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Characterization of Dysbiotic Changes of Skin Microbiota in Contact Sports Athletes

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Abstract Contact sports athletes often suffer from various skin disorders (inflammatory diseases of bacterial and fungal origin, atopic dermatitis, psoriasis, etc.) resulting in long breaks in training which ruin athletic performance. Wrestling implies intense skin-to-skin contact that creates perfect conditions for transmission of the infectious agents. Following the standard rules of hygiene (showering and handwashing directly after each competition and training) does not exclude the possibility to get an infection from sparring partner. To characterize the skin microbial composition of wrestlers who do not have current manifestation of any skin disorders, the metagenomic analysis was performed. Absolute predominance of Bacillus genus in metagenomic profiles of wrestlers' skin was observed in contrast with the existing literature data. Classic microbiological approaches allowed to detect hemolytic forms of microorganisms. Wrestlers' skin appeared to be colonized with hemolytic bacilli, whereas the non-wrestler athletes did not have such bacteria on their skin. Such dysbiotic shifts in the microbial community may cause the emergence of skin diseases. Revealed properties could help to design highly effective antiseptics for the contact sports hygiene.

Keywords Skin microbiota · Dysbiosis · Contact sport · Wrestlers · Bacillus

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1 Introduction

Microorganisms inhabiting different parts of the human body are known as microbiota. Abundance of four bacteria phyla (Actinobacteria, Firmicutes, Proteobacteria, and Bacteroidetes) in the microbiota reflects the tight coevolution of microorganisms and human [1]. This interaction implies the contribution of resident bacteria in a host's health maintenance and disease development. Numerous studies have shown involvement of microbiota in digestion of complex carbohydrate, vitamin synthesis, defense against pathogens, immune system regulation, etc. [2–5].

16S rRNA metagenome profiling of human skin has shown the presence of diverse groups of bacteria that colonize the surface of the human body [6]. One of the most important functions of skin microbiota is a defense against microbial and fungal pathogens by synthesis of antimicrobial compounds or modulating the host immune response [6, 7], and the skin dysbiosis is reported to be strongly associated with such medical conditions as atopic dermatitis and psoriasis, indicating connection between microbiota and dermatological diseases [8].

It is known that athletes involved in contact sports frequently suffer from skin diseases [9, 10]. For instance, wrestlers are at higher risk of developing dermatophytosis (tinea corporis, tinea pedis), impetigo, and herpes simplex virus infection [11, 12]. This high susceptibility rate can be accompanied with shifts in skin microbiome because these changes in bacterial community may cause predisposition to infection.

The aim of the present study is the characterization of dysbiotic changes of microbiota in contact sports athletes' skin.

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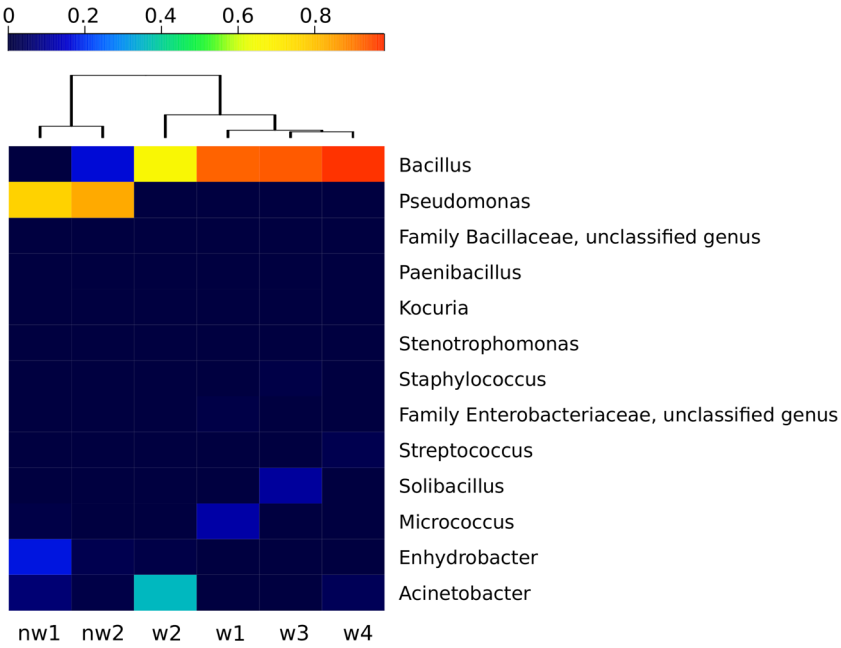

Fig. 1 Relative abundances of bacterial genera on the athletes' skin (*nw* non-wrestler, *w* wrestler). *Colors* indicate the percentage of sequences in each taxon, from 0% (*blue*) to 100% (*red*)

2 Material and Methods

Samples of skin microbiota were obtained before training by swabbing the intact skin of medial forearms of six athletes without visible manifestation of skin disorders: four Greco-Roman wrestlers and two non-wrestler athletes (karate fighter and arm wrestler). For metagenome analysis, DNA was extracted and sequencing of 16S rRNA V3-V4 variable regions was performed on the Illumina MiSeq instrument. After chimera filtering and rarefying steps, the number of reads per sample varied from 25,850 to 26,213. Sequences were assigned to OTUs at 97% similarity level using QIIME package (v. 1.9.1) with further alpha diversity estimation. Raw data for this project is stored on the Kazan Federal University servers and could be shared according to the Ethics Committee approval upon request.

To assess the presence of hemolytic forms of microorganisms in two studied groups of athletes, the skin bacteria were grown on a blood agar medium and on a vitelline-salt agar medium (VSA) for the growth and isolation of staphylococci. Colonies grown on VSA were then transferred to a blood agar medium, as well. Identification of species was performed using MALDI TOF MS Biotyper method as described previously [13].

3 Results and Discussion

The obtained 16S metagenomic sequences were grouped into four bacterial phyla: Proteobacteria, Firmicutes, Actinobacteria, and Cyanobacteria. The number of observed OTUs varied from 58 to 111. Alpha diversity analysis (Shannon index) of bacterial communities in samples indicates no significant differences in all analyzed groups (0.9–3.1 in wrestler group and 1.6–2.4 in non-wrestler group). Heat map plot (Fig. 1) demonstrates definite separation of the

Table 1 Hemolytic bacterial species inhabiting athletes' skin

Athlete ID	Sport	Blood agar medium	VSA → blood agar medium
nw1	Arm wrestling	*Pseudomonas luteola*	*Staphylococcus haemolyticus*
nw2	Karate	–	–
w1	Greco-Roman wrestling	*Bacillus cereus*	*Bacillus pumilus*
w2	Greco-Roman wrestling	*Bacillus cereus*	*Staphylococcus epidermidis*
		Bacillus flexus	*Bacillus pumilus*
		Staphylococcus haemolyticus	
		Acinetobacter lwoffi	
w3	Greco-Roman wrestling	*Bacillus pumilus*	*Staphylococcus epidermidis*
w4	Greco-Roman wrestling	*Bacillus cereus*	*Staphylococcus haemolyticus*

nw non-wrestler, *w* wrestler

samples into groups of wrestlers and non-wrestlers indicating different composition of skin microbiota in athletes. In the non-wrestler group, Proteobacteria is the most abundant phyla (83–98%), whereas on the skin microbiota of wrestlers, Firmicutes is the predominant phyla (63–99%). Analysis of bacterial composition on the level of genus shows prevalence of Bacillus in the wrestler group (62–92%), while Pseudomonas constitutes the most abundant group of microorganisms in non-wrestlers (73–80%). Thus, the metagenome of studied athletes' skin is characterized by domination of the one group of bacteria that implies the existence of certain conditions favoring the growth of specific microorganisms (sport activities, intense skin-to-skin contacts).

The presence of hemolytic bacteria in the skin microbiota often leads to the development of various diseases [14]. *Staphylococcus aureus*, *Pseudomonas aeruginosa*, and *Streptococcus pyogenes* are reported as the most common causes of skin diseases [15, 16]. Surprisingly, in the present study, it was discovered that the skin of all analyzed wrestlers was colonized by hemolytic bacilli, *Staphylococcus epidermidis*, and *S. haemolyticus* (Table 1). This result corresponds with our previous experiment in which *B. cereus*, *S. aureus*, and *S. epidermidis* were detected as prevailing hemolytic species in the skin microbiota of 15 wrestlers before and after training (data not shown). At the same time, hemolytic Bacillus was not detected on non-wrestler athletes' skin. There are only a few studies reporting about the association between skin disorders and Bacillus contamination [17, 18]. Thereby, we believe that the frequent manifestation of skin diseases in high-contact sports athletes may be caused by the presence of hemolytic bacilli, which could be detected by metagenomic approach.

4 Conclusions

In the present study, we characterized specific features of the skin microbiota of contact sports athletes, such as the predominance of Bacillus genus and the presence of diverse species with hemolytic properties. These attributes of the skin microbial community may serve as a basis for the selection of effective antiseptic agents for sports hygiene in the format of antibacterial wipes, spray, or gel.

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