
Diversity Of Culturable Bacteria On Natural Vs Artificial Fabrics

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Abstract

Bacterial sampling of clothing worn by a class of undergraduate microbiology students was performed over the course of one month. Microorganisms were cultured on nutrient agar, visually distinct colonies were subcultured, and subcultured colonies were tested for alpha haemolytic properties. Significant differences were found between the number of visually differentiable types of colony forming units on natural and artificial textiles, with mean diversity of cfus on artificial textiles exceeding those on natural by a factor of 2.3. Significant differences in the number of organisms capable of alpha haemolysis were also noted, with mean levels of such organisms on artificial textiles exceeding those on natural by a factor of 3.7.

INTRODUCTION

Clinical practices are important in reducing rates of nosocomial infection. Many studies have been done related to patient-centered aspects of nosocomial infection. For example, it is known that adherence to hand washing protocols results in reduced rates of nosocomial infection (1). Fomites also have the potential to transmit infection. Studies have shown that approximately 25% of the white coats worn by health care workers carry *Staphylococcus aureus*, including methicillin-resistant strains of the organism (2,3). Neckties have also been implicated as potential vectors, although conclusions as to the risks they present vary (4,5). They are no longer recommended for clinical wear in the UK (4).

The above referenced studies examine fomites such as white coats and neckties without breakdown as to material composition or microorganismal diversity. There is evidence to suggest that the type of textile used in clothing has a significant impact on the type and number of microorganisms that colonize the object. Microorganism populations have a significant impact on infection. Understanding these populations may allow superior control of nosocomial infections.

It is known that polyester and acrylic fibers bind Gram negative and Gram positive organisms at ratios exceeding 80%, whereas cotton fibers bind these organisms at ratios less than 10% (6). Synthetic textiles have been shown to collect more bacterial mass than cellulose-based textiles (7).

It has also been shown that while cellulose-based textiles are mostly colonized by bacteria normally found in human sweat, such as members of *Propionibacteria*, *Corynebacteria*, *Staphylococcus* and *Streptococcus*, while synthetic textiles are frequently colonized by genera that are not found in human sweat (8,7).

Studies addressing the type and quantity of bacteria that colonize textiles relative to their material composition have previously been done on textile and fiber samples under strictly controlled laboratory, ie in vitro conditions, usually with known quantities of microorganisms being artificially introduced to the fabric sample. This study looks at the relationship between the diversity of organisms on clothing and the type of material of which the clothing is composed under more typical, ie in vivo conditions, wherein the textiles sampled were worn by human beings during normal use, and acquired populations of microorganisms under real world conditions.

MATERIALS AND METHODS

In order to test if clothing composition affected the number of bacteria carried on that clothing, undergraduate students in a microbiology class at Illinois Wesleyan University examined the relationship between the number of organisms found on the cuffs of their classmates' sleeves and the material of which the clothing was made. Study participants gave informed consent; samples were anonymized and records relating individuals to their samples were destroyed.

Damp, sterile swabs were used to sample the bottom-most two inches of the sleeves of participants every class period. Material composition of the garments was recorded. If clothing was composed entirely of plant or animal-based fibers, it was recorded as a “natural fiber”. If clothing was composed all or in part of artificial fibers, it was recorded as “artificial fiber”. During swabbing, an area of approximately 2 cm² was sampled from the cuff of each garment’s right sleeve. The swabs were then immediately plated on nutrient agar and incubated for 48 hours at 37C. The same student researcher was responsible for swabbing and plating all trials to ensure consistency of technique.

The total number of visually distinguishable colony types were recorded. Each distinct type of colony was next subcultured on 5% sheep blood agar. Plates were incubated at 37C and analyzed at 24 and 48 hours for signs of haemolysis. Results were recorded and entered into SPSS for analysis. Independent sample t-testing was used to determine significance of results.

RESULTS

Significant differences were found in the diversity of organisms present on natural vs artificial fibers. Twenty-four artificial fiber cuffs and sixteen natural fiber cuffs were sampled over a three week period of time. Although several types of organisms were found on all types of clothing, there was significantly greater bacterial diversity on clothing composed of artificial fibers (Fig 1). When subcultured colonies were tested for haemolytic activity none showed beta haemolysis and a small percentage showed alpha haemolysis. There were relatively more types of alpha haemolytic bacteria on artificial as compared to natural fibers (Fig 2). The percentage of haemolytic bacteria out of the total population isolated was found to be 0.17% on artificial fibers and 0.10% on natural fibers. It should be noted that the sampling method utilized in this study excludes many fastidious haemolytic organisms.

Figure 1

Figure 1

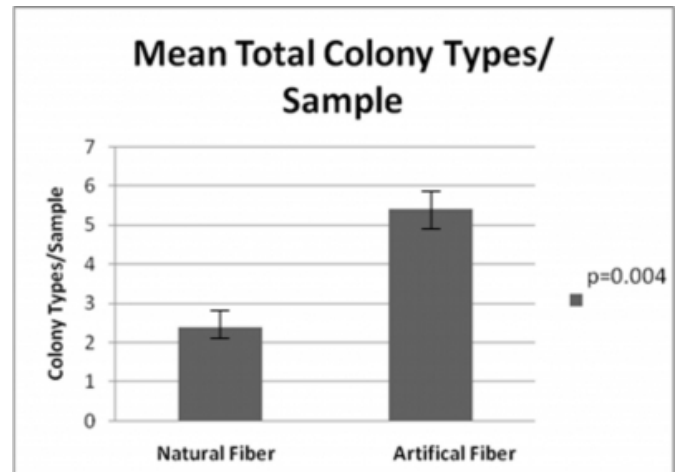
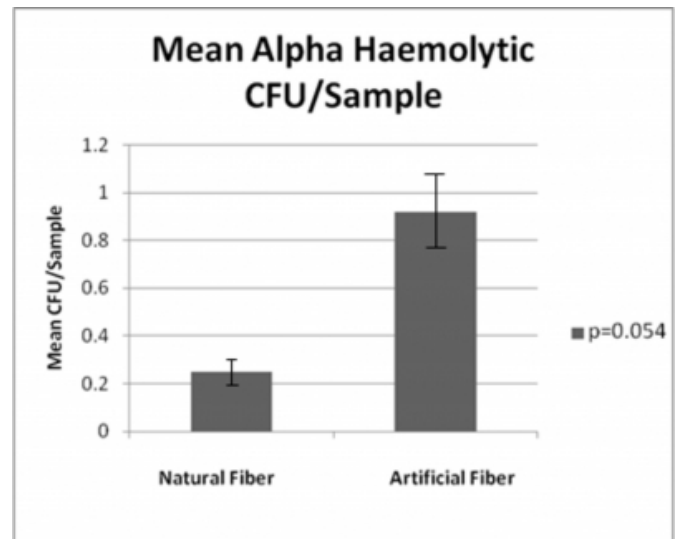


Figure 2

Figure 2



DISCUSSION

From the results it is apparent that the relationship between textile composition and bacterial diversity previously noted in vitro translates to in vivo conditions. Additionally, the fact that diversity was assayed through visual assessment of colony type means that more diversity may have existed within the samples than was noted due to visual similarities. Initial culturing of samples on nutrient agar also excluded the growth of fastidious organisms.

These two factors do limit the degree to which diversity observed fails to encapsulate total diversity, but as the same treatments were applied to both classes of textile samples it can be reasonably postulated that both classes of textiles would have their diversity reduced in similar degree. We

therefore propose that observed differences do reflect real differences in bacterial populations on the two classes of textiles. Additionally, though the length of the semester did not permit species identification, the higher incidence of alpha-haemolysing bacteria on the artificial textiles inconclusively suggests that these populations may contain more potential pathogens.

These results have implications for health care policy regarding composition of hospital-mandated garments, and can be applied to other studies related to hospital safety. For example, the 2000 study by Tammelin et al found data to support that tightly-woven textiles reduced MRSA transmission in the operating theater (9). Potentially, use of tightly-woven garments made of natural fibers would further reduce transmission due to their decreased pathogen load.

There are factors beyond fiber choice that influence the bacterial load of hospital garments. It has been shown that under the standard temperature conditions used in home washing machines, Gram positive bacteria were easily transferred from contaminated to previously sterile garments (10). Data also suggest that liquid and powdered laundry detergents are ineffective at preventing bacterial cross-contamination between garments or removing Gram positive microorganisms (11). The above studies demonstrate that protocols involving the appropriate care of hospital-mandated garments may provide an important contribution to the prevention of nosocomial infections. Regarding the development of such protocols, it is known that bleach-based cleaners are effective at removing microorganisms (11). However, cleaners in this category often damage or destroy artificial fibers. This information suggests another reason why natural fibers may be a superior choice when attempting to prevent transmission of potentially pathogenic microorganisms.

A recent study by Fernandez et al examines techniques that might improve cotton textiles by impregnating them with potentially antimicrobial chemicals such as chitosans and chitooligosaccharides (12). Current results suggest these chemicals are effective in vitro. Studies in Japan have shown the use of garments impregnated with the existing antimicrobial, digenite, by healthcare workers significantly reduced the number of febrile days experienced by their patients (13).

These results may suggest that it is possible for natural fibers to be improved on through the addition of antimicrobial chemicals. However, the ever-increasing levels of antibiotic-

resistant organisms and their impact on our society should perhaps cause us to exercise caution on this front. Routinely exposing bacteria to antimicrobials through the standardized use of chemically impregnated clothing is likely to rapidly increase resistance to these compounds. The use of standard natural fibers in healthcare workers' garments would not increase antimicrobial resistance in the bacterial population, and may reduce the incidence of nosocomial infection.

CONCLUSION

If the clothing of health care workers functions as a vector of transmission for infectious organisms, the use of textiles which are less hospitable to microorganisms would seem a reasonable means by which to reduce nosocomial infection rates. The use of natural cotton scrubs as opposed to cotton-poly blends would increase facility operating costs in the short term. However, if their use decreased the rate of nosocomial infection, facilities would ultimately reduce their costs while improving patient outcomes. A clinical trial based on these findings may lead to results that would impact patient health and reduce healthcare costs.

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