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PAPER



Scrubs contamination, domestic laundry effect and workwear habits of clinical staff at a referral hospital

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OBJECTIVE: To determine contamination rates of scrub suits worn by veterinary surgeons and nurses following a single shift.

MATERIALS AND METHODS: Cross-sectional preliminary study at a UK small animal referral centre. Sterilised scrub suits were distributed to veterinary surgeons (n = 9) and nurses (n = 9) at the beginning of their clinical shift and worn for at least 8 hours. They were then analysed for bacterial contamination before and after home laundry at 30°C. A questionnaire was distributed to hospital clinical staff regarding workwear habits.

RESULTS: Median bacterial counts were 47 (interquartile range: 14 to 162) and 7 (interquartile range: 0 to 27) colony forming units *per* cm² before and after laundering scrub suits. Bacteria identified included *Staphylococcus* sp., *Enterococcus* sp., *Escherichia coli*, *Bacillus* sp., *Pseudomonas aeruginosa*, *Micrococcus* sp., β -haemolytic Streptococci and a Group G Streptococcus. From 101 staff surveyed, 64.0% reported wearing fresh, clean scrub tops and 58.4% fresh, clean trousers each day, while 64.4% left the workplace wearing the same clothing in which they undertook clinical work.

CLINICAL SIGNIFICANCE: Workwear contamination risks spread of pathogens into the community and personnel compliance with workplace guidelines warrants further attention. Home laundry at 30°C significantly decreases, but does not eliminate, the bacterial burden after a single shift.

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INTRODUCTION

In human medicine, the spread of pathogens outside hospitals and into communities *via* contaminated health care worker (HCW) uniforms is a major public health concern because of the risk of cross infections with microorganisms resistant to standard cleaning methods and agents (Committee to Reduce Infection Deaths 2008). A pilot study in 2012 demonstrated bacteria on nurse uniforms 48 hours after a shift ended, posing a potential risk for patient cross contamination and spread of pathogens to the community (Sanon & Watkins 2012). Countries such as the UK, Belgium and Canada acknowledge and address this problem by prohibiting the wearing of hospital clothing outside the workplace (Conseil Superier d' Hygiene 2005, Nye *et al.* 2005, Jacob 2007, Treakle *et al.* 2009). These countries also require health service providers to sterilise and provide clean uniforms to HCWs (Conseil Superier d' Hygiene 2005, Nye *et al.* 2005, Jacob 2007, Treakle *et al.* 2009).

Veterinary personnel are identified as a high-risk group for carriage of methicillin-resistant *Staphylococcus aureus* and *pseud-intermedius* (MRSA and MRSP); carriers comprise 3.5–17.5% of veterinary staff (Loeffler *et al.* 2010, Singh *et al.* 2013, Worthing *et al.* 2018), compared with 0.95–1.5% of the general population (Abudu *et al.* 2001, Holtfreter *et al.* 2016, Peters *et al.* 2018),

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raising concerns about nosocomial cross infections and bacterial antibiotic resistance in small animal veterinary medicine facilities (Detwiler *et al.* 2013, Hopkins *et al.* 2019). Compared with human medicine, there are no specific guidelines for veterinary personnel regarding uniform hygiene.

There is much debate about the efficacy of home laundering for removing bacterial contamination from HCW uniforms. Some studies demonstrate adequacy of domestic laundry in significantly reducing bacterial contamination levels (Patel *et al.* 2006, Lakdawala *et al.* 2011), whereas others isolated statistically significantly higher bacteria counts from home-laundered scrubs and unwashed scrubs compared to new, hospital-laundered and disposable scrubs (Nordstrom *et al.* 2012). The use of tumbledrying or ironing influences contamination rates further (Patel *et al.* 2006). Even where laundry recommendations exist, staff compliance is poor; 44% of health care professionals do not adhere to recommended laundry protocols, presenting a potential route for cross contamination and infection (Patel *et al.* 2006, Munoz-Price *et al.* 2012, Riley *et al.* 2015).

Currently, there is no study in the veterinary literature examining the contamination of veterinary HCW uniforms with pathogens after a clinical shift and no information on contamination following home laundry of worn uniforms. The aims of the study were to: (1) document bacterial contamination levels on veterinary surgeon and veterinary nurse uniforms after a clinical shift; (2) investigate influence of home laundry on bacterial load after a clinical shift; and, (3) document veterinary surgeon and nurse habits regarding work attire during and after completion of a clinical shift.

MATERIALS AND METHODS

All veterinary surgeons and nurses at the Center for Small Animal Studies, Animal Health Trust (AHT) were asked to complete an anonymous questionnaire (Table 1) detailing their habits regarding work uniforms. Each of nine veterinary surgeons and nine registered veterinary nurses (Table 2) were provided with a sterilised, individually packaged uniform set consisting of scrub top and trousers. The nurses were selected randomly from the ward nursing group. The veterinary surgeons were randomly selected from each clinical discipline: dermatology, ophthalmology (n = 2), internal medicine, imaging, anaesthesia (n = 2), soft tissue surgery

Table 1. Survey questionnaire

- Do you wear a scrub/tunic top during your clinical shift?
- Do you wear scrub/tunic trousers during your clinical shift?
- Do you wear a fresh, clean top (either your own or a scrub/tunic) for every new day you are on clinics?
- Do you wear fresh, clean trousers (either your own or a scrub/uniform) for every new day you are on clinics?
- Do you leave the AHT campus after your clinical shift wearing the clothing (*i.e.* scrubs, uniform, or your own clothes if you did not wear scrubs) in which you undertook your shift?

Are you aware of the AHT guidelines for laundry of clothing/scrubs/ uniforms which are worn whilst on clinics? and neurology. The veterinary surgeons took part in the study whilst consulting, not operating, or whilst off-clinics.

Upon recruitment and receipt of informed verbal consent, the participants were then randomly assigned a number (nurse 1–9; vet 1–9, taken from numbers contained in an envelope). Uniforms were sterilised using an in-house autoclave (Logiclave LAB300V) at 138°C for 8 minutes before distribution and were confirmed to be sterilised using a type 2 indicator marker using class 6 diagnostic technology (3.5 min Helix Loadcheck, Medisafe). An additional unworn uniform set was used as a negative control. The participants were asked to change in the operating room changing rooms before and after the shift. Shift duration (in hours) was recorded and was a minimum of 8 hours.

Worn uniforms (pre-wash group) were collected at the end of the shifts in a sealed, labelled autoclave pouch and sent to the AHT bacteriology laboratory for analysis. Analysis was performed 36–48 hours after completion of the shift. Five analyses were conducted: (1) a heterotrophic growth plate count; (2) methicillin-resistant *Staphylococcus aureus* (MRSA) growth; 3) vancomycin-resistant enterococci (VRE); 4) identification of the heterotrophic plate counts (HPCs); and, 5) extended-spectrum beta-lactamases (ESBL).

The work undertaken at the laboratory mimicked that of Sanon & Watkins (2012). Upon receipt of the uniforms by the laboratory, a single 3×3 inch portion of each of the 19 uniforms was cut out with sterilised scissors from the front beltline/pocket area of each scrub. This is because the front beltline/pocket areas and the sleeves (for long sleeved coats) are more likely to be contaminated (Nye et al. 2005). For this study, all the uniforms were short sleeved so the focus remained on the front beltline/pocket area of the participants' uniforms. Unique to the present study was the inclusion of scrub trousers. A single 3×3 inch portion was removed from the right knee region, which was considered to be the most likely area to be contaminated. Gloves were changed and the scissors flame-sterilised between samples. After removing each sample, the fabric was cut into small pieces and placed in a sterile 100 mL container to which exactly 25 mL of sterile peptone water was added. The cloth in the peptone water was vigorously mixed to extract bacteria. After agitation, three volumes of each sample were placed on separate sterile Petri dishes (1 mL, $100\,\mu$ L and $20\,\mu$ L). Twelve to fifteen millilitres of tempered heterotrophic growth medium were added to each Petri dish, swirled and allowed to solidify and form plates. One millilitre of the peptone water extracted sample was also added to the top of a prepurchased chromogenic MRSA agar plate (Hardy Diagnostics G249) and 1 mL to a chromogenic VRE agar plate (Hardy Diagnostics G333). Prepared Petri dishes were sealed with parafilm and placed in an incubator at 35°C. After the designated growth interval was completed for each of the plates, the most prevalent bacteria were identified.

There were three control measures for this study: the negative control uniform set, the media control of the peptone water and the HPC agar black media. The latter two were tested for each batch of samples; two agar plates, one inoculated with the peptone water and one uninoculated, were incubated. There was no growth observed on any of the three controls, thereby verifying

| Participant | Shift (hours) | Age | Years qualified | No of patients handled | Barrier nursin |
|-------------|---------------|-----|-----------------|------------------------|----------------|
| /N 1 | Day (12) | 37 | 1.5 | 8 | Yes (HGE) |
| /N 2 | Day (8) | 25 | 3 | 10 | No |
| /N 3 | Day (8) | 49 | 23 | 4 | No |
| /N 4 | Night (12) | 22 | 4 | 20 | No |
| /N 5 | Day (8) | 32 | 10 | 8 | No |
| /N 6 | Day (8) | 32 | 9 | 9 | No |
| /N 7 | Day (8) | 27 | 4 | 6 | Yes (MU) |
| /N 8 | Day (8) | 25 | 0.5 | 12 | Yes (PL) |
| /N 9 | Night (12) | 46 | 24 | 25 | No |
| /S 1 (IM) | Day (12) | 30 | 5 | 4 | No |
| /S 2 (0) | Day (10) | 29 | 5 | 8 | Yes (DC) |
| /S 3 (DE) | Day (8) | 36 | 12 | 2 | No |
| /S 4 (DI) | Day (10) | 28 | 3 | 10 | No |
| /S 5 (N) | Day (12) | 24 | 2 | 7 | No |
| /S 6 (A) | Day (12) | 31 | 4 | 4 | No |
| /S 7 (STS) | Day (8) | 38 | 13 | 4 | No |
| /S 8 (0) | Day (8) | 46 | 15 | 6 | No |
| /S 9 (A) | Day (8) | 40 | 16 | 5 | Yes (D, POE) |

the sterilisation procedure and that there was no contamination of either the agar or the peptone water before sample collection and testing.

Thereafter, the efficacy of home laundry was assessed. All uniforms were returned to the primary author in sealed autoclave pouches, labelled nurse 1–9, vet 1–9 and control. Each scrub top/trousers pair was laundered individually in random order on the same day in a household laundry machine at 30°C using commercial non-biological washing powder and no fabric conditioner (post-wash group). Each scrub top/trousers pair was then left to dry individually on an outdoor washing line and returned to the AHT laboratory in sealed labelled autoclave pouches for analysis as above. Standard hand hygiene (washing with commercial hand soap and spraying with 70% isopropyl alcohol) was performed before handling of the air-dried uniforms. Fabric was harvested from the site adjacent to the previous site.

Our institution's Infection Control Group (IGC) adopts the guidelines advocated by the Department of Health (2010) for appropriate staff uniform or work wear management. These recommend either a 10-minute wash of uniforms at 60°C being sufficient to remove most microorganisms or use of detergents at lower temperatures (30°C) being sufficient to remove many of the microorganisms including MRSA. No drying method is clearly described in the guidance but it is stated that uniform fabrics must be capable of withstanding tumble-drying. The provision of sufficient uniforms to enable freshly laundered clothing to be worn for each shift or work session is also included in the guidelines; to ensure this, each member of the staff is provided with a minimum of five uniform sets.

A single pre- and post-wash heterotrophic growth plate count was calculated for each nurse and veterinary surgeon by averaging across bacterial counts of both top and trouser scrubs samples. Median (interquartile range [IQR]) heterotrophic growth plate count was estimated in the pre- and post-wash groups. The Wilcoxon signed rank test was used to compare median heterotrophic growth plate count between the pre- and post-wash groups. Within the pre-wash group, the Mann-Whitney U test was used to compare heterotrophic growth plate count across shift length (<8 hours *versus* >8 hours) and barrier nursing cases (yes/no). The Spearman's rank correlation coefficient was used to assess the relationship between heterotrophic growth plate count and the number of animals handled during a shift. These tests within the pre-wash group were conducted for all participants and separately for veterinary surgeons and nurses. A value of P < 0.05 was considered significant for all the tests. P-values were not adjusted for multiple comparisons (Perneger 1998). The software used for the statistical analysis was IBM SPSS Statistics v.20.

RESULTS

Results of bacterial growth achieved are shown in Table 3. Excluding the control, 45 of 72 (62.5%) samples yielded positive bacterial growth; of those, 32 (71.1%) were from the pre-wash group and 13 (28.9%) from the post-wash group. Fifteen (15 of 18, 83.3%) and 17 of 18 (94.4%) veterinary surgeon and nurse scrub suits yielded a positive culture in the pre-wash group compared to 8 of 18 (44.4%) and 5 of 18 (27.8%) in the post-wash group (Table 2). This result denotes a 1.9- and 3.4-fold decrease in the positive samples after home laundry for veterinary surgeons and nurses respectively. The demographics of the participants are presented in Table 3.

The heterotrophic growth plate count revealed a median bacterial count pre-wash of 47 (IQR 14 to 162) colony forming units per cm² (cfu/cm²) and post-wash of 7 (IQR 0 to 27) cfu/cm² (P = 0.025). No MRSA, VRE or ESBL were isolated. A group G streptococcus was isolated from one set of scrubs from a staff member caring for a dog from which the same bacterium was isolated. All control samples were negative for bacterial growth at all times. Within the pre-wash group, no significant difference in heterotrophic growth plate count was identified across length (in hours) of shift (P = 0.897) or with barrier nursing cases (P = 0.28) for all participants. Similarly, no significant and the

number of animals handled (P = 0.455) or years qualified of the participants (P = 0.47). When the same variables were separated according to role (*i.e.* veterinary surgeon or nurse) and re-analysed, no statistical differences were found.

Thirty (30 of 45, 66.7%) of the positive samples yielded a single growth each of *Staphylococcus* spp. (27 of 30, 90%), beta-haemolytic streptococci (1 of 30, 3.3%), *Escherichia coli* (1 of 30, 3.3%) or *Bacillus* (1 of 30, 3.3%) spp. Fifteen samples resulted in

| Table 3. Bacterial growth from scrub suits worn bypersonnel during a clinical shift before and after standarddomestic laundry | | | | | | | | |
|---|---|--|---|-------|--|--|--|--|
| Staff | Groups | Positive (%) | Negative (%) | Total | | | | |
| Nurses | Pre-wash Tops Trousers | 17 (94.4%) 8 (88.9%) 9 (100%) | 1 (5.6%) 1 (11.1%) 0 | 18 | | | | |
| | Post-wash Tops Trousers | 5 (27.8%) 0 5 (55.5%) | 13 (72.2%) 9 (100%) 4 (44.5%) | 18 | | | | |
| Total | | - () | . (| 36 | | | | |
| Vets | Pre-wash Tops Trousers Post-wash Tops Trousers | 15 (83.3%) 9 (100%) 6 (66.7%) 8 (44.5%) 4 (44.5%) 4 (44.5%) | 3 (16.7%) 0 3 (33.3%) 10 (55.5%) 5 (55.5%) 5 (55.5%) | 18 | | | | |
| Total | | · · · · | · · · · | 36 | | | | |
| Total staff | | | | 72 | | | | |
| Control | Pre-wash Tops Trousers | 0 0 0 | 2 (100%) 1 1 | 2 | | | | |
| | Post-wash Tops Trousers | 0 0 0 | 2 (100%) 1 1 | 2 | | | | |
| Total samples | | | | 76 | | | | |

mixed bacteria growth (Table 4), with the most frequent being a combination of *Staphylococci/Bacillus* spp. (9 of 15, 60%). On six occasions (nurses 1 and 4 and vets 3, 4, 5 and 7) the postwash bacterial growth was positive with different bacteria from the pre-wash sample (Table 4). In the post-wash group seven of 18 (38.9%) of the participants had negative bacteria growth from previously contaminated scrubs.

One hundred and one members of the clinical staff (veterinary surgeons and nurses) participated in the questionnaire. Up to 99.0 and 91.1% of the staff reported wearing scrub top and trousers respectively, during their clinical shift. Only 64.4 and 58.4% of the staff reported wearing fresh, clean uniform top and trousers respectively, for every new day on clinics. About two thirds (64.4%) replied that they leave the workplace after a clinical shift wearing the clothing in which they undertook the shift. Lastly, only 40.6% of the staff reported that they were aware of the AHT guidelines for home laundry of clothing/attire worn at the workplace.

DISCUSSION

Our findings mirror previous study results (Sanon & Watkins 2012) that bacterial contamination of uniforms occurs during clinical shifts. The bacteria we detected were *Staphylococcus* spp., *Bacillus* spp., *Pseudomonas aeruginosa*, β -haemolytic Streptococci and *E. coli*. A group G streptococcus was also detected; pathogenic species of streptococcus in dogs normally belong to Lance-field groups A, C, E or G (Markey *et al.* 2013), and are common opportunistic pathogens associated with a variety of diseases affecting multiple organ systems (Lamn *et al.* 2010). Bacterial contamination in a hospital environment can come from a variety of sources. *Staphylococcus* spp. are often carried on the skin

Table 4. Bacterial isolates and counts per participant in the pre- and post-wash groups

| Participants | No | Pre-wash isolates | | | Post-wash isolates | | |
|----------------|----|--|--------|-------------------|--|--------|-------------------|
| | | Genus/Species | Growth | Median cfu/cm² | Genus/Species | Growth | Median cfu/cm² |
| Nurses (n = 9) | 1 | Staphylococci | S | 49 | β-haemolytic Streptococci | S | 7 |
| | 2 | Staphylococci, Bacillus, E. coli, | М | 147.5 | Staphylococci | S | 35 |
| | 3 | Staphylococci | S | 13 | Staphylococci | S | 7 |
| | 4 | Coag-negative Staphylococci | S | 45.5 | Staphylococci, enterococci | М | 3.5 |
| | 5 | Staphylococci | S | 29 | - | N | 0 |
| | 6 | E. coli, Bacillus, Staphylococci | М | 68.5 | - | Ν | 0 |
| | 7 | Mixed Staphylococci, Bacillus | Μ | 81.5 | Staphylococci | S | 7 |
| | 8 | Staphylococci | S | 25.5 | - | Ν | 0 |
| | 9 | Coag-negative Staphylococci | S | 131 | - | N | 0 |
| Vets (n = 9) | 1 | Bacillus, mixed Staphylococci | M* | 665.5 | Staphylococci | S | 7 |
| | 2 | Bacillus, mixed Staphylococci | Μ | 406.5 | Staphylococci, Bacillus | Μ | 24.5 |
| | 3 | Bacillus | S | 3.5 | Coag-negative Staphylococci | S | 19.5 |
| | 4 | Mixed Staphylococci, Bacillus | Μ | 14 | Coag-negative Staphylococci | S | 65.5 |
| | 5 | Mixed Staphylococci, Bacillus | Μ | 14 | Coag-negative Staphylococci, Bacillus | Μ | 456 |
| | 6 | Group-G Streptococcus, Micrococcus, Coag-negative Staphylococcus | Μ | 6.5 | - | N | 0 |
| | 7 | Mixed Staphylococci, Bacillus | Μ | 41 | E. coli, P. aeruginosa , Staphylococci | Μ | 69 |
| | 8 | E. coli, Bacillus, Staphylococci | Μ | 207 | - | N | 0 |
| | 9 | Staphylococci | S | 257.5 | - | Ν | 0 |

S, single; M, mixed; N, negative; cfu/cm², colony forming units per centimetre square; median: average bacterial count for scrubs top and trousers for each participant; asterisk (*) denotes that mixed bacteria growth were isolated from both scrub top and trousers; post-wash isolates in **bold** are new isolates, not found in the pre-wash testing.

(Weese 2013), whilst *E. coli* and VRE are found most commonly in faeces (Huycke *et al.* 1998, Johnson & Russo 2002). *Bacillus* spp. contamination often comes from environmental sources (Logan 1988). Further identification of the staphylococcal species isolated or antimicrobial resistance profiles were not performed in our study. No MRSA was cultured; to the best of our knowledge, there was no patient with diagnosed MRSA-associated clinical disease in the hospital during this study. However, it is unknown whether any of the participants or the patients were carriers of MRSA.

The difference in bacterial load pre-wash and post-wash in this study was statistically significant (P = 0.025), which replicates other reports in which home laundry was efficacious at reducing bacterial load (Patel et al. 2006, Lakdawala et al. 2011). Our results demonstrated that domestic washing of uniform decreased counts of all bacteria and negative bacteria growth was achieved for 38.9% of the participants. The decision to use 30°C for home laundry was based on: (a) it being the lowest available temperature on many household washing machines programmes; and, (b) the addition of either a biological or non-biological detergent is beneficial in removing MRSA from experimentally contaminated uniform fabric (Lakdawala et al. 2011). Although it is reported that a high proportion of staff fail to comply with 60°C laundry recommendations (Patel et al. 2006, Munoz-Price et al. 2012, Riley et al. 2015), which our institution also adopts, no question on washing temperature was asked in our questionnaire. Additional studies are required to determine the optimal temperature and laundry cycle for washing of veterinary HCW uniforms.

On six occasions, bacteria isolated in the post-wash samples were not isolated in the pre-wash samples. This can be attributed to various reasons. First, the sampling sites for the pre- and postwash groups were not exactly the same and a bacterial population on one particular site is not necessarily representative of that across the entire surface. Secondly, contamination of the sample post-wash may have occurred, either from the washing mashing (Patel et al. 2006), the washing line, airborne contaminants, packaging and/or mishandling at the lab. The process of those six samples was randomly distributed throughout the study duration, thus making the possibility for cross contamination due to accumulation of bacteria (e.g. from the washing machine or washing line) less likely. Re-contamination of uniforms following laundry at home has been commonly reported previously, but ironing and tumble-drying has been reported to remove these contaminants (Patel et al. 2006, Lakdawala et al. 2011, Nordstrom et al. 2012). Uniforms were not tumble-dried or ironed and therefore their effect on bacterial count was not tested in our study. A relevant question for these procedures was not included in our staff questionnaire and so further investigation in a veterinary hospital is warranted.

Further detailed statistical analyses of our data revealed no significant differences or associations within the pre-wash group. The investigation of association of bacterial count in the prewash group with length of the shift, number of animals handled during shift and barrier nursing showed no significant findings for all the participants or separately for veterinary surgeons and nurses. Alternatively, lack of statistical significance may be attributed to the small sample size, which was likely not sufficient to identify smaller differences or weaker associations and, therefore, repetition of this study with larger cohorts could be beneficial.

The majority of veterinary staff at the AHT did not regularly change their attire after completion of a clinical shift, whilst only 64 and 58% of veterinary professionals wore clean scrubs top and trousers, respectively, every day. Veterinary staff appeared to have poor scrub hygiene practice based on our questionnaire and, surprisingly, 60% declared they were unaware of the AHT laundry guidelines for uniforms. Similarly, a recent study evaluating staff compliance with hospital guidelines on home laundering of uniforms in four NHS hospitals reported a compliance rate between 4 and 32% among the respondents to a questionnaire (Munoz-Price et al. 2012). Reasons for low staff compliance with our hospital guidelines were not investigated in this study but could include poor awareness of transmission of potential pathogens, lack of training or lack of suitable changing facilities. However, it is necessary to undertake more effective measures to increase awareness among health care personnel about the risks of uniform contamination both within and outside the workplace. Identification of such risks within a veterinary hospital setting requires further investigation such as the determination of the nature of bacterial populations carried on the skin of the staff and patients as well as their species-specific pathogenicity. Risk awareness as well as taking appropriate prophylactic measures (e.g. meticulous hand hygiene, use of personal protective equipment and avoiding wearing work uniforms outside work) will eventually help abate the spread of potential pathogens both inside and outside the workplace.

The findings of this study are important for various reasons. First, this is the only study to date describing veterinary HCWs uniform contamination during a clinical shift using heterotrophic growth plate count, as opposed to a recent study by Singh et al. (2013) that focused only on contamination of uniforms with MRSA and MRSP. Second, the use of sterilised uniforms allowed us to control for potential confounding factors that might have influenced the contamination of uniforms before the start of a clinical shift, as noted by Sanon & Watkins (2012). Third, our study investigated the influence of home laundry on the bacterial load. Although the post-wash uniforms were not handled strictly in an aseptic manner after the end of the laundry, normal hand hygiene (hand washing and spraying with 70% isopropyl alcohol) was pursued. Fourth, similarly to the study of Sanon & Watkins (2012), this study illustrated the longevity of the microorganisms isolated, with live bacteria confirmed ≥48 hours after the shifts ended. Previous human health care studies have been limited to detecting microorganisms during and immediately after shifts. The implications of these findings to bacterial contamination of the hospital, community areas and homes of veterinary HCWs remain to be elucidated.

One of the major limitations of this study was that participation in the study was voluntary with the participants aware of the purpose. This could have led them to alter their normal behaviour during work (*e.g.* being more vigilant with hand hygiene). However, in an attempt to reduce the bias, the participants were not aware of the sampling site. Additionally, the laboratory was not able to detect anaerobic organisms. Bacteria that are susceptible to oxygen (e.g. Clostridium haemolyticum) may have died before reaching the laboratory due to oxygen exposure during the 48 hours waiting period between the end of the shift and sampling. Also, although our study was based on methods reported by Sanon & Watkins (2012), in our study scrubs trousers were additionally examined. However, since a full depth sample of cloth was tested and not just the outer surface (such as by wiping an electrostatic cloth along the area of interest as used by Singh et al. 2013), it is uncertain whether a positive growth was due to contamination of the outer surface from the environment or the inner surface from the participant's skin, or both. This risk was of least concern for the scrub top where the samples were taken over the pocket. The cumulative effect of tumble-drying and ironing or steaming on further decreasing the bacteria burden after home laundering of scrubs at 30°C has been investigated before (Patel et al. 2006). However, since our primary aim was to assess 30°C domestic laundry impact on bacterial count the effect of tumble-drying and/or ironing was not tested. Another limitation is that the identification of risk factors associated with uniform contamination was not included in the aims of our study. However, it addresses the growing concern of veterinary staff uniforms as potential reservoirs for hospital-acquired infections or community infections.

Work attire contamination occurs in veterinary clinics and personnel should be vigilant about cross contamination and hygiene principles not only during clinical shifts but also before and afterwards. The importation of potential pathogens from the community to the workplace and *vice versa* is possible and, combined with the increasing emergence of multi-drug resistant bacteria, illustrates the necessity for development of and adherence to uniform hygiene standard operating procedures, policies and regulations. Nevertheless, we should highlight that our study did not investigate the pathogenicity of transferred bacteria. Lastly, adequate surveillance and provision of appropriate changing facilities at work should be investigated.

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Conflict of interest

No conflicts of interest have been declared.

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