A Systematic Review on *Escherichia coli* in Urinary Tract Infections: Prevalence, Resistance Patterns, and Virulence Factors

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Abstract:- ***Escherichia coli* is commonly known as the bacteria that causes Urinary tract infections. uropathogenic *E. coli* (UPEC) causes both uncomplicated and complicated UTIs. This study analyzes the recent studies to analyze the prevalence, resistance patterns, and virulence factors of *Escherichia coli* (E. coli) isolates in urinary tract infections (UTIs). With the use of the PRISMA methodology framework, 31 articles were initially gathered and narrowed to 10 articles after applying the inclusion criteria as well as screening the papers for eligibility according to the objectives. The findings highlight that E. coli is the primary bacterial cause of UTIs across diverse age groups, with the highest incidence in individuals aged 0-20. Data on antibiotic resistance patterns, analyzed from five key articles, revealed high resistance levels in E. coli, particularly against Ampicillin, which has a rate of 82.53% from 395 *E. Coli* isolates. Additionally, the review identified various virulence factors in uropathogenic E. coli (UPEC), with the fimH gene—an adhesin associated with type 1 fimbrial pili—exhibiting the highest prevalence (94.9%). This factor enhances UPEC's ability to adhere to and invade urinary tract epithelial cells, aiding its persistence and pathogenicity. The study's findings can inform clinical practices, supporting effective antibiotic choices and the development of targeted treatments for UTIs.**

Keywords:- *Antimicrobial; UTI Patients; Isolates; Uropathogenic; Gene; Immune System.*

I. INTRODUCTION

Urinary tract infections (UTIs) are the most common urological and renal issues, defined by the presence of microbial agents in any part of the urinary system, which includes the urethra, bladder, ureters, and kidneys. The urinary system is anatomically divided into the upper tract (which consists of the kidneys and ureters) and the lower tract (comprising the bladder and urethra). Upper UTIs, in particular, present substantial risks to kidney function and may result in serious complications, such as urosepsis, which occurs when bacteria from infected kidneys enter the bloodstream (Lin et al. 2022). These infections are often associated with considerable morbidity in both hospitalized and outpatient groups.

Staphylococcus aureus, and *Proteus mirabilis*. Notably, *E. coli* is responsible for approximately 85% of community-acquired UTIs and about 50% of hospital-acquired instances. Multiple factors, including age, gender, immunosuppression, and the use of urological devices, may affect the occurrence of UTIs (Sabir et al. 2014). While UTIs can arise from a wide range of pathogens, *Escherichia coli* remains the primary causative agent, accounting for a majority of such infections (Haghighatpanah & Mojtahedi, 2019).

Notably, uropathogenic *Escherichia coli* (UPEC), which accounts for 50-90% of uncomplicated UTIs, is a particularly significant concern. UPEC includes specific strains of *E. coli* that have moved away from their typical role in the intestinal microbiota, allowing them to grow and survive in the urinary tract, where they possess various virulence factors and mechanisms that promote infection (Shah et al. 2019).

The pathogenicity of UPEC is facilitated by a range of virulence factors, such as adhesins, toxins, iron acquisition mechanisms, and immune evasion strategies, which collectively improve their ability to invade, colonize, and persist within the urinary system (Hyun et al. 2021). Key virulence factors—like fimbriae, toxins, and siderophores—are vital in the colonization and pathogenicity of UPEC strains. These specialized traits enable *E. coli* to evade host immune responses and cause a variety of diseases (Neamati et al., 2015). Moreover, UPEC's ability to inhabit the bladder and resist antibiotic treatment is closely tied to several of these virulence factors, many of which also promote biofilm development. Adhesion factors, such as Type 1 fimbriae, P fimbriae, and S fimbriae, are especially significant in this regard (Whelan et al. 2023).

Identifying the pathogens responsible for UTIs, coupled with analyzing their resistance patterns against commonly used antibiotics in clinical settings, is crucial for improving the efficiency of empirical treatment strategies. The rise of multidrug-resistant (MDR) E. coli in UTI cases significantly raises healthcare costs, morbidity, and mortality, particularly in developing countries like India. Resistance rates among uropathogenic E. coli against various antibiotics have been reported, including beta-lactams (57.4%), co-trimoxazole (48.5%), quinolones (74.5%), gentamicin (58.2%), amikacin,

(33.4%), cefuroxime (56%), and nalidixic acid (77.7%). This systematic review aims to clarify the connection between virulence factors, resistance patterns, and the prevalence of Escherichia coli as the primary cause of urinary tract infections (UTI).

II. METHODOLOGY

The Preferred Reporting Items for Systematic Reviews and Meta-analyses (PRISMA system) was used as a guideline in selecting publications about the Prevalence, Virulence Factor, and Resistance Pattern of *Escherichia coli* in Urinary Tract Infection (UTI). This study uses a systematic review design.

➤ *Data Sources*

All published articles and studies were sourced from reputable search databases and publishers, including Google Scholar, Springer Nature, ScienceDirect (Elsevier), the National Center for Biotechnology Information (NCBI), the Indian Journal of Medical Research (IJMR), and Applied Microbiology International (AMI/SfAM). These sources were carefully reviewed and selected by the researchers in accordance with the PRISMA system guidelines.

➤ *Literature Search*

The researchers used a set of keywords to collect and gather data from the search engines. These sets of keywords were used as a strategy to obtain suitable reference studies. The first set of keywords is the general terms used in the researchers' study, such as "*E.coli*", "*Escherichia Coli*", "UPEC", "Uropathogenic", "UTI", and "Urinary Tract Infection". The second set of keywords is for the factors and behavior of the bacteria in the UTI such as, "VF", "Virulence Factor", "Resistance Patterns", "resistance", and "Prevalence".

The results of the searches from the online databases were limited to scientific papers and journal articles from 2014 - 2024. The collected references were narrowed down by selecting papers based on their titles, publication dates, and content information.

➤ *Inclusion and Exclusion Criteria*

The studies included in this systematic review were selected based on the following criteria: (1) Studies addressing various factors of *Escherichia coli*; (2) Studies reporting data on the antimicrobial resistance of *E. coli* to different antibiotics; (3) Studies detailing the prevalence of *E. coli* in different countries, including patient demographics such as age and sex; (4) Studies outlining methods for identifying *E. coli* genes; (5) Studies discussing the prevalence of identified virulence factors; (6) Quantitative studies only; (7) Studies published between 2014 and 2024; (8) Studies that are scientific papers or journal articles; (9) Studies available in full text; (10) Studies published in English or translated into English; (11) Studies from any country.

Exclusion criteria included: (1) Studies focusing on non-E. coli UTI pathogens; (2) Studies not involving human subjects; (3) Studies not related to UTIs; (4) Commentaries, case reports, or systematic reviews lacking original research data; (5) studies that do not provide at least one of the key aspects (prevalence, virulence factors, or resistance patterns of E. coli in UTI); (6) Studies not published in English; (7) Studies published before 2014.

➤ *Search Results*

The initial data for search results shows a total of 832: 361 in Google Scholar, 6 in Science Direct, 223 in Springer Nature, 226 in the National Center of Biotechnology Information, 14 in the Indian Journal of Medical Research, and 2 in Applied Microbiology International. The search results from these online directories were limited to English-language reviews and research articles published between 2014 and 2024, narrowing down the initial results to 31 studies. The 31 articles excluded 1 duplicate and then underwent a final screening according to the inclusion criteria. Following an additional review of titles, abstracts, and the availability of full-text materials, 10 articles were selected for quantitative analysis. The selection process and results are illustrated in the PRISMA flow diagram (Figure 1).
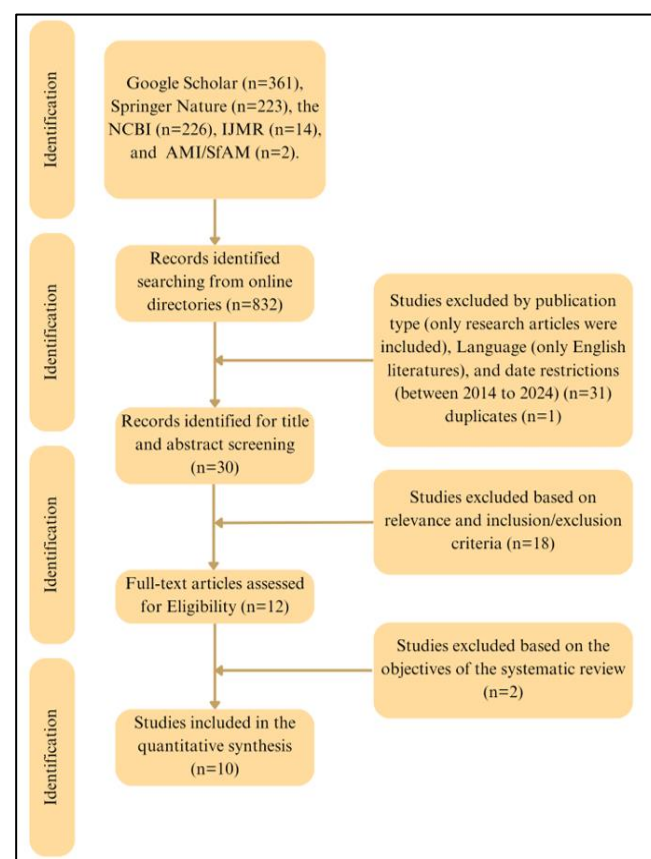

Fig 1 PRISMA Stages of Study Selection of Related Studies Flow Diagram

➤ *Data Extraction*

This study offers a systematic overview of the characteristics of *E. coli* in urinary tract infections (UTIs) and the factors influencing its presence. The studies included were systematically assessed based on their relevance to the topic. The data extracted from each study encompassed the

following: author and publication year, E. coli factors (such as virulence factors, resistance patterns, and prevalence), patient demographics (including age and sex), and the methods used to identify the virulence factors of E. coli.

➤ *Statistical Analysis*

Different selected literature is evaluated in terms of its qualitative characteristics for its suitability for quantitative analysis. Each selected journal and article indicates the *Escherichia coli* in urinary tract infection with its virulence factors that also include its results regarding prevalence and resistance patterns.

III. RESULTS AND DISCUSSION

➤ *Scientific Articles and Journals Related to the Prevalence, Resistance Patterns, and Virulence Factors of Escherichia Coli Isolates from UTI*

The retrieved articles are examined thoroughly from 31 initial articles down to 10 articles that are relevant to the interests of this review study by applying the PRISMA methodology framework. The scanning of relevant data is not only limited to studies conducted in particular region but instead taken into larger scope.

Results and outcomes from the collected papers from various sources are examined and tabulated in a comprehensive manner. Thus, the results suggest that urine samples from patients with urinary tract infections are mainly caused by *Escherichia coli,* and therefore the authors dove deep into determining the prevalence, resistance patterns, and virulence factors of *Escherichia coli* in urinary tract infection.

➤ *Prevalence of Urinary Tract Infection (UTI) Caused by Escherichia Coli*

The analysis presented in Figure 1 outlines ten scientific studies investigating the prevalence of urinary tract infections (UTIs) attributed to *Escherichia coli*, systematically categorized by age groups. According to the findings of Yun et al. (2014), UTIs emerge as the most prevalent bacterial infections among pediatric populations, with numerous affected infants exhibiting severe clinical manifestations, including lobar nephronia. Moreover, Haghighatpanah and Mojtahedi (2019) explain that while UTIs can manifest across

a broad spectrum of age cohorts, specific demographics—namely neonates, pregnant women, and the elderly—exhibit heightened susceptibility. Several factors, including age, gender, immunosuppression, and prior urological interventions, have been identified as influencing the prevalence of UTIs (Kulkarni et al. 2017).

In the summarized data illustrated in Figure 1, legends A through J represent the diverse scientific investigations reviewed. In study A conducted by Yun et al. (2014), from a total of 64 urine samples analyzed, 15 *E. coli* isolates were identified, originating from patients under the age of 18. Study B, by Kulkarni et al. (2017), reviewed 1,000 urine samples, revealing 395 *E. coli* isolates distributed across a broad age range from birth up to over 60 years old, segmented into age groups of 0-9, 10-19, 20-29, 30-39, 40-49, 50-59, and >60 years. For study C, Shah et al. (2019) identified 105 *E. coli* isolates from 1,142 samples, encompassing patients aged 18 to 87 years. In study D by Haghighatpanah and Mojtahedi (2019), 129 *E. coli* isolates were recorded from patients aged 1 to 90 years. Study E conducted by Lin et al. (2022), presented data from 907 randomly selected *E. coli* isolates, sourced from patients aged 0 to 100 years.

In addition, study F by Lee et al. (2015) identified 58 *E. coli* isolates from patients younger than 13 years. In study G, Hitzenbichler et al. (2018), reported 228 *E. coli* isolates from patients aged 20 to 70 years. Study H, conducted by Ny et al. (2019), analyzed 1,280 urine samples, identifying 775 *E. coli* isolates from patients aged 18 to 65 years. Study I by Neamati et al. (2015) found 150 *E. coli* isolates in patients aged 1 to 95 years. Lastly, in study J by Mohamed et al. (2019), 34 *E. coli* isolates were recorded from patients aged 20 to 40 years.

The comprehensive review of these ten studies presents a correlation between age and the incidence of UTI. Specifically, a frequency of twelve (12) infections was noted within the age group of 0-20 years, followed by 10 in the 21-40 age group, 9 in the 41-60 group, 7 in the 61-80 category, and a frequency of 5 recorded for the 81-100 age group. As illustrated in Figure 1, the highest prevalence of UTI was observed in the cohort aged 0-20 years, contrasting with the lowest prevalence documented in individuals aged 81-100 years.
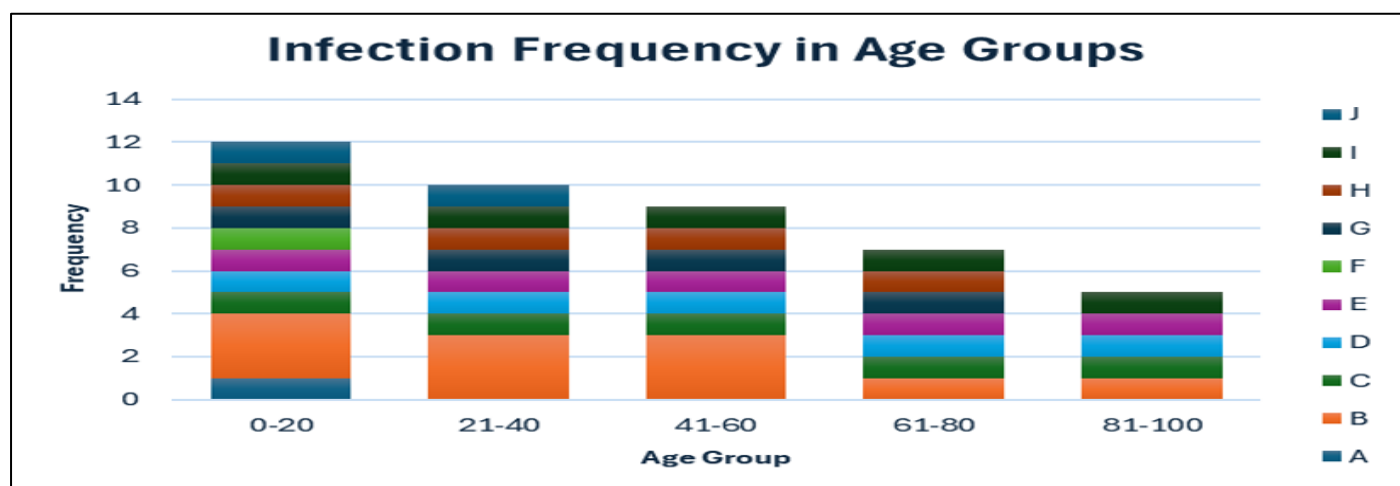

Fig 2 Infection Frequency in Age Groups Graph from Top 10 References.

➢ *Resistance Patterns of Escherichia coli in Urinary Tract Infection*

All scientific studies retrieved from different journals are carefully examined to determine the resistance patterns of *Escherichia coli* to various antibiotic drugs (See Table 1). There are a total of twenty-seven (27) antibiotic drugs listed from 5 out of 10 total articles. According to Schwartz (2015), the incidence of antibiotic resistance is increasing dramatically worldwide.

UTI, which affects numerous individuals yearly, is an infectious illness generated by bacteria with various antibiotic resistance patterns. In the collection of data (See Table 1), Amoxicillin/clavulanic acid, Ampicillin, Ciprofloxacin, and Trimethoprim/sulfamethoxazole (Yun et al. 2014; Kulkarni et al. 2017; Hitzenbichler et al. 2018; Ny et al. 2019; Neamati et al. 2015) is the most used antibiotic drug for testing of resistance of *Escherichia Coli.*

Article 1 shows the resistance patterns of *E. coli* to the following antibiotic drugs: Ampicillin (53.3%), Amoxicillin/clavulanate(6.7%), Piperacillin (33.3%), Piperacillin/tazobactam (0.0%), Cefazolin (6.7%), Cefotaxime (0.0%), Ceftriaxone (0.0%), Cefepime (0.0%), Aztreonam (0.0%), Gentamicin (26.7%), Tobramycin (0.0%), Tetracycline (13.3%), (SXT) Trimethoprim/sulfamethoxazole (20.0%), Ciprofloxacin (0.0%), and Levofloxacin (0.0%) (Yun et al. 2014).

Table 1 Resistance Patterns of *Escherichia coli* Isolated from Urine Samples from Patients with Urinary Tract Infection in Different Antibiotic Drugs

Article No.	Total number of *E. coli* isolates And Method Used	Antibiotics (%)																											Reference
		Am	Amc	Amp	Atm	Cfz	Fep	Ctx	Cfz	Cfx	Caz	Ctx	Cxm	Cip	Fo	Gm	Ipm	Lfx	Mpc	Mpm	Nil	Nit	Pip	Tzp	Sxt	Tc	TPV/r	Tpm	
1	15 Microdilution	-	6.7	53.3	0	-	0	-	6.7	-	-	-	0	0	-	26.7	-	0	-	-	-	-	33.3	0	20	13.3	0	-	Yun, K. et al., (2014)
2	395 Disk Diffusion	-	71.90	82.53	-	-	57.47	-	-	-	-	66.58	72.41	65.82	-	-	-	-	-	-	-	-	-	-	-	-	-	-	Kulkarni, S., Peerapur, B., and Sailesh, K. (2017)
3	228 MIC	90.7	19	-	-	-	-	-	-	-	-	13.8	19.1	39.4	-	-	0	-	-	0	-	6	-	5.3	45.6	-	-	-	Hitzenbichler, F. et al., (2018)
4	775 MIC	16.7	-	39.6	-	-	-	7.7	-	3.1	-	-	9.6	15.1	1.3	6.7	-	-	4.1	0	-	1.2	-	-	22.4	-	-	23.8	Ny, S. et al., (2019)
5	34 Disk Diffusion	-	-	-	-	-	-	-	-	-	-	97.1	-	32.4	-	-	-	50	-	-	-	14.7	-	-	-	-	-	-	Mohamed, M. A. et al. (2019)

• *Legend:*

Am = Amoxicillin, Amc = Amoxicillin/clavulanic acid, Amp = Ampicillin, Atm = Aztreonam, Cfz = Cefazolin, Fep = Cefepime, Ctx = Cefotaxime, Cfx = Cefoxitin, Caz = Ceftazidime, Ctx = Ceftriaxone, Cxm = Cefuroxime, Cip = Ciprofloxacin, Fo = Fosfomycin, Gm = Gentamicin, Ipm = Imipenem, Lfx = Levofloxacin, Mpc = Mecillinam, Mpm = Meropenem, Nil = Nalidixic acid, Nit = Nitrofurantoin, Pip = Piperacillin, Tzp = Piperacillin/tazobactam, Sxt = Trimethoprim/sulfamethoxazole (Cotrimoxazole), Tc = Tetracycline, TPV/r = Tobramycin, Tpm = Trimethoprim, MIC=Minimum Inhibitory Concentration Testing.

Article 2 shows the resistance patterns of *E. coli* to the following antibiotic drugs: Ampicillin (82.53%), Cefuroxime (72.41%), Amoxicillin-clavulanic acid (71.90%), Ciprofloxacin (65.82%), and Cefepime (57.47%) (Kulkarni et al. 2017).

Article 3 shows the resistance patterns of *E. coli* to the following antibiotic drugs: Ciprofloxacin (39.4%), Cotrimoxazole (45.6%), Amoxicillin/clavulanic acid (19%), Nitrofurantoin (6%), Amoxicillin (90.7%), Cefuroxime (19.1%), Ceftriaxone (13.8%), Piperacillin/tazobactam (5.3%), Imipenem (0%), and Meropenem (0%) (Hitzenbichler et al. 2018).

Article 4 shows the resistance patterns of *E. coli* to the following antibiotic drugs: Amoxicillin (16.7%), Ampicillin (39.6%), Cefotaxime (7.7%), Ceftazidime (7.3%), Cefotaxime (3.1%), Cefuroxime (9.6%), Ciprofloxacin (15.1%), Fosfomycin (1.3%), Gentamicin (6.7%), Mecillinam (4.1%), Meropenem (0%), Nitrofurantoin (1.2%), Trimethoprim (23.8%), and SXT (22.4%) (Ny et al. 2019).

Article 5 shows the resistance patterns of *E. coli* to the following antibiotic drugs: Ciprofloxacin (32.4%), Nitrofurantoin (14.7%), Levofloxacin (50%), and Ceftriaxone (97.1%) (Mohamed et al. 2019).

These results enable the researchers to evaluate the use of various antibiotic drugs and determine their ineffectiveness in treating UTIs caused by *E. coli.* These results are important to physicians as a basis for the prescription of effective antibiotics for UTI patients, preventing the emergence of new antibiotic-resistant strains by incorrect indications (Hossain. et al. 2020).

➢ *Antibiotic Drug with the Highest Resistance by Escherichia coli*

As seen in Table 1, *Escherichia coli*, commonly called *E. coli*, showed various resistant patterns after administering different antibiotic drugs using various methods of quantifying the resistance patterns—Disk diffusion, microdilution, and MIC. The highest resistance of *E. coli* is

in Ampilin, according to a study conducted by Kulkarni et al. (2017) using a disk diffusion method. It showed that 82.53% of 395 E. coli isolates (326 out of 395) are resistant to Ampicillin. Cleveland Clinic defined antibiotic resistance as when a particular bacteria changes so that antibiotic medicines can not kill or stop their growth, and as a result, bacterial infections become difficult to treat. In some cases, bacteria rapidly acquire antibiotic resistance at low antibiotic concentrations (Türkyılmaz and Darcan 2024).

➢ *Virulence Factors of Escherichia coli in Urinary Tract Infection*

A review of ten studies identified five articles focused on virulence factors and genes of uropathogenic Escherichia coli (UPEC). Key factors include fimbriae, toxins, and siderophores that help UPEC evade the host immune system. These virulence genes are found on transferable elements and pathogenicity islands, enabling gene exchange between strains. Major factors consist of adhesins that allow attachment to the urinary tract and cytotoxic factors that support persistence. Additionally, aerobactin, an iron-chelating agent, helps UPEC survive in low-iron environments (Neamati et al. 2015; Mulvey et al. 1998; Lee et al. 2015).

As shown in Table 2, aside from the virulence gene and factor, the prevalence of these and the method used are also included. For Article 1 (Shah et al. 2019), four virulence factors were determined; hemolysin, biofilm, hemagglutinin, and gelatinase. All of these factors were identified using the phenotypic method. From the 105 *E. coli* isolates, the following prevalence for Article 1 is identified: Hemolysin, 34 (32.3%); Biofilm, 65 (62%); Hemagglutinin– MRHA, 55 (52.3%), MSHA, 6 (5.7%); and Gelatinase, 0. For article 2 (Haghighatpanah and Mojtahedi 2019), four virulence factors were also identified along with several virulence genes in each factor through PCR amplification. Total *E. coli* isolates of 129 samples were determined. The prevalence of these factors and genes is; in the iron chelator factor, fyuA, 111 (86%); iutA, 32 (24.8%); iroN, 75 (58.1%); in adhesin factor, fimH, 96 (74.4%); pap G II, 92 (71.3%); papC, 72 (55.8%); in protective factor, traT, 113 (87.6%); kpsMT II, 98 (76%), and in invasion factor, usp, 88 (68.2%); cnf, 44 (34.1%). For article 3 (Lin et al. 2022), from 907 *E. coli* isolates, the prevalence of the virulence genes present are; fimH, 861 (94.9%); ompT, 703 (77.5%); aer, 570 (62.8%). For article 4 (Lee et al. 2015), from 58 *E. coli* isolates, the prevalence of the virulence factors and genes via PCR method is; Type 1 fimbriae, fimH, 58 (100%); (S family fimbriae, sfa, 58 (100%); ferrous iron transporter, feoB, 57 (98.2%). For Article 5 (Neamati et al., 2015), from 150 *E. coli* isolates, virulence genes were identified through the PCR method, traT, 111 (74%), pai, 92 (61.3).

➢ *Virulence Factor with the Highest Prevalence*

According to Table 2, the virulence factor with the highest prevalence is the type 1 fimbrial adhesin, specifically the virulence gene fimH, which appears with a prevalence of 861 (or 94.9%)

Table 2 Virulence Factors of *Escherichia Coli* Isolates from Urine Samples from Patients with Urinary Tract Infections.

Article No.	Virulence Factor	Gene	Prevalence	Method Used	Reference
1	Hemolysin		34 (32.3%)	Phenotypic	Shah, C., Baral, R., Bartaula, B., & Shrestha, L. B. (2019).
	Biofilm		65 (62%)	Phenotypic	
	Hemagglutinin	MRHA	55 (52.3%)	Phenotypic (Hemagglutination test)	
		MSHA	6 (5.7%)		
	Gelatinase		0	Phenotypic (Gelatinase test)	
2	Iron chelator	fyuA	111 (86%)	PCR amplification using a Veriti 96-well thermal cycler instrument (Applied Biosystems at Life Technologies, Foster City, CA, USA)	Haghighatpanah, M., & Mojtahedi, A. (2019)
		iutA	32 (24.8%)		
		iroN	75 (58.1%)		
	Adhesin	bmaE	35 (27.1%)		
		sfa/focDE	27 (20.9%)		
		sfaS	12 (9.3%)		
		focG	12 (9.3%)		
		afa/draBC	68 (52.7%)		

		papAH	39 (30.2%)		
		papC	72 (55.8%)		
		papEF	21 (16.3%)		
		papG II	92 (71.3%)		
		papG III	62 (48.1%)		
		fimH	96 (74.4%)		
	Protective	kpsMT II	98 (76%)		
		rfc	4 (3.1%)		
		traT	113 (87.6%)		
	Invasion	ibeA	31 (24%)		
		hlyA	39 (30.2%)		
		usp	88 (68.2%)		
		cnf1	44 (34.1%)		
3		PapG II	262 (28.9%)	PCR Method	Lin, W. H., Wang, M. C., Liu, P. Y., Chen, P. S., Wen, L. L., Teng, C. H., & Kao, C. Y. (2022)
		PapG III	125 (13.8%)		
		Sfa	65 (7.2%)		
		Foc	90 (9.9%)		
		Cnfl	183 (20.2%)		
		Aer	570 (62.8%)		
		Usp	566 (62.4%)		
		Iha	326 (35.9%)		
		OmpT	703 (77.5%)		
		Afa	481 (53%)		
		IroN	346 (38.1%)		
		FimH	861 (94.9%)		
		HlyA	209 (23%)		
		Sat	306 (33.7%)		
		K1 antigen	235 (25.9%)		
4	Type 1 fimbriae	fimH	58 (100%)	PCR Method	Lee, J. H., Subhadra, B., Son, Y., Kim, D. H., Park, H. S., Kim, J. M., Koo, S.
	S family fimbriae	sfa	58 (100%)		

	P family fimbriae	papA	23 (39.6%)		H., Oh, M. H., Kim, H., & Choi, C. H. (2015)
	a-Haemolysin	hylA	36 (62%)		
	Cytotoxic-necrotizing factor	cnfI	38 (65.5%)		
	Aerobactin protein	aer	47 (81%)		
	Afimbrial adhesins	afaC	5 (8.6%)		
	Ferrous iron transporter	feoB	57 (98.2%)		
	Yersiniabactin biosynthesis	irp2	55 (94.8%)		
	Catecholate siderophores receptor	iroN	23 (39.6%)		
	IrgA homologue adhesin	iha	30 (51.7%)		
	Escherichia coli attaching and effacing	eae	6 (10.3%)		
	Heat-stable enterotoxin b	stb	25 (43.1%)		
	Enterotoxins	lt-1	–		
5		pai	92 (61.3%)	PCR Method	Neamati, F., Firoozeh, F., Saffari, M., & Zibaei, M. (2015).
		pap	25 (16.6%)		
		traT	111 (74%)		

Virulence factors are distinct characteristics that enable *E. coli* to evade the host's immune system and cause a range of diseases (Neamati et al. 2015). In the context of urinary tract infections (UTIs), fimH, located at the tip of type 1 pili, is recognized as one of the most critical virulence factors for uropathogenic *E. coli* (UPEC). This adhesin facilitates the bacteria's adhesion to mannosylated receptors on bladder epithelial cells due to its strong affinity for urinary tract receptors. Once binding occurs, fimH plays a pivotal role in the colonization, invasion, and persistence of UPEC within the bladder (Derakhshandeh et al. 2020).

IV. CONCLUSIONS

The review of ten scientific articles highlights the significant prevalence, varied resistance patterns, and critical virulence factors associated with *Escherichia coli* in urinary tract infections (UTIs). *Escherichia coli* is established as the predominant pathogen responsible for UTIs across various demographics, particularly affecting pediatric populations and vulnerable groups such as neonates, pregnant women, and the elderly. The analysis of age-specific data reveals that UTI prevalence is highest among younger patients (0-20 years) and declines progressively with age, pointing to age as a crucial factor in UTI susceptibility. The studies consistently demonstrate that *E. coli* exhibits resistance to a range of antibiotics commonly used for UTI treatment. Ampicillin, in particular, shows high resistance rates, reaching up to 82.53% of 395 E. coli isolates (326 out of 395) are resistant to Ampicillin. These results emphasize the need for managing the selection of antibiotics carefully for treating UTIs to mitigate further resistance. Five of those ten articles are focused on the virulence factor and genes of the *E.coli*. The virulence factor with the highest prevalence is the type 1 fimbrial adhesins (fimH). Its prevalence appears to be 861 (94.9%) that adheres to the bladder epithelial cell. These results show how the adhesion of this gene plays an important role on the colonization, invasion, and persistence of the uropathogenic *E.coli* in the bladder causing urinary tract infection (UTI).

This systematic review offers insights into the prevalence, virulence factors, and resistance patterns of *Escherichia coli* in cases of urinary tract infection (UTI). It provides a valuable resource for future researchers and serves as background knowledge on this bacterium. However, ongoing research is essential to deepen our understanding of its characteristics and implications. Moreover, future findings regarding novel treatments could potentially offer alternative solutions in preventing risks associated with antibiotic resistance and improving the management of UTIs.

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