



Prevalence of *Proteus mirabilis* in Clinical Samples of UTI Patients with Rheumatoid Arthritis, Molecular Screening and Antibiotic Susceptibility Tests in Association with Interleukin-8 Analysis .

¹ZeinabJasem AL- Azzawi , ²Ashwak Basim AL-Hashimy

^{1,2} Institute of Genetic Engineering and Biotechnology for Postgraduate Studies, University of Baghdad

Received: February 20, 2025 / Accepted: July 23, 2025 / Published: November 16, 2025

Abstract: Rheumatoid arthritis (RA) is one of the more common autoimmune diseases, affecting individuals of middle age groups of the population worldwide. The exact cause of RA is not known however, initiation of disease seems to cause by an interaction among genetic susceptibility, environmental triggers, and chance. Different immunological and microbiological studies results support that there could be a link between urinary tract infections (UTI) and RA, the occurrence is found in females more than males, which mainly caused by microorganisms especially Gram-negative *P.mirabilis* bacterium aetiopathogenesis of RA which activate inflammation and production of cytokines and chemokines as IL-8 an important biomarker of the inflammatory immune response to pathogens. A total of 116 urine samples were collected from urinary tract infection patients with RA from different hospitals in Baghdad (Baghdad Teaching Hospital/ Medical City and Al-Nuaman Teaching Hospital) at a period of study from beginning of September 2023 to the end of March 2024. The clinical urine samples which collected were cultured on blood agar and MacConkey agar. Six of the specimen were identified as *P.mirabilis*, but only five isolated was confirmed depend on the automated VITEK2 system used for farther identification. Molecular methods using PCR technique targeting *16SrRNA*, the results indicated that only 5 isolates was diagnosed as *Proteus mirabilis*, further diagnosis using *UreC* gene was done, the results found that out of 6 samples only 2 were positive for identification *UreC*. The *P. mirabilis* samples were also characterized for antibiotic resistance and the results showed that *Proteus mirabilis* isolates 1,2,3 and 5 resists to 6 different antibiotics (Ampicilline/Sulbactam, Cefotaxime, Gentamicin, Tigecycline with a percentage reach (100%), but Rifampicin and Trimethoprim / Sulphamethazole with a prevalence rate of (80%) respectively. While all these isolates showed sensitivity to 7-4 antibiotics Amikacin, Ceftazidime, Ceftolozane, Ciprofloxacin with a percentage of (100%), while Piperacillin/ Tazobactam, Meropenem and Imipenem showed moderately sensitivity with a rate ranging from (80-60%) respectively, with non significant differences ($P \geq 0.05$). Haematological and immunological tests for RA patients to detect anti-pathogens antibody like Rheumatoid factor (RF+), also ESR, CRP and Anti-CCP tests were done. The results show positive reaction and increasing the levels of all these tests against pathogens. The level of IL-8 was measured and the mean level was elevated non significantly ($P \geq 0.05$) in RA patients with UTI more than control (83.74 pg/ml vs 74.09 pg/ml), also the level of IL-8 in RA patients' sera with UTI who infected by *P.mirabilis* is increased significantly, it gave mean level (126.3 pg/ml) in their serum.

Keywords: *Proteus mirabilis*, UTI, *UreC*, Antimicrobial susceptibility, Interleukin -8.

Corresponding author: (Email: zainab@uodiyala.edu.iq)

Introduction

Rheumatoid arthritis (RA) is a chronic inflammatory joint disease, which affects millions of people all around the world, with a prevalence rate ranging from 0.5 to 1%. RA is a disabling poly arthritic disease, which affects individuals of middle age groups and occurs three times more frequently in women than in men.(1,2,3). RA is characterized by an inflammation of the synovium and a destruction of cartilage and bone. Scientific researches consider RA as an immune mediated disease that could possibly be triggered by an environmental (microbial) factor in a genetically susceptible individual. Extensive evidence based on the results of various microbial, immunological and molecular studies from different parts of the world, shows that a strong link exists between urinary tract infections (UTI) and RA, this has mainly caused by *P.mirabilis* microbes.(4,5,6). *Proteus mirabilis* is a Gram-negative facultative anaerobic rod shaped bacterium. It may be found as part of the normal flora in intestine. This bacterium is not usually a pathogen, but does become a problem when it comes into contact with urea in the urinary tract, so that, the infection can spread to the other parts of the body. (4,7,8). *Proteus mirabilis* bacteria have a significant role in causing urinary tract infection which can be defined as the inflammatory response of urothelium to bacterial invasion, which is usually associated with bacteriuria and pyuria. A UTI can occur anywhere in the urinary tract which is made up of kidneys, ureters, urinary bladder, and urethra. UTI includes (urethritis, cystitis, pyelonephritis, epididymitis, prostatitis, perinephritis) and it is considered as one among the most common infectious diseases that are widely seen among all age groups of

individuals. (9,10,11). Most UTIs only involve the urethra and bladder, in the lower tract. However, UTIs can involve the ureter and kidneys, in the upper tract also. The bladder urothelium plays an important role in the host innate immune response to UTI, and the fact that women are more prone to getting UTIs, the role of estrogen's effect on the urothelial defense mechanisms and the shorter distance from the urethral opening to the bladder, increases the chance that a potential uropathogen can rise to the bladder, multiply in the urine, and invade bladder wall or rise further to the kidneys causing UTI. Also it is proposed that sub-clinical *Proteus mirabilis* urinary tract infections are the main triggering factors and that the presence of molecular mimicry and cross-reactivity between these bacteria and RA-targeted tissue antigens assists in the perpetuation of the disease process through production of cytopathic auto-antibodies(12). Several studies show that exposure to specific strains of *P.mirabilis* could play a role in early stage seropositive RA pathogenesis according to RF status (13). This bacterium is well-known for its urease enzyme production and distinctive ability to differentiate into elongated swarm cells(14). The bacterial 16S rRNA gene encodes for the ribosomal RNA small subunit(15). It contains DNA sequences that are common to all bacteria and some that are unique to each species(16,17,18). Initial studies on bacterial taxonomy and phylogeny depend on the Sanger sequencing of the most common housekeeping marker which is the 16S rRNA gene (19). Since *Proteus mirabilis* had many virulence factors that were important for inflicting UTIs, these factors had an important role to make an infection in different areas of the urinary tract including toxins like

hemolysin and its function of pore formation, biofilm and regulation of the pathogenicity (20,21). Urease enzyme which causes kidney and bladder stones, as well as its ability to form crystalline biofilms on the outer surface and in the lumen of indwelling urinary catheters(22). The MR/P fimbriae are the most well-studied fimbriae of *P. mirabilis*, which are potentially involved in adhesion to the uroepithelium, contributes to the ability of an organism to establish infection in the urinary tract (23,24) in addition the role of cellular and humoral autoimmunity play role in the development of RA when *P. mirabilis* contact with host cells lead to stimulus release of urinary cytokines and chemokines like IL-8 which important apparatuses of the inflammatory immune response to this pathogen.

This study aimed to investigate the prevalence of *P.mirabilis* bacteria in UTI patients with RA, detection of *UreC* virulence gene and examine the antibiotics sensitivity of this pathogen with measurement of IL-8 in RA patients' sera.

Materials and Methods

1.Urin Samples Collection

In this study, 216 urine specimens were collected from (100 healthy control and 116 Rheumatoid arthritis patients suffering from urinary tract infections with different age groups of both sex from different hospitals. Samples were collected from patients during the period from the beginning of September 2023 to the end of March 2024 from Baghdad Teaching Hospital/Medical City and Al Nuaman, Teaching Hospitals in Baghdad/Iraq.

2.Isolation and Identification of Bacterial Isolates

The urine samples of RA patients was cultured. Isolates were identified by methods of routine tests: depending on

their morphology and physiology characteristics on the culture media and colony morphology on MacConkey, Nutrient agar and Blood agar. Biochemical tests including; catalase test, oxidase and urease reaction and also VITEK-2 system used for more identification. The suspected bacterial isolates were re-inoculated on to MacConkey agar plates and then incubated overnight at 37 °C. A single colony was then taken and suspended in to solution. The turbidity of the bacterial suspension was adjusted with VITEK-2 densitometer (Bio Merieux) to match the McFarland 0.5 standard in 0.45% sodium chloride (25). Then the VITEK-2 (IDGNB) Kit (gram negative card) and the bacterial suspension tubes were manually loaded into the VITEK-2 system. Following steps on the software were done according to the manufacturer's instructions (Bio Merieux, France) (26-27). This system used to give good results for identification and confirmation with conventional methods (28).

3.Antimicrobial Susceptibility Testing

The antibiotic susceptibility tests were carried out for all the *P.mirabilis* isolates using VITEK-2 method in accordance to the recommendations of the manufacturer's instructions. *Proteus mirabilis* isolates were tested for antibiotic sensitivity against 13 different antibiotics: Ampicillin/ Sulbactam, Amikacin, Piperacillin/Tazobactam, Cefotaxime, Ceftazidime, Cefotriaxone, Rifampicin, Imipenem, Gentamicin, Ciprofloxacin, Tigecycline, Meropenem, Trimethoprim/Sulphamethoxazole.

4.Molecular Methods

1.DNA Extraction and PCR Protocol

The extraction of genomic DNA from *P. mirabilis* growth for all five VITEK-2 diagnosed isolates was carried out according to the protocol of (EasyPure-Genomic DNA Kit from

Transgene (China). Bacterial genomic DNA extracted from activated pure culture of *P. mirabilis* isolates were grown in brain heart broth for 24 hr. at 37 °C. (Qubit 4.0) instrument was used to detect the concentration of extracted DNA in order to detect the validity of samples for downstream application. Detection of DNA bands using agarose gel electrophoresis with concentration 1% and voltage 75 volt for 1hr.(12).

2.Detection of *P.mirabilis* 16SrRNA gene and *UreC* gene Using Conventional PCR Technique

Specific primers for 16SrRNA were used for detecting the *P. mirabilis* bacteria in addition to (*UreC*) virulence

gene, that related to urease production, as shown in (Table1). The PCR amplification mixture which used for detection of each gene include one NEB(England) Master Mix ,5X (12.5 µl), 3µl of DNA template, 1 µl (1 mM) of each forwarded and reversed primers and 7.5 µl of nuclease free water to complete the amplification mixture to 25µl (Table3). After preparing the reaction volume in PCR tube the mixture was spin down and the PCR tube placed in the PCR thermocycler. The amplification reactions was started according to the program described in (Table 2).

Table (1): The Primers Sequences and Size were Used for PCR Detection of genes

Genes name	Sequences (5→3) primer		Size (bp)	Ref.
<i>16SrRNA P.mirabilis</i>	F	5'TTAGCTAGTAGGTGGGGTAAA'3	404	In this study
	R	5'AACCAGTTTCAGATGCAATTC'3		
<i>UreC</i>	F	5'CGAGCTGTTTCTTGAAATTGA'3	470	In this study
	R	5'CCTCTAACATGCGGTACATAT'3		

Table(2): The PCR Program for (16SrRNA and UreC) Genes Amplification

Steps	Cycles	Genes amplification conditions			
		16SRNA Temp. °C	Time	UreC Temp. °C	Time
Initial Denaturation	1	94	5.00 min	94	5.00 min
Denaturation	30 (16SRNA) 30 (<i>UreC</i>)	94	30 sec.	94	30 sec.
Annealing		48	45 sec	48	45 sec
Extension		72	45sec	72	45sec
Final Extension	1	72	7 min	72	7 min

Table (3): Component of PCR Reaction for (16SrRNA and UreC) genes

Component	Volume	Final Concentration
Master Mix , 5X	12.5 µl	1X
Forward primer	1 µl	1 Mm
Reverse primer	1 µl	1 Mm
DNA template	3 µl	25 ng
Nuclease free dH2O	7.5 µl	
Final volume	25 µl	

5.Haematological and Immunological Analysis

1.Blood Sample Collection

A total of 216 (116 RA patients with UTI and 100 apparently healthy control

blood samples). Five ml of venous blood sample with drawn from each individual under aseptic technique the blood samples were collected from the same people whom urine samples were

taken. ESR test was done by the Westergreen method and three milliliter of each samples were transferred to test tube, centrifuged at 25000 rpm for 10 minutes and separated serum was divided into eppendroff tubes and immediately frozen at -20 °C till further use, for CRP ,anti-CCp and RF analysis (4).

2. Interleukin -8(IL-8) Level Measurment

The study included (58 RA patients with UTI and 30 apparently healthy control individual) to carried out the test. Serum separated from 2 ml of venous blood and examined using ELISA technique. The level of IL8, was determined for all samples included the five samples of patients sera with positive cultures of *P.mirabilis* in strict accordance with the instructions for

each ELISA kit (ELK Biotechnology Co., Wuhan- Roche -Cobas, China).

Results and Discussion

Six isolates were suspected as *P.mirabilis* depend on their morphological characteristics of the colony, smooth colorless on MacConkey and Blood agar plate with swarming phenomena and distinct fishy odor on cultured media as shown in (fig1A+B). Recent study shown closely results with (Aneta Filipiak *et al.*,2020) (29). It was also found the isolate has inability to metabolize lactose and form smooth, pale, or colorless colonies (on MacConkey agar plate). In addition, biochemical tests were done, all 6 isolates gave negative result for oxidase, catalase and positive results for urease test. Out of 6 isolates, only 5 that diagnosed by VITEK-2 system.

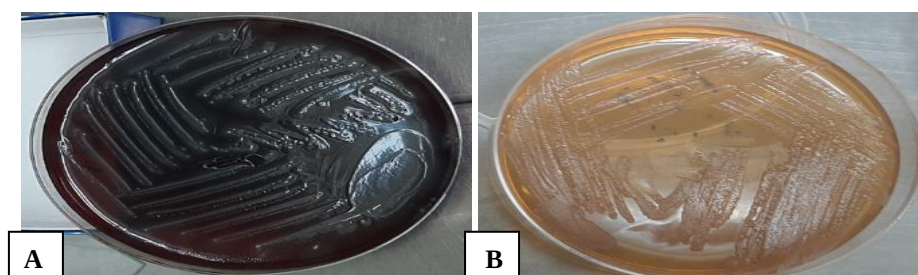


Fig.(1): The colonies of *Proteus mirabilis* on Blood agar (A) and MacConkey agar (B).

Antimicrobial Susceptibility Test

The information described in Table (4) explain the majority of the isolates showed multidrug resistance profiles. *Proteus mirabilis* isolate1,2,3 and5 resist to different antibiotics (Ampicilline/Sulbactum,Cefotaxime, Gentamicin,Tigecycline with a percentage reach(100%), but Rifampicin and Trimethoprim / Sulphamethazole with a prevalence rate of 80%) respectively. The results of the study agreed with what was informed as pathogens resistance to the antibiotic

Ampicillin-Sulbactam and Cefotaxime was high as it the important antibiotics of this group (30), also they showed resistant for Gentamicin and Tigecyclin respectively. These observations are in agreement with studies of (31,32). In addition, they showed approximately intermediate resistance for Rifampicin and Trimethoprim-sulphamethazol, those findings were in agreement with that mentioned by (33). While all these isolates showed sensitivity with a percentage of(100%), to

antibiotics (Amikacin, Ceftazidime, Ceftolozane, Ciprofloxacin, while Piperacillin/ Tazobactam, Meropenem and Imipenem showed moderate sensitivity with a rate ranging from 80-60% respectively, study agreed with the results that found the resistance pattern of the *P. mirabilis* was low rates and high susceptibility to the Amikacin, Piperacillin-Tazobactam, Ciprofloxacin, Ceftazidime and Ceftolozane antibiotics which was 100-90% respectively (34). The result of this study agree with (35,36,37) that showed moderate sensitive of bacteria to the antibiotic Imipenem and Meropenem are the antibiotics of this group with high ability and effectiveness against Gram-negative bacteria. Nonetheless, the total of isolated bacteria were sensitive to Ciprofloxacin, which disagree with the results recorded by

(38,39), while this result agrees with the researcher (40) with moderate resistant to Rifampicin, Trimethoprim and Piperacillin who test the susceptibility against antimicrobial agents for the *P. mirabilis* pathogenic isolates. The isolates did not reach statistical significance differences with ($P \geq 0.05$), which varied in different studies. This may be due to limited numbers of isolates and the antibiotics-abuse in countries from which those isolates were isolated. Researches were confirmed that Multi-drug resistance was defined as resistance to at least 3 antibiotics. All the five *Proteus* species were found to be MDR. Species identification in agreement with Jitendra Kumar *et al.*, 2013 (41). Therefore surveillance of antimicrobial resistance is essential in management and control of infections.

Table(4): The Result of Antibiotic Test for Each *Proteus mirabilis* Bacterial Isolates

Type of Isolates	AM P	AM K	PR I	CI X	CR O	CAZ	RIF	C N	IP M	CI P	TG C	SX I	ME M
<i>P. mirabilis</i> 1	R	S	S	R	S	S	R	R	S	S	R	R	S
<i>P. mirabilis</i> 2	R	S	S	R	S	S	R	R	I	S	R	R	S
<i>P. mirabilis</i> 3	R	S	S	R	S	S	R	R	S	S	R	R	S
<i>P. mirabilis</i> 4	R	S	I	R	S	S	I	R	I	S	R	I	I
<i>P. mirabilis</i> 5	R	S	S	R	S	S	R	R	S	S	R	R	S
Total Isolates =5 R=Resistance S=Susceptibility I= Intermediate													

Ampicillin=AMP, Amikacin=AMK, Piperacillin/Tazobactam=PRL, Cefotaxime=CIX, Cefotriaxon=CRO, Ceftazidime=CAZ, Rifampicin=RIF, Gentamycin=CN, Imipenem=IPM, Ciprofloxacin=CIP, Tigecycline=TGC, Trimethoprim/sulfamethoxazole=SXI, Meropenem=MEM.

Molecular Identification of *Proteus mirabilis* by 16S rRNA gene and *UreC* gene.

The total genomic DNA was extracted from five bacterial isolates that diagnosed positively by VITEK-2 system. The concentration of DNA was measured by (Qubit4.0) instrument

from Thermo fisher/USA). The results of gel electrophoresis showed the presence of DNA bands in the same level for all isolates in agarose gel, figure (3).

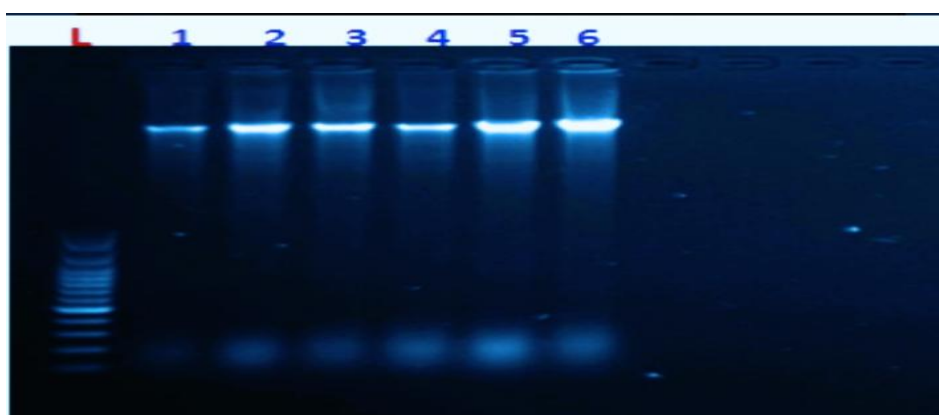


Fig.(3): Genomic DNA Extraction Electrophoresis for *P. mirabilis*(1%) agaros gel at 75 volt for 1 hr.

Further molecular diagnosis for *P.mirabilis* bacteria by using 16SrRNA gene specific primer with molecular size 404 bp , and the results were detected by gel electrophoresis on 2% agarose and exposed to U.V light in which the results indicates that all 5 isolates give the same result for biochemical diagnosis, this technique was rapid and accurate with high identification genomic rate (100%) as indicated by (GhufranJ.etall.,2019)

(42,4). Several studies referred to using of 16SrRNA for identification of *P.mirabilis* isolated,16SrRNA was described as a high discriminatory power for identification of bacteria and to differentiate between closely related genera because it exists in almost all bacteria, often existing as a gene cluster or operon, and also the function of this gene has not changed over time (43,44), figure (4).

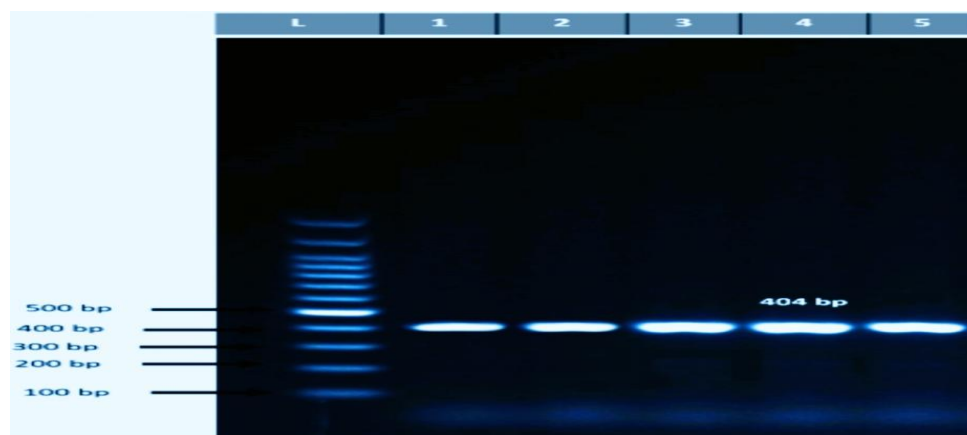


Fig.(4): The Agarose Gel Electrophoresis(2%) of PCR Amplified Products for 16sRNA gene of *P.mirabilis* isolates. Lane L: for 1000bp DNA ladder, lanes (1-5): DNA of positive result with expected size 404 bp (2 % Agarose, 75V for 1 hr)..

Clear correlation was appeared between PCR techniques and culturing methods whereas all positive samples with culturing method done with conventional PCR for identification of

all isolates of *P. mirabilis* depending on use of specific primers for *UreC* gene with molecular size (470bp), only two isolates exhibit the positive amplification results when the product

of conventional PCR was detected by using gel electrophoresis as showing in figure (5) which closely with traditional methods and VITEK-2 system, therefore this study agree with a previous study by (4,10,45). The *UreC* was the most prevalent gene and was identified in two isolates. The *UreC* gene is responsible for the elevation of pH of urine and resulting in stone formation, the study compared with another study by (46,47) that *P.mirabilis* generates urease, which catalyzes the hydrolysis of urea to ammonia and carbamate and elevates the pH of the urine to produce struvite or apatite crystals. Our results indicates the crucial role of *UreC* for the virulence of the *P.mirabilis*, regarding *UreC* gene a virulence factor, this result is in agreement with a previous study, indicating the presence of *UreC* approximately 40% among isolates obtained from patients with UTI (48,49). On the other hand, many studies demonstrate the high ability of *P. mirabilis* to produce urease (50,51) and

the study of Laurel *et al.* (52) found that all *P. mirabilis* isolates (100%) showed strong production of urease. Urease catalyzes the hydrolysis of urea to ammonia and carbonate then break down to carbon dioxide and another molecule of ammonia, as the following equation, $\text{Ureas (NH}_2\text{)}_2\text{CO} + 2\text{H}_2\text{O} \longrightarrow \text{CO}_2 + 2\text{NH}_3$

Hence, it breaks down one molecule of urea to two molecules of ammonia and one carbon dioxide molecule, that causes non physiological alkalization of urine as the pH rise, that result in sedimentation of urinary components such as Mg^{+2} and Ca^{+2} which are soluble at slightly acidic or neutral pH. As a result, struvite stones or carbonate apatite stones or both will form. Urease also assists *P. mirabilis* to develop bacteriuria, cystitis, and kidney, and bladder stones (48,53). Results agree with the studies that pointed out *UreC* as a major gene, it encodes the large subunit responsible for the production of urease enzyme of the *Proteus mirabilis* (54).

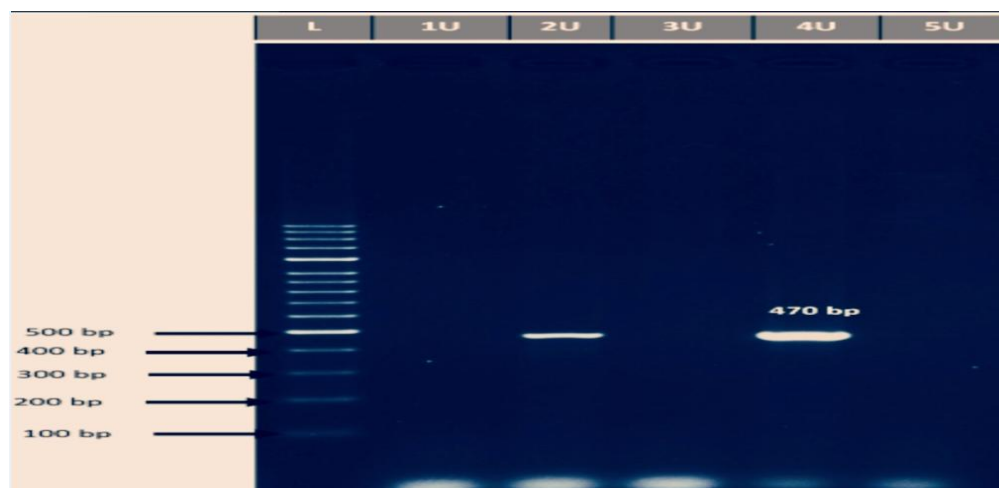


Fig.(5): The Agarose Gel Electrophoresis of PCR Amplified Products of *UreC* gene codify for urease enzyme of *P.mirabilis* isolates. Lane L: for 1000bp ladder, lanes (2,4): DNA of *P. mirabilis* positive result with expected size 470 bp (2 % Agarose, 75V for 1 hr).

Haematological and Immunological Analysis

1. Blood parameters tests

There is compelling evidence exists linking this microbe to RA, starting with recurrent sub-clinical *Proteus* UTIs and ending in the full development of RA(4). To prove the scientific logic of this possibility, many blood tests were done including (RF, ESR, CRP, RF and AcpA) all of these tests were high in the patients whom their urine are having *P.mirabilis* bacteria. Rheumatoid factor (RF) tests has shown that the pooled sensitivities of RF in the sera of RA patients infected with *P.mirabilis* as shown in Table (5A,5B) which agree with what indicated in previous study (4), among the study groups, it has been found that the mean level of the Erythrocyte Sedimentation Rate (ESR) was significantly higher between the case group than the controls (61.50mm/h vs16.97mm/h, $T=36.668$), respectively with a highly significant of ($P\leq0.01$), but the mean value of the (ESR) was increased significantly according to the bacterial infection of *P. mirabilis* (65.0mm/h $\pm$ 3.31) Similarly, the mean level of C- reactive protein (CRP) was substantially higher in the cases group compared to the controls (39.57mg/L vs9.45mg/L, $T=12.394$), respectively with highly significant ($P\leq0.01$), also the mean value of the (CRP) was elevated non significantly depend on the type of infected bacteria (75.83mg/L $\pm$ 13.22). Various metrics are utilized to measure the severity of rheumatoid arthritis (RA). These agreed with(55) that showed there was elevated (ESR, CRP and RF) as they that important in the diagnosis of inflammatory conditions .Although there is currently no clear consensus on when to administer one, the other, or both, the laboratory tests like the erythrocyte sedimentation rate (ESR)

and C-reactive protein (CRP) have been a crucial component of doctors' tools for many years. To measure acute disease activity among these tests, CRP has emerged as the most widely used serological marker (4,56). Likewise, all samples show positive results with rheumatoid factor test (RF), these findings by(23,57) has been shown that rheumatoid factor-(RF) positive patients with RA had significantly elevated levels of antibodies against *Proteus mirabilis*. In addition, the mean concentrations of anti-Citrullinated protein/peptide antibody (ACPA) were significantly higher among the cases group of rheumatoid arthritis than those of the rheumatoid arthritis free group (controls) (59.55 EU/mlvs19.20EU/ml, $T=19.015$) respectively with highly significant ($P\leq0.01$), respectively, but the mean value of ACPA was increased non significantly among infected patients with *P. mirabilis* (80/66 EU/ml $\pm$ 9.28) results are listed in Table(5A,5B). Also, T. Rasheed *et al.*, 2017, showed the citrullinated proteins recognised by ACPA antibodies was found to be highly abundant and more active within the synovial joints of patients with RA(10).The relatively constant associations of certain autoantibodies such as RFs and ACPAs with RA have been linked to *Proteus* microbes and all these might be involved in the aetiopathogenetic process and development of RA since they come before the start of disease symptoms and indicate a more severe disease course, therefore the combination of the two markers improves accuracy RA diagnosis(4).These extensive results provide a new approach to the treatment of this disease by combining the reduction of the *Proteus* microbial load together with the currently used biological approaches(10).

Table (5A): Mean Comparison of Haematological and Immunological Parameters Among Patients' Groups and Control (n=116 vs 100)

Cases	ESR	S.E.	CRP	S.E.	ACPA	S.E.
Patients	61.50	1.08	39.57	2.40	59.55	1.99
Control	16.97	0.54	9.45	0.37	19.20	0.72
T	36.668		12.394		19.015	
P-value	0.0001		0.0001		0.0001	
	(P≤0.01) Highly Significant		(P≤0.01) Highly Significant		(P≤0.01) Highly Significant	

Table (5B): Mean Comparison of Haematological and Immunological Parameters Among RA Patients Group with UTI (*P.mirabilis*) (n=116)

Cases	ESR	S.E.	CRP	S.E.	ACPA	S.E.
P.m.	65.0	3.31	75.83	13.22	80.66	9.28
T	2.28		1.182		1.012	
P-value	0.047		0.24		0.31	
	(P≤0.01) Highly Significant		P≥0.05: Non-Significant		P≥0.05: Non-Significant	

2. Interleukin-8 Levels Analysis.

The level of IL-8 differ significantly in RA patients sera with UTI according to their bacterial infection. The mean level of IL-8±SE increased non

significantly (P≥0.05) in RA patients with UTI (83.74pg/ml±6.48vs 74.09 pg/ml±14.94), (P=0.15) as shown in (Table 6).

Table(6): Mean Comparison of IL-8 Among Study Groups

Table (6). Mean Comparison of IE-6 Among Study Groups				
Cases	Conc.	S.E.	T-test	P-value
Patients =58	83.74	6.48	-1.454	0.15
Control =30	74.09	14.94		
P≥0.05: Non-Significant				

The mean level of IL-8 differ significantly in RA patients' sera who infected with *P. mirabilis* when it gave mean level (126.3 pg/ml) as shown in (Table7). Result is in agreement with a previous study by Tha'ir Abid D'asheesh *et al* ,(2020), which indicated a significant relationship between interleukin-8 (IL-8) production and urinary tract infection with *P.mirabilis* in RA patients (24,54).The level of IL-8 was influenced by bacterial virulence genes of *P.mirabilis*

and associated with ESR, RF and CRP elevation. The results agree with Naba *et al.*,2017(55) that showed a cytokine responses to urinary tract infection vary with the severity of infection and the cytokine activation is influenced by a variety of host and bacterial variable. Also IL-8 a potent neutrophil chemotactic molecule, the presence of neutrophils in the urine by bladder epithelial cells is a hallmark of UTIs. However, their action may also lead to the local tissue damage (59).

Table(7): Mean Comparison of IL-8 Parameters Among Infected Groups with *P.mirabilis*

Cases	NO	Conc.pg/ml	LSD
<i>P.mirabilis</i>	6	126.3	38.96

The IL-8 is a pro inflammatory cytokine which increased in reply to immune response for infected pathogens specially *P.mirabilis*. IL-8 is a chemokine reason to relocation of neutrophils to the apartment of irritation, causing the pyuria. in infected persons. During advanced stages of UTI and levels of cytokines will be a rise in blood and urine(24). As a result of the outcomes indicate most of *P.mirabilis* isolates showed MDR to antibiotics and two out of five isolates have positive screening for urease production gene(*UreC*) by coincide with IL-8 levels elevation in patient sera. These agree with other researchs showed that uropathogen *Proteus mirabilis* rapidly invades the bladder urothelium, its frequently forms extracellular clusters which form foci of mineral and calcium ions deposition consistent with development of urinary stones, result to elicit a robust neutrophil response, there are two virulence factors required for cluster development urease, which is required for urolithiasis, and mannose resistant *Proteus*-like fimbriae.(23). Studies of Poland showed that *P.mirabilis* produces urease and hemolysin, which contributes to the formation of a crystalline biofilm, considered to be one of the most important virulence factors of *P.mirabilis* strains, along with their ability to swarm on a solid surface, the strains which were able to form a stronger biofilm had broader antimicrobial resistance profiles. It was also found that the strongest swarming motility correlated with susceptibility to most antibiotics(54). Likewise, research indicated there is relationship of tested antibiotic resistance was observed in *P.mirabilis* with the ability of strong and moderate biofilm production and formation in the isolates (47). Also Milan Chromek *et al.*, (2005) found

that all isolates had the urease activity complicated urinary tract Infections *P.mirabilis* induce uroepithelial cells production, elicits both innate and adaptive immune responses, although an efficient host defense against urinary tract infection is reliant upon an early activation of the innate immune response like IL-8. This responses characterized by the production of a number of proinflammatory mediators, including cytokines and chemokines. Bladder and kidney epithelial cells appear to be a major source of interleukin-6 (IL-6) and interleukin-8 (IL-8) after infection with uropathogens, which are important in the development of local tissue damage Cytokine possesses a variety of proinflammatory functions, including activation of signals involved in neutrophils recruitment and production of acute phase proteins. IL-8 is a potent neutrophil chemotactic molecule and the appearance of neutrophils in the urine. Neutrophil recruitment to the site of infection has been shown to be critical for bacterial clearance from both the bladder and kidney, and the presence of neutrophils in the urine is a hallmark of UTI.(58,59). Therefore more investigation for hemolysin production virulence gene is required in other *P.mirabilis* isolates.

Conclusion

Molecular and immunological relation between the triggering aetiological factor, *Proteus mirabilis* antigens through MDR in recurrent UTIs, and damage targeted synovial tissue structures of RA patients in correlation of antibody-mediated cytotoxicity reactions and IL-8 production, RA patients should be treated early with anti-*Proteus* antibiotics as well as biological agents with restrictions for antibiotic prescription and susceptibility testing

must be done before antibiotic dispensing to avoid irreversible joint damages in RA patients.

References

- James, M. (2018). University of Illinois–Chicago, School of Medicine: What to know about urinary tract infections? Medical News Today, 2 pp.
- Fei, Y.; Huang, T.; Yang, G.; Wang, G.; Li, P.; Yang, B. and Li, J. (2021). Pathogenesis of *Proteus mirabilis* in catheter-associated urinary tract infections. *Urologia Internationalis*, 105, 354–361.
- Armbruster, C. E.; Smith, S. N.; Johnson, A. O.; De Ornellas, V.; Eaton, K. A.; Yep, A.; Mody, L.; Wu, W. and Mobley, H. L. T. (2017). The pathogenic potential of *Proteus mirabilis* is enhanced by other uropathogens during polymicrobial urinary tract infection. *Infection and Immunity*, 85, 1–23.
- Al-Hamdani, H. and Al-Hashimy, A. (2020). Molecular detection of ureC, hpmA, rsbA and mrpA genes of *Proteus mirabilis* urinary tract infection in patients with rheumatoid arthritis. *Iraqi Journal of Agricultural Sciences*, 5, 245–251.
- Ad'hiah, A. H.; Al-Mossawei, M. T.; Muhsin, H. and Mayouf, K. Z. (2015). Evaluating interferon- γ (IFN- γ) as biomarker for juvenile idiopathic arthritis and adult onset rheumatoid arthritis in samples of Iraqi patients. *Iraqi Journal of Biotechnology*, 14, 125–140.
- Smith, S. N.; Johnson, A. O.; Armbruster, C. E.; De Ornellas, V. and Eaton, K. A. (2018). The pathogenic potential of *Proteus mirabilis* is enhanced by other uropathogens during polymicrobial urinary tract infection. *Infection and Immunity*, 85, 1–23.
- Wellington, D. de O.; Barboza, M. G. L.; Faustino, G.; Inagaki, W. T. Y.; Sanches, M. S.; Takayama, R. K.; Kobayashi, E. C. V. and Rocha, S. P. D. (2021). Virulence, resistance and clonality of *Proteus mirabilis* isolated from patients with community-acquired urinary tract infection in Brazil. *Microbial Pathogenesis*, 152, 1–6.
- Abraham, S. and Shin, J. (2001). Complicated catheter-associated urinary tract infections due to *Escherichia coli* and *Proteus mirabilis*. *Clinical Microbiology Reviews*, pp. 1–55.
- Hussein, S. (2016). Biochemical and genetic study of virulence factor hemolysin of *Proteus mirabilis* isolated from urinary tract infection. *Clinical Microbiology Journal*, pp. 1–8.
- Rashid, T.; Ebringer, A. and Wilson, C. (2017). The link between *Proteus mirabilis*, environmental factors and autoantibodies in rheumatoid arthritis. *Clinical and Experimental Rheumatology*, 35, 865–871.
- Gama, C. R. B.; Pombo, M. A. G.; Nunes, C. P.; Gama, G. F.; Mezitis, S. G. E.; Suchmacher Neto, M.; Guimarães, O. R.; Geller, M.; Oliveira, L.; da Fonseca, A. S.; Sitnoveter, A.; Goldwasser, G.; Cunha, K. S. and Darrigo Junior, L. G. (2020). Treatment of recurrent urinary tract infection symptoms with urinary antiseptics containing methenamine and methylene blue: Analysis of etiology and treatment outcomes. *Research and Reports in Urology*, 12, 639–649.
- Al-Obaidi, S. A. and Al-Hashimy, A. B. (2022). Molecular screening for luxS and pml virulence genes of *Proteus mirabilis* isolated from Iraqi urinary tract infection patients. *Iraqi Journal of Biotechnology*, 21(2), 499–504.
- Newkirk, M. M.; Zbar, A.; Baron, M. and Manges, A. R. (2010). Distinct bacterial colonization patterns of *Escherichia coli* subtypes associate with rheumatoid factor status in early inflammatory arthritis. [Journal not specified].
- Girlich, D.; Bonnin, R. A.; Dortet, L. and Naas, T. (2020). Genetics of acquired antibiotic resistance genes in *Proteus* spp. *Frontiers in Microbiology*, 11, 256.
- Bloukh, S. I.; Hassan, N. A.; AlAni, R. S. and Gacem, S. A. (2021). Urinary tract infection and antibiotic resistance among pregnant and non-pregnant females in UAE. *Research Journal of Pharmacy and Technology*, 14(1), 461–465.
- Alves, D. F.; Magalhães, A. P.; Neubauer, D.; Bauer, M.; Kamysz, W. and Pereira, M. O. (2018). Unveiling the fate of adhering bacteria to antimicrobial surfaces: Expression of resistance-associated genes and macrophage-mediated phagocytosis. *Acta Biomaterialia*, 78, 189–197.
- Benga, L.; Benten, W. P. M.; Engelhardt, E.; Köhrer, K.; Gougoula, C. and Sager, M. (2014). 16S ribosomal DNA sequence-based identification of bacteria in laboratory rodents. *Laboratory Animals*, 48(4), 305–312.
- Janda, J. M. and Abbott, S. L. (2007). 16S rRNA gene sequencing for bacterial identification in the diagnostic laboratory: Pluses, perils, and pitfalls. *Journal of Clinical Microbiology*, 45(9), 2761–2764.

19. Abdul, F. R.; Raheem, I. A.; Subhi, H. T.; Fatah, H. R. and Muhammad, H. A. (2023). Immunological parameters of *Proteus mirabilis* isolates in rheumatoid arthritis patients with urinary tract infection. [Journal not specified].
20. Stankowska, D.; Kwinkowski, M. and Kaca, W. (2008). Quantification of *Proteus mirabilis* virulence factors and modulation by acylated homoserine lactones. *Journal of Medical Microbiology*, **57**, 125–131.
21. Hussein, A. R.; Khalaf, Z. Z. and Kadhim, M. J. (2017). Antibiofilm activity of bacteriocin produced by *Proteus mirabilis* against some bacterial species. *Current Research in Microbiology and Biotechnology*, **5**(3), 1071–1077.
22. Rocha, S. P. D.; Pelayo, J. and Elias, P. W. (2007). Fimbriae of uropathogenic *Proteus mirabilis*. *FEMS Immunology & Medical Microbiology*, **51**, 1–7.
23. Schaffer, J. N. and Pearson, M. M. (2016). *Proteus mirabilis* and urinary tract infections. In *Urinary Tract Infections: Molecular Pathogenesis and Clinical Management* (2nd ed.; Chap. 7).
24. D'asheesh, T. A.; Al-Kaabi, H. K. J. and Al-Khalidi, B. A. H. (2020). Investigation of IL-6, IL-8 and TNF- α among patients infected with *Proteus mirabilis* in UTI cases. *Journal of Physics: Conference Series*, **1664**, 012001.
25. Ahmed, Z. F. and Al-Daraghi, W. A. H. (2022). Molecular detection of *medA* virulence gene in *Staphylococcus aureus* isolated from Iraqi patients. *Iraqi Journal of Biotechnology*, **21**(1), 8–18.
26. Stock, I. (2013). Natural antibiotic susceptibility of *Proteus* spp.; with special reference to *P. mirabilis* and *P. penneri* strains. *Journal of Chemotherapy*, 12–26.
27. Shakir, Z. A.; Al-Draghi, W. A. H. and Mazin, H. (2023). Molecular identification, prevalence, and antibiotic resistance of *Pseudomonas aeruginosa* isolated from clinical and medical waste samples in Baghdad City, Iraq. *HIV Nursing*, **23**, 1216–1221.
28. Yahea, I. F. and Obaid, H. H. (2024). Role of DNA isolated from gut microbiota *Escherichia coli* in mice joints inflammation. *Iraqi Journal of Biotechnology*, **23**(1), 194–203.
29. Filipiak, A.; Chrapek, M.; Literacka, E.; Wawrzczak, M.; Głuszek, S.; Majchrzak, M.; Wróbel, G.; Łyseck-Gładysińska, M.; Gniadkowski, M. and Adamus-Białek, W. (2020). Pathogenic factors correlate with antimicrobial resistance among clinical *Proteus mirabilis* strains. *Frontiers in Microbiology*, **11**, 1–11.
30. Al-Khalidy, R. M. S. and Aburesha, R. A. (2023). Molecular detection of some virulence genes in *Proteus mirabilis* isolated from urinary tract infection in Iraq. *Iraqi Journal of Agricultural Sciences*, **54**(3), 709–715.
31. Kadhum, W. N. and Zaidan, I. A. (2020). Synergistic effects of chitosan–alginate nanoparticles loaded with doxycycline against multidrug resistant *Proteus mirabilis*, *Escherichia coli* and *Enterococcus faecalis*. *Iraqi Journal of Science*, **61**(12), 3187–3199.
32. Umar, M.; Yaya, A. A.; Yusuf, G.; Tafinta, Y.; Aliko, A. A.; Jobbi, D. Y. and Lawal, G. (2016). Biochemical characterization and antimicrobial susceptibility trends of *Proteus mirabilis* isolated from patients with urinary tract infections in Zaria, Nigeria. *Annals of Biological Sciences*, **4**(2), 1–8.
33. Serry, F. M.; Abdel-Latif, H. K.; Gomaa, S. E. and Abbas, H. A. (2018). Antimicrobial resistance of clinical *Proteus mirabilis* isolated from different sources. *Zagazig Journal of Pharmaceutical Sciences*, **27**(1), 57–63.
34. Maharaul, H.; Mehta, F.; Shah, K. and Asokan, A. (2021). A clinico-microbiological profile of diabetic foot patients. *Medico-Legal Update*, **21**(2), 633–638.
35. Al-Khateeb, A. F. (2014). Role of *Proteus mirabilis* DNA in comparison to *Candida albicans* DNA in rats' joints infection (M.Sc. thesis).
36. Girlich, D.; Bonnin, R. A.; Dortet, L. and Naas, T. (2020). Genetics of acquired antibiotic resistance genes in *Proteus* spp. *Frontiers in Microbiology*, **11**, 256.
37. Al-Azawy, A. N.; Al-Taai, H. R. R. and Al-Rajab, I. A. M. (2015). Biological study of *Proteus mirabilis* isolated from different clinical sources in Al-Muqdadia city. *Diyala Journal for Pure Science*, **11**(2).
38. Attallah, N. A. (2020). Investigation of some virulence factors of *Proteus mirabilis* isolated from patients with urinary tract infection by biochemical and molecular methods (M.Sc. thesis).
39. Al-Jumaily, E. and Zgaer, S. H. (2016). Multidrug-resistant *Proteus mirabilis* from urinary tract infection in Baghdad City. *International Journal of Current Microbiology and Applied Sciences*, **5**(9), 390–399.

40. Khudhair, D.; Al-Zubaidi, F. and Raji, A. (2019). The effect of board characteristics and audit committee characteristics on audit quality. *Management Science Letters*, 9(2), 271–282.
41. Pandey, J. K.; Narayan, A. and Tyagi, S. (2013). Prevalence of *Proteus* species in clinical samples, antibiotic sensitivity pattern and ESBL production. *International Journal of Current Microbiology and Applied Sciences*, 2(10), 253–261.
42. Shamkhi, G. J.; Saadedin, S. M. K. and Jassim, K. A. (2019). Detection of the prevalence of some chromosomal efflux pump genes in MRSA isolated from Iraqi patients. *Iraqi Journal of Biotechnology*, 18(3), 33–42.
43. Kamil, T. D. and Jarjes, S. F. (2021). Molecular characterization of *Proteus* spp. from patients admitted to hospitals in Erbil City. *Polytechnic Journal*, 11(2), 95–99.
44. Jacobsen, S. M.; Stickler, D. J.; Mobley, H. L. T. and Shirtliff, M. E. (2008). Complicated catheter-associated urinary tract infections due to *Escherichia coli* and *Proteus mirabilis*. *Clinical Microbiology Reviews*, 21(1), 26–59.
45. Jombo, G. T. A.; Emanghe, U. E.; Amefule, E. N. and Damen, J. G. (2012). Nosocomial and community-acquired uropathogenic isolates of *Proteus mirabilis* and antimicrobial susceptibility profiles at a university hospital in Sub-Saharan Africa. *Asian Pacific Journal of Tropical Disease*, 2(1), 7–11.
46. Cohen-Nahum, K.; Saidel-Odes, L.; Riesenber, K.; Schlaeffer, F. and Borer, A. (2010). Urinary tract infections caused by multidrug-resistant *Proteus mirabilis*: Risk factors and clinical outcomes. *Infection*, 38, 41–46.
47. Mirzaei, A.; Habibi, M.; Bouzari, S. and Asadi Karam, M. R. (2019). Antibiotic-susceptibility patterns, virulence factor profiles and clonal relatedness in *Proteus mirabilis* isolates from UTI patients in Iran. *Infection and Drug Resistance*, 12, 3967–3979.
48. Pathirana, H. N. K. S.; De Silva, B. C. J.; Wimalasena, S. H. M. P.; Hossain, S. and Heo, G. J. (2017). Comparison of virulence genes in *Proteus* species isolates from humans and pet turtles. *Iranian Journal of Veterinary Research*, 19(1), 48–52.
49. Ali, H. H. and Yousif, G. M. (2015). Detection of some virulence factor genes of *Proteus mirabilis* isolated from urinary tract infection. *International Journal of Advanced Research*, 3, 156–163.
50. Jones, B. D. and Mobley, H. L. (1988). *Proteus mirabilis* urease: Genetic organization, regulation, and expression of structural genes. *Journal of Bacteriology*, 170(8), 3342–3349.
51. Jones, S. M.; Yerly, J.; Hu, Y.; Ceri, H. and Martinuzzi, R. (2007). Structure of *Proteus mirabilis* biofilms grown in artificial urine and standard laboratory media. *FEMS Microbiology Letters*, 268(1), 16–21.
52. Laurel, S. B.; Janette, M. H.; Xin, L.; Virginia, C. L.; Stephanie, D. H.; Richard, J. H., *et al.* (2004). *Proteus mirabilis* genes that contribute to pathogenesis of urinary tract infection: Identification of 25 signature-tagged mutants attenuated at least 100-fold. *Infection and Immunity*, 72, 2922–2938.
53. Al-Atrash, A. K. M. and Al-Yasseen, A. K. (2017). Detection of ureR and ureC among *Proteus mirabilis*. *Asian Journal of Pharmaceutical and Clinical Research*, 10(8), 386–389.
54. Wang, J.-T.; Chen, P.-C.; Chang, S.-C.; Shiau, Y.-R.; Wang, H.-Y.; Lai, J.-F.; Huang, W.; Tan, M.-C.; Yang, T.-L. Y. and TSAR Hospitals. (2014). Antimicrobial susceptibilities of *Proteus mirabilis*: A longitudinal nationwide study from the Taiwan Surveillance of Antimicrobial Resistance (TSAR) program. *BMC Infectious Diseases*, 14, 486.
55. Nama, N. A.; Alsaffar, J. M. J. and Alosami, M. H. M. (2017). Serum and urine level of interleukin-8 in Iraqi reactive arthritis patients. *Current Research in Microbiology and Biotechnology*, 5(5), 1254–1257.
56. Youssef, A.; Elshabacy, F.; Abdelrahman, S. and Mohamed, T. (2015). Comparison between ESR and C-reactive protein as markers of disease activity in rheumatoid arthritis. *Egyptian Journal of Rheumatology and Clinical Immunology*, 3, 77.
57. Khudhair, S. Y. J.; Al-Badri, R.; Al-Muslih, R. and Al-Khafaji, J. T. (2014). Correlation between anti-*Proteus* antibodies and isolation rates of *Proteus mirabilis* in rheumatoid arthritis Iraqi patients. *Al-Mustansiriyah Journal of Pharmaceutical Sciences*, 14(2), 48–54.
58. Chromek, M.; Stankowska, D.; Dadfar, E.; Kaca, W.; Rabbani, H. and Brauner, A. (2005). Interleukin-8 response in human urinary tract cells induced by LPS of *Proteus mirabilis* O3 and O18. *Journal of Urology*, 173(4), 1208–1213.

59. Bien, J.; Sokolova, O. and Bozko, P. (2012). Role of uropathogenic *Escherichia coli* virulence factors in development of urinary tract infection and kidney damage. *International Journal of Nephrology*, 2012, 681473.