ABSTRACT

Mitigation of infectious diseases in developing countries like India is an important healthcare objective. In hospital environments, microorganisms interact with various hospital textiles such as lab coats, bedsheets, and curtains. The spread of infections through fabrics used in the hospital sector is well known. However, there is a lack of systematic studies in this area and the mechanisms involved in spread of nosocomial infections due to textiles are not well understood. Effect of textile properties on microbial adhesion and interactions between fabrics and bacteria have not been studied extensively. Such information is essential to formulate guidelines for the use of textile materials in the healthcare and hospitality sectors, which is currently missing, especially in the Indian context.

The present work focused on assessing factors affecting bacterial adhesion on different types of fibres. Four clinically relevant bacterial genera, viz. *Staphylococcus aureus*, *Acinetobacter calcoaceticus*, *Escherichia coli*, and *Pseudomonas aeruginosa* were studied for their adherence to different fabric types, viz. polyester, wool, polypropylene, viscose, silk, and cotton in laboratory conditions. Surface properties of bacteria and fibres were measured. Adhesion between fibres and bacterial strains was assessed by incubating sterile fibres of each type with the pure culture of bacterial species. Bacterial adhesion was correlated with the nano-roughness of the fibres. Scanning electron microscopy was done to assess the visualization of bacterial adhesion on fibres. Subsequently, the assessment of biofilm formation was performed on seven fabrics (polyester, cotton, polyester-cotton (70:30) blend, silk, wool, viscose, and nylon fabrics) commonly used in hospitals. Fabric characterization was done. Qualitative and quantitative assessment of biofilm formation on different fabrics was performed. Exopolysaccharides (EPS) produced by bacteria were extracted and different functional groups were determined using Fourier Transform Infrared Spectroscopy. The effect of sweat on bacterial abundance on different fabrics (polyester, cotton, polyester-cotton [70:30] blend, silk, wool, viscose, and nylon) was examined. In the first set, the suspension of each bacterial species was inoculated on each type of fabric in the presence of sweat and incubated. In the second set, each bacterial species was inoculated on fabrics in the absence of sweat suspension. Bacterial count was determined for each set of experiment. The effect of sweat, type of bacteria, and incubation time was examined.

Next, the work was extended to study the bacterial load on hospital fabrics under real-life conditions. Two studies were conducted at a primary health care facility in Delhi, one on nurses' coats and the other on hospital bedsheets in the emergency ward of the facility. Patch test method

was used for bacterial sampling in the two studies. In the first case, the effect of fabric type (polyester, cotton and polyester-cotton blend) and temporal variation on bacterial load on nurses' white coats was studied. In the second study, the bacterial load was assessed on patients' bedsheets by employing both culture-dependent and culture-independent approaches. In the culture-dependent approach, seven bacterial species of significance in such settings (*Acinetobacter baumannii*, *S. aureus*, *E. coli*, *Salmonella* spp., *Klebsiella pneumoniae*, *Enterococcus faecalis*, and Group A *Streptococcus*) were enumerated on blend fabrics stitched on patients' bedsheets. Studies were conducted across different seasons using group-specific culture media. In the culture-independent approach, DNA was extracted from the patches and specific bacterial phyla (*α-Proteobacteria*, *ß-Proteobacteria*, *Firmicutes* [*Bacillota*], and *Actinobacteria* [*Actinomycetota*]) were quantified by qPCR. Amplicon sequencing of the 16S rRNA gene was performed for profiling of the total bacterial community.

A direct correlation was observed between textile properties and the extent of bacterial adhesion. Biofilm formation by bacterial species was found to be highest on wool fabric, and minimum on silk fabric. The presence of different functional groups in EPS of bacteria might affect the adhesion of bacteria on textile surfaces by interaction with functional groups present on fabrics. The nano-roughness of the fabrics was also found to affect bacterial adhesion, with a rougher surface proving more favourable for biofilm formation. The count of *E. coli*, *A. calcoaceticus*, and *P. aeruginosa* was observed to be maximum with sweat on polyester fabrics, while least on viscose fabrics. In the presence of sweat, the abundance of *S. aureus* was maximum on wool, and minimum on viscose. The studies conducted at the healthcare facility indicated that the abundance of bacterial adhesion depends on the type of fabric used, the duration of use, as well as the ambient conditions. In particular, high ambient humidity attracted higher bacterial load on polyester-cotton blended fabrics compared to cotton and polyester fabrics. Several bacterial species (*A. baumannii*, *S. aureus*, *E. coli*, *Salmonella* spp., *K. pneumoniae*, *Enterococcus faecalis*, Group A *Streptococcus*) isolated from fabric patches stitched on patients' bedsheets were found to be resistant to several broad-spectrum drugs.

These results highlight the need for a stricter protocol to minimize contamination in healthcare facilities across the country. Newer strategies like physical and chemical modification of fabrics, functionalization of fabrics, etc. can be done to engineer the fabrics to minimise microbial adhesion on fabrics and prevent transfer of infection through fabrics. Specific guidelines could also be formulated based on this data for selecting suitable fabrics which harbour minimal bacterial load.