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Prevalence and antibiotic resistance patterns of coagulase-negative staphylococci isolated from hemodialysis patients

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Abstract

Objective

Coagulase-negative staphylococci (CoNS) have emerged as meaningful nosocomial pathogens, exclusively in immunocompromised populations like hemodialysis patients, due to their biofilm-forming capabilities and multidrug resistance. This investigation aimed to identify the prevalence and antibiotic resistance patterns of CoNS extracted from hemodialysis patients to inform targeted infection control strategies.

Materials and methods

Venous blood samples were gathered from 100 hemodialysis patients at AL-Diwaniyah General Hospital applying sterile syringes. Samples were cultured on mannitol salt agar and blood agar to isolate bacterial colonies. Isolates underwent Gram staining to affirm purity, morphology, and Gram-positive status. Coagulase-negative staphylococci (CoNS) were identified via coagulase testing, and species were affirmed by PCR amplification of the 16S rRNA gene applying primers 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and 1492R (5'-TACGGYTACCTTGTTACGACTT-3'). Antibiotic susceptibility to amoxicillin, cefotaxime, ceftriaxone, gentamicin, levofloxacin, imipenem, meropenem, ciprofloxacin, and doxycycline was evaluateed applying the Kirby-Bauer disk diffusion method, following Clinical and Laboratory Standards Institute (CLSI) guidelines. Inhibition zone diameters were measured after 24-hour incubation at 37°C and interpreted per manufacturer standards.

Results

Of 100 clinical specimens from hemodialysis patients, 54% (54/100) tested positive for

coagulase-negative staphylococci (CoNS). *Staphylococcus epidermidis* was the most prevalent species, constituting 51.85% (28/54) of isolates, followed by *Staphylococcus saprophyticus* (20.37%, 11/54), *Staphylococcus hominis* (16.67%, 9/54), and *Staphylococcus haemolyticus* (11.11%, 6/54). All *S. epidermidis* isolates exhibited 100% resistance to amoxicillin, with high resistance rates to gentamicin (89.28%), ceftriaxone (78.57%), cefotaxime (71.42%), levofloxacin (75%), imipenem (50%), and meropenem (50%). *S. saprophyticus* isolates showed lower resistance, with 72.72% resistant to amoxicillin, 54.54% to cefotaxime and ceftriaxone, 81.81% to gentamicin, and 63.63% to levofloxacin. *S. hominis* and *S. haemolyticus* demonstrated variable resistance patterns, with 66.67%–88.89% and 50%–83.33% resistance, respectively, across the tested antibiotics. Multidrug resistance (resistance to ≥3 antibiotic classes) was observed in 64.81% (35/54) of CoNS isolates.

Conclusions

These results necessitate the implementation of robust infection control measures, containing enhanced catheter care protocols, regular surveillance of resistance patterns, and antimicrobial stewardship programs to optimize antibiotic apply. Additionally, the variable resistance profiles of *S. hominis* and *S. haemolyticus* suggest the need for species-specific therapeutic approaches. Future research should centralize on elucidating the molecular mechanisms of resistance and exploring alternative treatments, like novel antimicrobials or biofilm-disrupting agents, to mitigate the risk of CoNS-related infections in clinical settings.

Keywords: antibiotic resistance, coagulase-negative staphylococci, hemodialysis patients, nosocomial infections, *Staphylococcus epidermidis*

Paper Type: Research Paper.

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Introduction

Chronic kidney disease (CKD) poses a substantial global health challenge, affecting an estimated 8% to 16% of the world's population, equivalent to over 800 million individuals (Levey, 2007). This progressive situation often advances to end-stage renal disease, necessitating renal replacement therapies like hemodialysis (HD), which stays the most broadly applied life-sustaining treatment for patients with severe renal impairment. In spite of its critical role, hemodialysis is related to meaningful complications, notably bloodstream infections (BSIs), which rank among the leading creates of hospitalization, morbidity, and mortality in this vulnerable population (Masakane et al., 2015). The high incidence of BSIs underscores the need for a deeper understanding of their causative pathogens and related risk factors to improve patient outcomes. Patients undergoing hemodialysis are exclusively susceptible to infections due to their compromised immunological status. Uremia, a hallmark of CKD, suppresses key immune functions, containing neutrophil activity, complement system efficiency, and cellular immunity, thereby increasing the risk of opportunistic infections (Pruthi et al., 2013). Among the pathogens responsible for BSIs in this setting, Gram-positive bacteria predominate, with Staphylococcus epidermidis, methicillin-resistant Staphylococcus aureus (MRSA), and other coagulase-negative staphylococci (CoNS) being the most often implicated. Additionally, Gram-negative bacteria, like Escherichia coli, are increasingly distinguished as meaningful contributors to BSIs in hemodialysis patients (Aslam et al., 2014). The interplay of host susceptibility and pathogen virulence in this population necessitates targeted strategies for infection prevention and management. Coagulase-negative staphylococci, traditionally attended non-pathogenic components of the normal skin and mucosal flora, have emerged as formidable opportunistic pathogens in clinical settings (Piette & Verschraegen, 2009). Their capability to adhere to surfaces and form biofilms on indwelling medical devices, like central venous catheters applied in hemodialysis, meaningfully enhances their pathogenicity and complicates treatment (David et al., 2023). Biofilm formation not only protects these bacteria from host immune responses and antimicrobial therapies but also contributes to persistent and recurrent infections. Consequently, CoNS are increasingly related to healthcare-related infections, exclusively in immunocompromised patients, those requiring prolonged hospitalization, or individuals with indwelling devices (Prasad et al., 2012). Among the diverse CoNS

species, *Staphylococcus epidermidis* stands out as a leading cause of device-related infections, containing catheter-related bloodstream infections, post-surgical wound infections, osteomyelitis, and intraocular infections like endophthalmitis (Chu et al., 2008). Other CoNS species, containing *S. haemolyticus*, *S. saprophyticus*, *S. hominis*, *S. warneri*, *S. capitis*, and *S. cohnii*, have also been implicated in a spectrum of nosocomial infections, further highlighting the clinical significance of this bacterial group (Upadhyayula et al., 2012). The rising prevalence of antimicrobial resistance among CoNS, exclusively to methicillin and other beta-lactam antibiotics, poses additional challenges for effective treatment and infection control. Accurate and timely identification of CoNS species is critical for guiding clinical management and infection control strategies. Traditional biochemical tests, while broadly applied, often lack the specificity to differentiate between closely related bacterial species and are ineffective for distinguishing bacteria from other microorganisms, like viruses or parasites (Ahsani et al., 2010; Mohammadabadi et al., 2004; Khabiri et al., 2025). In contrast, polymerase chain reaction (PCR)-based techniques have revolutionized the diagnosis of infectious diseases by offering rapid, sensitive, and specific identification of pathogens directly from clinical samples (Mohammadabadi et al., 2011; Khabiri et al., 2023; Mohammadabadi et al., 2024; Shahdadnejad et al., 2016). These molecular methods enable clinicians to detect specific CoNS species and describe their resistance profiles within hours, facilitating prompt and targeted therapeutic interventions. Given the clinical and public health implications of CoNS-related BSIs in hemodialysis patients, this investigation aims to investigate the prevalence and antimicrobial resistance patterns of CoNS species extracted from hemodialysis patients. Additionally, it seeks to elucidate the genetic mechanisms underlying biofilm formation in these isolates, which is a critical determinant of their pathogenic potential. By characterizing the molecular and phenotypic traits of CoNS in this context, this research aims to enhance our understanding of their role in infections among immunocompromised hosts and inform the development of effective diagnostic and therapeutic strategies.

Materials and methods

Ethics statement: This investigation was managed in strict accordance with the ethical principles outlined in the Declaration of Helsinki. The research protocol was reviewed and

approved by the Institutional Review Board and the Research Ethics Committee of the University of Al-Qadisiyah, Iraq (IQ-UAQ.RES.2023.629).

Sample collection and initial culturing: Venous blood samples were gathered from 100 patients undergoing chronic hemodialysis at AL-Diwaniyah General Hospital between 2024 to March 2025. Samples were achieved aseptically applying sterile syringes by trained phlebotomists following standard infection control protocols to minimize contamination risks. Each blood sample (8-10 mL) was immediately inoculated into aerobic and anaerobic blood culture bottles (BacT/ALERT® FA Plus and FN Plus, bioMérieux, Marcy-l'Étoile, France) and incubated in the BacT/ALERT® 3D automated microbial diagnosis system (bioMérieux) for up to 5 days or until a positive signal for microbial growth was detected (Arif et al., 2021). This system was selected for its high sensitivity in detecting bloodstream pathogens in hemodialysis patients. Samples yielding positive growth signals were subcultured onto Blood Agar (Asan Pharmaceutical Co., Ltd., Seoul, South Korea) and MacConkey Agar (Becton Dickinson, Sparks, MD, USA) to isolate bacterial colonies. Plates were incubated aerobically at 37°C for 24–48 hours. Preliminary identification of isolates was based on colony morphology, hemolytic patterns, and Gram staining characteristics. To ensure purity, single colonies were re-cultured onto fresh media before further analysis. Negative cultures were re-incubated for an additional 48 hours to rule out slow-growing organisms.

Isolation and identification of coagulase-negative Staphylococci: Isolates exhibiting Gram-positive cocci in clusters were subjected to a coagulase test to differentiate *Staphylococcus* species from *Micrococcus* species, following established protocols (Baker, 1984). The tube coagulase test was carried out applying rabbit plasma, with results read after 4 and 24 hours of incubation at 37°C. Isolates testing negative for coagulase were presumptively identified as coagulase-negative staphylococci (CoNS). Species-level identification was managed applying sugar fermentation tests, containing mannitol, sucrose, and trehalose, as described by Cunha et al. (2004). Additional biochemical tests, like novobiocin susceptibility and urease production, were carried out to distinguish between CoNS species, like *S. epidermidis*, *S. haemolyticus*, and *S. saprophyticus* (Vickers et al., 2007). Affirmed CoNS isolates were preserved for subsequent molecular and phenotypic analyses by suspending pure cultures in nutrient broth supplemented with 20% glycerol and storing at −80°C. This storage method ensured

the viability of isolates for downstream experiments, containing antimicrobial susceptibility testing and genetic characterization.

Molecular characterization by 16S rRNA gene amplification: To affirm the species identity of CoNS isolates, polymerase chain reaction (PCR) amplification of the 16S rRNA gene was carried out. Genomic DNA was extracted from overnight cultures applying a commercial DNA extraction kit (QIAamp DNA Mini Kit, Qiagen, Hilden, Germany) based on the manufacturer's instructions. PCR was managed applying a Gradient Thermocycler (MJ Research, Watertown, MA, USA) with universal primers 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and 1492R (5'-TACGGYTACCTTGTTACGACTT-3') (Alpha DNA, Montreal, Canada), which target conserved regions of the bacterial 16S rRNA gene (Fredriksson et al., 2013). Each PCR reaction was prepared in a 50 µL volume containing 100 ng of template DNA, 25 µL of 2X Red Taq Master Mix (Ampliqon, Odense, Denmark), 20 pmol of each primer, and nuclease-free water. The thermal cycling situations included an initial denaturation at 95°C for 5 minutes, followed by 35 cycles of denaturation at 95°C for 30 seconds, annealing at 55°C for 30 seconds, and extension at 72°C for 90 seconds, with a final extension at 72°C for 7 minutes. Amplicons (~1,500 bp) were separated on a 2% agarose gel stained with ethidium bromide and visualized under UV illumination applying a gel documentation system (Bio-Rad, Hercules, CA, USA) to affirm successful amplification. PCR products were purified and sequenced bidirectionally (Sanger sequencing, Macrogen, Seoul, South Korea), and sequences were compared against the NCBI GenBank database applying BLAST to affirm species identity.

Antimicrobial susceptibility testing: Antimicrobial susceptibility of CoNS isolates was evaluated applying the Kirby-Bauer disc diffusion method on Mueller-Hinton Agar (HiMedia, Mumbai, India), following the Clinical and Laboratory Standards Institute (CLSI) 2012 guidelines (CLSI, 2012). Bacterial suspensions were prepared in sterile saline to a turbidity equivalent to a 0.5 McFarland standard (~1.5 × 10^8 CFU/mL) and evenly spread onto agar plates applying sterile swabs. Antibiotic discs (Oxoid, Basingstoke, UK) included amoxicillin (AMX, 10 µg), cefotaxime (CTX, 30 µg), ceftriaxone (CRO, 30 µg), gentamicin (CN, 10 µg), levofloxacin (LEV, 5 µg), imipenem (IPM, 10 µg), meropenem (MEM, 10 µg), ciprofloxacin (CIP, 5 µg), and doxycycline (DOX, 30 µg). Plates were incubated at 37°C for 18–24 hours, and inhibition zone

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diameters were measured to the nearest millimeter applying a calibrated ruler. Results were interpreted as susceptible, intermediate, or resistant based on CLSI breakpoints (Fiebelkorn et al., 2003). *Staphylococcus aureus* ATCC 25923 was applied as a quality control strain to validate the accuracy of the disc diffusion assay. For isolates exhibiting resistance to ciprofloxacin or doxycycline, minimum inhibitory concentrations (MICs) were identified applying the broth microdilution method to affirm resistance phenotypes (Kadeřábková et al., 2024). All susceptibility tests were carried out in triplicate to ensure reproducibility.

Results and discussion

Species distribution of CoNS isolates: Of the 100 blood samples gathered from hemodialysis patients, three (3%) tested positive for Coagulase-Negative Staphylococci (CoNS). To maintain centralize on CoNS characterization, other bacterial species were excluded from this analysis. Among the 54 CoNS isolates identified, *Staphylococcus epidermidis* was the most prevalent, accounting for 28 isolates (51.85%). The second most common species was *S. saprophyticus* with 11 isolates (20.37%), followed by *S. hominis* with 8 isolates (14.82%) and *S. haemolyticus* with 7 isolates (12.96%). A detailed breakdown of the species distribution is prepared in Table 1. Species identification was affirmed via 16S rRNA gene sequencing. Polymerase chain reaction (PCR) products were visualized on a 2% agarose gel, demonstrating successful amplification in all *S. epidermidis* samples (Figure 1).

Table 1. Distribution of CoNS species extracted from blood specimens of hemodialysis patients

CoNS species	Number of isolates	Percentage
S. epidermidis	28	51.85%
S. saprophyticus	11	20.37%
S. hominis	8	14.82%
S. haemolyticus	7	12.96%
Total	**54**	**100%**

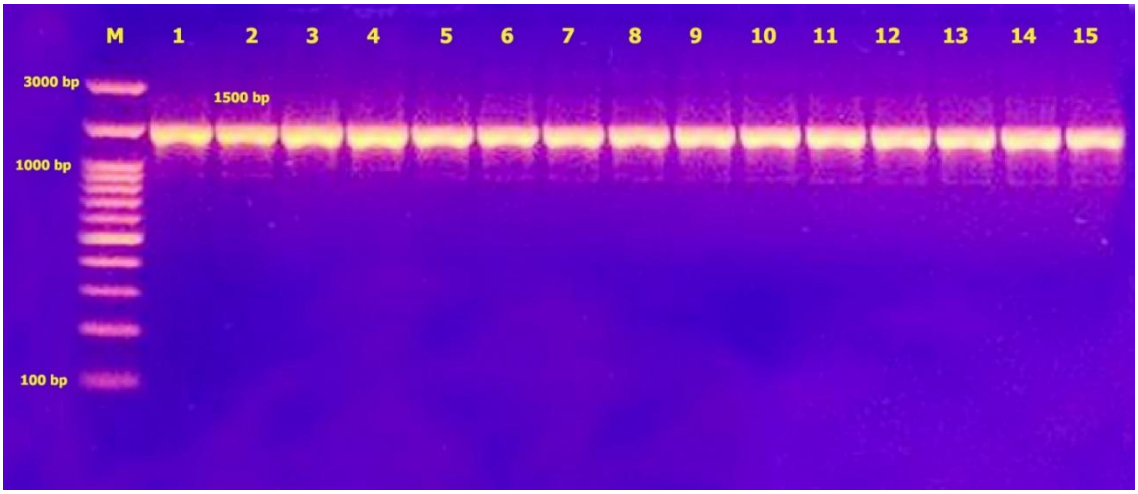

Figure 1. Visualization of 16S rRNA gene amplification in *Staphylococcus epidermidis* isolates applying 2% agarose gel electrophoresis. Lane M shows the molecular weight marker (100–3000 bp). Lanes 1 to 15 display PCR products from *S. epidermidis* isolates, each exhibiting bands at the expected fragment size

Antibiotic resistance profiles: Antibiotic susceptibility testing revealed diverse resistance patterns among CoNS species. All *S. epidermidis* isolates (100%) were resistant to amoxicillin. High resistance was also observed for cefotaxime (71.43%), ceftriaxone (78.57%), gentamicin (89.29%), and levofloxacin (75.00%). Moderate resistance was noted for imipenem and meropenem (each 50.00%). In contrast, *S. saprophyticus* exhibited lower resistance rates, with 72.73% of isolates resistant to amoxicillin, 54.55% to cefotaxime and ceftriaxone, and 81.82% to gentamicin. Resistance to meropenem was the lowest at 27.27%. *S. hominis* demonstrated complete sensitivity to imipenem and meropenem (0% resistance), with resistance to other antibiotics ranging from 37.50% (levofloxacin) to 75.00% (gentamicin). *S. haemolyticus* showed consistently high resistance across all tested antibiotics, with 100% resistance to levofloxacin and elevated resistance to amoxicillin (85.71%), cefotaxime (71.43%), ceftriaxone (71.43%), and gentamicin (85.71%). These results highlight a concerning prevalence of multidrug-resistant CoNS, exclusively *S. epidermidis*, among hemodialysis patients. The observed resistance patterns underscore the need for targeted antimicrobial stewardship and routine surveillance in dialysis units to curb the spread of resistant strains.

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Table 2. Antibiotic resistance profile of CoNS isolates from hemodialysis patients

Antibiotic	*S. epidermidis*	*S. saprophyticus*	*S. hominis*	*S. haemolyticus*
AMX (10 µg)	100%	72.73%	62.50%	85.71%
CTM (30 µg)	71.43%	54.55%	50.00%	71.43%
CTX (30 µg)	78.57%	54.55%	50.00%	71.43%
CN (10 µg)	89.29%	81.82%	75.00%	85.71%
LFN (5 µg)	75.00%	63.64%	37.50%	100%
IMI (5 µg)	50.00%	45.45%	0%	28.57%
MEM (10 µg)	50.00%	27.27%	0%	14.29%

The predominance of *Staphylococcus epidermidis* among CoNS isolates in this investigation aligns with previous reports, containing those by Mohan et al. (2002), Cuevas et al. (2004), and Keogh et al. (2015), which similarly identified *S. epidermidis* as a leading cause of nosocomial infections in clinical settings. In contrast, some investigations, like D'Azevedo et al. (2008), announced *S. haemolyticus* as the dominant CoNS species. These discrepancies may stem from variations in sample types, patient populations, or geographical regions, highlighting the importance of local epidemiological data. The high prevalence of *S. epidermidis* in this investigation underscores its role as a meaningful opportunistic pathogen, exclusively in hemodialysis patients undergoing invasive procedures. Its ubiquitous presence on human skin, coupled with its capability to form biofilms on medical devices, enhances its pathogenicity (Piette and Verschraegen, 2009; David et al., 2023). Although *S. epidermidis* is a commensal organism, its increasing involvement in nosocomial infections, especially among immunocompromised patients, poses a meaningful clinical challenge (Prasad et al., 2012). *S. saprophyticus*, the second most common species in this investigation, is typically related to urinary tract infections but was detected in bloodstream infections here, suggesting its adaptability as an opportunistic pathogen. Its moderate resistance levels indicate partial susceptibility to antibiotics, but vigilance is warranted to prevent the emergence of resistant strains. Similarly, *S. hominis* and *S. haemolyticus*, though less often extracted, exhibited meaningful multidrug resistance, consistent with results by

Kavitha and Shaik (2014) and Daniel et al. (2014). Notably, the complete sensitivity of *S. hominis* to imipenem and meropenem suggests these agents may stay effective therapeutic options for certain CoNS infections. The 100% resistance of *S. epidermidis* to amoxicillin observed in this investigation exceeds the 85.7% announced by Jiyad (2023). Resistance to cefotaxime, ceftriaxone, and meropenem was also higher than previously announced, denoting an alarming trend in multidrug resistance. These results are consistent with global reports of *S. epidermidis* resistance to beta-lactam antibiotics, driven by mechanisms like β-lactamase production and alterations in penicillin-binding proteins (Otto, 2014). CoNS, exclusively *S. haemolyticus*, are known reservoirs for antibiotic resistance genes, facilitating their dissemination through horizontal gene transfer via mobile genetic elements like plasmids and transposons (Barros et al., 2012; Miragaia et al., 2002; Ventola, 2015). Additionally, efflux pumps, which actively expel antibiotics from bacterial cells, contribute meaningfully to resistance, reducing the efficacy of antibacterial agents (Nikaido, 2003; Orna, 2018). These mechanisms highlight the genetic adaptability of CoNS and their potential to drive resistance in clinical settings. To address the rising threat of multidrug-resistant CoNS, this investigation emphasizes the need for stringent infection control measures, containing enhanced hygiene protocols and regular monitoring of resistance patterns in dialysis units. Routine surveillance can inform empirical therapy choices and limit the spread of resistant strains. Furthermore, molecular investigations targeting resistance genes and their transfer mechanisms are critical to developing novel therapeutic strategies.

Conclusions: This investigation reaffirms the clinical significance of CoNS, exclusively *S. epidermidis*, in bloodstream infections among hemodialysis patients. The high prevalence of multidrug resistance underscores the growing threat of these nosocomial pathogens. Their frequent involvement in dialysis-related infections and robust resistance to commonly prescribed antibiotics highlight the urgent need for routine antimicrobial resistance monitoring in dialysis units. Implementing rigorous infection control measures, applying antibiotics judiciously, and conducting molecular investigations to track resistance gene dissemination are essential steps to mitigate the spread of resistant CoNS. Addressing these challenges is critical to improving patient outcomes and reducing treatment complexities in this vulnerable population.

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Author contributions

Conceptualization: L.A. and B.A.; Methodology: L.A. and B.A.; Validation: L.A.; Formal Analysis: L.A. and B.A.; Investigation: L.A.; Data Curation: B.A.; Writing—Original Draft: L.A. and B.A.; Writing—Review and Editing: L.A. and B.A.; Visualization: B.A.; Supervision: L.A.; Project Administration: L.A.; Funding Acquisition: L.A. and B.A. All authors have reviewed and approved the final manuscript for submission.

Data availability statement

The datasets generated and analyzed through this investigation are not publicly available due to ethical and privacy restrictions. Requests for access to the data may be directed to the corresponding author and will be attended subject to approval by the institutional authorities at the University of Al-Qadisiyah.

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Ethical considerations

This investigation adhered strictly to the ethical principles set forth in the Declaration of Helsinki. The research protocol was approved by the Institutional Review Board and the Research Ethics Committee at the University of Al-Qadisiyah, Iraq (IQ-UAQ.RES.2023.629). Written informed consent was achieved from all participants prior to their inclusion. Participants were fully informed about the investigation's objectives, procedures, potential risks, and benefits and were assured of their right to withdraw at any time without repercussions. All personal and sensitive data were anonymized and managed with the highest standards of confidentiality to safeguard participant privacy.

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Conflict of interest

The authors declare no conflicts of interest related to this research. No financial, personal, or professional relationships exist that could have biased the design, conduct, or reporting of this investigation.

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شیوع و الگوهای مقاومت آنتی‌بیوتیکی استافیلوکوک‌های منفی‌کوآگولاز جدا شده از بیماران همودیالیزی

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چکیده

هدف: استافیلوکوک‌های منفی‌کوآگولاز (CoNS) به‌عنوان پاتوژن‌های بیمارستانی مهم، به‌ویژه در جمعیت‌های دارای نقص ایمنی مانند بیماران همودیالیزی، به دلیل توانایی تشکیل بیوفیلم و مقاومت چندگانه به آنتی‌بیوتیک‌ها، برجسته شده‌اند. این مطالعه با هدف تعیین شیوع و الگوهای مقاومت آنتی‌بیوتیکی CoNS جدا شده از بیماران همودیالیزی برای اطلاع‌رسانی به استراتژی‌های هدفمند کنترل عفونت انجام شد.

مواد و روش‌ها: نمونه‌های خون وریدی از ۱۰۰ بیمار همودیالیزی در بیمارستان عمومی الدیوانیه با استفاده از سرنگ‌های استریل جمع‌آوری شد. نمونه‌ها روی آگار نمک مانیتول و آگار خون کشت داده شدند تا کلنی‌های باکتریایی جدا شوند. ایزوله‌ها تحت رنگ‌آمیزی گرم قرار گرفتند تا خلوص، مورفولوژی و وضعیت گرم‌مثبت تأیید شود. استافیلوکوک‌های منفی‌کوآگولاز (CoNS) از طریق آزمایش کوآگولاز شناسایی شدند و گونه‌ها با استفاده از تکثیر PCR ژن 16S rRNA با استفاده از پرایمرهای 27F -(5' AGAGTTTGATCMTGGCTCAG-3') و 1492R (5'-TACGGYTACCTTGTTACGACTT-3') تأیید شدند. حساسیت آنتی‌بیوتیکی به آموکسی‌سیلین، سفتاکسیم، سفتریاکسون، جنتامایسین، لووفلوکساسین، ایمی‌پنم، مروپنم، سیپروفلوکساسین و داکسی‌سایکلین با استفاده از روش دیسک دیفیوژن Kirby-Bauer و بر اساس دستورالعمل‌های موسسه استانداردهای بالینی و آزمایشگاهی (CLSI) ارزیابی شد. قطر مناطق مهار پس از ۲۴ ساعت انکوباسیون در دمای ۳۷ درجه سانتی‌گراد اندازه‌گیری و بر اساس استانداردهای سازنده تفسیر شد.

نتایج: از ۱۰۰ نمونه بالینی بیماران همودیالیزی، ۵۴ درصد (۱۰۰/۵۴) برای استافیلوکوک‌های منفی‌کوآگولاز (CoNS) مثبت بودند. استافیلوکوک اپیدرمیدیس شایع‌ترین گونه بود که ۵۱.۸۵ درصد (۲۸/۵۴) از ایزوله‌ها را تشکیل می‌داد، پس از آن استافیلوکوک

ساپروفیتیکوس (۲۰.۳۷ درصد، ۱۱/۵۴)، استافیلوکوک هومینیس (۱۶.۶۷ درصد، ۹/۵۴) و استافیلوکوک همولیتیکوس (۱۱.۱۱ درصد، ۶/۵۴) قرار داشتند. تمام ایزوله‌های استافیلوکوک اپیدرمیدیس مقاومت ۱۰۰ درصدی به آموکسی‌سیلین نشان دادند و نرخ‌های مقاومت بالایی به جنتامایسین (۸۹.۲۸ درصد)، سفتریاکسون (۷۸.۵۷ درصد)، سفتاکسیم (۷۱.۴۲ درصد)، لووفلوکساسین (۷۵ درصد)، ایمی‌پنم (۵۰ درصد) و مروپنم (۵۰ درصد) داشتند. ایزوله‌های استافیلوکوک ساپروفیتیکوس مقاومت کمتری نشان دادند، به‌طوری‌که ۷۲.۷۲ درصد به آموکسی‌سیلین، ۵۴.۵۴ درصد به سفتاکسیم و سفتریاکسون، ۸۱.۸۱ درصد به جنتامایسین و ۶۳.۶۳ درصد به لووفلوکساسین مقاوم بودند. استافیلوکوک هومینیس و استافیلوکوک همولیتیکوس الگوهای مقاومت متغیری نشان دادند، به ترتیب با ۶۶.۶۷ تا ۸۸.۸۹ درصد و ۵۰ تا ۸۳.۳۳ درصد مقاومت به آنتی‌بیوتیک‌های آزمایش‌شده. مقاومت چندگانه (مقاومت به سه یا بیشتر کلاس آنتی‌بیوتیکی) در ۶۴.۸۱ درصد (۵۴/۳۵) از ایزوله‌های CoNS مشاهده شد.

نتیجه‌گیری: این یافته‌ها لزوم اجرای اقدامات قوی کنترل عفونت، از جمله پروتکل‌های بهبودیافته مراقبت از کاتتر، نظارت منظم بر الگوهای مقاومت و برنامه‌های مدیریت آنتی‌بیوتیکی برای بهینه‌سازی استفاده از آنتی‌بیوتیک‌ها را ضروری می‌سازد. علاوه بر این، پروفایل‌های مقاومت متغیر استافیلوکوک هومینیس و استافیلوکوک همولیتیکوس نیاز به رویکردهای درمانی خاص برای هر گونه را نشان می‌دهد. تحقیقات آینده باید بر روشن‌سازی مکانیسم‌های مولکولی مقاومت و بررسی درمان‌های جایگزین، مانند آنتی‌بیوتیک‌های نوین یا عوامل مختل‌کننده بیوفیلم، برای کاهش خطر عفونت‌های مرتبط با CoNS در محیط‌های بالینی تمرکز کند.

کلمات کلیدی: مقاومت آنتی‌بیوتیکی، استافیلوکوک‌های منفی‌کوآگولاز، بیماران همودیالیزی، عفونت‌های بیمارستانی، استافیلوکوک اپیدرمیدیس

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