A microbiome study reveals the potential relationship between the bacterial diversity of a gymnastics hall and human health

Z. Liang1, C. B. Dong2, H. Liang3, Y. X. Zhen1, R. L. Zhou1, Y. F. Han2* & Z. Q. Liang2*

Currently, investigations on the microbiota of sports centers and related facilities have been carried out in some countries, which showed that Microsporum gypseum, Trichophyton mentagrophytes and T. tonsurans are important dermatophyt fungi. In China, some research on athletes and sports equipment between the fungal community and public health has made some interesting achievements. However, the bacterial group among them has not been reported. Therefore, the aim of this study was to uncover (I) gymnastic equipment is there potential pathogenic factors and (ii) is there any difference in the biomarker of bacterial in different types of gymnastic room? The samples were collected from the gymnastics halls of one university in western China and main sports equipment, including gymnastics carpets, moving barres, hoops and balls, as well as wall bars, parallel bars and horizontal bars. The 16S rDNA of all the samples was sequenced, and the analyses were performed using FaproTax, Bugbase function prediction and Line Discriminant Analysis (LDA) Effect Size. A 16S rDNA sequence analysis revealed abundant bacterial species biodiversity on gymnasts and apparatuses from two gymnastics halls at a university in western China. An analysis using the FaproTax and Bugbase functional prediction platforms showed that there were some opportunistic pathogens on the athletes and equipment from the Rhythmic Gymnastics (RG) and Artistic Gymnastics (AG) halls, such as Staphylococcus and Corynebacteriaceae. Infectious agents associated with cancer induction and development, such as Ruminococcaceae, Veillonellaceae and Moraxellaceae, as well as microbial toxin producers with a potential impact on human health, were also detected. According to a line discriminant analysis (LDA effect size), the bacterial biomarker groups of the two gymnasiums were different at the phylum-genus level: for RG, Erysipelatoclostridium, Lachnospiraceae and Bacteroidales, while for AG, Rhizobiales. Based on the results of the investigation, we suggest that more comprehensive consideration should be given to indoor microbial biodiversity and related public health problems in school gymnasiums.

At present, 55% of the world’s population has moved from rural to urban areas1. The referenced study observed that people living in towns and cities interact with microbes in markedly different ways from those living in rural areas. Microorganisms in a built-up environment have been considered a possible source of infection2,3. Obviously, living in a city has a significant impact on human health, and the mechanism of that impact varies greatly4.

Urban transportation systems, including subways and buses, are utilized daily by billions of urban residents. Travelers, in turn, move around the city carrying their symbiotic microbes, adding to the complexity of urban microbes. At present, studies on urban environmental microbiota in transportation systems5, hospitals6,7, soil8, and sewage9 have been performed. For example, Danko et al.4 found 10,928 viruses, 1302 bacteria and 2 archaea in a survey of 4728 metagenomic samples from mass transit systems. All of these studies show that public urban public spaces contain abundant microbes. However, there are many other indoor public places where people...
often gather, such as karaoke halls, airports and bus stations, as well as sports venues and other facilities, for which research reports are uncommon.

In recent years, the correlation between the diversity, relative abundance, and function of microbiota and respiratory diseases in the campus environment (including dormitories and classrooms) has been studied in some countries\textsuperscript{10–13}. These studies observed that the highest abundance of Actinobacteria, Gammaproteobacteria and Alphaproteobacteria was in urban schools, and Actinobacteria and Cyanobacteria were more abundant in rural schools\textsuperscript{14–17}. Fu et al.\textsuperscript{12} also found that \textit{Izhakiella} and \textit{Robinsoniella} were positively correlated with the severity of asthma in a study of classroom floor dust in junior middle schools in Malaysia.

By the 2020s, some countries had also carried out microbiota studies on swimming pools, showers, saunas, wardrobes, wrestling mats, gymnastics carpets and pillowcases in sport centers. In most cases, dermatoprotrophic fungi such as \textit{Microsporum gypseum}, \textit{Trichophyton mentagrophytes} and \textit{T. tonsurans} were found\textsuperscript{14}. Sports venues and corresponding equipment have become carriers or storehouses of pathogenic fungi\textsuperscript{18}. Liang et al.\textsuperscript{16–18} from China conducted the first investigation based on the rDNA-ITS sequence to study the structure, dynamics and potential public health problems of fungi on some participants and sports equipment of school soccer teams and rhythmic gymnastics in China. However, there are few reports on the bacterial microbiome structure of such sports venues and its relevance to public health.

In this study, athletes and the main apparatuses in two gymnasiums from a university in western China were selected as the research subjects. Based on the 16S rDNA sequence, the bacterial community structure and function will be analyzed to uncover that gymnastic equipment was there potential pathogenic factors and was there any difference in the biomarker of bacterial in different types of gymnastic room.

**Materials and methods**

**Test items and sampling methods.** \textit{Rhythmic gymnastics group} (RG). Thirty female RG students at a university in western China were used in this study (age: 20.70 years; height: 165.20 cm; weight: 52.96 kg; training period: 7.16 years).

**Tested items.** Rhythmic gymnast palms (n = 30 persons), one rhythmic gymnastics carpet (13 × 13 m\textsuperscript{2}), 3 barres (length: 4 m/barre), rhythmic gymnastics hoops (n = 30) and balls (n = 30).

**Sampling method.** Athlete. A small amount of sterile water was poured into a sterile medical bag to moisten the gauze. The tester wore disposable gloves (replaced for each sampled subject), wiped both of the subject's palms 4–5 times with gauze after exercise, and then immediately put the gauze into a sterile plastic bag.

Sport equipment. The gymnastics carpet was sampled after training. The carpet was divided into 9 rectangles (diagonal: 30 cm × 30 cm) with wide adhesive tape. Three pieces of gauze were used to sample each rectangle. A gloved tester wiped each rectangle with wet gauze 4–5 times. The gauze was put into a sterile plastic bag. To compensate for insufficient biological samples obtained by wiping the carpet, some of the fibers on the surface of the carpet were cut as a sample at any three places in each sampling rectangle area.

RG apparatus. The hoop, ball and barre were sampled after gymnast training. A gloved sampler wiped the hoops and balls' surface 2–3 times with wet gauze; each barre was wrapped with two pieces of wet gauze and wiped 2–3 times. After all the samples were collected, they were mixed into 5 pooled samples.

RG sample code. Carpet (aa), barre (ab), hoop (ac), ball (ad), palm (ae).

**Artistic gymnastics group** (AG). Thirty-seven AG students at a university in Western China were included in the study, including 12 boys and 25 girls (age: 20.81 years; height: 165.97 cm; weight: 55.88 kg; training period: 4.57 years).

**Tested items.** Artistic Gymnast's palms (37 persons), one gymnastics carpet (14 × 14 m\textsuperscript{2}), 3 sets of gymnastics wall bars, 10 bars per set (length: 77 cm/bar), 3 pairs of horizontal bars (length: 23.7 cm/bar) and 4 pairs of parallel bars (length: 35 cm/bar).

**Sampling method.** Athletes. The same as the sampling method for rhythmic gymnasts.

Sports equipment. One gymnastics carpet was sampled after training. The carpet was divided into 9 rectangles (diagonal: 47 cm × 47 cm) with wide adhesive tape. Three pieces of gauze were used to sample each rectangle. A gloved tester wiped each rectangle with wet gauze 4–5 times. The gauze was put into a sterile plastic bag. To compensate for insufficient biological samples obtained by wiping the carpet, some of the fibers on the surface of the carpet were cut as a sample at any three places in each sampling rectangle area.

Gymnastic equipment. Samples were collected from the wall bars, parallel bars and horizontal bars after training. A gloved sampler whose gloves were replaced for each sampled piece of equipment wrapped each wall bar with two pieces of wet gauze and wiped the surface 2–3 times. The same method as for the wall bars was used to sample the parallel bars and horizontal bars. After all samples were collected, they were mixed into 5 pooled sample bags.
AG sample code. Carpet (ba), wall bars (bb), horizontal bar (bc), parallel bars (bd), palm (be).

**DNA extraction, amplification and sequencing.** DNA extraction and PCR amplification. Total DNA was extracted using a FastDNA Spin Kit for Soil (MP, USA) according to the manufacturer’s instructions. DNA concentration and purity were detected using a NanoDrop2000, in which nucleic acid was selected after placing the 2 μL DNA sample and the DNA extraction quality was detected by 1% agarose gel electrophoresis. The PCR experiment used 338F (5′-ACTCTACGGGAGGCAGCAG-3′) and 806R (5′-GGAATTTCCTACGGGAGGCAGCAG-3′) primers for PCR amplification of the v3–v4 variable region. The amplification procedure was as follows: pre-denaturation for 3 min at 95 °C, 27 cycles (95 cyclic denaturation for 30 s, 55 s annealing for 30 s, 72 for extended 30 s), and a maximum extension of 10 min (PCR: ABI GeneAmp 9700). The amplification system was 20 μL, 4 μL 5×FastPfu buffer, 2 μL 2.5 mm dNTPs, 0.8 μL primer (5 μM), and 0.4 μL FastPfu polymerase. Briefly, 10 ng DNA template. PCR products were recovered using a 2% agarose gel, purified using the AxyPrep DNA Gel Extraction Kit (Axygen Biosciences, Union City, CA, USA), eluted with 10×TE buffer, and detected by 2% agarose electrophoresis. Quantification was performed using QuantiFluor uantiPromega, USA). PE 2×300 libraries were constructed from the purified amplified fragments according to the Illumina MiSeq platform (Illumina, San Diego, USA) standard operating procedures.

**Data quality control.** fastp (https://github.com/OpenGene/fastp, version 0.20.0) software was used for quality control of the original sequencing sequence, and FLASH (http://www.cbc.ca/software/flash, Version 1.2.7) software splicing was employed. For OTU sequence clustering, UPARSE software (http://drive5.com/uparse/, version 7.1) was used with a similarity of 97%, and chimeras were eliminated. Species classification annotation was performed using the RDP classifier (http://rdp.cme.msu.edu/, Version 2.2), and the comparison threshold was set to 70% for the Silva 16S RNA database (V138).

**Data processing.** Functional prediction. FAPROTAX is a functional prediction software based on 16S sequencing. It integrates multiple prokaryotic functional databases of published culturable literature. The database contains 7600 functional information for over 4600 species, including 80 functional groups including potential pathogenesis, methanogenesis, fermentation, and so on. When using, the annotated OTU table in Greengenes or Silva database is read, and the annotated OTU information is compared with the species information in the database through Python program, and the results of predicting various functions are output. BugBase is another tool for predicting the phenotypic function of the 16S microbiome. Based on OTU tables and Mapping files, BugBase uses existing databases, annotations and frameworks to compare and measure a large amount of information, providing users with organism-level related phenotypic prediction of the microbiome. Including Pathogenic Potential, Biofilm Forming, Gram Positive and Gram Negative and so on. BugBase also provides grouped statistics and visualization. BugBase can be used as a web application (http://bugbase.ccm.umn.edu) to use, also can be downloaded for free (https://github.com/knights-lab/BugBase).

Bar chart of microbial composition and relative abundance of samples, Venn and KRONA Annotation, FapRoTax and Bugbase function prediction analysis as well as LeSe analysis (http://huttenhower.sph.harvard.edu) were performed using BMKCloud (http://www.biocloud.net/). Specifically, for species analysis with significant differences (known as biomarker analysis) between groups, the LeSe was used to estimate the impact of the abundance of each component (species) on the differential effect. The LDA score for significant differences was set to 3.0 and p < 0.05.

The Ethics committee of Chengdu Sport University approved the study protocol. The study was conducted in accordance with relevant guidelines and regulations.

**Informed consent.** Informed consent was obtained from all individual participants included in the study.

**Results and analysis**

**The bacterial community of gymnasts and commonly used instruments has abundant species diversity.** A total of 1926 OTUs were obtained by 623,404 clustering effective sequences, and these OTUs were annotated as 847 species of microorganisms belonging to 41 phyla, 99 classes, 225 orders, 374 families, and 746 genera of archaea and bacteria. These data indicate a rich diversity of bacteria on athletes’ palms and the commonly used gymnastic apparatus (Fig. 1, Table 1). Some of these groups, such as Muribaculaceae, are anaerobic bacteria that specifically inhabit the gut. The abundance of these bacteria correlates with animal longevity. Lactobacillus is the main probiotic in the human stomach and small intestine. Of these, a mixture of Lactobacillus acidophilus and Bifidobacterium sp. is good for regulating gastrointestinal dysfunction. Sphingomonas has multiple ecological functions ranging from remediation of environmental pollution to the production of highly beneficial plant hormones. Other taxa, such as the order chloroplasts in Archaea and Lachnospiraceae, also have various ecological functions and application prospects.

In the RG hall, the dominant bacteria on the carpet (aa) was Staphylococcus, with a relative abundance of 25%, followed by Corynebacterium (14%) and Enhydrobacter (5%) (Fig. 1). The bacterial composition of the AG hall carpet (ba) was similar to that of the carpet (aa), and the dominant groups were as follows: Staphylococcus 22%, a species of Cyanobacteria belonging to the order chloroplast 15%, Corynebacterium 13%, Craurococcus 2%, and Acinetobacter 2%.

On the carpet, except for a chloroplast (15%) in the AG hall, opportunistic pathogenic bacteria, Staphylococcus and Corynebacterium were predominant. Other equipment (except the wall bars [bb]) also generally contained Staphylococcus (including STRAIN S31), Corynebacterium, Acinetobacter, Streptococcus, Lachnospiraceae and an unidentified genus of Enterobacteriaceae.
Opportunistic pathogenic factors were found in two gymnasiums and the main apparatus. To confirm the existence of opportunistic pathogens in all analyzed bacterial groups, the Faprotax and Bugbase functional prediction platforms were used to predict the potential pathogens of humans in all samples from the two gyms (Fig. 2a–c). There were some differences in the relative abundance and opportunistic pathogen taxa. The overall trend indicated that the relative abundance in the AG hall was higher than that in the RG hall. BugBase phenotypic function prediction also confirmed the existence of potential human pathogens in the two gyms. Visualizations (Fig. 2c) further showed that the specific taxa were Veillonellaceae, Ruminococcaceae, Moraxellaceae, Lachnospiraceae, Propionibacteriaceae and Staphylococci. Comamonas, Klebsiella, Rothia, Acinetobacter, and Micrococcus are cancer-related microbial factors.

Shared bacterial groups and biomarker groups in different gymnasiums. A Venn diagram analysis showed that there were 226 taxa in all samples at the genus level, accounting for 30.3% of the total 746 genera (Fig. 3a). A KRONA species note diagram is further shown in detail (Fig. 3b). The relative abundance of Staphylococci,
lococcus, Corynebacterium and Enhydrobacter in the two gymnastic halls was 5–25%. In addition, other groups with a relative abundance of 2% were Class Chloroflexi, Rhizobiales, Micrococcales, Muribaculaceae, Ruminococcaceae, Burkholderiaceae, Enterobacteriaceae, and Lactobacillus. Acinetobacter, Acidobacteria, Oxyphotobacteria. Chloroflexi is a typical member of the anaerobic photosynthetic taxa, mostly from hot spring-associated environments26.

Line discriminant analysis (LDA effect size) can identify biomarkers with significant differences between different groups. Figure 4a and b show the different microbial groups in the two gyms. In the AG hall (in red), the biomarker microorganism is Rhizobiales, while in the RG hall (in green), the biomarker microorganisms are Erysipelatoctrostridium and Lachnospiraceae. E. ramosum, a species in the genus Erysipelatoctrostridium, is a normal member of the human gut microbiota and only causes invasive infections in rare cases27. The members

Figure 2. Bar chart of FaproTax function prediction of microbiome in two gyms, (a) (TOP 20 in functional abundance; P: 0.05). (b) Phenotypic functional maps of the microbiome of the two gyms predicted by BugBase algorithm; (c) opportunistic pathogens or dominant microbiota associated with cancer displayed at the family-level.
of Lachnospiraceae are the core taxa of the intestinal tract and have a high species abundance and relative abundance in the life cycle of the host. Although they are the main producers of short-chain fatty acids, different taxa are also associated with different enteral and extracellular diseases. The AG hall had only one biomarker microbial group, Rhizobiales. A member of this order, Agrobacterium, can be used in genetic engineering. Genera associated with human and animal diseases include \textit{Bartonella}, \textit{Brucella}, \textit{Pedomicrobium} and \textit{Xanthobacter}. The first two genera were not found in our current survey.

**Discussion**

The skin is home to millions of bacteria, fungi and viruses. In a survey of healthy adults, Byrd et al.\textsuperscript{28} found that on drier parts of the hand, such as the palm and forearm, the main bacteria were \textit{Staphylococcus}, \textit{Streptococcus}, \textit{Corynebacterium} and \textit{Propionibacterium} (\textit{Cutibacterium}). On the more moist antecubital fossa and popliteal fossa, \textit{Corynebacterium}, \textit{Enhydrobacter}, \textit{Propionibacterium} and \textit{Staphylococcus} were found. For the lipid-based...
check and retroauricular crease, Corynebacterium, Propionibacterium, Staphylococcus and Streptococcus were dominant. The main bacteria on the feet are Corynebacterium and Staphylococcus. Kim et al. studied the surface microbes of different populations in South Korea and found that Enhydrobacter was dominant in the skin microbiome of the elderly, while Lawsonella was more prevalent in a younger group. Staphylococcus and Corynebacterium were dominant in males, while Lactobacillus was dominant in females.

In our study (Fig. 5), the dominant taxa in the palm front of 9 female gymnasts (RG) and male and female gymnasts (AG), in addition to chloroplasts, were Streptococcus, Staphylococcus, Corynebacterium and Cutibacterium, which was basically consistent with the report of Byrd et al. RG athletes have Lactobacillus, which is consistent with the report of Kim et al. AG, which contains a combination of male and female team members, contains more specific groups, including Lawsonella, Acinetobacter, Micrococcus, Sphingomonas, Order Chloroplas and Kocuria. The reason may be related to the physiology of male and female athletes and this AG openness to the outside world. Acinetobacter, for example, often comes from contaminated dairy products, raw fruits and vegetables.

In the two carpets of GR and AR that had more contact with athletes’ hands and feet, the dominant microbiota similar to hands, including Staphylococcus. Corynebacterium and Enhydrobacter have increased, while Streptococcus has decreased (Fig. 5c,d). The hydrophilic bacteria Enhydrobacter are more abundant. The skin microbiome composition of the dominant types of bacteria is considerably stable; the diversity of the gym microbiome is closely related to the human body surface microbiome.

Cyanobacteria are widely found in seawater, fresh water, soil and the bark of some plants. Some of these cyanobacteria can produce harmful toxins, such as microcystins (characteristic hepatotoxins), nodularins and cylindrospermopsin. Anatoxin A and saxitoxins are neurotoxins, and their formation shows no strain specificity. Common toxin-producing algae include Microcystis spp., Anabaena spp., Aphanizomenon, Planktothrix and Oscillatoria. Radkova et al. reported that Microcystis produced microcystin in shallow water in Bulgaria, which is the cyanobacterial toxin found with the highest frequency; it has a wide distribution and high toxicity in cyanobacterial water blooms. Archaea have been detected on human skin, and they mainly belong to Methanobacteriota and Halobacteriota, which have relatively low abundance. Umbach et al. evaluated the relative abundance and taxonomic distribution of archaea on human skin based on 16S rRNA gene sequence data. Their results showed that only 5.9% of the 1,688 skin samples contained archaea. The dominant bacteria on computer keyboards in contact with finger skin are members of Nitrososphaeria. Our study found some rare groups of Cyanobacteria, such as Chroococcidiopsaceae, Calothrix, Microcoleus PC-7113, Scytonema UTEX 2349, Tychonema CCAP-459-11 and Nostocales and Afrocarpus, Nannochloropsis, and Trachysdiscus.

Figure 5. Composition of dominant taxon (top 10 taxa) of palms and carpets from RG and AG group. (a) palm of RG athlete, (b) palm of AG athlete, (c) RG carpet, (d) AG carpet.
hands and carpets of RG and AG athletes. These taxa were not consistent with the groups reported by Svirčev et al. and Umbach et al. In addition to the differences in environmental conditions of sampling sites, an important reason for such inconsistency was that Svirčev et al. and Umbach et al. found that the reported microbes were common taxa with high relative abundance, whereas we found that the reported microbes were all with relative abundance < 0.001% rare taxa. The prediction based on the FapTax and Bugbase functional platforms (Fig. 2) reveals that there are some opportunistic human pathogens in the gymnastic stadium. The opportunistic pathogens detected were Lawsonella spp. and Corynebacterium pseudodipthericum. Streptococcae are widely found in nature and in human and animal feces, and most of them do not cause disease. We found that the relative abundance St. mutans was extremely low, but it is a key species in the caries process. Acinetobacter baumannii contaminates dairy products, fruits and vegetables and increases the risk of infection in immunocompromised individuals and young children. Some microorganisms are not directly opportunistic agents but are carcinogenic agents. Yu et al. confirmed that Fusobacterium nucleatum and Peptostreptococcus stomatis are related to colorectal cancer. Several other species, including Parvimonas micra and Solobacterium moorei, have also been significantly associated with colorectal cancer. Some of the other microbes that we found by using functional prediction, such as Neisseriaceae, Ruminococcaceae, Veillonellaceae and Moraxellaceae, are also associated with the occurrence and development of cancer. The multifaceted biodiversity of the microbiome on gymnastics, gyms and apparatuses should be fully understood and recognized by managers, teachers and athletes. In daily activities, participants should pay attention to the cultivation of personal and public health habits and regularly clean and disinfect equipment and instruments used. Some researchers and administrators have proposed their inclusion in health education programs and curricula. Some schools have even set up ultraviolet sterilization lamps in gymnastic halls to improve the protection of athletes. These ideas and methods are worth learning from school administrators.

Conclusions

Based on rDNA-16S sequencing, the results of this study showed that gymnasts and commonly used equipment had abundant species diversity, and the potential pathogenic factors involved not only opportunistic pathogens but also microbial infectious factors related to the occurrence and development of cancer. Some rare species of cyanobacteria merit more attention, such as Calothrix, Microcoleus, Tychonema, Affrocarpus and Trachydiscus, which were found in our survey. Whether these cyanobacteria produce toxins harmful to humans is still a concern.

Received: 9 October 2021; Accepted: 8 March 2022
Published online: 05 April 2022

References

1. Ritchie, H. & Roser, M. Urbanization. Our World in Data. https://ourworldindata.org/urbanization (2019).
2. Nicolaou, N., Siddique, N. & Custovic, A. Allergic disease in urban and rural populations: Increasing prevalence with increasing urbanization. Allergy 60, 1357–1360 (2005).
3. Neiderud, C. J. How urbanization affects the epidemiology of emerging infectious diseases. Infect. Ecol. Epidemiol. 5, 27060 (2015).
4. Danko, D. et al. A global metagenetic map of urban microorganisms and antimicrobial resistance. Cell 184, 3376–3393 (2021).
5. Kang, K. et al. The environmental exposures and inner- and intercity traffic flows of the metro system may contribute to the skin microbiome and resistome. Cell. Rep. 24, 1190–1202 (2018).
6. Brooks, B. et al. Strain-resolved analysis of hospital rooms and infants reveals overlap between the human and room microbiome. Nat. Commun. 8, 1814 (2017).
7. Lax, S. et al. Bacterial colonization and succession in a newly opened hospital. Sci. Transl. Med. 9, 6500 (2017).
8. Joyner, J. L. et al. Green infrastructure design influences communities of urban soil bacteria. Front. Microbiol. 10, 982 (2019).
9. Maritz, J. M., Ten Eyck, T. A., Elizabeth, A. S. & Carlton, J. M. Patterns of protist diversity associated with raw sewage in New York City. ISME J. 13, 2750–2763 (2019).
10. Laurent, J. G. C., Allen, J. G., McNeely, E., Dominici, F. & Spengler, J. D. Influence of the residential environment on undergraduate students’ health. J. Exp. Sci. Environ. Epidemiol. https://doi.org/10.1038/s41370-019-0196-4 (2019).
11. Fu, X. et al. Associations between respiratory infections and bacterial microbiome in student dormitories in Northern China. Indoor Air 30, 816–826 (2020).
12. Fu, X. et al. Indoor microbiome, environmental characteristics and asthma among junior high school students in Johor Bahru, Malaysia. Environ. Int. 138, 105664 (2020).
13. Fu, X. et al. Indoor bacterial, fungal and viral species and functional genes in urban and rural schools in Shaxi Province, China: association with asthma, rhinitis and rhinoconjunctivitis in high school students. Microbiome. 9, 138 (2021).
14. Mahmoudabadi, A. Z. & Rahmaeini, S. Dermatophytic contaminations in sport centers of Jundishapur University of Medical Sciences, Ahvaz. Iran. Turk. J. Med. Sci. 42, 177–178 (2012).
15. Ayan, S. The hidden danger for the users of playgrounds and sport complexes. Turk. J. Med. Sci. 55, 125 (2012).
16. Liang, H. et al. Diversity analysis of fungal community composition in shoe cavity of campus football players based on DNA meta-barcoding technology. Chin. J. Sports Med. 38, 131–136 (2019).
17. Liang, H., Liang, Z., Cao, Y., Zhang, Z. Y. & Liang, Z. Q. Fungal community composition on the rhythmic gymnast’s partial positions and gymnastic blankets. Mycosistema 39, 280–288 (2020).
18. Liang, Z., Zhang, Z. Y., Liang, H., Han, Y. F. & Liang, Z. Q. Fungal community diversity and correlation analysis of gymnasts as well as sports equipment in the gymnasium. Mycosistema 39, 1281–1290 (2020).
19. Louca, S., Parfrey, L. W. & Doebeli, M. Decoupling function and taxonomy in the global ocean microbiome. Science 353(6305), 1272 (2016).
20. Sibai, M. et al. Microbiome and longevity: High abundance of longevity-linked muribaculaceae in the gut of the long-living rodent Spalax leucodon. OMICS J. Integr. Biol. 24, 592–601 (2020).
21. Smith, B. J. et al. Changes in the gut microbiome and fermentation products concurrent with enhanced longevity in acaerbose-treated mice. BMC Microbiol. 19, 130 (2019).
22. Asaf, S., Numam, M., Khan, A. L. & Al-Harrasi, A. Spingomonas: from diversity and genomics to functional role in environmental remediation and plant growth. Crit Rev. Biotechnol. 40, 138–152 (2020).
23. Rafiee, P., Ebrahimi, S., Hosseini, M. & Tong, Y. W. Characterization of soluble algal products (SAPs) after electrocoagulation of a mixed algal culture. Biotechnol. Rep. 25, e00433 (2020).

24. Yacca, M. et al. The controversial role of human gut Lachnospiraceae. Microorganisms. https://doi.org/10.3390/microorganisms8040573 (2020).

25. Jin, Y. G. & Quan, S. G. Diagnostic kits and methods for lung cancer by bacterial metagenomic analysis. Chinese patent. CN, 108265115A (2018).

26. Saghaı, A., Zivanovic, Y., Moreira, D., Tavera, R. & López-Garcı’a, P. A novel microbialite-associated phototrophic chloroflexi lineage exhibiting a quasi-clonal pattern along depth. Genome Biol. Evol. 12, 1207–1216 (2020).

27. Milosavljevic, M. N. et al. Antimicrobial treatment of Erysipelotoclostridium ramosum invasive infections: A systematic review. Rev. Inst. Med. 63, e30 (2021).

28. Byrd, A. L., Belkaid, Y. & Segre, J. A. The human skin microbiome. Nat. Rev. Microbiol. 16, 143–155 (2018).

29. Kim, J. H. et al. Taxonomic profiling of skin microbiome and correlation with clinical skin parameters in healthy Koreans. Sci. Rep. 11, 16269 (2021).

30. Moreira, C., Vasconcelos, V. & Antunes, A. Phylogeny and biogeography of cyanobacteria and their produced toxins. Mar. Drugs. https://doi.org/10.3390/md111114350 (2013).

31. Radkova, M., Stefanova, K., Uzunov, B., Gärtner, G. & Stoyneva-Gärtner, M. Morphological and molecular identification of microcystin-producing cyanobacteria in nine shallow Bulgarian water bodies. Toxins. 12, 39. https://doi.org/10.3390/toxins12010039 (2020).

32. Umbach, A. K., Stegelmeier, A. A. & Neufeld, J. D. Archaea are rare and uncommon members of the mammalian skin microbiome. mSystems. 6, e0064221 (2021).

33. Švicev, Z. et al. Global geographical and historical overview of cyanotoxin distribution and cyanobacterial poisonings. Arch. Toxcol. 93, 2429–2481 (2019).

34. Eriksson, L., Holgerson, P. L., Esberg, A. & Johansson, I. Microbial complexes and caries in 17-year-olds with and without Streptococcus mutans. J. Dent. Res. 97, 275–282 (2018).

35. de Amorim, A. M. B. & dos Santos, N. J. Acinetobacter: An underrated foodborne pathogen?. J Infect. Dev. Ctries. 11, 111–114 (2017).

36. Thomas, R. M. & Jobin, C. Microbiota in pancreatic health and disease: The next frontier in microbiome research. Nat. Rev. Gastroenterol. Hepatol. 17, 53–64 (2020).

37. Yu, J. et al. Metagenomic analysis of fecal microbiome as a tool toward targeted noninvasive biomarkers for colorectal cancer. Gut 66, 70–78 (2017).

38. Denna, I. et al. Evaluation of environmental health knowledge and practice among youth football players in Benghazi, Libya. Rehabil. Sci. 3, 23–27 (2018).

39. LaBelle, M. W. et al. Infection risk reduction program on pathogens in high school and collegiate athletic training rooms. Sports Health. 12, 51–57 (2019).

Acknowledgements
This work was supported by the Program of High-level innovative scientific talents of Guizhou Province [(2020)6005], the National Natural Science Foundation of China (32060011), and the Construction Program of Biology First Class Discipline in Guizhou [GNYL(2017)009].

Author contributions
H.Y.F. and Z.Q.L. wrote, reviewed, and edited the manuscript. All authors have read and agreed to the published version of the manuscript.

Competing interests
The authors declare no competing interests.

Additional information
Correspondence and requests for materials should be addressed to Y.F.H. or Z.Q.L.

Publisher’s note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

Open Access This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article’s Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit http://creativecommons.org/licenses/by/4.0/.

© The Author(s) 2022