156.
- 15. ŞENCAN, İ., KARABAY, O., ALTAY, F. A., YILDIZ, S. S., ŞİMŞEK, H., GÖZÜKARA, M. G., ... & SAYAR, M. S. (2023). Multidrug resistance in pathogens of community-acquired urinary tract infections in Turkey: a multicentre prospective observational study. Turkish Journal of Medical Sciences, 53(3), 780-790.

- Swamy, S. (2023). Missed urinary tract infection in patients with chronic recalcitrant LUTS and recurrent cystitis (Doctoral dissertation, UCL (University College London)).
- 17. Vaez, H., Kalarestaghi, H., Sahebkar, A., & Khademi, F. (2022). Prevalence of antibiotic resistance of Proteus species in urinary tract infections in Iran: A systematic review and meta-analysis. Gene Reports, 27, 101632.
- 18. Velioglu, A., Guneri, G., Arikan, H., Asicioglu, E., Tigen, E. T., Tanidir, Y., ... & Tuglular, S. (2021). Incidence and risk factors for urinary tract infections in the first year after renal transplantation. Plos one, 16(5), e0251036.