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Research article

Microbial profile of T-shirts after a fitness session of Chinese students

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ABSTRACT

Clothing textiles could protect our human skin against external factors, but the microbial population, including conditional pathogens, in clothing, would cause unpleasant odor, Skin inflammation, and textile deterioration. Several studies have reported that microbiomes on clothes are affected by skin microorganisms of individuals, the local environment and the types of textile fabrics, but little is known about how the textile microbial community is shaped in the Chinese population. In this study, 10 healthy young students were recruited to successfully wear the T-shirts made with 3 different fabrics (polyester, cotton, and blending fabrics of polyester and cotton) during physical exercise. Total deoxyribonucleic acid (DNA) was extracted from 30 T-shirts and 16s rRNA gene amplicon sequencing was applied to estimate the absolute abundances of bacteria in the samples. The main bacteria on wore T-shirts were *Staphylococcus* (21.66%) *Enhydrobacter* (13.81%), *Pantoea* (8.14%), *Acinetobacter* (7.81%), *Pseudomonas* (6.18%), *Cutibacterium* (4.99%). However, no difference of α and β diversity was observed among the three textile fabrics. Further analysis found that *Pantoea* and *Pseudomonas*, mainly from the environment, enriched on the polyester, but not on cotton, while *Enhydrobacter*, from human skin, has the growth advantage on cotton, and the blending fabric in between. Collectively, our study preliminary explored the clothes microbiome in Chinese young students, contributing to helping understand the role of clothing microorganisms on human health.

1. Introduction

Clothes could keep a warm and moist environment on our skin to make us feel comfortable, but it also creates a suitable environment for the growth of bacteria, especially in the summer season. The textiles of clothes can affect our skin's microbiome, and specific ranges of bacteria or fungi may induce potentially unhealthy effects, including unpleasant odors, fabric deterioration, and even skin allergies and infections (Szostak-Kotowa, 2004; Van Herreweghen et al., 2020). The skin has various small niches, but each of them is a specific bacterial community, indicating that the diversity of bacteria varies on different parts of skin surfaces (Callewaert et al., 2014; Fredricks, 2001). In dry areas, such as the forearm and legs, only 10^2 bacteria per cm^2 exist, while the moist parts (axillae, umbilicus, and toe) contain about 10^7 bacteria per cm^2 (Leyden et al., 1981; Sterndorff et al., 2020). Moreover, the skin bacterium types are complex and diverse, previous research reported that up to 19 different phyla are present on human skin, and even more than 9 different phyla could be detected in one niche of the axillary region (Callewaert et al., 2013; Grice et al., 2009). Microorganisms can transfer between skin and the clothing fibers, but the growth of adhered bacteria can be affected by clothing fibers, skin desquamation, sweat secretions, season or nutrition from the environment and natural particles. Among them, the composition of the clothing textile and bacterium-fiber interaction are important factors determining the microbiome.

The adhering ability of bacteria to natural or synthetic fibers is different, it is generally accepted that microbiota could more easily adhere and grow on natural fibers, having natural nutrients present in clothing and a high ability to adsorb and retain sweat components (Liao et al., 2020). Due to these absorbent properties, fabrics made from wool, cotton and other similar protein and cellulose fibers are ideal substrates for bacterial adherence and growth (El-Tahlawy et al., 2005). However, these natural fibers can be also degraded by cellulolytic enzymes released by special bacteria and fungi (Khoddami et al., 2002; McQueen and Vaezafshar, 2020). Synthetic fibers do not absorb moisture on the fibers

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themselves while retaining it in the space between fibers, therefore they are less susceptible to growth (Varshney et al., 2020). Besides these two textiles, the blending fabric made from various proportions of natural and synthetic fibers are created by advanced textile technology, but varied blending fabric holds different abilities to support bacteria growth. Much research has been conducted on eliminating all microorganisms on textile fabrics by adding various antimicrobials to prevent against the potential damage to skin (Alonso et al., 2009; Kathirvelu et al., 2009; Maguire and Maguire, 2017), but several questions are still needed to be explored, including whether there are any differences of microbial profiles among T-shirts made by different fabrics, what are the main factors affecting microbial profiles on T-shirts.

Previous researches reported that the microbial profile of T-shirts varied due to the different individuals and local environments, involved in the determination of microbiome, but their results were not all consistent. Recent studies on the microbiome data of various locations in the human body in 35 countries in the Forensic Microbiome Database (FMD) (http://www.fmd.jcvi.org) found that the microbiome distribution differed according to the body part as well as the geographic location. In the case of skin samples, *Staphylococcus* species were higher than *Corynebacterium* species among Asians compared with Americans. *Holdemanella* and *Fusobacterium* were specific in the saliva of Korean and Japanese populations (Cho and Eom, 2021). To our knowledge, no study has been conducted on the Chinese population. Thus, in the current study, the microbial profile of T-shirts made with different fabrics (polyester, cotton and blending fabric) after a fitness session was investigated by 16S rRNA gene sequencing in young individuals from China.

2. Methods

2.1. Study design

10 students (19–25 years), 8 males and 2 females lived in the Qiaokou District of Wuhan, Hubei Province, China, where the climate type is Koppen's CWA. All recruited participants met the following specific requirements. (1) No antiperspirant or deodorant was used 48 h before the experiment and during the experiment (the use of antiperspirant and deodorant has an impact on skin bacteria); (2) volunteers reported no body odor, confirmed in the hospital; (3) No local or systemic antibiotics were used 2 months before or during the experiment; (4) volunteers did not suffer from any skin diseases, such as psoriasis, atopic dermatitis or skin infection; (5) volunteers did not suffer from any chronic or systemic diseases; (6) general health and mental condition of the volunteers are good. The study protocol was approved by the Medical Ethics Committee of Tongji Medical College, Huazhong University of Science and Technology and informed consent was obtained from every participant before data collection in the current study.

The T-shirts made with pure cotton, blended fabrics (35% cotton, 65% polyester) or polyester from one factory used in the experiment were purchased from the website. Before use, new T-shirts shall be washed uniformly before distribution to remove stains and chemicals. They were first washed with 4 g/l ECE non-phosphate standard detergent at 25 °C through standard washing procedures for 22 min, which consist of washing and drying. Then, the T-shirts were washed again through standard washing procedures without detergent to remove the residual laundry detergent from the clothes. The prewashed T-shirts were placed in clean plastic bags before wearing them.

Volunteers are required to wear each T-shirts next to the skin and exercise until sweating. The time of physical exercise (running or playing badminton) ranges from 8 to 90 min (Table 1). No significant differences in exercise time were observed among the three groups (polyester, Cotton and blending fabric). After exercising, volunteers quickly take off the T-shirts, then put the clothes into a sterile sampling bag strictly following the same procedures, and fill in the information collection form truthfully. Finally, the clothes were put into a black plastic bag immediately and stored protected from light at room temperature for 72 h.

2.2. DNA extraction

The bacterial extraction was conducted using the method from Callewaert et al. (2014) with some modifications. Briefly, the bacterial extraction occurred on the complete T-shirts, using deionized water (Teufel et al., 2008). 300 mL of water was added into the plastic bag with the clothes, firmly sealed with tape, and vortexed for 15 min. Then, the buffer was subsequently manually pressed out and transferred into sterile 50 mL reaction tubes. The extracts were used for isolation of bacteria and extraction of DNA respectively. The method focused on the extraction of the bacteria from the whole clothes, not from one region (e.g., the axillary region). The extractions of bacteria DNA were performed according to the instructions of the D5525-01 Water DNA Kit (Omega Bio-Tek). The concentration of extracted DNA was measured using ND-1000 NanoDrop (Thermo Fisher) and DNA was stored in the freezer at -20 °C before experiments.

2.3. 16S rRNA gene amplicon sequencing

Sequencing libraries were prepared using a dual-PCR setup, targeting variable regions V3 and V4 of the 16S rRNA gene, approx. 460 bp. In the first step (30 cycles), general primers (F-ACTCCTACGGGAGGCAGCAG, R-GGACTACHVGGGTWTCTAAT (Behrendt et al., 2012; Klindworth et al., 2013) were used. In the second step (15 cycles) the primers additionally included sequencing adaptors and barcode tags (Nunes et al., 2016). PCR reactions were performed using Taq PCR Kit (E5000, NEB), modified to 20 μL reactions (with 2 μL template), following the manufacturer's instructions. After each PCR reaction the amplicon products were purified using QIAquick Gel Extraction Kit (28704, Qiagen). The pooled library concentration was determined using the Qubit™ dsDNA HS Assay Kit (Thermo Fisher Scientific, CA, US). Paired-end

Table 1. Characteristics of volunteers.

Subject	Gender	Age (y)	BMI	Types of physical exercise	Time of physical exercise (min)		
					Poly	Cotton	Blending
1	Male	20	24.80	Badminton	50	50	60
2	Male	21	23.31	Badminton	50	40	60
3	Female	20	18.83	Running	75	90	80
4	Male	21	20.20	Running	20	10	15
5	Male	19	20.98	Running	15	25	20
6	Male	20	18.14	Running	10	10	10
7	Male	20	21.22	Running	20	20	20
8	Male	20	21.20	Running	25	30	30
9	Female	24	21.97	Running	70	85	70
10	Male	21	20.52	Running	8	10	15

Amplicon sequencing was performed on the Illumina NovaSeq Sequencer 6000 (Illumina Inc., CA, US) with the denatured libraries.

2.4. Data analysis and data availability

QIIME2 software was used to further de-noise, splice and filter chimera of clean data obtained from data quality control by using the DADA2 method. species annotation, including Domain, Phylum, Class, Order, Family, Genus, Species, etc. (the default confidence is 0.7), were performed by QIIME2 software and SILVA database, and the relative abundance of each sample at genus levels was log10-transformed (Quast et al., 2013). Since our data was collected through repeated measurement, we chose a linear mixed model to analyze by selecting groups (polyester, cotton and blending fabric) as fixed effectors and individuals as random effectors. While the differences in specific genus relative abundance among three groups were analyzed using Paired FREIDMAN test with multiple comparisons test by controlling the false discovery rate (Plachokova et al., 2021). The statistical analysis was performed by QIIME2, SPSS 22.0 and the statistical graphs were generated from Graphpad Prism 8.0 and R 3.4.1.

2.4.1. α Diversity

α Diversity is represented by a series of indices, and the level of community species diversity can be judged by comparing these indices. QIIME2 software was used to calculate the α diversity index of each sample. Species richness (Chao1 and ACE index), Species diversity (Shannon and Simpson index), community evenness (Simpson's evenness and Pielou's Evenness), and sequencing depth indexes (Observed Features and Good's Coverage) were compared among groups using the Kruskal-Wallis method analyzed.

2.4.2. β Diversity

β Diversity is used to compare the diversity between different ecosystems, namely diversity between samples, and is an indicator of similarity in microbial composition between individuals. A PERMANOVA (999 permutations) with Bonferroni correction for multiple testing was applied to calculate the Unweighted UniFrac distances (a quantitative measure of community dissimilarity incorporating phylogenetic distance and taxon abundance) among three groups. The heat map of the distances between every two samples was shown in a heat map. Principle coordinates analysis (PCoA) plot using the Bray–Curtis dissimilarity was generated from the unweighted UniFrac distances.

3. Results

3.1. Characteristics of volunteers

The current study recruited 10 young and healthy students, as the average age was 20.6 ± 1.4 years old and the average BMI was 21.1 ± 2.0. Volunteers wearing T-shirts made of polyester, cotton or blending fabric, participated in physical exercise outside, including running and playing badminton, for varied times, but there was no difference in physical exercise duration among the three groups ($p = 0.34$) (Table 1).

3.2. α Diversity among polyester, cotton and blending textiles

A total of 4452520 high-quality sequences were obtained for the 16S rRNA gene V3, and V4 region across all 30 samples. In the total samples, 3 domains, 41 phyla, 88 classes, 210 orders, 354 families and 802 genera were detected. The microbial composition and diversity of each textile fabric were quantified on genus levels, as the 16s rRNA sequence method does not work well at the level of species. α diversity, referring to the diversity in a specific region or ecosystem, is a comprehensive index reflecting species richness and evenness in the group. By comparing these α diversity indices, a series of indices should be calculated according to the data from 16s rRNA sequencing. Generally, the indexes of species richness mainly include Chao1 and ACE index; the indexes of species diversity include Shannon and Simpson index; species evenness indexes mainly include Simpson's evenness and Pielou's Evenness. In addition, Observed Features and Good's Coverage are sequencing depth indexes, and the index of Faith's PD reflects the pedigree diversity by considering evolutionary distance (Shu and Huang, 2021). As shown in Figure 1A, The ACE values of polyester, cotton and blending fabric groups were respectively 478.1 ± 370.1, 653.1 ± 499.4 and 452.1 ± 401.5, but no difference was observed among their groups. Consistent with Chao1, there was no difference among polyester (463.1 ± 358.9), cotton (633 ± 476.4) and blending fabric groups (438.9 ± 392.2) (Figure 1B). Analysis of the Shannon index found that there was no difference in species diversity among the three groups (polyester 4.991 ± 1.097, cotton 5.3 ± 1.564, blending fabric 4.778 ± 1.549) (Figure 1C). Consistently, the analysis of Simpson's evenness index (polyester 0.05277 ± 0.04656, cotton 0.02767 ± 0.009537, blending fabric 0.04699 ± 0.03682) and Pielou's Evenness (polyester 0.6075 ± 0.07774, cotton 0.5948 ± 0.1083, blending fabric 0.5816 ± 0.1185) got the same result, indicating that different fabrics did not affect the Species evenness (Figure 1D and E). Results of Observed Features (polyester 401.9 ± 317.1, cotton 551.9 ± 384.7 and blending fabric 378.9 ± 347.4) and Good's Coverage (polyester 0.9931 ± 0.00615, cotton 0.9912 ± 0.00929, blending fabric 0.994 ± 0.006184) indicated that sequencing depth index was not different among three groups (Figure 1F and G). Moreover, analysis of Faith's PD (polyester 140 ± 69.6, cotton 111 ± 43.8, blending fabric 109.1 ± 48.14) showed pedigree diversity was identical (Figure 1H). Collectively, the different fabrics of T-shirts worn by Chinese young students did not affect the α diversity after sweating exercise.

3.3. β Diversity among polyester, cotton and blending textiles

β Diversity is used to compare the diversity between different groups, and is an indicator to measure the similarity of microbial composition between individuals. Beta diversity uses the evolutionary relationship and abundance information of sample sequence to calculate the distance between two samples and obtain the distance matrix to reflect whether there are significant community differences between samples (groups) (Shu and Huang, 2021). We ran a PERMANOVA (999 permutations) with Bonferroni correction for multiple testing to calculate the Unweighted Unifrac among samples in the study. As shown in Figure 2A, the distances between every two samples ranged from 0.5 to 0.7 and no difference in unweighted UniFrac distances were observed among the three groups. Further PCoA analysis showed that PC1, PC2 and PC3 accounted for 12.38 %, 9.065 % and 7.334 %, respectively. β diversity was not different on T-shirts made with different textiles (polyester, cotton and blending fabric) (Figure 2B).

3.4. Taxa that differed in abundance among polyester, cotton and blending textiles

As shown in Figure 3A, an assessment of the bacterial composition of the most abundant Taxa showed that the top 20 genera were listed and the dominated 6 genera in descending order were *Staphylococcus* (21.66%), *Enhydrobacter* (13.81%), *Pantoea* (8.14%), *Acinetobacter* (7.81%) *Pseudomonas* (6.18%) and *Cutibacterium* (4.99%). for each group, the enriched genera in the polyester group were *Staphylococcus* (26.94%), *Pseudomonas* (15.74%), *Pantoea* (9.67%), *Cutibacterium* (8.48%), *Acinetobacter* (7.92%) and *Enhydrobacter* (2.03%). In cotton group, the dominated bacteria were *Staphylococcus* (18.19), *Enhydrobacter* (13.96%), *Cutibacterium* (6.97%), *Acinetobacter* (6.88%), *Corynebacterium* (4.40%), Sphingomonas (3.65%), *Pseudomonas* (2.91%), Chryseobacterium (2.17%) and *Pantoea* (1.67%); in blending fabric group, *Staphylococcus* (31.39%), *Pantoea* (17.08%), *Acinetobacter* (9.20%), *Enhydrobacter* (5.04%), *Pseudomonas* (3.33%), *Micrococcus* (2.91%), *Corynebacterium* (2.00%) and *Cutibacterium* (1.77%) were dominant bacteria.

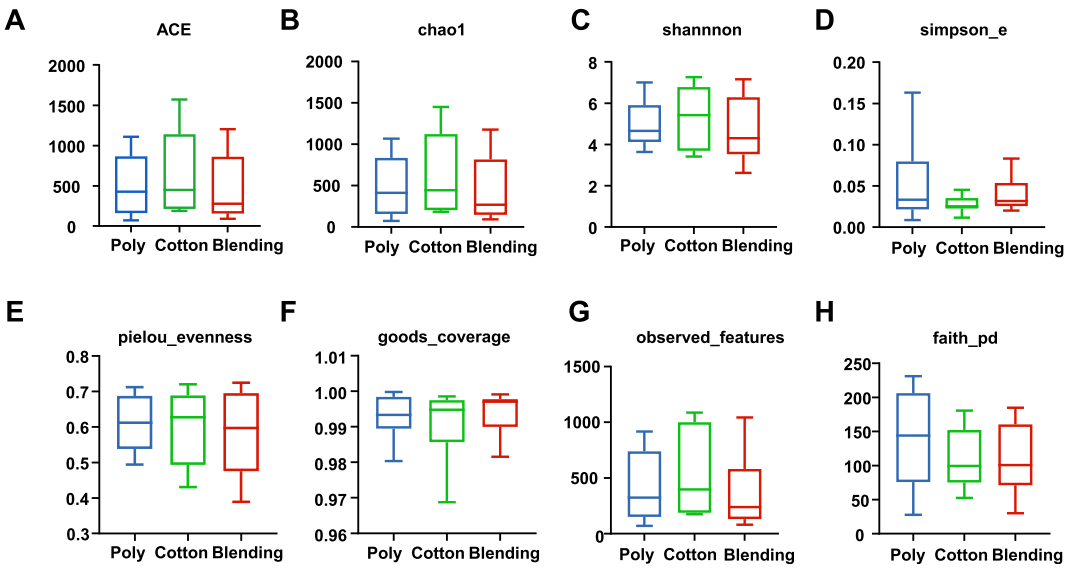

Figure 1. α-Diversity indices of microbial community of different textile fabrics. T-shirts made with different fabrics (polyester, cotton and blending fabric) after a fitness session was investigated by 16S rRNA gene sequencing, α-diversity indices, including ACE (A), chao1 (B), shannnon (C), simpson_e (D), pielou_evenness (E), goods_coverage (F), observed_features (G) and faith_pd (H), were acquired.

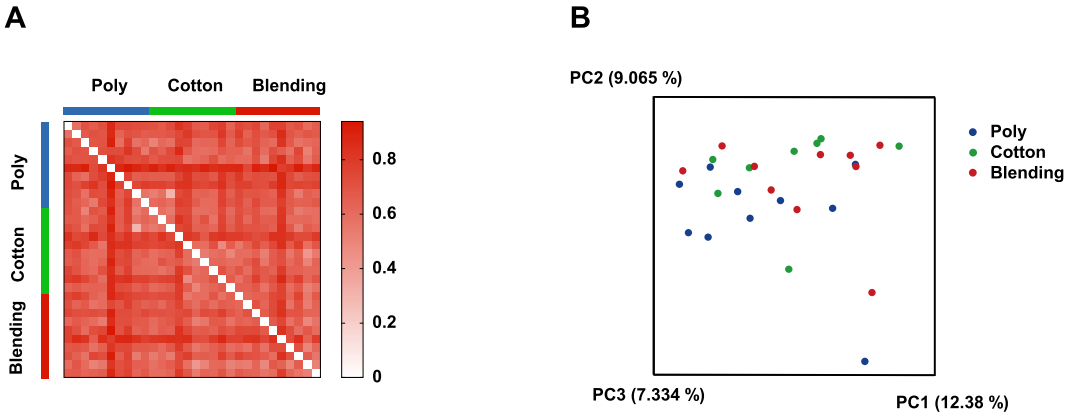

Figure 2. β-Diversity in textile samples. (A) The heat map of the distances between every two samples. (B) PCoA plot using the Bray-Curtis dissimilarity. The percentage of the axis represents the amount of variance explained by the principal component.

Though there were no differences in α or β diversity among the three fabric groups, further analysis found that the composition of bacteria on three textiles were not identical. The relative abundance was Log10-transformed and analyzed by using a mixed effect model. Statistical results showed that no difference in relative abundance of *Cutibacterium*, *Staphylococcus* and *Pantoea* were observed among the three groups. However, the blending group had a lower level of *Pseudomonas* than the polyester group, a higher level of *Pantoea* than the cotton group and a lower level of *Enhydrobacter* than the polyester group, while the polyester group had a lower level of *Enhydrobacter* than the cotton group and higher level of *Pantoea* than the cotton group (Figure 4A). By using Paired Freidman method, we also found that less *Pantoea* and more *Enhydrobacter* grew on cotton fabric compared with blending fabric and polyester, respectively (Figures 4B–E).

4. Discussion

Fabrics could have a great impact on the microbiome of clothes. In the current study, 30 samples from different fabrics of T-shirts worn by 10 Chinese students were collected and analyzed by 16s rRNA sequencing. We did not find any statistical significance of species richness, evenness, diversity and pedigree diversity among polyester, cotton and blending fabric groups, indicating that no differences were observed in α diversity. In addition, the β diversity of the three groups are identical too. Further analysis found that *Staphylococcus* was often able to gain dominance on three textile fabrics. Polyester textiles showed an enrichment for *Pseudomonas*, *Pantoea*, but less *Enhydrobacter* compared with cotton textiles.

The clothes microbiomes are shaped mainly by the individual wearing them and the air particles carrying microorganisms are adsorbed on textiles fabrics (Perez et al., 2016). Previous studies of polyester and cotton clothes after fitness in Belgium, Western Europe, have found that certain species were able to grow in more abundant quantities on the textile fibers. *Micrococci* were selectively enriched on textile of polyester and wool but were inhibited on fleece or viscose. An enrichment of *Enhydrobacter* and *Cutibacterium* (*Propionibacterium*) were observed on polyester textiles. Cotton and polyester textiles showed an enrichment of *Staphylococcus* seen in the fitness clothes. Another study also reported a high affinity of *Staphylococcus* for cotton and polyester in close correlation with these findings. Inconsistent with these results, the current study found *Staphylococcus* enriched on all fabrics (polyester, cotton and blending fabric), composed about 20% of the total microorganism. *Staphylococcus* is a common microorganism widely distributed in nature

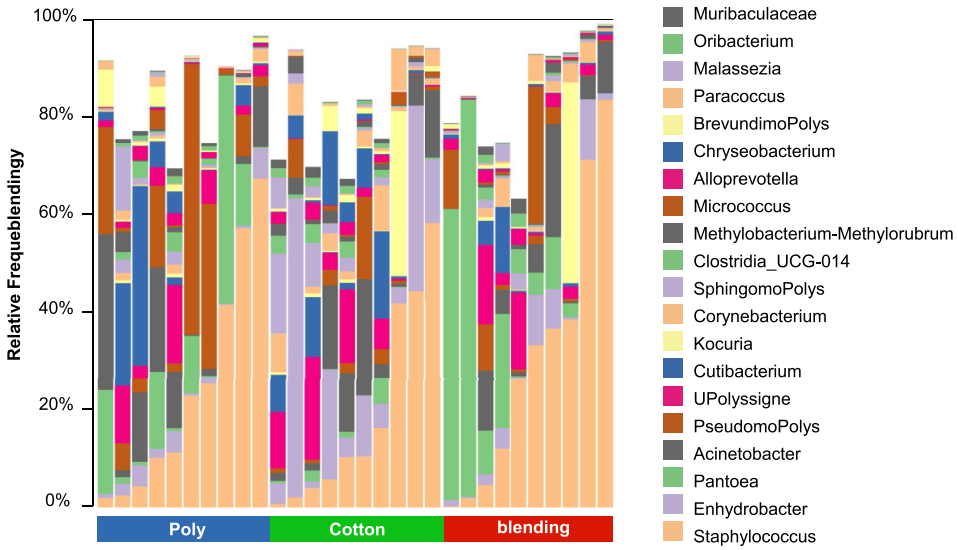

Figure 3. Community composition of textile samples. Relative abundance of the top 20 abundant genera across all samples. Missing bars are due to samples with too few reads determined by 16s rRNA sequencing.

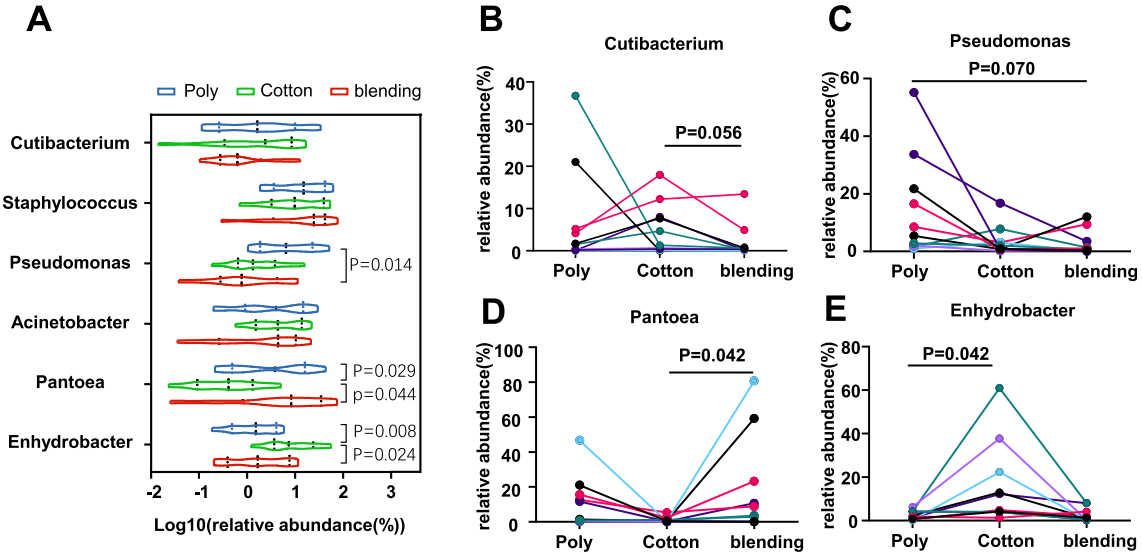

Figure 4. Differentially abundant sequences among polyester, cotton and blending fabric groups. (A) The relative abundances are log10-transformed and the distribution of groups' abundances is shown as a Tukey's boxplot. P values for analysis by linear mixed model comparing mean log relative abundance among three groups. (B–E) Relative abundance of each individual was shown and analyzed by using Paired FREIDMAN test with multiple comparisons test by controlling the false discovery rate.

and exists on the skin, feathers, eyelids, mucous membranes and intestines of healthy birds. We also observed an enrichment of *Enhydrobacter* on cotton and blending fabric groups textiles but not on polyester, inconsistent with previous study. *Enhydrobacter* are generally found in human skin, mucous membrane, and in great abundance of intestine. In addition, the *Cutibacterium,* a known skin commensal, was also observed in three groups, the proportion is only 1–3%, our results were consistent with previous results. However, according to the study of the skin microbiota in a healthy Chinese population (Zhai et al., 2018), the common and dominant bacterial genera in skin microbiota profile were *Cutibacterium*, *Staphylococcus*, *Streptococcus, Moraxella* and *Corynebacterium*, thus the abundance of *Cutibacterium* should be much higher than the proportion in the current study (4.99%–8.48%). *Cutibacterium* plays a key role in the skin ecosystem as they can protect microbiota disequilibrium by fighting pathogens and participating in skin homeostasis by producing beneficial bacterial metabolites. It also acts as an opportunistic pathogen, causing either superficial or invasive infections, including but not limited to breast infections, infective endocarditis, skin abscesses, or device-related infections (Fourniere et al., 2020). Studies in children or adolescents found the relative abundance of *Cutibacterium* was lower, as the sebaceous glands develop and have a high level of secretion in neonates in childhood (Zouboulis and Boschnakow, 2001). Another study reported that *Cutibacterium* utilized glycerol as carbon source, produced from the catabolism of sebaceous triglycerides, maintaining the skin pH by the remaining fatty acids and inhibiting growth of *Staphylococcus* and *Streptococcus* (Webster, 2007). In addition, the skin microbiota reflects differences in terms of the relative abundance of dominant species between different skin, sites, ages and gender. The elderly had more species richness and diversity than other age groups (Shropshire and Bordenstein, 2016; Zhai et al., 2018). Collectively, the

low abundance of *Cutibacterium* may be due to the young age of individuals participating in this study.

We also observed certain amounts of *Pseudomonas* (0–24%) and *Pantoea* (0–32%), which were not reported before in different textiles of T-shirts after sporting. Members of the *Pseudomonas* genus including more than 200 species endowed with diverse biological properties, are saprophytic bacteria widespread in the environment, and are readily isolated from soil and moist environments (Llamas et al., 2014). *Pseudomonas* is a frequent causative bacteria of healthcare-associated diseases, and some genera have been recognized to induce human colonization and infection (Iseppi et al., 2020). *Pantoea*, an environmental Gram-negative bacterium, comprises many versatile species, isolated from a multitude of environments. Although most of the previous research on *Pantoea* normally focused on its parasitic association with plants, including maize, cotton, melon and onion, recent evidence suggests that *Pantoea* has been frequently found in the nosocomial environment, with considerable debate as to its effect on human health (Raza et al., 2021; Walterson and Stavrinides, 2015). These two genera found on special textile fabrics are mainly from environmental media, indicating that the microorganism from outside environment could shape the microbiome on clothes. Previous studies did not find high proportion of these microbiota from the environment, because the microbiome was analyzed immediately after sample collecting, while in the current study, the collected T-shirts were placed in clean bags for 72h incubation before detection, thus the microorganism from the skin and outside environment compete for survival during incubation, *Pseudomonas* and *Pantoea* have the survival superiority in these condition on certain textile fabrics. Hence, these bacteria might affect each other during the growth on textile.

Certain species of organisms were able to grow on special textile fibers, depending on the type of textile fibers and the type of bacterial. Polyester textiles showed enrichment for *Pantoea* but less *Enhydrobacter* compared with Cotton textiles. These results are in close correlation with previous results that a high enrichment of *Staphylococcus* spp. for cotton and polyester was reported (Broadhead et al., 2021). In addition, *Staphylococcus* was often able to gain dominance on cotton textiles, as reported in another fitness experiment. However, this was not seen for synthetic clothing textiles. *Micrococci* were selectively enriched on polyester and wool but were inhibited on fleece and viscose. Polyester textiles showed an enrichment for *Micrococcus*, *Enhydrobacter*, and *Propionibacterium*. Cotton, a natural fiber, originates from the plants of Gossypium cotton, and have a high adsorbing capacity as cotton fibers consist of cellulose. While polyester, a petroleum-based synthetic fiber, has no natural properties, and synthetic fibers have a very poor adsorbing capacity due to their molecular structure (Jacksch et al., 2021; Levitt, 1947). It is widely believed that textile fabrics made from cotton, wool, and other similar protein and cellulose fibers are suitable substrates for bacterial growth, as bacteria grow more rapidly in a moist environment (Massaroni et al., 2015).

In the current study, bacteria from the skin, including *Enhydrobacter*, *Cutibacterium* and *Staphylococcus*, preferred to grow on the cotton fabrics, while environmental bacteria, *Pantoea* and *Pseudomonas,* enriched on the polyester fabrics. The composition of bacteria on blending fabric was normally considered between the cotton and polyester fabrics, but in certain specials the bacteria had different tendentiousness. On blending fabrics, growth of *Pseudomonas* was inhibited the same as in cotton fabrics, while *Pantoea* and *Enhydrobacter* were enriched in polyester fabric. These differences may be associated with the bacteria specials. A previous study reported that *Staphylococcus* strains considerably persisted for over 90 days on polyester fabrics longer than on cotton fabrics, but we did not observe the difference (Neely and Maley, 2000). The composition of bacteria on polyester is not completely consistent with nylon, another man-made fabric. Nylon showed a very selective bacterial growth, with the enrichment noted for *Staphylococcus* and *Enhydrobacter* same as cotton, while the growth of *Micrococcus* and *Corynebacterium* were inhibited (McQueen et al., 2007). These differences among various fabrics need further studies to clarify.

5. Limitation

There are several limitations to current study. (1) We only investigated the bacteria composition on different textiles, but the total number of bacteria was not evaluated. Thus, the different ability to support bacteria growth among the polyester, cotton and blending fabrics is not able to acquire. (2) There are only 10 young students recruited and the bacteria composition variation within groups is large, resulting in less identification of bacteria, although we did our best to control bias through recruitment of individuals from one campus and repeated measurement in current study. (3) The impact on environment was not evaluated or controlled, as the results showed that environmental bacteria played an important role in the process. Several environmental samples should be collected and investigated. (4) How these different compositions of bacteria on varied textile fabrics affect humans was not clear, further studies are needed to clarify these questions.

6. Conclusion

The textile fabrics did not affect the α diversity and β diversity on the T-shirts worn by young students from China after a fitness session. *Pantoea* and *Pseudomonas* mainly from the environment enriched on the polyester fabric, while *Enhydrobacter*, from human skin, has the Growth advantage on cotton fabric. Our study primarily explored the microbial profile of T-shirts worn by young individuals from China, providing the evidence to further clarify how microorganisms on clothes affect the skin health of Chinese individuals.

Declarations

Author contribution statement

Huizhen Yan: Conceived and designed the experiments; Performed the experiments; Analyzed and interpreted the data; Wrote the paper.

Yuxing Ren: Performed the experiments.

Bihong Zhou: Contributed reagents, materials, analysis tools or data.

Fang Ye: Analyzed and interpreted the data; Wrote the paper.

Zhigang Wu: Conceived and designed the experiments.

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Data availability statement

Data will be made available on request.

Declaration of interest's statement

The authors declare no conflict of interest.

Additional information

No additional information is available for this paper.

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