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By Huda J. Mohemmad

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Molecular detection of virulence genes for multi drug resistance *Klebseilla pneuminae* in patients with urinary tract infections, Thi-Qar Provenance, Iraq

Huda J. Mohemmad[1*], Semaa H.Shalal[1], Rawaa Bannay Zubairi[2]

[1]Department of Pharmaceutical Sciences, College of Pharmacy, Thi-Qar University, Iraq

[2]Sothern Technical University, Basrah Technical Institute, Iraq

*Correspondence author

Medicalresearch100@yahoo.com

Abstract

An agent that contributes to hospital acquired illnesses is *Klebsiella pneumoniae*. In community-acquired infections and illnesses of the urinary tract, it is the primary and most frequent causal agent. The strains were detected by using Analytical Profile Index (Api-20 E) and 16s rRNA techniques, fifteen trains of *K.pneumoniae* were obtained from eighteen Urine samples collected from patients in Al-Hussein Hospital, Thi-Qar Governorate, Iraq. This research sought to identify the antibiotic resistance of *K. pneumoniae* to Aztreonam, Ceftriaxone, Trimethoprim, Amikacin, Ciprofloxacin, Meropenem, and Piperacillin., the resistance was high and ranged between (86.6-100)%. The multidrug resistance percentage was 100%, in addition the investigation aimed to detect some virulence genes, (i.e. *HtrA* and *MrkA* gene) in *K. pneumonia*. The *HtrA* and *MrkA* genes were found using the PCR method, which revealed that 6 (40%) of the isolates had the HtrA gene and that all strains under study lacked the MrkA gene.

Keywords: MDR, *Klebsiella pneumoniae*, Urinary tract infections, *HtrA* gene, *MrkA* gene

Introduction

In most nations around the world, urinary tract infections rank second to respiratory tract infections in terms of frequency of health issues [1]. These infections are the most often reported bacterial illnesses in the community and have been estimated to impact up to 150 million people worldwide annually [2], affecting both men and women of all ages [3]. UTIs are a group of illnesses that can affect the kidneys, renal pelvis, or lower urinary tract alone (urethritis, cystitis, and urethrocystitis), and are all caused by the presence of microorganisms in the urine [4]. UTIs can also be divided into uncomplicated and complicated infections as a result of the infection, depending on a number of variables that may help to distinguish between these two classifications, such as the type and length of antibiotic therapy as well as a more thorough examination of the urinary tracts. *Escherichia coli* is one of the most frequent agents (around 80%) of UTI in individuals [5] and one of the most frequent causes of Gram-negative bacteremia in hospitalized patients [6]. Some of the other bacteria involved are *Proteus mirabilis*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterococcus* species, *Enterobacter* species, group B Streptococcus, and *Staphylococcus saprophyticus* [7]. The second most frequent cause of urinary tract infections after Escherichia coli is *K. pneumoniae*, which is frequently brought on by the use of indwelling catheters [8]. It is an important nosocomial pathogen that can lead to potentially lethal septic shock, pneumonia, uti, and other infections [9]. Pathogenic *Klebsiella pneumoniae* is a Gram-negative bacteria that causes wound infections, urinary tract

infections, and community-acquired illnesses. The emergence of MDR strains of this bacterium is quite alarming [10].

K. pneumoniae has the capacity to penetrate the host due to a variety of virulence factors, such as capsular polysaccharide, lipopolysaccharide, siderophores synthesis, fimbriae, and other factors such the development of urease and enterotoxin [11].

The majority of *Klebsiella* strains produce type 3 fimbriae, which are responsible for bacterial adhesion to host mucosal surfaces [12]. Type 3 fimbriae's main structural element is the *MrkA* protein, while *MrkD* adhesion determines whether type 3 fimbriae can bind to collagen molecules [13]. High temperature requirement A, or *htrA*, is a gene that plays a role in the virulence of other species including *Salmonella enterica* serovar Typhimurium, *Brucella abortus*, and *Yersinia enterocolitica*. *HtrA* mutant strains of several gram-negative bacteria have been shown to be attenuated in animal models and can also be used as vaccines [14]. Mice and macrophages with *htrA* mutations from these species had lower survival rates: Their 50% fatal doses (LD50) plummeted between 2 and 5 log units, likely due to their increased vulnerability to oxidative stress, which makes them more susceptible to the oxygen-dependent host death mechanisms. However, the methods by which the pathogenicity of *htrA* mutants is reduced are not completely understood [15,16]. In this investigation, we looked for the existence of the *mrkA* and *HtrA* genes in *Klebsiella pneumoniae*, a pathogen that is susceptible to the oxygen-dependent death mechanisms of the host.

Methods

The Isolation and Detection of *Klebsiella pneumoniae*

80 urine samples from patients with UTIs were taken between October and December 2022 when they were enrolled in Al-Hussein Hospital in Thi-Qar Province, Iraq. UTI sufferers sent their urine samples to the relevant hospital laboratory in accordance with their doctor's orders. The bulk of urine samples from adult patients were taken using the clean-catch midstream method. In the morning, the urine was preferred. The samples were maintained in a 4 °C refrigerator until processing [17] .Different bacterial strains were identified using various growth conditions, API20 E tests, and 16srRNA studies.

Antimicrobial susceptibility testing

On Muller-Hinton agar, the identified isolates underwent an antibiotic sensitivity test. Aztreonam (ATM) 30 μg, Ceftriaxone(CRO) 10 μg, Trimethoprim (TMP) 10 μg, Amikacin (AK) 30 μg, Ciprofloxacin (CIP) 10 μg, Meropenem (MEM) 10 μg, Piperacillin (PRL)100 μg (Bioanalyse,

Turkey) were used in the current study. According to CLSI 2020 recommendations, data from the susceptibility assay were interpreted [18].

DNA extraction and Purification Kit

The genomic DNA was recovered from bacterial growth using the DNA Purification Kit, Transgene /China technique in the following ways:

The bacteria were re-suspended by overtaxing after being centrifuged at 12,000 g for one minute with a 1.5 ml tube containing 1 ml of overnight Gram-negative bacteria, 100 μl of LB11, and 20 l of Proteinase K. At 55 ºC, it was incubated for 15 minutes.

If the solution isn't clear after incubation, the incubation was extended by 30 minutes with a vortex every five minutes. 400 μl of BB11 (verify that 96-100% ethanol has been supplied) were added and vortexed for 30 seconds after 20 μl of RNase A had been mixed and incubated in the tube at room temperature for 2 minutes. (At this step, there may be white flocculent precipitate or translucent gelatinous materials; this will not affect DNA extraction), The whole thing was moved to a spin column, spun at 12,000 g for 30 seconds, and the flow-through was thrown away. The flow-through was then removed after centrifuging 500 μl of CB11 for 30 seconds at 12,000 g. WB11 was diluted to 500 l, centrifuged at 12,000 g for 30 seconds, and the flow-through was discarded (make sure 96–100% ethanol was supplied).The sample was centrifuged at 12,000 g for 2 minutes to remove any leftover WB11. The spin column was contained in a 1.5 ml microcentrifuge tube that was sterile. 50–200 μl of elution buffer (preheated to 65 °C) or sterile, distilled water (pH > 7.0) were added to the center of the column. 2 minutes of room temperature incubation. After 1 minute of centrifugation at 12,000 g, genomic DNA was eluted. The isolated DNA was preserved at -20 ºC. By measuring the absorbance at (260/280 nm) on a Nanodrop spectrophotometer, the purity of the isolated genomic DNA was evaluated [19].

Primer pairs preparation

The lyophilized primers are dissolved in TE (Tris-EDTA) buffer to create a stock solution with a concentration of 100 pM/l, and the primer working solution is created by dilution with TE buffer, spinning down, and storing it at 4°C for the duration of the following day, as per the manufacturer's instructions (Alph, Canada). For each primer, (10 pM/l) Table 1.

Preparation of the PCR master mix reaction

Using (one taq quick-load) PCR Kit, a reaction of PCR master mix was created, and this master mix was carried out in accordance with the manufacturer's instructions as given in Table 2. Then, these PCR master mix reaction components that are listed below are added to typical PCR tubes that already have all of the other components required for a PCR reaction, such as Taq DNA Polymerase, dNTPs, 6 mM MgCl2, and pH 8.7. For three minutes in the Exispin vortex centrifuge, the tube was then spun. The Multigene PCR thermocycler was then transferred.

Polymerase Chain Reaction (PCR)

Using particular primer pairs listed in Table 1, conventional PCR was employed to amplify the target DNA. It consists of three sequential processes that are repeated for a predetermined number of cycles (about 35–38 cycles) in order to produce PCR result (amplicon), which can then be seen following agarose gel electrophoresis.

Table 1: Primers used in the recent study

Target Gene	Oligonucleotide Sequence (5'-3')	Size (bp.)	References
16srRNA	F:GCAAGTCGAGCGGTAGCACAG R:CAGTGTGGCTGGTCATCCTCTC	216	[20]
HtrA	**F: CGTTCTGCCAGGATGGTTCT** **R: CCCCAATGATGACATCGCCT**	1071	[21]
mrkA	**F: AGTGCTTTCACCCCCTCCT** **R:GAGTGACTGGGGTGAGCAAA**	862	[21]

Table 2: Components of PCR Master Mix preparation

Component	25µl reaction
10 μM Forward Primer	0.5 μl
10 μM Reverse Primer	0.5 μl
Template DNA	1.5 μl

OneTaq Quick-Load 2X Master Mix with Standard Buffer	12.5 µl
Nuclease-free water	10 µl
Total	25 µl

Results and Discussion

The gram-negative, lactose-fermenting bacillus *Klebsiella pneumoniae* is a rod-shaped member of the *Enterobacteriaceae* family with a distinct capsule. It is a clever pathogen that mostly attacks people with immune systems that are resistant and frequently causes nosocomial infections [22]. After performing the Biochemical and 16srRNA tests Figures 1 and 2.

In the current investigation, a total of 80 samples taken from patients with UTIs at Al-Hussein hospital in Thi-Qar origin yielded fifteen isolates of *Klibsiella pneumoniae*. *Escherichia coli*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and other species of UTI bacteria were the pathogens that were most frequently found. These findings supported the assertion that *E. coli* is the primary bacterium responsible for UTIs, which was also supported by findings from other research carried out internationally. This outcome is analogous to a study by [23] from Zakho, Iraq, where they discovered that the higher percentage of *E. coli* isolates, and another study by [24] was consistent with our findings. One of the most significant causes of bacteremia, burns, urinary tract infections, fees, and respiratory tract infections is *K. pneumoniae* [25]. *K.pneumoniae* recorded high resistance in all tested antibiotics i.e. Ampicillin (AM), Piperacillin (PRL), Trimethoprim (TMP), Amikicin (AK), Meropenem (MEM), Aztreonam (ATM), Ceftriaxone (CRO), and Ciprofloxin (CIP) the resistance percentage was ranged between 86.6%-100% Table 3, these results were in line with [26,27]. Since there are many different causes of urinary tract infections and antibiotic resistance patterns evolve over time, evaluating antimicrobial sensitivity is crucial. This will let doctors provide safe and effective

empiric treatments to halt the growth and dissemination of bacteria that cause urinary tract infections [28]. Self-medication, noncompliance with therapy, the spread of resistant isolates between people, the selling of faulty medications, and most importantly the fact that antibiotics are affordable and widely available without a prescription may all be factors in the rise in antibiotic resistance. A strain was termed MDR if it demonstrated resistance to at least three different types of antibiotics [29]. *K. pneumoniae* resistance to both classes of antibiotics may be caused by the -lactamase enzymes cephalosporinase and penicillinase, which can inactivate pencillins and cephalosprins by cleaving the drug's -lactam ring [30]. The B-lactamase gene is found on chromosomes or plasmids, the majority of which are self-transmitting plasmids. Additionally, due to a lack of penicillin binding proteins (PBPs), bacteria may change their susceptibility to the antibiotic or acquire a resistance to penicillins [31].

In *Klebsiella* isolates harboring extended spectrum -lactamase enzymes, aminoglycosides resistance was reported, according to [32]. Quinolone resistance is brought on by alterations in the antibiotic-enzyme (GyrA) binding site, while carbapenem resistance is brought on by the Carbapenemase enzymes produced by *K. pneumoniae* [33].

The MDR resistance percentage in the recent study was 100%. Multidrug-resistant Gram-negative bacterial infection is a widespread issue that is linked to higher rates of morbidity and mortality. Antibiotic overuse and abuse, particularly in patients receiving broad-spectrum or multiple medications, may result in unique changes that make the bacteria resistant to other antibiotics [34].

Recent study recorded that 6 (40%) of *K.pnemoniae* were harbor *HtrA* gene Figure 3, this is in agreement with (35), they stated that about 27% of *K.pnemoniae* from urine were carry the *HtrA* gene whereas all isolates were recorded negative results for *MrkA* gene Figure 4 and that's in some text similar to the results reported by [35], that's mean that the studied isolated may contain other genes responsible for

attachment or the primer doesn't pick up the presence gene or we must increase the sample size to get positive *MrkA* gene in *K.pnemoniae*.

Figure 1: Api 20E test for *Klebseilla pneumoniae*.

Table 3: Antibiotic Resistance for MDR *K.pneumoniae*

No.	Antibiotics	Resistance NO. (%)
1.	ATM	13 (86.6)
2.	CRO	14(93.3)
3.	TMP	14 (93.3)
4.	AK	13 (86.6)
5.	CIP	15 (100)
6.	MEM	14 (93.3)
7.	PRL	15 (100)

Figure 2: The 216 bp Primer TM from the K. pnuemuniae primer was electrophoresed on a gel at 55 ºC with 1% Agarose for 10 minutes at 100 volts before being decreased to 70 volts for 60 minutes. Following ethidium bromide staining and visualization under ultraviolet light, Lane L represents a DNA ladder (100–1500 bp), Lanes 5–39 indicate positive results, and Lane (N) represents a negative control.

Figure 3: 1071 bp are seen on the gel electrophoresis for the PCR product of the (ntrA primer) at 63°C (Agarose 1%, 10 min. at 100 voltage, decreased to 70 volts, 60 min.). Visualized under ultraviolet lighting following ethidium bromide staining. Lane L: DNA ladder (100-1500 bp), good findings were represented by lanes 5, 11, 13, 26, 27, and 39, whereas negative results were represented by lanes 6, 10, 14, 23, and 29. Lane (N) stood for the adverse control.

Figure 4: Gel electrophoresis was performed at 59°C for the PCR product of the mrkA primer, which produced no results (Agarose 1%, 10 min. at 100 volts, followed by 60 min. at 70 volts).After being stained with ethidium bromide and viewed under ultraviolet light, Lane L represents the DNA ladder (100–1500 bp), while Lane (5–39) represents the negative result. Negative control was symbolized by Lane (N).

Conclusions

The most prevalent isolates from Urinary Tract Infections were Gram Negative bacteria, high resistance to various antibiotics was recorded in the studied isolates due to random use of antibiotics. An acceptable percentage from *K.pneumoniae* contain *HtrA* genes and none of the studies isolates were contain *MrkA* gene.

Ethical approval

Approval from University of Thi-Qar (#602).

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Nil

Conflicts of interest

There aren't any competing interests.

References

1. Najar M.S , Saldanha C.L. and Banday K.A . Approach to urinary tract infections . Indihar Journal of Nephro logy . 2009 ; 19(4) : 128- 139

2. Picozzi SC, Casellato S, Rossini M, Tejada M, Costa E, and Carmignani L. Extended-spectrum beta-lactamasepositive Escherichia coli causing complicated upper urinary tract infection: Urologist should act in time. Urology Annals.2014; 6:107

3. Thass, N., M. Kumar and R. Kaur. Prevalence and antibiogram of bacterial pathogens causing urinary tract infection in a tertiary care hospital. Int. J. Med. Sci. Public Health,2019; 8: 53-57. DOI: 10.5455/ijmsph.2019.0926517102018

4. Kayser, F. H., K. A. Bienz, J. Eckert, R. M. Zinkernagel. Medical Microbiology, 1st Ed. New York. Thieme, Stuttgart ,2005.

5. Hooton, T. M. Pathogenesis of Urinary Tract I nfections: an Update. J Antimicrob Chemother .2000;46.S1: 1-7

6. Foxman, B. Epidemiology of urinary tract infections: Incidence, morbidity, and economic costs. Am. J. Med. 113 (Suppl. 1A),2002; S5–S13. 3.

7. Nicolle, L. Urinary tract infection in long-term-care facility residents. Clin. Infect. Dis. 2000; 31, 757–761.

8. Ronald A. The etiology of urinary tract infection: traditional and emerging pathogens. Am. J. Med.2002; 113

9. Hentschke, M., Wolters, M.,Sobottka, I., Rohde, H and Aepfelbacher M:RamR mutation in clinical isolates of *K. pneumoniae* with reduced susceptibility to tigecycline. Antimicrb.Agent chemother.,2010; 54: 2720-2723.

10. Moradigarav D. Evolution and epidemiology of multidrug resistant *Klebsiella pneumoniae* in the United Kingdom and Ireland. mBio.2017; 8(1):e01976-e2016.

11. Kim H, Chon J, Kim Y. Prevalence and characterization of extended-spectrum-βlactamase-producing Escherichia coli, and Klebsiella pneumoniae, in ready-to-eat vegetables. Int. J. Food Microbiol. 2015; 207: 83–86.

12 Schroll C, Barken KB, Krogfelt KA, Struve C .Role of type 1 and type 3 fimbriae in Klebsiella pneumoniae biofilm formation. BMC Microbiol,2010;10:179.

13. Langstraat J, Bohse M, Clegg S .Type 3 fimbrial shaft (MrkA) of Klebsiella pneumoniae, but not the fimbrial adhesin (MrkD), facilitates biofilm formation. Infect Immun,2001;69(9):5805-12.

14. Chatfield S, H Strahan, D Pickard, IG Charles. Molecular characterization of the PhoPQPmrDPmrAB mediated pathway regulating polymyxin "B" resistance in *Klebsiella pneumoniae* CG43. J. Biomedical Sci. 2010; 17(60): 2-6.

15.Baumler,A.J.,J.G.Kusters,I.Stojiljkovic,andF.Heffron.*Salmonella typhimurium* loci involved in survival within macrophages. Infect. Immun. 1994; 62:1623–1630.

16. Li, S. R., N. Dorrell, P. H. Everest, G. Dougan, and B. W. Wren. Construction and characterization of *Yersinia enterocolitica* O:8 high-temperature requirement (htrA) isogenic mutant. Infect. Immun. 1996; 64:2088–2094.

17. Shigemura K, Tanaka K, Okada H, Nakano Y, Kinoshita S, Gotoh A, et al. Pathogen occurrence and antimicrobial susceptibility of urinary tract infection cases during a 20-year period (1983-2002) at a single institution in Japan. Japanese Journal of Infectious Diseases.2005; 58:303

18. Clinical Laboratory Standard "CLSI" .M100 .Performance Standerds for Antimicrobial suscebtibilty test .2020; 40(1): 32-40.

19. Mai M. Zafer, Mai M. Zafer, Hadir A. El-Mahallawy, Magdy A. Amin, and Mohammed Seif El-Din Ashour. Antimicrobial Resistance Pattern and Their Beta-Lactamase Encoding Genes among Pseudomonas aeruginosa Strains Isolated from Cancer Patients. BioMed Research International;2010; 14(8): 1-8.

20. Miller, C.S.; Handley, K. M.; Wrighton, K. C.; Frischkorn, K. R.; Thomas, B. C. & Banfield ,J. F. Short-Read Assembly of FullLength 16S Amplicons Reveals Bacterial Diversity in Subsurface Sediments. PLoS ONE ,2013;8(2): e56018. doi:10.1371.

21.Kadhim,N.J., Al-Janabi,H.S.,& Kadhim,M.J. Molecular detection of Virulence Factors genes Associated with Immune Resistance in *Klebsiella pneumonia*. Medico-legal Update,2020; 20(3):1460.

22. Chaudhary, U. & Aggarwal, R. Extended spectrum lactamases (ESBL) - an emerging threat to clinical therapeutics. Indian Journal of Medical Microbiology,2004; 22(2), 75-80.

23.Polse, R.F.; Yousif, S.U. and Assafi, M.S. Prevalence and antimicrobial susceptibility patterns of uropathogenic E. coli among people in Zakho, Iraq. International Journal of Research in Medical Sciences. Int J Res Med Sci. 2016; 4(4): 1219-1223.

24.Beyene,G. and Tsegaye, W. Bacterial Uropathogens in Urinary Tract Infection and Antibiotic Susceptibility Pattern in Jimma University Specialized Hospital, Southwest Ethiopia, Ethiop J Health Sci.2011; 21(2) :142.

25.Lee, P.Y.;Costumbrado, J.;Hsu, C. and Kim, Y.H.(2012). Agarose Gel Electro phoresis for the Separation of DNA Fragments. J.Vis. Exp.2012; 62:5pp.

26. Kadher ,M.K. and Jarallah ,E.M. Detection OF β- lactamase genes in clinical Klebsiella pneumonia strains isolated from hilla hospitals. IOP Conf. Series: Journal of Physics: Conf. Series 1294 ;2019, 062073. doi:10.1088/1742-6596/1294/6/062073.

27. Kuinkel ,S. , Acharya , J., Dhungel ,B. , Adhikari,S. , Adhikari ,N. & Shrestha,U.T.Biofilm Formation and Phenotypic Detection of ESBL, MBL, KPC and AmpC Enzymes and Their Coexistence in Klebsiella spp. Isolated at the National Reference Laboratory, Kathmandu, Nepal. Microbiol. Res.2021; 12, 683–697. https://doi.org/10.3390/microbiolres12030049

28. Sime, W.T., Biazin, H. , Zeleke,T.A. & Desalegn,Z . Urinary tract infection in cancer patients and antimicrobial susceptibility of isolates in Tikur Anbessa Specialized Hospital, Addis Ababa, Ethiopia,2020; 15(12). https://doi.org/10.1371/journal.pone.0243474.

29. Magiorakos, A.P., Srinivasan, A., Carey, R.B., Carmeli,Y., Falagas, M.E., Giske, C. G, Harbarth, S., Kahlmeter, G., Olsson-Liljequist, B., Monnet, D.L. Multidrug-

resistant, extensively drug-resistant and pandrug-resistant bacteria: an international expert proposal for interim standard definitions for acquired resistance. Clin. Microbiol. Infect.,2012; 18 : 268-281.

30. Pagani, L.; Migliavacca, R.; Luzzar, F.; Giacobone, E.; Perille, M.; Micheletti, P. and Amicosante, G. Comparative activity of Pipracillia/Tazabactum agents clinical isolate of extended–spectrum Blactamases producing Enterobacteriacea. J. Clin. Microbiol., 2006; 22: 61-68.

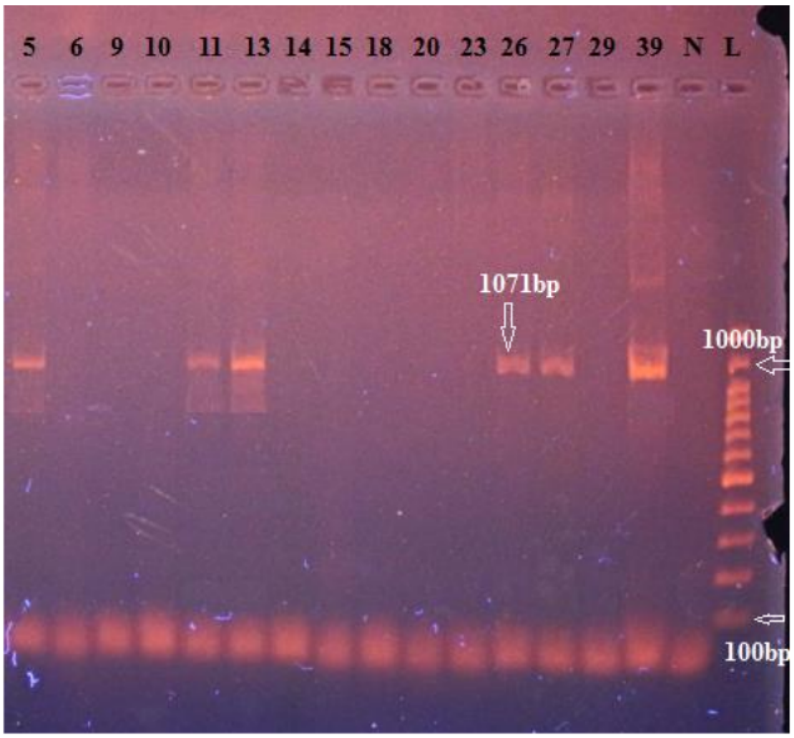
31. Bermudes, H.; Jude, F., Chaibl, E.; Arpin, C.; Labia, R. and Quantum, C. Molecular Characterization of TEM-59 (IRT-17) Anoval Inhibitor – Resistant TEM–Derived β-lactamases in Clinical Isolates of Klebsiella oxytoca. Antimicrob. Agent Chemother.,1999; 43(7): 1667-1681.

32. Feizabadi, M.; Etemadi, G. and Rahmati, M. Antibiotic resistance patterns and genetic analysis of Klebsiella pneumoniae isolates from the respiratory tract. Tanaffos.,2007; 6: 20-25.

33. Deshpande, P.; Rodrigues, C.; shetty, A.; kapadi, F; Hedge, A. and soman, R. New Delhi Metallo–B–lactamases (NDM-1) in Enterobacteriaceae: Treatment option with carbapenems compromised. journal of the Assocition of physicians of India.,2010; 58.

34. Munita, J.M. and Arias, C.A. Mechanisms of antibiotic resistance. Microbiol. spectrum.2016;4(2).

35.Kadhim ,N.J., Al-Janabi ,H.S.,and Kadhim ,M.J. Medico-legal Update, July-September 2020;20(3):1458.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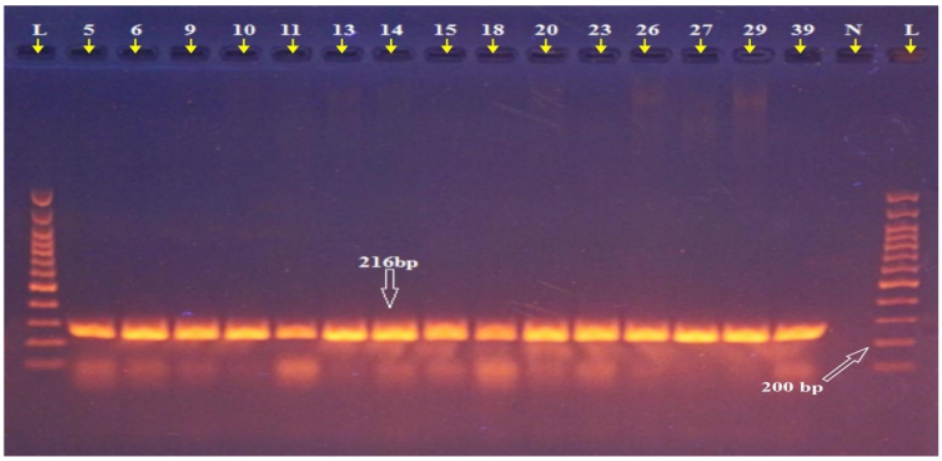
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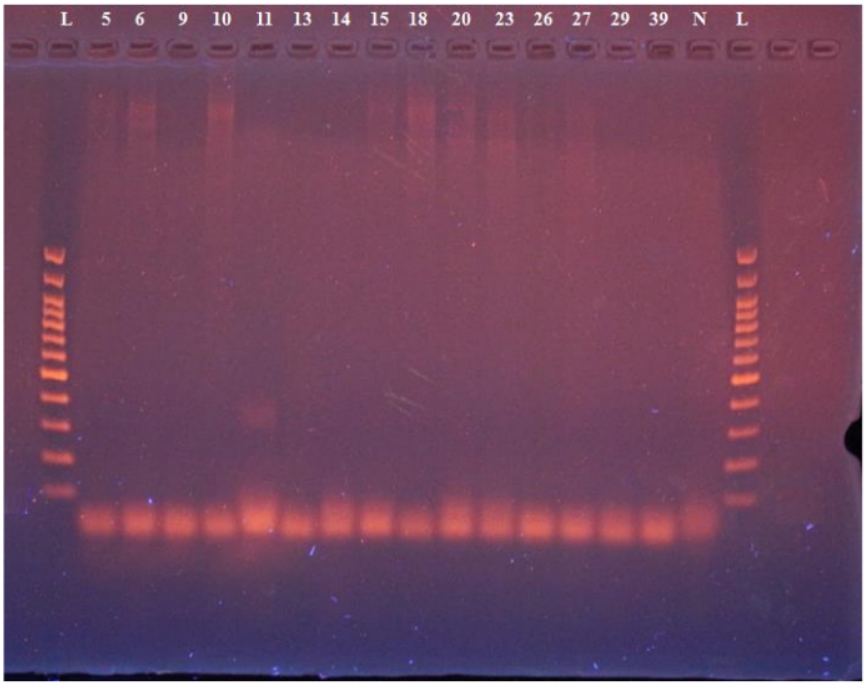
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29	C. H. Jones, T. C. Bolken, K. F. Jones, G. O. Zeller, D. E. Hruby. "Conserved DegP Protease in Gram-Positive Bacteria Is Essential for Thermal and Oxidative Tolerance and Full Virulence in Streptococcus pyogenes", Infection and Immunity, 2001 Crossref	6 words — < 1%
30	Mahde S. Assafi, Fawwaz F. Ali, Reem Fouad Polis, Nisreen Jawad Sabaly, Sozan Muhsin Qarani. "An Epidemiological and Multidrug Resistance Study for E. coli Isolated from Urinary Tract Infection (Three Years of Study)", Baghdad Science Journal, 2022 Crossref	6 words — < 1%
31	Vuotto, Claudia, Francesca Longo, Maria Balice, Gianfranco Donelli, and Pietro Varaldo. "Antibiotic Resistance Related to Biofilm Formation in Klebsiella pneumoniae", Pathogens, 2014. Crossref	6 words — < 1%

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