

Bacterial Profile of the Hands of Healthcare Professionals Working in ICUs and Wards of a Tertiary Healthcare Setup

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ABSTRACT

Background: Bacterial contamination on the hands of healthcare workers (HCWs) acts as a critical transmission bridge for healthcare-associated infections (HAIs). Monitoring the bacterial profiles and antimicrobial resistance (AMR) patterns on HCWs' hands is vital for strengthening hospital infection control workflows. **Materials and Methods:** This prospective study evaluated hand swabs from 100 active on-duty HCWs across ICUs and wards over a six-month period (February–July 2023). Swabs were processed on blood agar media, and bacterial strains were identified via phenotypic and biochemical screening. Antibiotic sensitivity profiling was executed utilizing the Kirby-Bauer disk diffusion method. **Results:** Of the 100 processed samples, 27% were sterile, 31% showed monomicrobial growth, and 42% yielded polymicrobial growth. Out of 126 valid microbial growths isolated, Gram-positive cocci (GPC) were highly dominant at 85.7% (n=108), comprising Coagulase-Negative Staphylococci (CoNS; (n=81), 64.3%), *Micrococcus* (n=26), 20.6%), and *Staphylococcus aureus* (n=1), 0.8%). Phenotypic AMR detection highlighted that 11.1% of the CoNS isolates were methicillin-resistant (MR-CoNS) via cefoxitin disk testing. The single *S. aureus* strain was methicillin-sensitive (MSSA), and two *Acinetobacter* spp. isolates were fully pan-susceptible. **Conclusion:** While normal skin flora and benign commensals predominated, the isolation of opportunistic pathogens like MR-CoNS underlines the perpetual risk of cross-contamination and the continuous need for rigorous hand hygiene enforcement.

Keywords: Healthcare-associated infections; Hand hygiene; Healthcare workers; Coagulase-negative Staphylococci; Methicillin resistance; Antimicrobial susceptibility.

INTRODUCTION

The term healthcare-associated infections (HAIs) presents a significant threat to global patient health, notably appearing 48 hours or more post-admission¹. Hospital environments like Intensive Care Units (ICUs) and acute surgical wards handle highly vulnerable, immunocompromised populations undergoing continuous invasive procedures². Transient and resident bacterial flora persisting on the hands of healthcare providers act as primary vectors for spreading pathogens between contaminated patient surroundings and sterile bodily sites³.

While a large portion of skin microflora acts as beneficial commensals that control pathogenic colonization, continuous exposure to the hospital environment can allow virulent bacteria or multi-drug resistant organisms (MDROs) to establish residency on HCWs' skin. Although institutional hand hygiene models like the World Health Organization (WHO) "Five Moments for Hand Hygiene" are widely acknowledged, real-world compliance frequently dips below 50%⁴. This study maps the microbiological landscape and AMR baseline trends of active clinical staff at a major tertiary care center in

Uttarakhand to improve regional infection control frameworks.

MATERIALS AND METHODS

Study Design and Participant Selection

This prospective cross-sectional study was carried out at the Department of Microbiology, Government Medical College, Haldwani, spanning six months from January to June 2026. A sample size of 100 non-repetitive, on-duty healthcare workers actively handling patient care was selected. The cohorts included doctors (30%), nurses (33%), medical interns/students (20%), attendants (9%), housekeeping personnel (4%), and laboratory technicians (4%). Informed, signed, or thumb-imprinted consent was captured from every participant prior to sampling.

- **Inclusion Criteria:** Active clinical staff on regular shifts who had not washed or sanitized their hands for at least 10 minutes prior to evaluation.
- **Exclusion Criteria:** Individuals with visibly wet hands, those who sanitized within the 10-minute window, or those refusing voluntary participation.

Sample Collection and Isolation

Sterile cotton swabs pre-moistened with normal saline (0.9% NaCl) were rubbed vigorously across defined anatomical target sites on both hands, covering the palms, interdigit finger webs, fingertips, and thenar zones. Swabs were immediately transferred to the microbiology laboratory, streaked across 5% sheep blood agar plates, and incubated under aerobic conditions in a biochemical oxygen demand (BOD) incubator at 37°C for 24 hours.

Phenotypic Characterization and Biochemical Identification

Grown macro-colonies were analyzed based on morphological attributes and evaluated via Gram staining. Standard systematic biochemical panels were run for comprehensive identification, utilizing catalase testing,

slide/tube coagulase assays, mannitol fermentation, triple sugar iron (TSI) agar, citrate utilization, Christensen's urease testing, phenyl-alanine deaminase (PPA), Voges-Proskauer (VP), Methyl Red (MR), indole production, and cytochrome oxidase reactions.

Antimicrobial Susceptibility Testing (AST)

Pure sub-cultures were subjected to in-vitro disk diffusion tracking using the Kirby-Bauer method on Mueller-Hinton media according to Clinical and Laboratory Standards Institute (CLSI) references. Phenotypic methicillin-resistance testing among *Staphylococcus* isolates was verified using a cefoxitin (30µg) disk, acting as the validated surrogate marker for tracking the *mecA* gene layout⁵.

Ethical Approval

The study protocol was reviewed and approved by the Institutional Ethics Committee of Government Medical College & Dr. Susheela Tiwari Government Hospital, Haldwani. Written informed consent was obtained from all participants before sample collection.

Statistical Analysis

Data were entered into Microsoft Excel and analyzed using SPSS version 26.0. Descriptive statistics were expressed as frequencies and percentages. Associations between categorical variables were assessed using the Chi-square test. A p-value <0.05 was considered statistically significant.

RESULTS

The sampling split effectively captured the tiered staffing hierarchy of the facility. Out of the 100 distinct processed profiles, 27% (n=27) yielded completely sterile results with no microbial growth. Monomicrobial isolation was noted in 31% (n=31) of samples, while polymicrobial growth was confirmed in 42% (n=42) of cases.

Table 1: Distribution of Healthcare Worker Categories (N=100)

Staff Category	Participant Count	Percentage Representation (%)
Nurses	33	33
Doctors	30	30
Students / Interns	20	20
Clinical Attendants	9	9
Housekeeping Staff	4	4
Lab Technicians	4	4

A total of 127 initial microbial isolates were recovered. One contaminant environmental fungal growth (*Rhizopus*) was excluded from the analytical baseline, leaving a finalized active cohort of(N=126) bacterial cultures. Gram-positive cocci (GPC) formed the large majority at 85.7% (n=108). Biochemical testing divided the 108 GPC strains into three clear clusters: Coagulase-Negative Staphylococci (CoNS; (n=81, 64.3%), *Micrococcus* spp. (n=26, 20.6%), and *Staphylococcus*

aureus (n=1, 0.8%). Non-GPC strains included 13 Aerobic Spore Bearers (ASB; 10.3%), 3 Diphtheroids/Gram-positive bacilli (GPB; 2.4%), and 2 Gram-negative *Acinetobacter* spp. (1.6%).

DISCUSSION

This evaluation shows that hand contamination among active staff remains well-managed at this tertiary setup compared to historical studies. For instance, comparative literature by Singh *et al.* reported an *S. aureus* carriage rate of 47.5% across 200 subjects, with over half (52.6%) confirmed as MRSA⁶. Similarly, ICU baselines tracked by Mathew *et al.* highlighted a 16.67% *S. aureus* colonization rate⁷. In contrast, this cohort displayed a low *S. aureus* prevalence of 0.8% (n=1), with zero incidence of phenotypic MRSA.

The high prevalence of CoNS (64.3%), *Micrococcus* (20.6%), Aerobic Spore Bearers (10.3%), and Diphtheroids (2.4%) reflects typical resident human skin flora. Out of 81 valid CoNS isolates, 11.1% (n=9) demonstrated resistance against the cefoxitin (30 µg) threshold, classifying them as Methicillin-Resistant CoNS (MR-CoNS). When introduced into deep sterile tissues via central lines or surgical access points, these opportunistic, resistant commensals can cause severe device-associated infections (DAIs).

Limitations

This study was conducted at a single tertiary care hospital with a relatively small sample size. Molecular characterization of resistance genes such as *mecA* was not performed, and only culture-based methods were employed. Therefore, the findings may not be generalizable to all healthcare settings.

Strengths of the Study

This study provides baseline data on the bacterial flora present on the hands of healthcare workers in a tertiary care hospital in Uttarakhand, a region where such data are limited. The inclusion of different categories of healthcare professionals working in ICUs and wards offers a comprehensive overview of hand contamination patterns across various clinical settings. Standard microbiological techniques and CLSI-guided antimicrobial susceptibility testing were used to ensure reliable identification of bacterial isolates and resistance patterns. The findings can assist hospital infection control committees in strengthening hand hygiene practices and antimicrobial stewardship programs.

CONCLUSION

This study shows that while benign resident flora and commensal organisms dominate the hands of active healthcare professionals at the facility, a persistent fraction of methicillin-resistant strains (MR-CoNS) remains active. Hand hygiene compliance continues to be the primary barrier against the selection and transmission

of healthcare-associated pathogens. To maintain these favorable patterns, the institution should focus on regular educational reviews for clinical students, continuous compliance tracking, and accessible bedside alcohol-based rubs.

Future Recommendations

Regular surveillance of hand flora, periodic antimicrobial resistance monitoring, reinforcement of WHO hand hygiene practices, and molecular characterization of resistant isolates are recommended.

Data Availability Statement

The datasets generated during the current study are available from the corresponding author upon reasonable request.

Author Contributions

Shambhavi Singh: Conceptualization, study design, sample collection, laboratory investigations, data analysis, manuscript drafting, and corresponding author responsibilities.

Neha Kaushal: Study supervision, methodology development, interpretation of microbiological findings, critical revision of the manuscript, and final approval.

Reeta: Laboratory support, data collection, validation of results, manuscript review, and final approval of the submitted version.

All authors read and approved the final manuscript and agree to be accountable for all aspects of the work.

Conflict of Interest

The authors declare no conflict of interest.

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