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Bacterial Contamination Burden, Site Distribution and Cumulative Wearing-Day Changes on Long-Sleeved Nurses' Uniforms in a Respiratory Ward: A Real-World Repeated-Measures Observational Study

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Research Article

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Abstract

Background

Evidence remains limited on how bacterial contamination burden is distributed across sites on long-sleeved nurses' uniforms and how it changes during cumulative wearing under real-world nursing conditions. This study evaluated site distribution, cumulative wearing-workday changes and high-contamination patterns of bacterial burden on long-sleeved nurses' uniforms in a respiratory ward.

Methods

This single-centre repeated-measures observational study included 12 registered nurses in a respiratory ward of a tertiary teaching hospital. Each nurse wore the same hospital-laundered long-sleeved uniform. Samples were collected from seven predefined uniform sites on the 3rd, 5th and 7th cumulative wearing workdays at 10:00 and 16:00, yielding 504 valid sampling points. Total bacterial colony counts were measured by standardized area swabbing and expressed as CFU/100 cm². A linear mixed-effects model (LMM) was used to analyse contamination burden.

Results

Bacterial growth was detected in 90.9% of sampling points. The median colony count was 80.0 CFU/100 cm², with a right-skewed distribution and extreme high-contamination values. Unadjusted analyses showed significant differences across sampling sites and cumulative wearing workdays. In the mixed-effects model, the 5th and 7th cumulative wearing workdays were associated with higher contamination burden than the 3rd workday, whereas no significant difference was observed between 10:00 and 16:00.

Conclusions

Long-sleeved nurses' uniform contamination in a respiratory ward was common and characterized by uneven site distribution, wearing-workday-related changes and a skewed burden pattern. Uniform monitoring should focus on contamination burden, high-contact sites and cumulative wearing stages rather than bacterial detection alone.

Introduction

Microbial contamination of healthcare workers' uniforms is a practical concern in nursing infection prevention and control. During patient care, uniforms are repeatedly exposed to clinical environments and may come into contact with nurses' hands, patients, bedside surfaces and care-related devices [1, 2]. Unlike fixed environmental surfaces, nurses' uniforms are wearable textile surfaces that move with healthcare workers across bedsides and care locations. Their contamination may therefore be

influenced not only by textile material, laundering processes and microbial characteristics, but also by actual use conditions and cumulative exposure during clinical work [3–5].

Respiratory wards may be particularly relevant for studying nurses' uniform contamination. Patients in these wards often require close nursing care related to cough, sputum production, oxygen therapy, nebulization, repositioning and respiratory device use. These activities create repeated opportunities for contact between uniforms, nurses' hands, patients, bedside environments and care-related devices. For long-sleeved uniforms, areas such as pockets, sleeves, the abdomen and waist may be exposed differently during routine respiratory nursing care.

Previous studies have shown that healthcare workers' attire, including white coats, scrubs and nurses' uniforms, can become contaminated during clinical work [6, 7]. Contamination has been detected on high-contact areas such as pockets, sleeves, cuffs, abdominal areas and waist areas [8, 9]. Systematic reviews and guidance documents have also suggested that healthcare personnel attire should be considered in infection prevention discussions, although the clinical significance of attire contamination remains incompletely defined [10]. These findings suggest that the important question is not only whether healthcare attire can be contaminated, but also where contamination occurs and how the contamination burden changes during real-world use.

However, evidence remains limited. Many studies assessed uniform contamination at a single time point or after work shifts, and some were conducted in intensive care or other non-respiratory settings [11, 12]. Studies evaluating contamination after an 8-hour workday or comparing antimicrobial and conventional scrubs have not repeatedly examined the same type of long-sleeved nurses' uniform across predefined cumulative wearing workdays [13, 14]. Although studies on bacterial transfer after patient contact and on the influence of uniform type and wearing duration suggest that exposure conditions may affect healthcare apparel contamination, repeated-measures evidence from respiratory wards and multiple predefined uniform sites remains scarce [15–18].

This evidence gap is relevant to nursing practice. In many clinical settings, uniform monitoring and replacement decisions are based mainly on routine management practices rather than on site-specific or wearing-stage-related contamination data. Understanding how bacterial contamination burden differs across uniform sites and cumulative wearing stages may help identify priority areas for monitoring and inform future nursing infection prevention strategies.

To address this gap, we conducted a single-centre real-world repeated-measures observational study in a respiratory ward. Seven predefined sites on hospital-laundered long-sleeved nurses' uniforms were repeatedly sampled on the 3rd, 5th and 7th cumulative wearing workdays at two predefined daytime observation points. This study aimed to describe bacterial contamination burden and analyse its site distribution, cumulative wearing-workday-related changes and high-contamination patterns under real-world respiratory nursing conditions.

Methods

Study design and setting

This single-centre repeated-measures observational study was conducted in a respiratory ward of a tertiary teaching hospital from April to May 2026. The study was performed under real-world nursing conditions without changing routine nursing procedures, uniform wearing practices, hospital laundering processes or ward infection prevention and control measures. The reporting was guided by the STROBE statement.

Study participants

Registered nurses who provided routine clinical care in the respiratory ward and wore hospital-issued long-sleeved uniforms managed through the hospital's centralized laundering process were eligible. Twelve nurses were included and anonymized using codes A–L. Each nurse wore the same long-sleeved uniform throughout the predefined sampling schedule. Sampling would be terminated if the uniform was changed early because of visible contamination, damage, clinical work requirements or personal reasons, or if the predefined sampling schedule could not be completed.

Sampling design

A cumulative wearing workday was defined as a workday on which the same uniform was worn by the same nurse during routine nursing work after centralized laundering and return to clinical use. The first clinical wearing day was defined as the 1st wearing workday. Surface sampling was performed on the 3rd, 5th and 7th cumulative wearing workdays. Seven predefined sampling sites were selected: abdomen, left waist, right waist, left sleeve, right sleeve, left pocket and right pocket **(Fig. 1**).

Sampling was performed at 10:00 and 16:00 on each sampling day. These were predefined daytime observation points, not strict pre-shift or post-shift points. Each nurse was scheduled to contribute 42 sampling points, yielding 504 planned sampling points in total.

Uniform laundering and storage

All uniforms were centrally laundered and managed by the hospital. The routine laundering process included sorting, two prewash cycles at 45 °C, a main wash at 75–80 °C, rinsing and neutralization, drying, folding, packaging and delivery. During the study period, uniforms were used and stored according to routine ward practice. After work, uniforms were not taken out of the ward and were not personally washed, disinfected or otherwise treated. Routine hygienic monitoring during the same period showed that 35 clean medical textile samples met WS/T 508—2025 requirements [19]. No separate baseline sampling was performed for each uniform before clinical use.

Microbiological methods

Bacterial contamination was measured using a standardized area swabbing method with reference to routine hygienic monitoring procedures [20]. Samples were collected from the outer surface of uniforms. For each site, a disposable bacterial sampling swab was used to swab a 10 cm × 10 cm area, corresponding to 100 cm². The swab was placed into 10 mL of neutralizing sampling solution containing sodium thiosulfate and sent for microbiological testing.

After mixing, two 1-mL aliquots were inoculated into two sterile Petri dishes. Nutrient agar medium was added, and samples were cultured using the pour plate method at 36 ± 1 °C for 48 h. Colonies on the two plates were counted, and the mean colony count was used for calculation. The total bacterial colony count was calculated as CFU/100 cm² = mean colony count of the two plates × 10. Only total bacterial colony counts were measured; species identification, antimicrobial susceptibility testing and molecular typing were not performed.

Outcome definitions

The primary outcome was the total bacterial colony count on nurses' uniforms, expressed as CFU/100 cm². Bacterial growth positivity was defined as > 0 CFU/100 cm². A colony count > 200 CFU/100 cm² was defined as a research-defined high-contamination sampling point according to the hygienic requirement for clean medical textiles in WS/T 508—2025 [19]. A colony count > 1000 CFU/100 cm² was defined as a research-defined extreme high-contamination sampling point according to the ≤ 10 CFU/cm² limit for class III environmental object surfaces in WS/T 367—2012, converted to a 100 cm² sampling area [21]. These thresholds were used only for research-based stratification and were not intended to determine the qualification status of in-use uniforms or infection risk.

Statistical analysis

Colony counts were expressed as CFU/100 cm². Because colony counts were right-skewed, continuous variables were described using medians and interquartile ranges. Categorical variables were described using frequencies and percentages. Raw colony count distributions were compared using the Kruskal–Wallis test across sampling sites and cumulative wearing workdays, and the Mann–Whitney U test between the two predefined daytime sampling points.

For model analysis, colony counts were transformed using $\log_{10}$(CFU/100 cm² + 1). A linear mixed-effects model (LMM) was used to analyse the associations of sampling site, cumulative wearing workday and predefined daytime sampling point with contamination burden, with nurse code included as a random intercept.Generalized estimating equation logistic regression models were used as supplementary analyses for research-defined high-contamination and extreme high-contamination sampling points, with nurse code as the clustering variable. Sensitivity analysis repeated the main model after excluding the six highest colony counts. All tests were two-sided, and $p < 0.05$ was considered statistically significant. Analyses were performed using R software version 4.4.1.

Ethics approval and consent to participate

This study was approved by the Clinical Research Ethics Committee of the First Affiliated Hospital of Wenzhou Medical University (Acceptance No. KY2026-280; Approval No. 2026-280). The study was conducted in accordance with the principles of the Declaration of Helsinki. All participating nurses provided informed consent and were recorded using anonymous study codes.

Results

Sample structure and overall contamination burden

A total of 12 registered nurses were included, yielding 504 valid sampling points. Each nurse contributed 42 sampling points. The dataset was balanced across the study design, with 72 points for each sampling site, 168 points for each cumulative wearing workday and 252 points for each predefined daytime sampling point.

The overall colony count ranged from 0 to 9520 CFU/100 cm². The median colony count was 80.0 CFU/100 cm² (IQR, 30.0–232.5), and the mean was 299.8 ± 788.2 CFU/100 cm² (**Table 1**). Bacterial growth was detected in 458 of 504 sampling points, corresponding to a positivity rate of 90.9%. The proportions of sampling points with colony counts > 200 CFU/100 cm² and > 1000 CFU/100 cm² were 27.4% and 6.2%, respectively (**Table 2**). The distribution was right-skewed, as indicated by the marked difference between the mean and median values and the presence of extreme high values.

Table 1 Distribution of bacterial contamination burden on long-sleeved nurses' uniforms

Group	*n*	Median	IQR	Mean ± SD	Max
Overall	504	80.0	30.0–232.5	299.8 ± 788.2	9520
Abdomen	72	90.0	30.0–370.0	289.3 ± 444.1	2350
Left waist	72	55.0	20.0–217.5	217.2 ± 509.1	3960
Right waist	72	50.0	20.0–135.0	199.2 ± 732.5	6170
Left sleeve	72	65.0	30.0–217.5	225.3 ± 489.9	3360
Right sleeve	72	55.0	30.0–175.0	302.5 ± 674.1	3620
Left pocket	72	120.0	50.0–252.5	460.8 ± 1248.1	9520
Right pocket	72	135.0	60.0–242.5	404.2 ± 1046.7	6240
Wearing day 3	168	55.0	20.0–150.0	248.7 ± 928.4	9520
Wearing day 5	168	110.0	40.0–252.5	335.6 ± 745.8	6240
Wearing day 7	168	90.0	30.0–290.0	315.1 ± 670.0	5310
10:00	252	80.0	30.0–210.0	257.4 ± 607.8	6170
16:00	252	80.0	30.0–240.0	342.2 ± 933.7	9520

Note: Colony counts are expressed as CFU/100 cm². IQR, interquartile range; SD, standard deviation.

Table 2 Bacterial growth positivity and high-contamination sampling points

Group	*n*	Bacterial growth positivity, %	> 200, %	> 1000, %
Overall	504	90.9	27.4	6.2
Abdomen	72	90.3	31.9	6.9
Left waist	72	86.1	29.2	4.2
Right waist	72	87.5	20.8	1.4
Left sleeve	72	95.8	27.8	2.8
Right sleeve	72	88.9	23.6	8.3
Left pocket	72	93.1	27.8	13.9
Right pocket	72	94.4	30.6	5.6
Wearing day 3	168	86.9	17.9	3.0
Wearing day 5	168	91.1	32.1	7.1
Wearing day 7	168	94.6	32.1	8.3
10:00	252	88.1	25.8	5.6
16:00	252	93.7	29.0	6.7

Note: Bacterial growth positivity was defined as a colony count > 0 CFU/100 cm². Colony counts > 200 CFU/100 cm² and > 1000 CFU/100 cm² were used as research-defined stratification thresholds.

Contamination distribution by sampling site

In the unadjusted comparison, colony count distributions differed significantly across sampling sites (Kruskal–Wallis test, $p = 0.0025$; **Fig. 2**). The right and left pockets showed the highest median colony counts, followed by the abdomen (**Table 1**). The proportion of sampling points with colony counts > 1000 CFU/100 cm² was highest on the left pocket (**Table 2**). These results indicated uneven site distribution.

When sampling site and cumulative wearing workday were examined together, site-specific patterns were not uniform over time. The median colony count on the left pocket increased across cumulative wearing workdays, whereas the right pocket, left sleeve and some waist areas showed higher values on the 5th cumulative wearing workday followed by lower values on the 7th cumulative wearing workday (**Fig. 3**).

Colony counts are shown as $\log_{10}(\text{CFU}/100\ \text{cm}^2 + 1)$. Boxes indicate interquartile ranges, horizontal lines indicate medians and dots indicate individual sampling points.

Colour intensity represents the median colony count for each combination of sampling site and cumulative wearing workday. Values within cells indicate median colony counts, expressed as CFU/100 cm².

Contamination changes by cumulative wearing workday and daytime sampling point

In the unadjusted comparison, colony count distributions differed significantly across cumulative wearing workdays (Kruskal–Wallis test, $p = 0.0003$; **Fig. 4**). Median colony counts were higher on the 5th and 7th cumulative wearing workdays than on the 3rd cumulative wearing workday (**Table 1**). The proportion of sampling points with colony counts > 200 CFU/100 cm² increased from 17.9% on the 3rd cumulative wearing workday to 32.1% on both the 5th and 7th cumulative wearing workdays (**Table 2**). However, the 7th cumulative wearing workday was not higher than the 5th cumulative wearing workday, and no monotonic increase in contamination burden was observed.

No significant difference in colony count distribution was observed between the two predefined daytime sampling points, 10:00 and 16:00 ($p = 0.5384$; **Fig. 4**). The median colony count was 80.0 CFU/100 cm² at both time points (**Table 1).**

The y-axis shows $\log_{10}$(CFU/100 cm² + 1)-transformed colony counts. Points indicate medians and error bars indicate interquartile ranges. The 10:00 and 16:00 sampling points were predefined daytime observation points rather than strict pre-shift or post-shift points.

Adjusted associations with contamination burden

In the LMM, cumulative wearing workday remained associated with bacterial contamination burden after adjustment for sampling site, predefined daytime sampling point and within-nurse repeated sampling correlation (**Table 3**). Compared with the 3rd cumulative wearing workday, both the 5th cumulative wearing workday ($\beta = 0.286$, 95% CI: 0.126–0.445, $p < 0.001$) and the 7th cumulative wearing workday ($\beta = 0.309$, 95% CI: 0.150–0.469, $p < 0.001$) were associated with higher contamination burden. No significant difference was observed between 16:00 and 10:00 ($\beta = 0.092$, 95% CI: -0.039 to 0.222, $p = 0.168$). Compared with the abdomen, the right waist showed a lower contamination burden, whereas pocket sites were not independently associated with higher contamination burden in the adjusted model. Thus, site-related findings were interpreted mainly as descriptive evidence of uneven distribution rather than independent site effects.

Table 3 Linear mixed-effects model for bacterial contamination burden on long-sleeved nurses' uniforms

Variable	*β* coefficient	Standard error	95% CI	*p* value
Intercept	1.676	0.131	1.419–1.933	< 0.001
Abdomen	Reference	—	—	—
Left waist	-0.230	0.124	-0.474–0.013	0.064
Right waist	-0.286	0.124	-0.529–-0.042	0.022
Left sleeve	-0.070	0.124	-0.314–0.173	0.571
Right sleeve	-0.149	0.124	-0.392–0.095	0.232
Left pocket	0.112	0.124	-0.132–0.355	0.368
Right pocket	0.134	0.124	-0.110–0.377	0.280
Wearing day 3	Reference	—	—	—
Wearing day 5	0.286	0.081	0.126–0.445	< 0.001
Wearing day 7	0.309	0.081	0.150–0.469	< 0.001
10:00	Reference	—	—	—
16:00	0.092	0.066	-0.039–0.222	0.168

Note: The dependent variable was $\log_{10}$(CFU/100 cm² + 1). Sampling site, cumulative wearing workday and predefined daytime sampling point were included as fixed effects, and nurse code was included as a random intercept. The abdomen, wearing day 3 and 10:00 were used as reference groups. A β value > 0 indicates a higher contamination burden compared with the reference group, whereas a β value < 0 indicates a lower contamination burden. CI, confidence interval.

High-contamination sampling points and sensitivity analysis

When colony counts > 200 CFU/100 cm² were defined as research-defined high-contamination sampling points, GEE logistic regression showed higher odds on the 5th and 7th cumulative wearing workdays than on the 3rd cumulative wearing workday, although these differences did not reach statistical significance (**Table 4**). When colony counts > 1000 CFU/100 cm² were defined as research-defined extreme high-contamination sampling points, the 7th cumulative wearing workday was associated with increased odds compared with the 3rd cumulative wearing workday (OR = 3.06, 95% CI: 1.08–8.68, p = 0.036). The predefined daytime sampling point was not significantly associated with either high-contamination or extreme high-contamination sampling points. Given the limited number of nurse-level clusters and extreme high-contamination events, the GEE logistic regression results were interpreted as supplementary evidence to the main LMM.

Table 4 GEE logistic regression analysis of high-contamination and extreme high-contamination sampling points

Variable	> 200 CFU/100 cm² OR	95% CI	*p* value	> 1000 CFU/100 cm² OR	95% CI	*p* value
Abdomen	Reference	—	—	Reference	—	—
Left waist	0.87	0.50–1.52	0.632	0.58	0.17–2.01	0.388
Right waist	0.55	0.28–1.11	0.095	0.18	0.03–1.13	0.068
Left sleeve	0.82	0.43–1.55	0.532	0.38	0.09–1.64	0.194
Right sleeve	0.65	0.35–1.23	0.185	1.22	0.44–3.40	0.700
Left pocket	0.82	0.41–1.61	0.556	2.20	0.55–8.77	0.266
Right pocket	0.94	0.42–2.06	0.869	0.79	0.22–2.77	0.707
Wearing day 3	Reference	—	—	Reference	—	—
Wearing day 5	2.19	0.99–4.84	0.052	2.57	0.84–7.83	0.096
Wearing day 7	2.19	0.93–5.14	0.072	3.06	1.08–8.68	0.036
10:00	Reference	—	—	Reference	—	—
16:00	1.18	0.87–1.60	0.288	1.24	0.53–2.93	0.623

Note: GEE, generalized estimating equation; OR, odds ratio; CI, confidence interval. Nurse code was used as the clustering variable. Sampling site, cumulative wearing workday and predefined daytime sampling point were included in the model. The abdomen, wearing day 3 and 10:00 were used as reference groups. Colony counts > 200 CFU/100 cm² and > 1000 CFU/100 cm² were used as research-defined stratification thresholds.

Sensitivity analysis was performed after excluding the six sampling points with the highest colony counts: 9520, 6240, 6170, 5310, 3960 and 3960 CFU/100 cm². The remaining 498 sampling points were included in the analysis. Compared with the 3rd cumulative wearing workday, the 5th cumulative wearing workday (β = 0.284, 95% CI: 0.129–0.439, $p < 0.001$) and the 7th cumulative wearing workday (β = 0.331, 95% CI: 0.177–0.485, $p < 0.001$) remained associated with higher contamination burden. No significant difference was observed between 16:00 and 10:00 (β = 0.082, 95% CI: -0.044 to 0.208, p = 0.204) (**Table**

5), indicating that the main findings were stable after excluding these extreme high-contamination values.

Table 5 Sensitivity analysis of the linear mixed-effects model after excluding approximately the highest 1% of colony counts

Variable	*β* coefficient	95% CI	*p* value
Wearing day 5 vs day 3	0.284	0.129–0.439	< 0.001
Wearing day 7 vs day 3	0.331	0.177–0.485	< 0.001
16:00 vs 10:00	0.082	-0.044–0.208	0.204

Note: The sensitivity analysis was performed after excluding the six sampling points with the highest colony counts. The dependent variable was $\log_{10}(\text{CFU}/100\ \text{cm}^2 + 1)$. The fixed-effect and random-effect structures were consistent with those used in the main analysis.

Discussion

Main findings and contribution

This real-world repeated-measures observational study evaluated bacterial contamination burden on long-sleeved nurses' uniforms in a respiratory ward. Bacterial growth was detected in 90.9% of sampling points, and contamination burden showed an uneven distribution across uniform sites. Contamination levels were higher on the 5th and 7th cumulative wearing workdays than on the 3rd cumulative wearing workday, although the 7th workday was not higher than the 5th workday. Colony counts were clearly right-skewed, with a small number of extreme high-contamination values. No significant difference was observed between the two predefined daytime sampling points, 10:00 and 16:00. Overall, these findings indicate a site- and wearing-stage-related contamination burden with a right-skewed distribution pattern.

This study contributes to the literature by shifting the focus from whether nurses' uniforms are contaminated to how contamination burden is distributed across uniform sites and cumulative wearing stages. By repeatedly sampling seven predefined sites on the same type of long-sleeved nurses' uniform across predefined wearing workdays, this study provides real-world evidence that may help inform more targeted uniform monitoring strategies in respiratory nursing settings.

Interpretation and comparison with previous studies

The high frequency of bacterial growth observed in this study is consistent with previous studies showing that healthcare workers' attire, including nurses' uniforms, routinely worn attire and long-sleeved attire, can become contaminated during clinical care [4, 8, 17, 18]. Previous studies have also reported that contamination is often detected on high-contact areas of healthcare attire, such as pockets, sleeves, cuffs and abdominal areas [6, 8, 10, 11]. These findings support the view that nurses'

uniforms are not passive clothing items but wearable textile surfaces that are repeatedly exposed during routine care. Compared with earlier studies that mainly assessed contamination at a single time point, after work shifts or across different attire types, the present study further described total bacterial contamination burden across multiple predefined sites and cumulative wearing workdays on the same type of long-sleeved nurses' uniform in a respiratory ward.

The uneven site distribution observed in this study has practical implications for understanding nurses' uniforms as wearable textile surfaces that are repeatedly exposed during routine nursing care. Pocket areas showed relatively higher median colony counts in descriptive analysis, while abdominal, sleeve and waist areas also showed high contamination values. Earlier studies and attire-focused research have identified high-contact areas such as pockets, sleeves, cuffs and abdominal areas as relevant sampling sites [6, 8, 10, 11, 18]. In the present study, this site-related pattern may be explained by plausible contact behaviours during routine nursing care: pockets are frequently touched and may be used to store pens, scissors, adhesive tape or documentation tools, while sleeves and abdominal areas may repeatedly contact patient surroundings, bedrails, bedside equipment or care-related devices during close nursing care. Previous evidence has shown that healthcare worker clothing can acquire pathogenic bacteria during patient care, and recent textile-transfer evidence suggests that microbial transfer to and from textiles may vary according to transfer mechanism, moisture, friction and contact conditions [23, 24]. In respiratory wards, oxygen therapy management, nebulization assistance, sputum-related care, repositioning and bedside care may further increase opportunities for local contamination. However, in the adjusted model, pocket sites were not independently associated with higher contamination burden. Therefore, the site-related findings should be interpreted as evidence of uneven contamination distribution rather than proof that any single site independently drives contamination.

The association between cumulative wearing workday and contamination burden was another important finding. Previous studies have examined uniform contamination after work shifts, after an 8-hour workday, in comparisons of antimicrobial and conventional scrubs, or in relation to uniform type and days of use [11, 13, 14, 16]. In the present study, the 5th and 7th cumulative wearing workdays were associated with higher contamination burden than the 3rd cumulative wearing workday, and this association remained stable after excluding approximately the highest 1% of colony counts. This finding suggests that contamination burden may become more pronounced after several cumulative wearing workdays, making the later wearing stage a relevant point for uniform monitoring.

However, the 7th cumulative wearing workday was not higher than the 5th cumulative wearing workday, indicating that contamination may not simply increase in a linear manner with wearing duration. Instead, contamination may be influenced by episodic high-exposure events, patient care intensity, hand-to-uniform contact, environmental exposure, textile contact conditions and storage conditions after work [24]. From a nursing management perspective, the 5th cumulative wearing workday may serve as a practical reference point for evaluating whether earlier uniform replacement or targeted contamination monitoring could reduce bacterial contamination burden. Future intervention studies are needed to

determine whether changing uniforms before or around this stage can effectively reduce contamination under real-world nursing conditions.

No significant difference was observed between 10:00 and 16:00. Because these were predefined daytime observation points rather than strict pre-shift and post-shift sampling points, this finding should not be interpreted as evidence that contamination does not change during a work shift. Rather, it indicates that no measurable difference was detected between the two observation points used in this study. Future studies with true pre-shift and post-shift sampling, combined with structured nursing activity records, may better clarify within-shift contamination dynamics.

Nursing implications

The right-skewed distribution of colony counts is practically relevant for contamination monitoring. Most sampling points showed low to moderate bacterial burden, whereas a small number had very high colony counts. Therefore, mean values or positivity rates alone may not adequately represent contamination burden. Uniform contamination assessment may need to consider high-contact sites, cumulative wearing stages and extreme high-contamination events.

These findings may support more targeted monitoring strategies for nurses' uniforms. Pocket, sleeve and abdominal areas may be considered priority sites for observation in future studies, and the 5th and 7th cumulative wearing workdays may serve as reference time points for evaluating wearing-cycle management. In daily practice, the findings suggest the potential value of reinforcing hand hygiene after high-contact care activities, improving pocket item management and considering timely uniform replacement after visible or suspected contamination exposure. Future studies may further evaluate whether textile design optimization, laundering and storage strategies or antimicrobial textile approaches can reduce uniform contamination burden under real-world nursing conditions [22, 25]. These implications should be interpreted as risk-management considerations rather than evidence that uniform contamination directly causes healthcare-associated infections.

Strengths and limitations

This study has several strengths. It was conducted under real-world nursing conditions without changing routine care, uniform wearing practices or infection prevention measures. In addition, the repeated-measures design included 504 valid sampling points from seven predefined sites, three cumulative wearing workdays and two daytime observation points, allowing a more detailed description of site distribution and wearing-stage-related changes than a single cross-sectional assessment. The analysis also accounted for repeated sampling within nurses and included a sensitivity analysis to assess the influence of extreme high-contamination values.

Several limitations should be acknowledged. First, only total bacterial colony counts were measured; species identification, antimicrobial susceptibility testing and molecular typing were not performed. Therefore, the clinical pathogenic significance and transmission relevance of the detected

contamination could not be determined. Second, detailed nursing activity data, hand hygiene behaviour, patient contact intensity, pocket item use and environmental surface contamination were not recorded, limiting interpretation of the mechanisms underlying site differences and wearing-workday changes. Third, this was a single-centre study with 12 nurse-level clusters, which limits generalizability and the ability to analyse individual-level contamination trajectories. Fourth, separate baseline sampling of each uniform before clinical use was not performed, and repeated sampling at the same predefined sites may have introduced overlap or removal effects. Finally, the thresholds used for high-contamination and extreme high-contamination sampling points were research-defined stratification indicators rather than validated clinical risk thresholds for in-use nurses' uniforms.

Conclusion

Under real-world repeated-measures conditions in a respiratory ward, bacterial contamination burden on long-sleeved nurses' uniforms showed site-related uneven distribution, cumulative wearing-workday-related non-linear changes and a clearly right-skewed pattern. These findings suggest that uniform contamination should not be assessed only as detected or not detected, but should be evaluated as a quantifiable wearable textile contamination interface across three dimensions: contamination burden, priority sites and wearing stage. Future studies should incorporate pathogen identification and structured nursing exposure records to clarify the sources of high contamination burden and its potential infection prevention relevance.

Abbreviations

CFU: Colony-forming unit

CI: Confidence interval

GEE: Generalized estimating equation

IQR: Interquartile range

LMM: Linear mixed-effects model

OR: Odds ratio

SD: Standard deviation

STROBE: Strengthening the Reporting of Observational Studies in Epidemiology

Declarations

Ethics approval and consent to participate

This study was conducted as a stage-specific analysis of the project “Microbial contamination characteristics of healthcare workers’ uniforms in a respiratory department and evaluation of antimicrobial interventions,” which was approved by the Clinical Research Ethics Committee of the First Affiliated Hospital of Wenzhou Medical University (Acceptance No. KY2026-280; Approval No. 2026-280). The study was conducted in accordance with the principles of the Declaration of Helsinki. All participating nurses were informed of the study purpose, sampling procedures and data use, and voluntarily agreed to participate. Nurses were recorded using anonymous codes. This study did not collect patient-identifiable information, patient biological samples or patient clinical outcome data.

Consent for publication

Not applicable. This study does not contain any identifiable personal information, images, case details or other materials requiring separate consent for publication.

Availability of data and materials

The datasets generated and analysed during the current study are not publicly available because they contain ward-level operational information and anonymized staff sampling records, but are available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests.

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Authors’ contributions

DX was responsible for manuscript drafting, sample collection and coordination of study implementation. LL was responsible for microbiological testing, data analysis and study protocol design. SYL contributed to manuscript review, revision and critical appraisal of important intellectual content. QL contributed to manuscript revision and critical review of important intellectual content. FL contributed to manuscript revision and critical review of important intellectual content. ZG, as the corresponding author, supervised the study, reviewed the study protocol, critically revised the manuscript and coordinated the submission process. All authors read and approved the final manuscript.

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Authors' information

DX is the deputy head nurse of Ward C191 at the First Affiliated Hospital of Wenzhou Medical University and is mainly involved in research related to respiratory nursing and healthcare-associated infection prevention and control.

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Figures

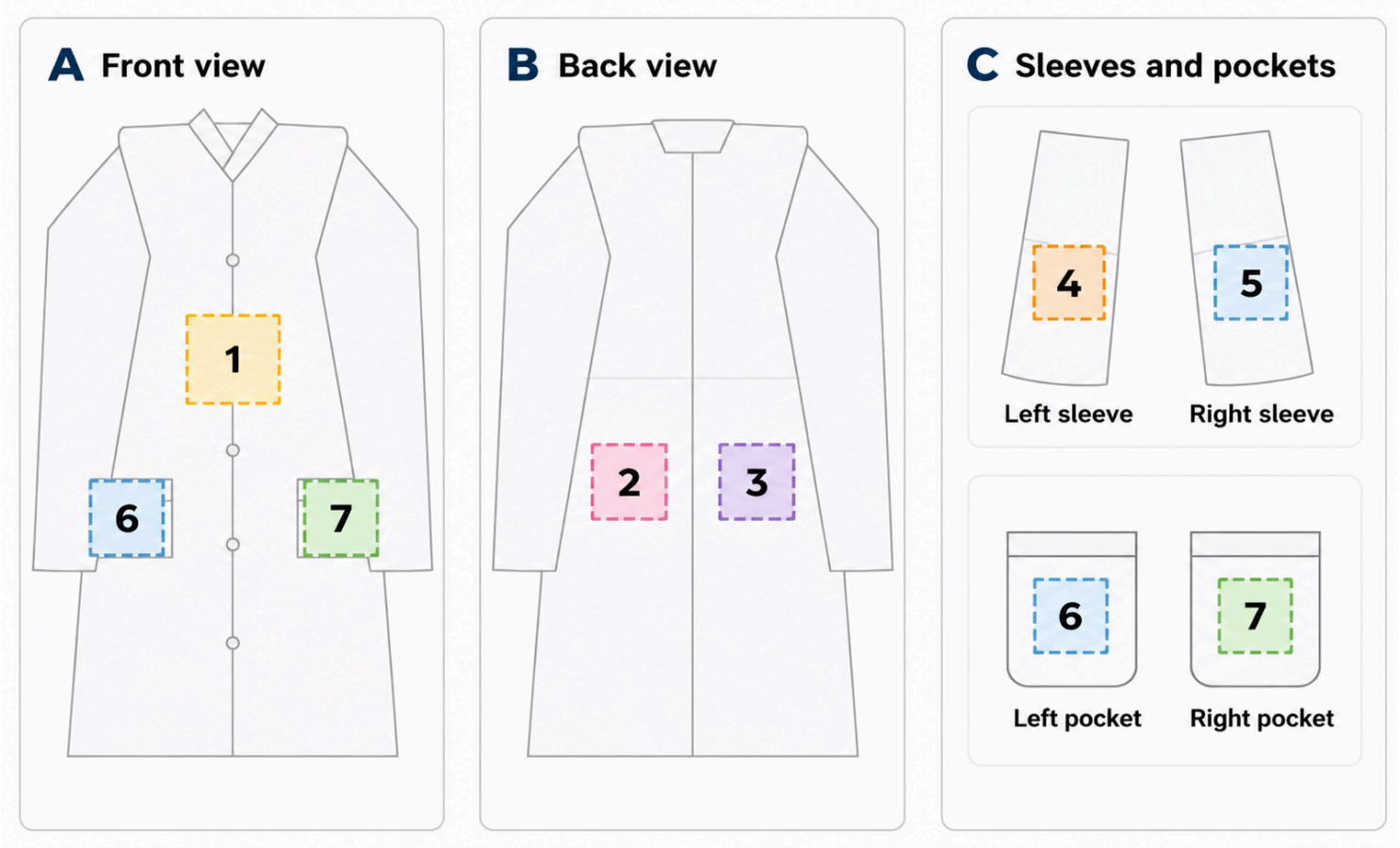


Figure 1

Predefined sampling sites on long-sleeved nurses' uniforms.
The seven predefined sampling sites included the abdomen, left waist, right waist, left sleeve, right sleeve, left pocket and right pocket. Each sampling site covered an area of 10 cm × 10 cm.

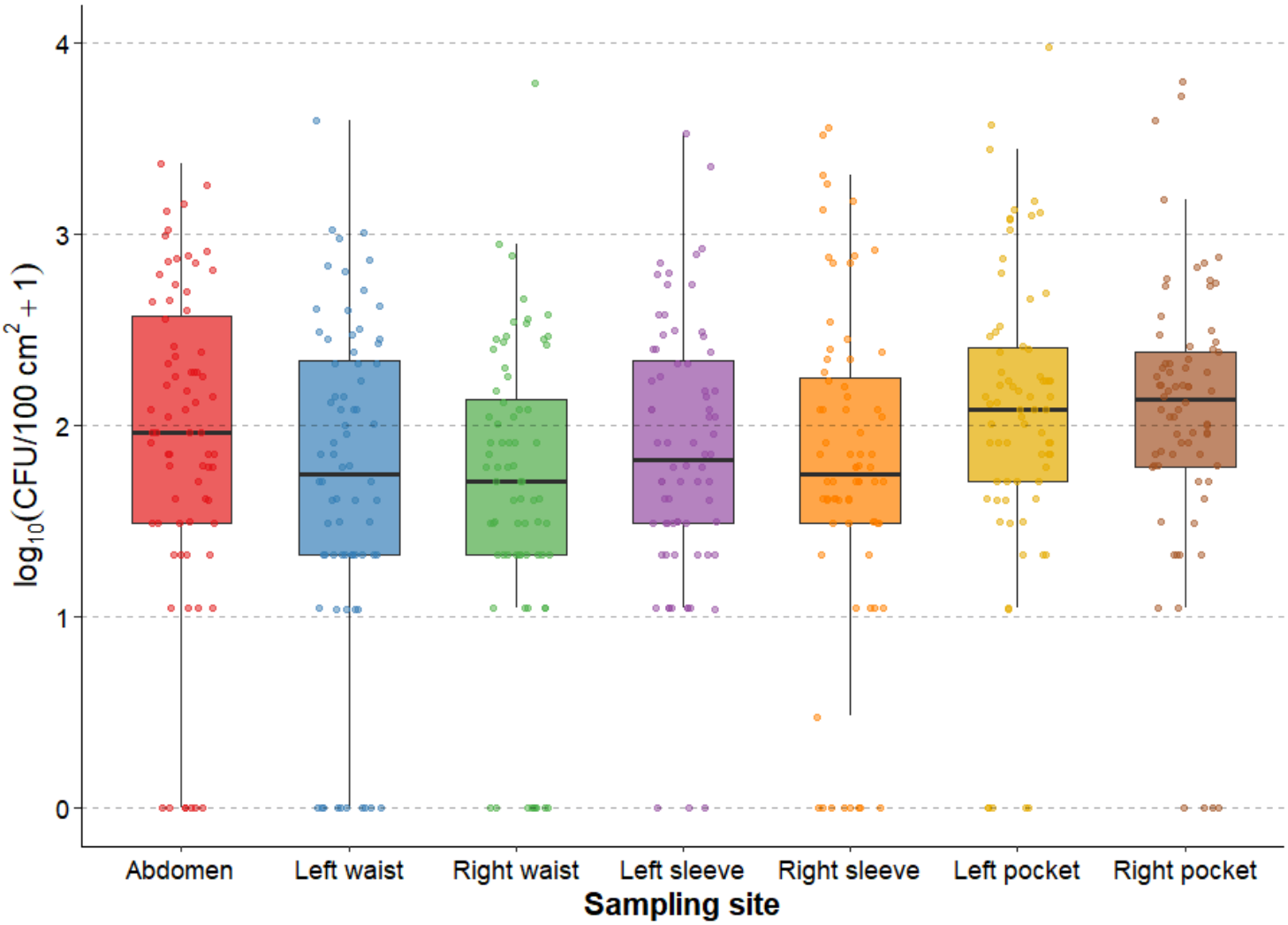


Figure 2

Distribution of bacterial contamination burden by sampling site.

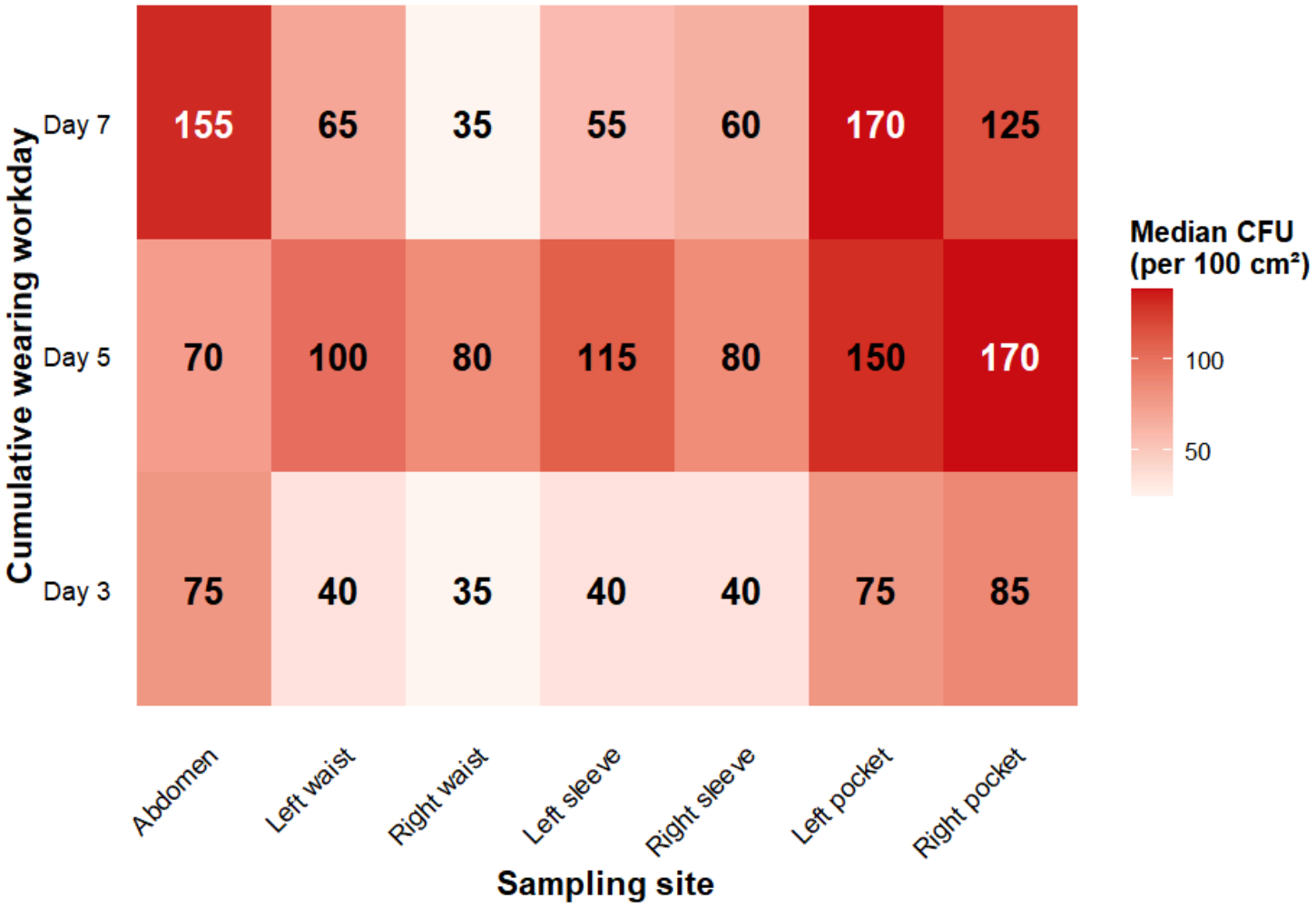


Figure 3

Heatmap of median bacterial colony counts by sampling site and cumulative wearing workday.

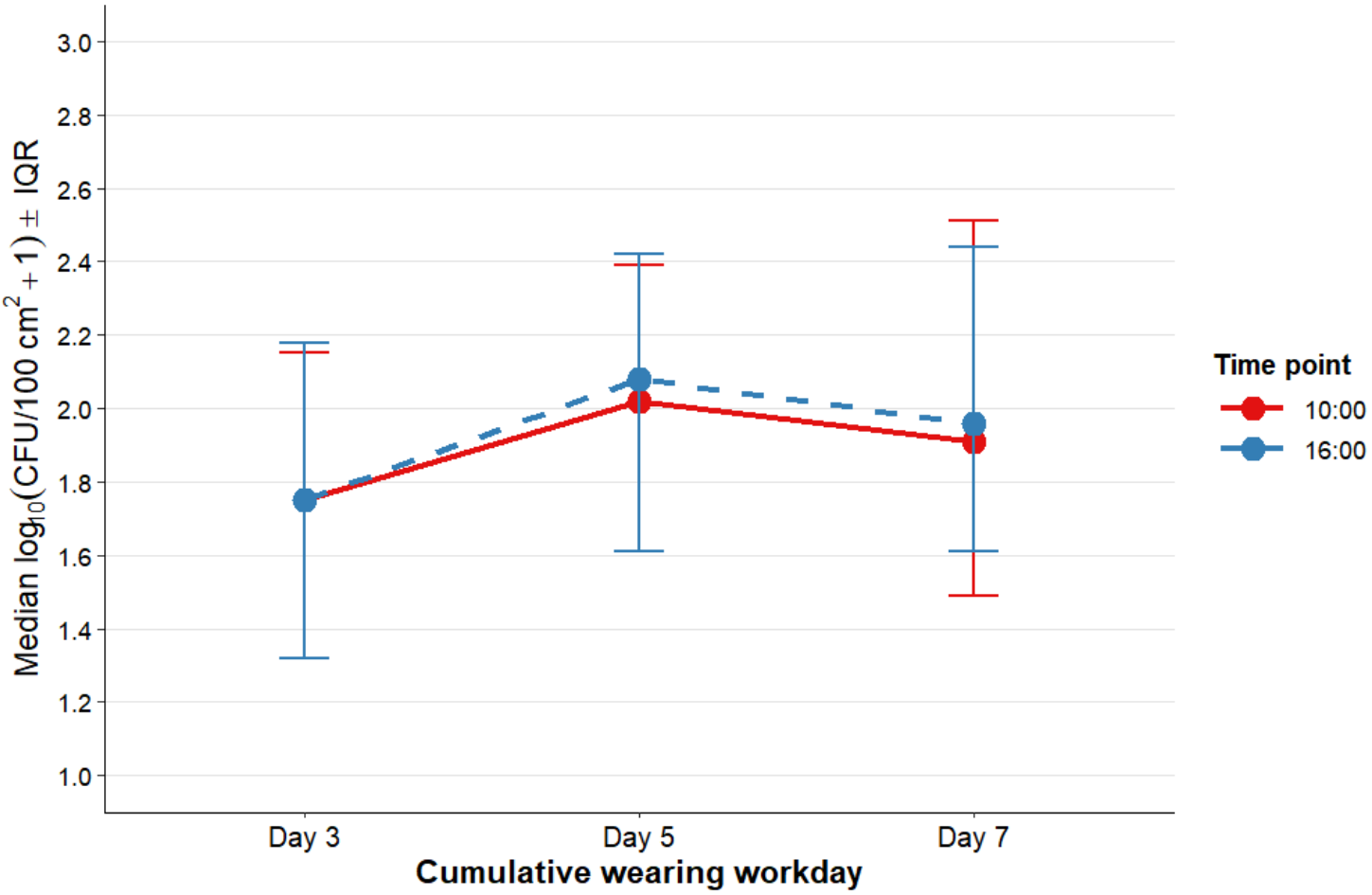


Figure 4

Bacterial contamination burden by cumulative wearing workday and predefined daytime sampling point.

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