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The Correlation Between Capsular Serotypes and Some Virulence Factors of Classical and Hyper Virulent *Klebsiella Pneumoniae* Isolated from Urinary Tract Infections

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Abstract

Background: *Klebsiella pneumoniae* is a major pathogen in urinary tract infections (UTIs), with its virulence influenced by specific capsular serotypes and strain types.

Objectives: This study aims to investigate the association between virulence factors and capsular serotypes in classical (cKp) and hypervirulent (hvKp) *K. pneumoniae* isolates from UTIs.

Patients and Methods: A total of 280 urine samples were collected from patients at Medical City Hospital in Baghdad, Iraq, between November 2023 and May 2024. Polymerase chain reaction (PCR) was used for molecular identification and capsular serotyping. Virulence factors assessed included biofilm formation, hemolytic activity, serum resistance, and siderophore production.

Results: Among 41 classical cKp, 19 were identified as serotypes K1 or K2, while the remaining 22 belonged to other serotypes. Of the 21 hypervirulent hvkp, 18 were associated with serotypes K1, K2, K20, or K54. All isolates exhibited biofilm formation with no significant difference between cKp and hvKp. However, hvKp strains demonstrated significantly higher hemolytic activity, particularly in K1 and K2 serotypes, although differences between K1 and K2 within hvKp were not statistically significant. Serum resistance was significantly greater in hvKp strains ($p > 0.05$), with K2 showing higher resistance than K1 in both groups. Siderophore production was also significantly elevated in hvKp, with K1 strains exhibiting the highest levels.

Conclusion: Capsular serotyping may offer valuable insights for clinical diagnostics and therapeutic decision-making in UTIs caused by *K. pneumoniae*.

Keywords: Capsular serotypes, Virulence factors, *Klebsiella pneumoniae*, Hypervirulent, UTI.

Introduction

Urinary tract infections (UTIs) are among the most prevalent healthcare-associated infections, especially in immunocompromised patients. *K. pneumoniae* is a major opportunistic pathogen responsible for a significant proportion of these infections. The bacterium exists in two distinct forms: classical *K. pneumoniae* (cKp), which is commonly associated with nosocomial infections, and hypervirulent *K. pneumoniae* (hvKp), which can cause severe, life-threatening community-acquired infections even in otherwise healthy individuals. The pathogenic potential of *K. pneumoniae* is largely driven by multiple virulence factors that enable the bacterium to colonize host tissues, evade immune responses, and cause systemic infections. These virulence traits include capsular polysaccharide

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production (crucial for immune evasion), biofilm formation (important for persistence on medical devices), hemolysin activity (which contributes to tissue damage), serum resistance (which enhances survival in host blood), and siderophore production (which facilitates iron acquisition) (1–3). Colonization typically begins in the gastrointestinal tract but can extend to the respiratory, circulatory, and urinary systems (4). Biofilm development on indwelling medical devices such as catheters further increases the risk of persistent infections (5). Capsular serotypes, particularly K1, K2, K20, and K54, have been strongly linked to increased virulence in hvKp strains (6). These serotypes not only provide resistance to phagocytosis and complement-mediated killing but are also believed to influence the activity and prevalence of other virulence factors. The primary aim of this study is to explore the relationship between specific capsular serotypes and the activity of key virulence traits-namely biofilm formation, hemolytic activity, serum resistance, and siderophore production-in both cKp and hvKp isolates from UTIs.

Patients and Methods

Patients and isolation of bacteria: A total of 280 urine samples were collected from Medical City Hospital, Baghdad Iraq, in period extending from November 2023 to May 2024. Urine samples from patients with urinary tract infection (UTI) symptoms-including dysuria, burning sensation, and hematuria-were collected following clinical examination by a physician. The samples were obtained from both male and female patients aged 18 to 65 years. Each sample was cultured on nutrient agar, MacConkey agar, blood agar, and UTI medium (HiMedia, India), and incubated at 37 °C for 24 hours to facilitate bacterial growth for further analysis. Relevant patient data, including name, age, sex, smoking status, and history of antibiotic use, were recorded.

Inclusion criteria: Patients with UTI symptoms.

Exclusion criteria: Patient treated with antibiotics for UTIs for less than 1 month.

Identification of bacteria: Patient urine samples were cultured on MacConkey agar, nutrient agar, blood agar, and UTI medium (HiMedia, India), to facilitate bacterial growth. The cultures were incubated at 37°C for 24 hours. Following incubation, turbidity was adjusted to match the 0.5 McFarland standard and measured using a DensiChek™ Plus visible spectrophotometer. The standardized bacterial suspension was then used to inoculate the VITEK 2 system (bioMérieux, France). Identification of bacterial species and strains was carried out using the VITEK 2 compact system specialized software using GN kit) Catalog no. 21341).

String test: The string test was employed to differentiate hypervirulent hvKp from cKp. A positive result was indicated an inoculation loop could pull a viscous string of bacterial colonies on a blood agar plate extending 5 mm or more. If the string measured 5 mm or less, or was absent entirely, the result was considered negative (7).

Genomic DNA extraction: Genomic DNA was extracted from Klebsiella pneumoniae isolates using the Wizard® Genomic DNA Purification Kit (Promega, USA), following the manufacturer's instructions. Specific primers targeting capsular serotype-related genes were used, including magA (mucoviscosity-associated gene A, associated with the K1 serotype), K2wzy (capsular polysaccharide synthesis gene specific to the K2 serotype), K5wzx (polysaccharide transport gene specific to the K5 serotype), wzyK20 (biosynthesis gene for the K20 capsular serotype), and wzxK54 (transport gene associated with the K54 serotype). Polymerase chain reaction (PCR) was performed using primers from Alpha (USA) as listed in Table 1. The PCR conditions included an initial denaturation at 95 °C for 5 minutes, followed by 35 cycles of denaturation at 95 °C for 20 seconds, annealing at

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58–62 °C for 30 seconds (depending on primer Tm), and extension at 72 °C for 30 seconds. A final extension step was carried out at 72 °C for 5 minutes. Amplified PCR products were separated by electrophoresis on a 2% agarose gel, and the presence of bands at the expected sizes indicated successful amplification of the target genes.

Table 1. PCR primers used for the detection of Capsular serotype.

Primer Name	Seq.	Size	Tm. (°C)	Reference
MagAF1 MagAR1	5' GGTGCTCTTTACATCATTGC 3' 5' GCAATGGCCATTTGCGTTAG 3'	1,283	62	(8)
K2wzy-F1 K2wzy-R1	5'GACCCGATATTCATACTTGACAGAG3' 5'CCTGAAGTAAAATCGTAAATAGATGGC3'	641	60	(9)
K5wzxF360 K5wzxR639	5'TGGTAGTGATGCTCGCGA 3' 5'CCTGAACCCACCCCAATC 3'	280	59	(10)
wzyK20F wzyK20R	5'CGGTGCTACAGTGCATCATT 3' 5'GTTATACGATGCTCAGTCGC 3'	741	58	
wzxK54F wzxK54R	5'CATTAGCTCAGTGGTTGGCT 3' 5'GCTTGACAAACACCATAGCAG 3'	881	60	

Biofilm assay: Bacterial cultures were incubated overnight in LB broth at 37 °C for 24 hours. The culture was then diluted to a 0.01 McFarland standard. A volume of 50 µl of the adjusted bacterial suspension was added to 150 µl of LB broth in each well of a tissue culture plate (96 well), followed by incubation at 37 °C for another 24 hours. After incubation, the medium was gently removed, and each well was rinsed twice with µL of 0.2% crystal violet solution was added to each well and incubated for 10 minutes at room temperature (25°C). Wells were then washed 2–3 times with distilled water and allowed to air dry. Finally, 200 µl of 95% ethanol was added to dissolve the stain. The optical density (OD) was measured at 630 nm, and the results were interpreted accordingly (11).

Siderophores production: Both qualitative and quantitative methods were employed to evaluate the siderophore production of various *Klebsiella pneumoniae* isolates. The assay was conducted following a modified version of the method described by Hu and Xu (2011) (12). To prepare the agar plates, 100 mL of Chrome Azurol S (CAS) reagent was combined with 900 mL of sterile LB agar medium. Four different bacterial isolates were spot-inoculated onto each plate. A control plate was also prepared using standard positive and negative control strains- *Acinetobacter baumannii* (positive control) and *Proteus spp*. (negative control). Following inoculation, the plates were incubated aerobically at 28°C for five to seven days. Siderophore production was indicated by the development of an orange halo surrounding the bacterial colonies, including those of the positive control strain. The presence of this color change signified a positive result for siderophore activity, reflecting the ability of the strain to chelate iron in the growth medium (13).

Serum resistance: Serum resistance was examined using the method outlined by (14). In 96-well polystyrene, round-bottomed microtiter plates (Greiner bio-one), 75 µL of normal human serum drawn from healthy volunteers was mixed with 25 µL of inoculum containing 2.5 x 106 colony-forming units (CFU)/mL of a mid-log phase culture. The combination was incubated for 1, 2, and 3 hours at 37°C. Following incubation, the cell count was ascertained using standard plating in LB agar and 10-fold serial dilutions.

Hemolysis: To assess the hemolytic activity of bacterial isolates on previously prepared red blood cells (RBCs), 0.2 ml of an 18-hour culture

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grown in brain heart infusion (BHI) broth was added to 2 mL of fresh BHI broth, along with 0.2 ml of a 5% standardized suspension of human erythrocytes. The mixture was incubated at 37 °C for 3 hours, then centrifuged at 1500 × g. Hemoglobin release in the supernatant was quantified by measuring optical density at 540 nm using a spectrophotometer. A sample blank was prepared using the same components, but it was measured immediately before incubation (time zero). The positive control consisted of 2.2 ml of 1% Triton X-100 mixed with 0.2 ml of 5% RBC suspension, incubated for 3 hours. The negative control consisted of 2.2 mL of Ringer's solution (normal saline) and 0.2 mL of the same RBC suspension, both of which were incubated for 3 hours. Blanks for both controls were similarly composed but measured before incubation (at zero time). All tests, including those for the bacterial isolates and both controls, were performed in triplicate (15).

Statistical Analysis

Version 23 of the SPSS software was used to analyze the data. The frequency and proportion of capsular serotypes and virulence factors among *K. pneumoniae* isolates were compiled using descriptive statistics. The Independent Samples t-test and the Chi-square test for categorical variables (such as serotype distribution and biofilm formation strength) were used to compare classical (cKp) and hypervirulent (hvKp) strains. Within each group (cKp and hvKp), variations between serotypes (K1, K2, etc.) were assessed using one-way ANOVA.

Results

Bacterial isolation: A total of 280 urine samples were collected from patients with UTI symptoms such as itching, dysuria and burning sensation. Culturing of urine samples revealed that 209 out of 280 (74.64%) samples were positive for bacterial growth, including various species of bacteria. Bacterial growth was obtained from ordinary culture media including blood agar media, nutrient agar media, MacConkey agar media and chromogenic agar UTI media. The vast majority of isolated bacteria were Gram negative bacteria, 191/209(91.39%), while Gram positive was 18/209(8.61 %). Females were more infected with UTI than males, mean age 54±12 years. Primary bacterial diagnosis is based on colony morphology, blood hemolysis, lactose fermentation, and gram staining. Biochemical tests such as Catalase, Oxidase, and IMViC are then used to further identify the bacteria, and the final diagnosis is made using the VITIK 2 Compact System, which confirms the identification of bacteria based on 49 biochemical tests. *Escherichia coli* was the most predominant bacteria isolated from patients with UTI, then *Klebsiella pneumoniae*. Other bacterial species included *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Enterococcus faecalis*, and finally less bacterial species frequency was *Acinetobacter baumannii* as in Table 2.

Table 2. Identification of Bacterial Species

Bacterial Species	Number	%
Klebsiella pneumoniae	62	22.14
E. coli	75	26.79
Pseudomonas aeruginosa	14	5.00
Proteus mirabilis	31	11.07
Acinetobacter baumannii	9	3.21
Enterococcus faecalis	18	6.43
No growth	71	25.36
Total	280	100

Serotyping: A total of 62 *Klebsiella pneumoniae* isolates were identified, of which 83.8% were obtained from female patients and 17.2% from male patients. Based on the results of the modified loop test, hypervirulent phenotypes were found in 21 (33.9%) of the 62 isolates. A total of 66.1% of cKp strains were isolated. The proportion of patients with cKp was much higher. Sex did not associate with the positive string test (both P >0.05), Table 3.

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Table 3. Distribution of cKp and hvKp Isolates by Patient Sex.

Sex	cKp (n = 41)	hvKp (n = 21)	Total (n = 62)
Male	6 (14.6%)	4 (19.0%)	10 (16.1%)
Female	35 (85.4%)	17 (81.0%)	52 (83.9%)
Total	41 (100%)	21 (100%)	62 (100%)

Detection for capsular genes: The capsular encoding genes of *K. pneumoniae* was detected using PCR, cKp stains only 19/41 belong to serotype K1, K2 and the other 22/41 may related to other serotype isolates while hvKp strains showed 18/21 isolates belong to K1, K2, K 20, K54 and 3/21 belong to another serotype, as in Table 4 and Figure 1, and 2.

Table 4. Molecular identification of capsular genes in *K. pneumoniae*.

Tested serotypes	k1 (%)	k2 (%)	k20 (%)	k54 (%)	Another serotype	Total
cKp (%)	11(57.9)	8(42.1)	0	0	22	41
hvKp (%)	7(39)	9(50)	1(5.5)	1(5.5)	3	21

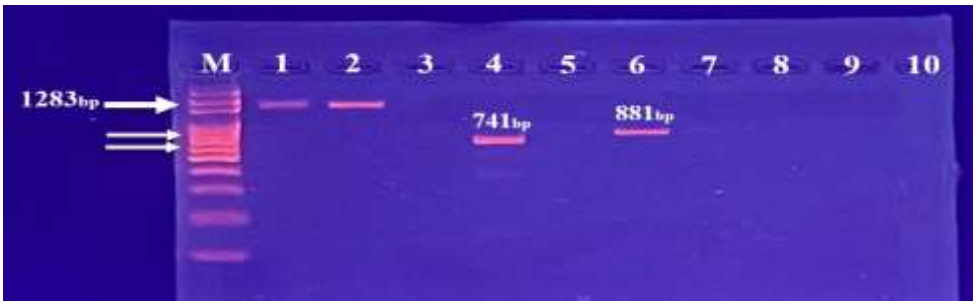

Figure 1. Multiplex PCR amplification of Klebsiella pneumoniae isolates visualized on 2% (w/v) agarose gel. Lane M: DNA ladder (100–1500 bp); Lanes 1–2: positive for the magA (K1) gene (1283 bp); Lane 4: positive for the wzyK20 gene (741 bp); Lane 6: positive for the wzxK54 gene (741 bp).

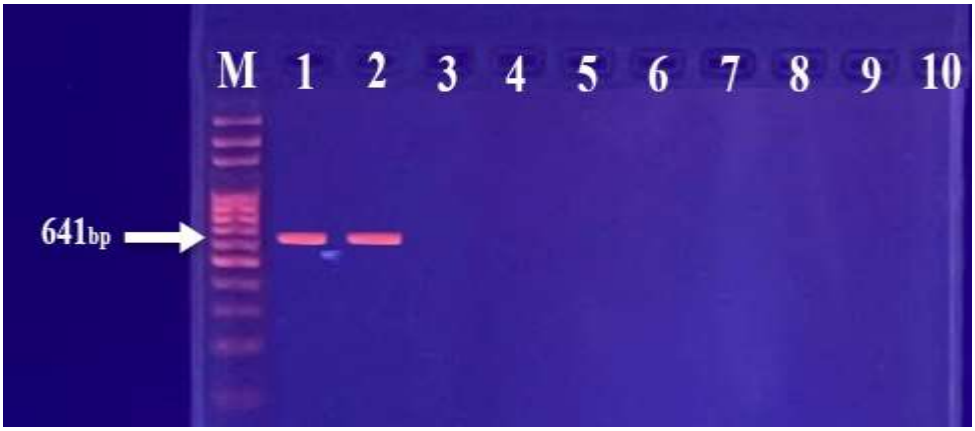

Figure 2. PCR amplification of Klebsiella pneumoniae isolates visualized on a 2% (w/v) agarose gel. Lane M: DNA ladder (100–1500 bp); Lanes 1–2: positive for the K2wzy gene (641 bp).

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Biofilm formation: The results showed all strains have the ability for biofilm formation either strong, moderate or low, and there were no significant differences between cKp and hvKp, Table 5.

Table 5. Biofilm profile.

Biofilm profile distribution				
Isolates	**Tested serotypes**	**L**	**M**	**H**
cKp	K1 N (%) =11	4(36)	7(63.6)	0(0)
	K2 N (%) =8	2(25)	6(75)	0(0)
hvKp	K1 N (%) =7	3(42.8)	3(42.8)	1(14.4)
	K2 N (%) =9	1(11.1)	7(77.8)	1(11.1)
	K20 N (%) =1	0 (0)	1 (100)	0 (0)
	K54 N (%) =1	0 (0)	0 (0)	1 (100)
*L: Low, M: Moderate, H: High				

Hemolysis: hvKp demonstrated significantly greater hemolytic activity than cKp. However, no significant differences were detected between the K1 and K2 serotypes within the hvKp group, as illustrated in Figure 3.

Serum resistance: In the current study human serum was used to test the *K. pneumoniae* serum resistance. The serum resistance p value ≤ 0.05 of hvKp was much higher than that of cKp, and for both cKp and hvKp, the serum resistance of K2 was significantly higher than that of K1, Figure 4.

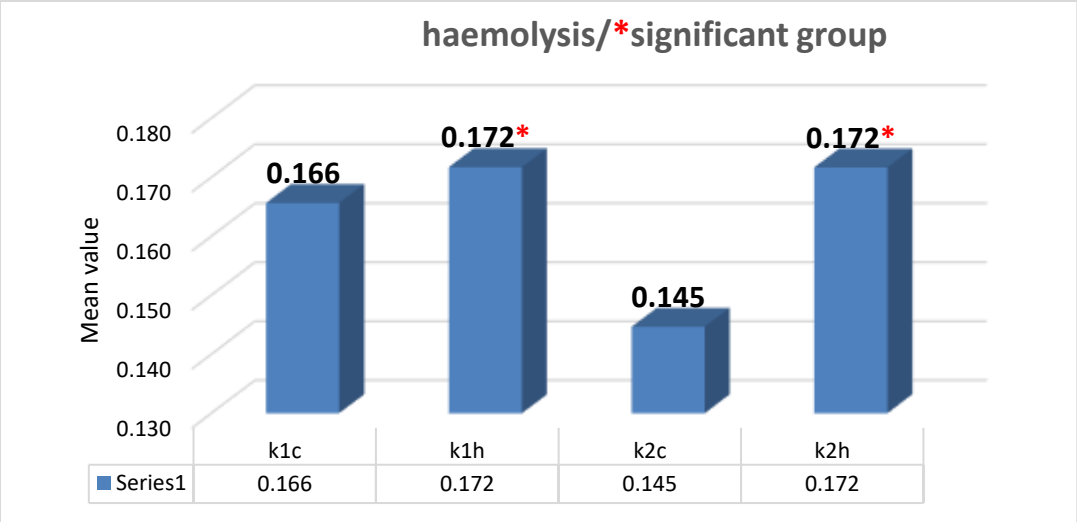

Figure 3. Hemolysis activity for cKp and hvKp serotypes.

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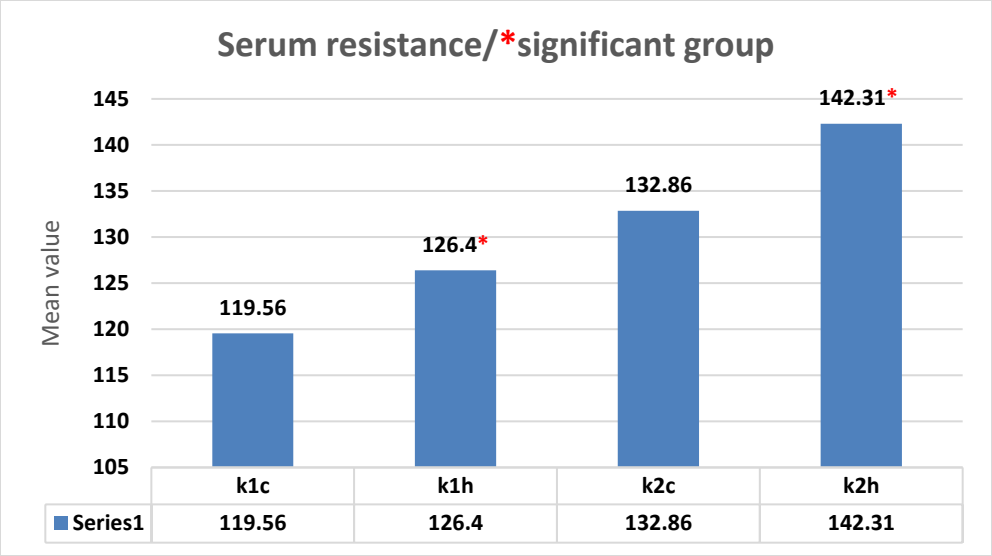

Figure 4. Serum Resistance for cKp and hvKp serotypes.

Siderophore production: To find siderophores, a CAS agar plate was used. Siderophore production was demonstrated by all isolates and detected by diameter of production zone. In the current study, with a significant increase at p value $p \leq 0.05$ in siderophore production of hvKp compared to cKp and a significant increase in siderophore production of K2 compared to K1 for hvKp, Figure 5, and 6.

Figure 5. Siderophore production positive phenotype.

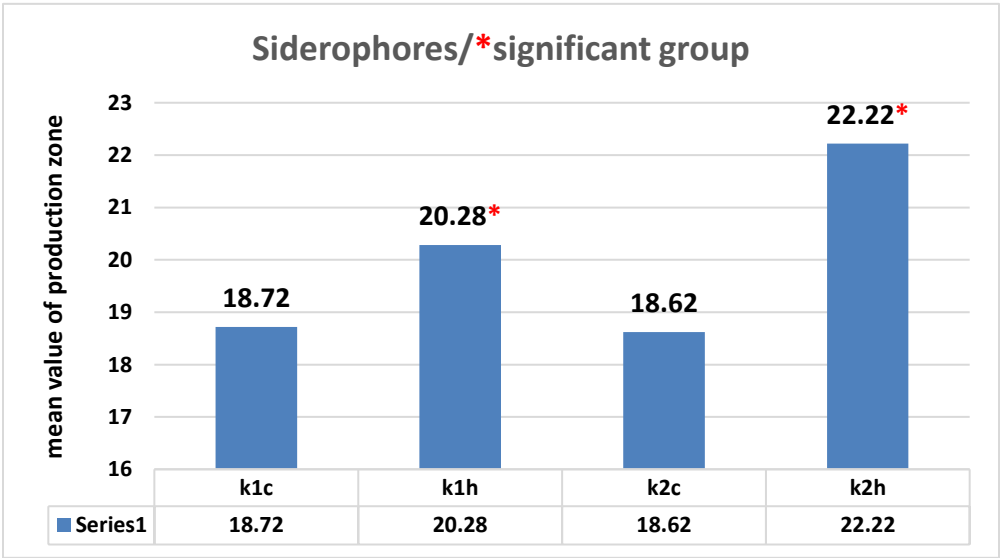

Figure 6. Siderophore production.

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Discussion

The majority of isolated bacteria being Gram negative and Female were more infected with UTI than male. The high prevalence of UTI in females compared with males may be due to the proximity of the anus to the shorter urethra tube in females. Additionally, the female's urethral tube is small, which reduces the organism's travel distance to the bladder. Low socioeconomic position, poor hygiene, and a lack of resources all contribute to the increased risk of UTIs (16). In the current study the most prevalent causative agent of UTI was *E. coli* followed by *K. pneumoniae* and less prevalence bacteria was *Acinetobacter baumannii* that related to nature *E.coli* which possesses a virulence factors enable the bacteria to invade the urinary tract and adapted to survive in such environments. The percentage was accepted as proved by previous study such as a local study in Baghdad included 62 patients with UTI concluded the most prevalence bacteria was *E. coli* (17). While a study in Nepal aimed to determine the prevalence of UTIs among patients with chronic kidney disease (CKD), included four hundred eighty-two midstream urine samples were collected from CKD patients they found 15.8% of the 482 CKD patients had a positive culture, and the majority were in the older age range. *K. pneumoniae* accounted for 11.84% of the bacterial isolates, *Pseudomonas aeruginosa* for 15.80%, Enterococcus species for 15.80%, while the majority for *E.coli* as estimated 50% (18). *K. pneumoniae* is an opportunistic pathogen, with hypervirulent strains exhibiting greater virulence than cKp, making it a rapidly emerging clinical threat. It is commonly associated with a range of severe infections, including liver abscesses, pneumonia, osteomyelitis, endophthalmitis, and meningitis. In some cases, the infection can involve multiple sites or progress to metastatic dissemination (19). The novel hypervirulent and hypermucoviscous *K. pneumoniae* phenotype (Hmv) a physical characteristic where colonies appear mucoid and produce a viscous string >5 mm, which is primarily associated with serotypes K1 and K2, is becoming more commonplace globally. Because biofilm formation ability can be directly impacted by capsular thickness (20). Serotyping of isolates for both classical isolates and hyper virulence isolates and the results revealed serotype K1 was predominant. A study in Iran investigated the prevalence of magA gene (mucoviscosity-associated gene A) of *Klebsiella spp*. isolated from clinical samples, showed that only (3.8%) of *K. pneumoniae* isolates harbor magA gene (21). The results showed all strains have the ability for biofilm formation either strong, moderate or weak, and there were no significant differences between cKp and hvKp. It is well recognized that biofilms are essential to the resistance and duration of bacterial diseases (22). hvKp had significantly higher hemolytic activity than cKp (K1 and K2), and no significant differences between K1 and K2 of hvKp. The production of hemolysin among gram-negative bacteria is indicative of other virulence and enterotoxigenic factors. *K. pneumoniae* has been found to have the oxygen-labile hemolysin (23). Many bacterial pathogens have hemolysis, or the capacity to lyse red blood cells, which contributes to their virulence by facilitating immune evasion and nutrient acquisition. Increased hemolytic activity in hvKp strains directly affects the severity of the clinical illness. Because hemolysis releases iron for bacterial consumption, it can cause tissue damage, inflammation, and aid in the spread of bacteria. Given their comparable virulence profiles, K1 and K2 hvKp strains ought to be regarded as similarly hazardous in clinical settings and need swift, intensive therapy. These strains frequently possess virulence plasmids that encode several harmful characteristics that improve their capacity to elude the immune system and induce systemic infections (24). According to a Turkish study that used blood agar

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to examine the hemolytic activity of *K. pneumoniae*, 30 (67%) of 45 isolates had this activity (25). In the current study human serum was used to test the *K. pneumoniae* serum resistance. Serum resistance was significantly higher in hvKp compared to cKp. Moreover, within both cKp and hvKp groups, strains with the K2 serotype exhibited significantly greater serum resistance than those with the K1 serotype. These results imply that both capsular serotype and hypervirulence promote survival in host serum, most likely by avoiding complement-mediated killing. *K. pneumoniae* uses serum resistance as a vital virulence mechanism that enables the bacteria to avoid the complement system, which is an essential part of innate immunity. Resistance to complement-mediated lysis enhances the ability of the bacteria to survive in the bloodstream and disseminate to extraintestinal sites (26). Although hvKp and cKp both show variable levels of serum resistance, hvKp typically shows a higher degree of evasion because of its improved virulence characteristics (27). Studies have consistently shown that hvKp strains exhibit greater serum resistance than classical strains due to the presence of additional virulence determinants (28). A cross-sectional Saudi Arabian study examined the virulence factors of bacteria in 120 intensive care unit patients with *K. pneumoniae* infections found that the hypermucoviscous phenotype was more strongly found in the hvKp group than in the cKp group. The rate of resistance to several antimicrobial agents was substantially higher in the cKp group than that in the hvKp group. The hvKp isolates were strongly related with moderate and strong biofilm development than cKp isolates. The hvKp isolates were substantially related with intermediate sensitivity and resistance to serum in the serum resistance assay. The K1, and K2 genes were substantially linked to hvKp. Due to their capacity to cause infections that are more severe and potentially fatal than those caused by cKp, the hvKp strains have become a new threat to patients in intensive care units (29). In this study, the finding that K2 serotypes produced more siderophores than K1 in hvKp groups, suggesting that K2 strains may be more aggressive in acquiring iron, potentially explaining their association with more severe infections. Cheng et al. (2010) and Bachman et al. (2012) showed a direct correlation between siderophore production and bacterial survival, replication, and host immunity resistance (30, 31). According to a United state investigation, *K. pneumoniae* siderophores can affect host survival during infection, localized tissue injury, and widespread bacterial dispersion. Additionally, they showed that siderophores can maintain the host master transcription factor (hypoxia-inducible factor-1α), promote bacterial spread, and trigger cytokine release as a risk factor for sepsis development (23). It has been shown in earlier research that hvKp strains generate more siderophores than cKp strains. In a mouse sepsis model, Russo et al. found that a siderophore generation of ≥30 μg/mL was significantly linked to severe illness or mortality. These results imply that siderophore synthesis is linked to a higher risk of sepsis in *K. pneumoniae* bacteremia patients (32).

Conclusion

The hvKp isolates were more frequently associated with capsular serotypes K1, K2, K20, and K54, and exhibited enhanced hemolytic activity, serum resistance, and siderophore production. These findings suggest that capsular serotyping could play a valuable role in guiding both diagnostic strategies and therapeutic decisions, while also providing critical insights into the pathogenic potential of *K. pneumoniae*. It is recommended that healthcare facilities incorporate routine capsular serotyping to facilitate early detection of hvKp strains.

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Ethical clearance: The current study was approved by Ethical Committee of College of Medicine-AL-Iraqia University (No. 218 - Date 12/10/2023).

Conflict of interest: None.

Use of Artificial Intelligence (AI): The authors state they did not use any generative AI tools for creating or editing the manuscript's language.

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دراسة الارتباط بين الأنماط المصلية للكبسولة وبعض عوامل الضراوة في سلالات كليب سيلا الرئوية الكلاسيكية وفائقة الضراوة المعزولة من حالات التهابات المسالك البولية

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الملخص

الخلفية: تُعد كليبسيلا الرئوية أحد الممرضات الرئيسية المسببة لالتهابات المسالك البولية (UTIs)، وتتأثر ضراوتها بأنماط مصلية كبسولية محددة وأنواع السلالات.

الأهداف: تهدف هذه الدراسة إلى استقصاء العلاقة بين عوامل الضراوة والأنماط المصلية الكبسولية في عزلات كليبسيلا الرئوية الكلاسيكية (cKp) وفائقة الضراوة (hvKp) المسببة لالتهابات المسالك البولية.

المرضى والطرق: تم جمع ما مجموعه ٢٨٠ عينة بول من مرضى في مستشفى مدينة الطب في بغداد، العراق، خلال الفترة من نوفمبر ٢٠٢٣ إلى مايو ٢٠٢٤. استُخدم تفاعل البلمرة المتسلسل (PCR) للتشخيص الجزيئي وتحديد الأنماط المصلية الكبسولية. وشملت عوامل الضراوة المدروسة تكوين الغشاء الحيوي، والنشاط الحالّ للدم، ومقاومة المصل، وإنتاج السيدروفورات.

النتائج: من بين ٤١ عزلة من النمط الكلاسيكي (cKp)، تم تحديد ١٩ عزلة على أنها من النمطين المصليين K1 أو K2، بينما انتمت الـ ٢٢ المتبقية إلى أنماط مصلية أخرى. أما من بين ٢١ عزلة فائقة الضراوة (hvKp)، فقد ارتبطت ١٨ عزلة بالأنماط المصلية K1 وK2 وK20 وK54. أظهرت جميع العزلات قدرة على تكوين الغشاء الحيوي دون وجود فروق معنوية بين cKp وhvKp. في المقابل، أظهرت سلالات hvKp نشاطًا حالًا للدم أعلى بشكل معنوي، خصوصًا في النمطين K1 وK2، مع عدم وجود فروق ذات دلالة إحصائية بين K1 وK2 ضمن hvKp. كما كانت مقاومة المصل أعلى بشكل معنوي في سلالات hvKp ($p > 0.05$)، مع تفوق النمط K2 على K1 في كلا المجموعتين. كذلك كان إنتاج السيدروفورات أعلى بشكل معنوي في hvKp، حيث سجلت سلالات K1 أعلى المستويات.

الاستنتاج: يمكن أن يوفر تحديد الأنماط المصلية الكبسولية رؤى مهمة في التشخيص السريري واتخاذ القرارات العلاجية لالتهابات المسالك البولية الناجمة عن كليبسيلا الرئوية.

الكلمات المفتاحية: الأنماط المصلية الكبسولية، عوامل الضراوة، كليبسيلا الرئوية، فائقة الضراوة، التهابات المسالك البولية.

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