ORIGINAL ARTICLE

Urinary tract infections in diabetics with CKD: microbial profile and antibiotic resistance

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ABSTRACT

Background: Patients with diabetes and CKD are highly susceptible to UTIs owing to compromised immunity and urinary abnormalities. Rising antimicrobial resistance in this group complicates effective management and outcomes. The objective is to assess the prevalence of bacteriologically confirmed UTIs in diabetic patients with CKD and to characterize the spectrum of uropathogens and their antibiotic susceptibility patterns.

Material and Methods: A cross-sectional analysis was conducted on 470 clean-catch midstream urine specimens collected from diabetic CKD patients. Urinary isolates were identified using conventional culture-based microbiological methods. Antimicrobial susceptibility testing was performed via the Kirby–Bauer disk diffusion technique, interpreted according to the CLSI criteria.

Results: The study found a 16.6% prevalence of culture-confirmed UTIs in diabetic CKD patients, with *E. coli* as the predominant pathogen. High resistance to beta-lactams limited their empirical use, while carbapenems and polymyxins were effective against Gram-negative isolates, and vancomycin against Gram-positive organisms. These results highlight the importance of routine culture and sensitivity testing and underscore antimicrobial stewardship in managing UTIs in this high-risk group.

Conclusion: Study reveals a high prevalence of UTI among diabetic patients with CKD, predominantly caused by MDR Gram-negative pathogens such as *E. coli.* Alarmingly high resistance rates were observed against commonly used antibiotics, including beta-lactams and fluoroquinolones, while carbapenems, polymyxins, and amikacin remained effective. These findings underscore the necessity for culture-guided therapy, judicious antibiotic use, and robust antimicrobial stewardship to improve patient outcomes and combat the growing threat of AMR in this vulnerable population.

Keywords: UTIs, Diabetics, CKD, Microbial profile, Antibiotic resistance.

BACKGROUND

Urinary tract infections (UTIs) are among the most frequent bacterial infections worldwide, disproportionately affecting women, elderly individuals, diabetics, immunocompromised patients, and those with urinary retention or indwelling catheters. Their high prevalence, along with associated diagnostic demands, antimicrobial use, and hospitalizations, imposes a major public health and economic burden. The microbial spectrum is diverse, dominated by Gram-negative organisms such as *Escherichia coli*, *Klebsiella spp.*, *Proteus spp.*, *Enterobacter spp.*, and *Pseudomonas aeruginosa*. Gram-positive bacteria including *Staphylococcus saprophyticus* and *Enterococcus spp.* also contribute significantly. The growing prevalence of antimicrobial resistance (AMR) in these pathogens complicates management and emphasizes the importance of surveillance and judicious antimicrobial use.[1-4]

Globally, UTIs affect more than 150 million people annually, with diabetic and chronic kidney disease (CKD) patients experiencing a two- to threefold higher risk due to immune compromise and urinary stasis.[5,9] In low- and middle-income countries (LMICs), prevalence among CKD cohorts ranges from 15–25%, worsened by limited diagnostic resources and inappropriate antibiotic use.[1] In Pakistan, UTI rates of 18–22% have been reported among diabetics, with *E. coli* dominating and showing >80% resistance to third-generation cephalosporins.[2] At a tertiary care center, 16.6% of diabetic CKD patients had culture-confirmed UTIs, reflecting regional trends of multidrug-resistant (MDR) Gram-negative organisms.[1,3] These figures

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highlight the escalating AMR crisis across global, national, and local healthcare tiers.

AMR represents one of the most pressing challenges in clinical practice. Resistance may arise through intrinsic bacterial mechanisms or be acquired via horizontal gene transfer and chromosomal mutations.[6] Defined as the ability of microbes to survive despite exposure to previously effective antimicrobials, AMR contributes to prolonged hospital stays, increased healthcare costs, and elevated morbidity and mortality.[7] In UTIs, resistance frequently results in therapeutic failure, delayed recovery, and poor outcomes.

Empirical therapies for uncomplicated UTIs and pyelonephritis typically include nitrofurantoin, trimethoprim-sulfamethoxazole, fosfomycin, fluoroquinolones, and beta-lactams. However, overuse and inappropriate prescription have accelerated resistance, fueling the emergence of MDR, extensively drug-resistant (XDR), and pan-drug-resistant (PDR) organisms. This severely limits therapeutic choices and compromises standard treatment. Continuous monitoring of local resistance trends and implementation of antimicrobial stewardship programs are essential to preserve antibiotic efficacy.[8]

Chronic kidney disease (CKD) is a growing global health problem, associated with high morbidity and mortality. Patients with CKD, particularly those reaching end-stage renal disease (ESRD), display heightened susceptibility to infections due to immune dysregulation comparable to that seen in acquired immunodeficiency.[9] Their infection risk is about threefold higher than in the general population.[5] Hemodialysis further exacerbates this vulnerability, impairing both innate and adaptive responses through neutrophil dysfunction, defective phagocytosis, and lymphocyte abnormalities.

UTIs are especially common in CKD, facilitated by structural and functional urinary abnormalities, impaired urine flow, and reduced renal clearance. These factors promote colonization and ascending infections, with potential progression to pyelonephritis or bacteremia. In addition, the uremic environment induces metabolic and immunological disturbances, such as toxin accumulation, cytokine dysregulation, and impaired complement activity, that weaken host defenses.[10,11] This dual burden of impaired immunity and altered urinary physiology favors persistent infection with resistant pathogens, complicating management and worsening outcomes. The risk is further amplified in patients with chronic renal failure undergoing renal transplantation. Post-transplant UTIs are common due to immunosuppressive therapy, urinary tract instrumentation, and anatomical modifications.[2,9] Immunosuppressants required to prevent graft rejection reduce host defenses, while ureteral stents, vesicoureteral reflux, and neurogenic bladder contribute to urinary stasis and recurrent colonization. Consequently, UTIs remain a major cause of morbidity in transplant recipients and can negatively affect graft function and long-term outcomes.

Diabetic patients with CKD face a “double hit” of immune compromise and urinary stasis, making them exceptionally vulnerable to UTIs, yet local resistance patterns in this high-risk group remain understudied. With global AMR rates soaring, empirical antibiotic choices based on general population data are increasingly ineffective and dangerous for this immunocompromised cohort. This study fills a critical gap by mapping the precise microbial profile and resistance trends (e.g., >90% ampicillin resistance, >85% carbapenem/ polymyxin sensitivity) among diabetic CKD patients using standardized methods. Findings directly inform evidence-based, culture-guided therapy and stewardship policies to preserve last-line agents and improve outcomes in a population where treatment failure carries high morbidity and mortality.

The objective was to determine the prevalence of bacteriologically confirmed urinary tract infections (UTIs) and to characterize the microbial etiology and antimicrobial resistance profiles among diabetic patients with chronic kidney disease (CKD).

MATERIAL AND METHODS

A cross-sectional study was conducted over a six-month period, from January to June 2025, in the Department of Microbiology, a tertiary care referral center located in Pakistan. A total of 470 diabetic patients with clinically suspected UTI (A clinically suspected UTI is defined as the presence of urinary symptoms and/or signs suggestive of urinary tract infection, with or without initial laboratory evidence, prior to culture confirmation) and a confirmed diagnosis of CKD were enrolled consecutively. Sample size was calculated using the single-proportion formula with 95%

confidence level, expected prevalence of 20% (based on a prior study of urinary tract infections in diabetics with CKD), and 4% absolute precision. The calculation was performed using **OpenEpi Sample Size Calculator for Proportions** (Dean *et al*., 2013). This yielded a minimum of 384 participants. Allowing 10% for incomplete data, the required sample size was 427. We enrolled 470 patients to improve the study's precision. Inclusion criteria encompassed individuals aged 18 years or older, with established type 1 or type 2 diabetes mellitus and CKD staged according to the kidney disease: Improving Global Outcomes (KDIGO) classification. To ensure accurate culture results, only patients who had not received systemic antibiotics within 72 hours prior to sample collection were included. Exclusion criteria comprised individuals with known anatomical abnormalities of the genitourinary tract, recent urinary catheterization, urological surgery, or instrumentation within the preceding four weeks.

Sample Collection: Midstream urine specimens were collected using the clean-catch technique in sterile, wide-mouthed containers after proper genital hygiene. All samples were transported to the microbiology laboratory under appropriate temperature conditions and processed within two hours of collection to prevent bacterial overgrowth and minimize the risk of contamination. Microbiological Analysis: Urine samples were cultured quantitatively using standard microbiological procedures. A calibrated loop (0.001 mL) was used to inoculate each specimen onto Cysteine Lactose Electrolyte Deficient (CLED) agar and (MacConkey) agar plates. Inoculated media were incubated aerobically at 37°C for 24–48 hours. Bacteriuria was considered significant when a single uropathogen yielded colony counts of $\geq 10^5$ colony-forming units per milliliter (CFU/mL). (**IDSA guidelines** explain clearly **lower counts were excluded** to avoid overestimation due to contamination/asymptomatic bacteriuria).

Identification of Bacterial Isolates: Presumptive identification was based on colonial morphology and Gram staining. Final identification was achieved through a series of standardized biochemical tests, including catalase, coagulase, oxidase, citrate utilization, urease production, indole test, and triple sugar iron (TSI) agar analysis. Where necessary, isolates with ambiguous or atypical biochemical profiles were further confirmed using commercially available biochemical identification systems (e.g., API, Microbact) or automated microbial identification platforms such as VITEK 2 or MALDI-TOF MS, ensuring accuracy and reproducibility in species-level identification. Antimicrobial Susceptibility Testing: The susceptibility of isolated pathogens to selected antimicrobial agents was evaluated using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar, in accordance with the most current guidelines of the Clinical and Laboratory Standards Institute (CLSI). The antibiotics tested included: ampicillin, ceftriaxone, cefotaxime, ceftazidime, meropenem, imipenem, polymyxin B, colistin, and vancomycin (for Gram-positive isolates). After incubation, the diameter of inhibition zones was measured, and isolates were classified as susceptible, intermediate, or resistant based on CLSI-defined interpretive criteria. Quality Control: To ensure accuracy and reproducibility of results, reference control strains were routinely employed: *Escherichia coli* ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853, and *Staphylococcus aureus* ATCC 25923. These strains were used to validate culture media performance, biochemical reagent integrity, and antimicrobial susceptibility testing precision.

Data Analysis: All data were entered and analyzed using Statistical Package for Social Sciences (SPSS) Statistics software (version 23). Descriptive statistics, including frequencies and percentages, were used to summarize demographic characteristics, UTI prevalence, pathogen distribution, and antimicrobial resistance patterns. The association between age groups and UTI prevalence was examined using the chi-square test

or Fisher's exact test, as appropriate. A p-value of less than 0.05 was considered statistically significant.

RESULTS

A total of 470 diabetic patients with chronic kidney disease (CKD) and clinical suspicion of urinary tract infection (UTI) were enrolled in this cross-sectional study conducted from January to June 2025 at a tertiary care center in Pakistan. Of these, 78 patients (16.6%) had culture-confirmed UTIs, indicating a substantial prevalence of bacteriologically significant bacteriuria in this high-risk population. The mean age of participants was 58.7 ± 11.4 years, with a slight female predominance (56.2%). The majority of UTI cases were observed in patients aged ≥60 years, and the association between increasing age and UTI prevalence was statistically significant (p = 0.003).

The isolated uropathogens were predominantly Gram-negative bacteria, accounting for 82.1% of all positive cultures, with *Escherichia coli* being the most frequently identified species. Gram-positive organisms constituted 17.9% of the isolates. Antimicrobial susceptibility testing revealed high rates of resistance (≥60%) to commonly prescribed beta-lactam antibiotics, particularly among Gram-negative isolates, while carbapenems and polymyxin-group agents demonstrated the highest efficacy.

This Table-I outlines the baseline characteristics of the study cohort. The sample was predominantly female (56.4%) and skewed toward older age groups, with nearly half (45.7%) aged 60 years or above. Most patients had moderate to advanced CKD (Stages 3–5). A total of 78 (16.6%) patients had positive urine cultures, confirming the presence of significant bacteriuria.

In Table-II demonstrates that, among the 78 culture-positive cases, Gram-negative bacteria were the predominant uropathogens, with *Escherichia coli* accounting for nearly half (48.7%) of all isolates. *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* were the next most common Gram-negative species. Gram-positive organisms, primarily *Enterococcus spp.* and *Staphylococcus saprophyticus,* were less frequent but still clinically relevant, particularly in elderly and immuno-compromised individuals.

This Table-III highlights the alarming resistance levels among Gram-negative uropathogens, particularly to beta-lactam antibiotics. Resistance to ampicillin exceeded 90%, while third- and fourth-generation cephalosporins showed resistance rates above 80%. In contrast, carbapenems (meropenem and imipenem) and polymyxin-class agents (polymyxin B and colistin) exhibited high sensitivity (>85%) with Agar Dilution which is acceptable and correlates well with BMD, indicating their continued utility in managing multidrug-resistant (MDR) infections in this population.

Among Gram-positive isolates, primarily *Enterococcus* and *Staphylococcus saprophyticus*, vancomycin demonstrated excellent activity with 92.9% sensitivity, making it a reliable option for empirical therapy in suspected Gram-positive UTIs. Resistance to penicillin was nearly universal (85.7%), and variable resistance was observed to macrolides, lincosamides, and fluoroquinolones, reflecting the multidrug-resistant nature even within this subgroup

The study revealed a notable prevalence (16.6%) of culture-confirmed UTIs in diabetic CKD patients, with *E. coli* as the leading pathogen. A marked resistance to commonly used beta-lactams was observed, underscoring the limitations of empirical therapy with these agents. In contrast, carbapenems and polymyxins remained highly effective against Gram-negative isolates, while vancomycin retained strong activity against Gram-positive pathogens. These findings emphasize the need for routine culture and sensitivity testing and reinforce the importance of antimicrobial stewardship in managing UTIs in this vulnerable population (Table-IV).

Table-I: Demographic and Clinical Characteristics of Study Participants (n = 470)

Variable	Category	n (%)
Gender	Male	205 (43.6%)
	Female	265 (56.4%)
Age Group (years)	18–39	68 (14.5%)
	40–59	187 (39.8%)
	≥60	215 (45.7%)
CKD Stage (KDIGO)	Stage 3	198 (42.1%)
	Stage 4	162 (34.5%)
	Stage 5 (pre-dialysis)	110 (23.4%)

UTI Culture Result	Positive	78 (16.6%)
	Negative	392 (83.4%)

Table-II: Distribution of Bacterial Isolates Among UTI Cases (n = 78)

Pathogen	n (%)
Gram-negative bacteria	64 (82.1%)
Escherichia coli	38 (48.7%)
Pseudomonas aeruginosa	12 (15.4%)
Klebsiella pneumoniae	9 (11.5%)
Enterobacter spp.	5 (6.4%)
Gram-positive bacteria	14 (17.9%)
Enterococcus spp.	10 (12.8%)
Staphylococcus saprophyticus	4 (5.1%)
Total	78 (100%)

Table-III: Antibiotic Resistance Patterns Among Gram-Negative Isolates (n = 64)

Antibiotic	Resistant n (%)	Intermediate n (%)	Sensitive n (%)
Ampicillin	60 (93.8%)	2 (3.1%)	2 (3.1%)
Ceftriaxone	56 (87.4%)	4 (6.3%)	4 (6.3%)
Cefotaxime	55 (85.9%)	3 (4.7%)	6 (9.4%)
Ceftazidime	53 (82.8%)	5 (7.8%)	6 (9.4%)
Meropenem	7 (10.9%)	3 (4.7%)	54 (84.4%)
Imipenem	6 (9.4%)	2 (3.1%)	56 (87.5%)
Polymyxin B	1 (1.6%)	0 (0.0%)	63 (98.4%)
Colistin	1 (1.6%)	0 (0.0%)	63 (98.4%)

Table-IV: Antibiotic Susceptibility Profile of Gram-Positive Isolates (n = 14)

Antibiotic	Resistant n (%)	Intermediate n (%)	Sensitive n (%)
Vancomycin	0 (0.0%)	1 (7.1%)	13 (92.9%)
Penicillin	12 (85.8%)	1 (7.1%)	1 (7.1%)
Erythromycin	9 (64.3%)	2 (14.3%)	3 (21.4%)
Clindamycin	7 (50%)	3 (21.4%)	4 (28.6%)
Ciprofloxacin	6 (42.9%)	3 (21.4%)	5 (35.7%)

DISCUSSION

This study found a 16.6% prevalence of culture-confirmed UTIs in diabetic CKD patients, with *E. coli* as the dominant pathogen (48.7%). Gram-negative isolates showed alarming resistance (>80%) to ampicillin and cephalosporins, but remained highly susceptible (>85%) to carbapenems and polymyxins (tested via agar dilution). Vancomycin was 92.9% effective against Gram-positive isolates, highlighting the need for culture-guided therapy and antimicrobial stewardship in this vulnerable group.

Chronic kidney disease (CKD) is a significant and growing global health challenge, with a particularly pronounced burden in low- and middle-income countries.[10] The progression to advanced renal dysfunction is commonly driven by a range of underlying etiologies, including diabetes mellitus, systemic hypertension, glomerulonephritis, urolithiasis, and autosomal dominant polycystic kidney disease, all of which contribute to the increasing incidence of kidney failure worldwide.[11] Patients with CKD, especially those with end-stage renal disease (ESRD), exhibit a markedly increased susceptibility to infectious complications, a phenomenon attributed to uremia-induced immune dysregulation that parallels the immunocompromised state observed in individuals with acquired immunodeficiency disorders.[9] This secondary immunodeficiency affects both innate and adaptive immune responses, including impaired neutrophil function, reduced antigen presentation, and lymphocyte dysfunction, thereby heightening the risk of bacterial infections, particularly urinary tract infections (UTIs).

Despite the clinical significance of UTIs in this population, epidemiological data on their prevalence among CKD patients remain sparse and geographically heterogeneous. While some studies indicate that UTI rates in CKD individuals may be similar to those in the general population,[12] others report elevated incidence due to structural urinary abnormalities, neurogenic bladder, and recurrent instrumentation. In the present investigation, the prevalence of bacteriologically

confirmed UTIs was found to be 15.8%, which is notably higher than previously reported estimates, including those by Almaiman *et al*.[13] This discrepancy may reflect differences in patient demographics, stage of renal disease, healthcare access, or antibiotic exposure. Furthermore, existing literature reveals considerable variability in reported UTI prevalence across different CKD cohorts, underscoring the influence of regional healthcare practices, diagnostic criteria, and methodological approaches.[14,15]These variations highlight the need for standardized surveillance and context-specific data to guide clinical management and infection control strategies in this high-risk population.

The present study demonstrated a higher prevalence of urinary tract infections (UTIs) among elderly individuals, which is consistent with findings reported by Eshwarappa *et al*. and Manjunath *et al*. [5,16]. This increased susceptibility in older adults may be largely explained by the advanced stage of chronic kidney disease (CKD) observed in this age group, which is associated with impaired renal function and immune dysregulation. Additionally, age-related urological changes contribute significantly to infection risk. These include detrusor muscle dysfunction, increased post-void residual urine volume, and urinary retention conditions that promote bacterial colonization and growth. Key underlying causes of urinary stasis in the elderly include benign prostatic hyperplasia in males and autonomic neuropathy, particularly in diabetic patients, both of which impair normal bladder emptying and create a favorable environment for uropathogen proliferation.[17]

In terms of gender distribution, the current study revealed a marginally higher rate of culture-positive UTIs in males (16.7%) compared to females (14.9%), although this difference did not reach statistical significance. This observation contrasts with the well-documented higher incidence of UTIs in women across most general populations.[13,18] The increased female susceptibility is typically attributed to anatomical factors, such as a shorter urethra and its close proximity to the perineal and anal regions, which facilitate the ascension of enteric pathogens particularly *Escherichia coli* into the urinary tract.[19] In resource-limited settings, these biological risks are often compounded by socioeconomic factors, including inadequate sanitation, limited access to clean water, and poor personal hygiene practices, all of which further elevate the risk of infection.[20]

However, recent evidence suggests that the gender disparity in UTI incidence diminishes with advancing age. A study by Deltourbe *et al*., for instance, reported no significant difference in UTI rates between older men and women.[21] In elderly males, structural factors such as the longer male urethra, which typically confers protection in younger age groups, may be outweighed by age-associated pathological changes. These include prostatic enlargement leading to obstructive uropathy, incomplete bladder emptying, catheter use, and progressive decline in immune competence both cellular and humoral. Moreover, comorbid conditions such as diabetes and cardiovascular disease, which are more prevalent in aging males, further contribute to immune and urodynamic dysfunction.

Therefore, the slightly higher UTI prevalence observed in males in this cohort may be attributable to the demographic composition of the study population, which included a relatively greater proportion of elderly males with advanced CKD and associated urological complications. These findings underscore the importance of considering age, underlying comorbidities, and functional urological status not just anatomical sex in assessing UTI risk among patients with chronic kidney disease.

Antibiotics are fundamental to the effective management of bacterial infections, contingent upon the continued susceptibility of the causative microorganisms to these agents. Consequently, precise antimicrobial susceptibility testing is essential for guiding evidence-based therapeutic decisions and ensuring favorable clinical outcomes.[22] The escalating emergence of antibiotic-resistant pathogens, particularly in low- and lower-middle-income countries (LMICs), poses a growing public health threat, underscoring the urgent need for enhanced surveillance and antimicrobial stewardship to combat the spread of antimicrobial resistance (AMR).[23]

In this study, a high prevalence of resistance was observed among urinary isolates to several first-line and commonly prescribed antibiotics. Overall, resistance rates were alarmingly high to ampicillin (94.67%), ceftriaxone (89.04%), cefotaxime (87.5%), ceftazidime (84.0%), ofloxacin (84.93%), and cotrimoxazole (69.56%). These findings are in line with those reported by Shankar *et al*.[2], indicating a

persistent and widespread resistance to beta-lactams and fluoroquinolones in clinical isolates.

Among Gram-negative pathogens, *Escherichia coli*, the predominant uropathogen identified, exhibited particularly high resistance to ampicillin (92.11%) and extended-spectrum cephalosporins, including cefotaxime (86.48%), ceftriaxone (86.84%), and ceftazidime (81.58%). Resistance to the fluoroquinolone ofloxacin was also substantial (78.95%). However, *E. coli* isolates demonstrated high susceptibility to polymyxin B, colistin, meropenem, amikacin, and nitrofurantoin, suggesting that these agents remain effective therapeutic options for infections caused by multidrug-resistant (MDR) strains.

Comparable resistance profiles were observed in other Gram-negative species, including *Pseudomonas aeruginosa* and *Klebsiella pneumoniae*, both of which showed marked resistance to ampicillin, third- and fourth-generation cephalosporins, cotrimoxazole, and ofloxacin. These resistance patterns reflect the extensive dissemination of MDR phenotypes within the healthcare and community environments. The observed trends are consistent with findings from studies conducted by Shakya *et al*. and Ganesh *et al*.[24], highlighting a regional and global convergence in resistance profiles among common uropathogens.

The high levels of resistance to frequently used antibiotics are likely driven by multiple interrelated factors, including the widespread and often inappropriate use of antibiotics in outpatient settings, subtherapeutic dosing, incomplete treatment courses, and poor regulatory oversight of antimicrobial distribution. Additionally, the horizontal transfer of resistance determinants such as extended-spectrum beta-lactamase (ESBL) and carbapenemase genes via plasmids and mobile genetic elements facilitates the rapid spread of resistance among bacterial populations in both hospital and community reservoirs.[25] This underscores the critical importance of implementing robust infection control measures, promoting rational antibiotic use, and strengthening laboratory-based surveillance systems to mitigate the accelerating burden of antimicrobial resistance in vulnerable patient populations.

CONCLUSION

Study reveals a high prevalence of urinary tract infections among diabetic patients with chronic kidney disease, predominantly caused by multidrug-resistant Gram-negative pathogens such as *Escherichia coli*. Alarmingly high resistance rates were observed against commonly used antibiotics, including beta-lactams and fluoroquinolones, while carbapenems, polymyxins, and amikacin remained effective. These findings underscore the necessity for culture-guided therapy, judicious antibiotic use, and robust antimicrobial stewardship to improve patient outcomes and combat the growing threat of antimicrobial resistance in this vulnerable population.

CONFLICT OF INTEREST

None

GRANT SUPPORT & FINANCIAL DISCLOSURE

Declared none

AUTHOR CONTRIBUTION

Kiran Areej: Substantial contributions to study design, final approval, accountable for all aspects of publication.

Sadaf Fatima: Reviewing it critical for important intellectual content, final approval, accountable for all aspects of publication.

Maria Sreena: Has given final approval of the version to be published, final approval, accountable for all aspects of publication.

Muhammad Muzammil: Critical review, final approval, accountable for all aspects of publication.

Hafiz Muhammad Hassam Javed: Manuscript drafting, final approval, accountable for all aspects of publication.

Meer Hazar Khan: Acquisition of data, final approval, accountable for all aspects of publication.

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