TOCHUKWU ANSELEM UJU

FOOT MICROBIOTA OF FOOTBALL PLAYERS IN COMPARISM WITH NORMAL WORKING PEOPLE

MASTER THESIS

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NEAR EAST UNIVERSITY
INSTITUTE OF GRADUATE STUDIES
DEPARTMENT OF MEDICAL MICROBIOLOGY
AND CLINICAL MICROBIOLOGY

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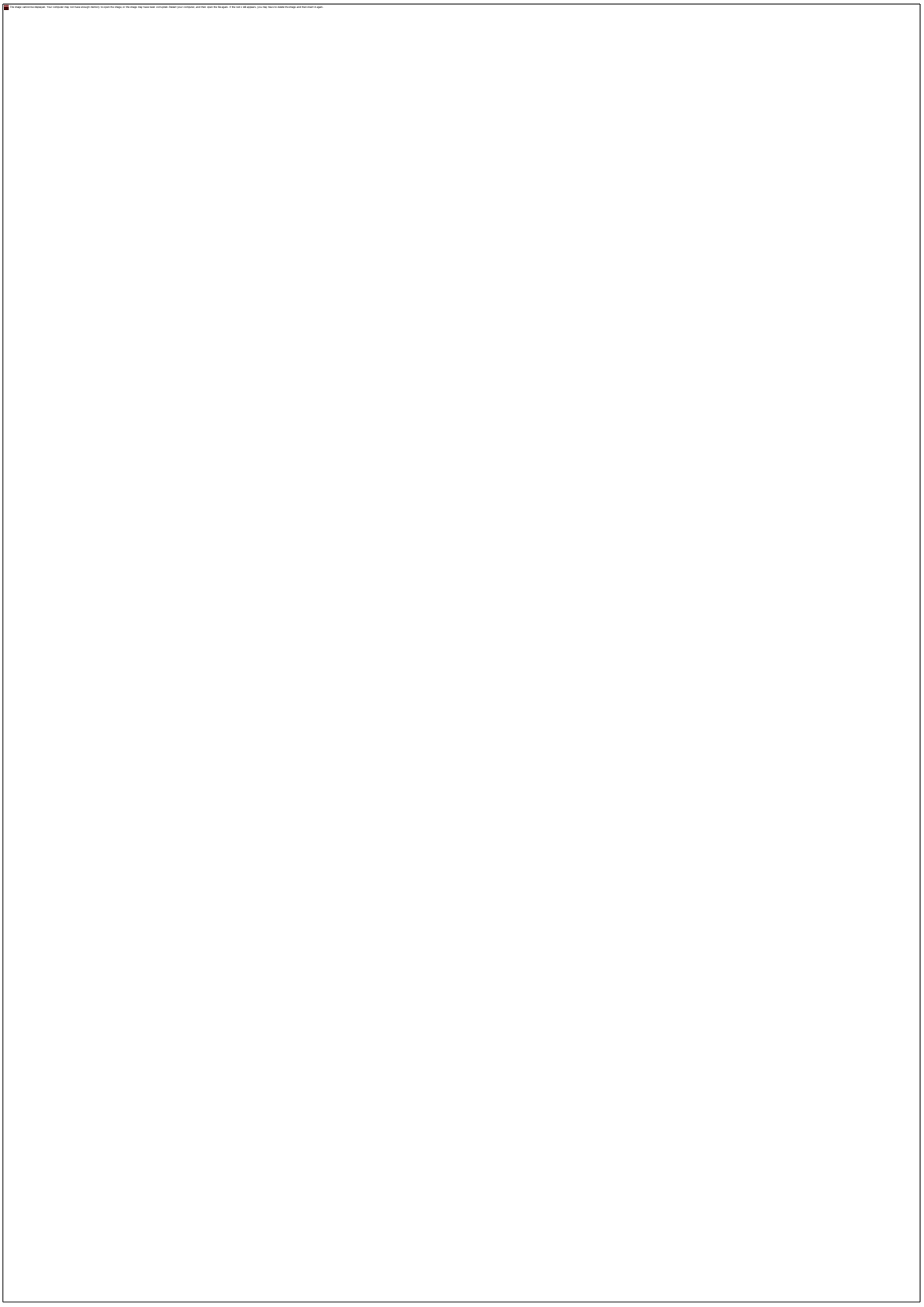
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I hereby certify that all information, documents, examinations, and results in this thesis were collected and presented in accordance with the Near East University Institute of Graduate Studies' ethical guidelines and academic rules. I further declare that I have properly referenced and cited any data and information that are not original to this work, as required by these rules and conduct.

TochukwuAnselem UJU

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Abstract

FOOT MICROBIOTA OF FOOTBALL PLAYERS IN COMPARISM WITH NORMAL WORKING PEOPLE IN LAFIA NIGERIA.

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Foot microbiota represents bacteria and fungi inhabiting the foot. This study was conducted to evaluate the occurrence of microbiota inhabiting the feet of soccer players and to compare results obtained with those in non-athlete individuals. A total of 300 participants was used in this study within the age range of 18-35 years. Swab were taken from the nails, soles and interdigital areas and bacterial and fungi isolation was done.bacterial identification was achieved using molecular techniques and fungi were identified based on microscopic features. The bacterial microbiota comprised of *Staphylococcus aureus*, *Staphylococcus haemolyticus*, *Micrococcus luteus* and *Bacillus licheniformis* while the fungal microbiota comprised *Aspergillus* sp., *Penicillium* sp., *Candida* sp., *Epidermophyton* sp., and *Cladosporium* sp. *Staphylococcus aureus* (60%) was the most prevalent bacteria for all three studied while *Bacillus*. *Candida* sp (66.6%) isolated from the sole of the feet where the most prevalent fungi and *Cladosporium*sp (66.6%) isolated from interdigital areas were the most prevalent bacteria in both Lafia athletes and non-Lafia athletes while *Cladosporium*sp (0%) and *Epidermophyton*sp (0%) were the least prevalent for all sampled area for non-athlete The most commonly found bacteria was Staphylococcus aureus, while the most prevalent fungi were Aspergillus sp. The study observed the presence of bacteria and fungi on the foot, some of which may raise public health concerns.

Key Words*:*Prevalence of *Staphylococcus aureus, Aspergillus spp.* Football players none athletes

ÖZET

FUTBOLCULARIN AYAK MİKROBİYOTALARI

NORMAL ÇALIŞAN İNSANLARLA KARŞILAŞTIRMA

LAFIA NİJERYA'DA.

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Ayak mikrobiyotası ayakta yaşayan bakteri ve mantarları temsil eder. Bu çalışma, futbolcuların ayaklarında mikrobiyota oluşumunu değerlendirmek ve elde edilen sonuçları sporcu olmayan bireylerle karşılaştırmak amacıyla yapılmıştır. Bu çalışmada 18-35 yaş aralığında toplam 300 katılımcı kullanıldı. Tırnak, ayak tabanı ve parmak arası bölgelerden sürüntü alınarak bakteri ve mantar izolasyonu yapıldı. bakteriyel tanımlama moleküler teknikler kullanılarak yapıldı ve mantarlar mikroskobik özelliklere göre tanımlandı. Bakteriyel mikrobiyota Staphylococcus aureus, Staphylococcus haemolyticus, Micrococcus luteus ve Bacillus licheniformis'ten oluşurken, mantar mikrobiyotası Aspergillus sp., Penicillium sp., Candida sp., Epidermophyton sp. ve Cladosporium sp.'den oluşmuştur. Staphylococcus aureus (%60) incelenen her üç bakteri için de en yaygın bakteri olurken, Bacillus bakterisi de en yaygın bakteriydi. Hem Lafia sporcularında hem de Lafia dışı sporcularda ayak tabanından izole edilen Candida sp (%66,6) ve parmak arası bölgelerden izole edilen Cladosporium sp (%66,6) en yaygın mantar iken Cladosporium sp (%0) ve Epidermophyton sp (%0) sporcu olmayanlar için tüm örneklenen alanlarda en az yaygın olanlardır. En sık bulunan bakteriler Staphylococcus aureus iken, en yaygın mantarlar Aspergillus sp. Çalışmada ayakta bakteri ve mantarların varlığı gözlemlendi; bunların bazıları halk sağlığı açısından endişelere neden olabilir.

Anahtar Kelimeler: Staphylococcus aureus, Aspergillus spp. prevalansı. Futbolcular hiçbiri atlet değil

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CHAPTER I

Introduction

The entire collection of bacteria and their genomes that are present in an individual at any one moment is known as the human microbiome. (Shukla *et al.,* 2017) The human microbiota, comprising the collective genome of all microorganisms residing in and on the human body, has gained significant attention in recent years due to its profound influence on human health and disease (Martinez *et al*., 2021; Adamczyk*et al.*, 2020). Although a great deal of research has been done on the gut microbiome, little is known about the microbiota of other body locations, like the foot. This study aims to provide a comprehensive investigation into the microbiota of the foot, shedding light on its composition, diversity, and potential implications for foot-related disorders and overall well-being. The human foot is a complicated anatomical structure that is subjected to a lot of mechanical stress and different climatic conditions. It is home to a varied microbial ecosystem that is essential to preserving the health of the feet and avoiding infections.(Bay *et al.*, 2020; Jnana *et al;* 2022). However, dysbiosis, or an imbalance in the microbial composition, has been associated with several foot-related conditions, including athlete's foot, toenail fungal infections, and diabetic foot ulcers (Loeshce*et al.*, 2017; Jnana *et al.*, 2022; Adamczyk*et al*., 2020).Athlete's foot, also known as tinea pedis, is a common fungal infection caused by dermatophytes, primarily Trichophyton rubrum and Trichophyton mentagrophytes. These fungi thrive in warm, moist environments, such as sweaty feet, and can lead to itching, scaling, and cracking of the skin between the toes and on the soles of the feet. Toenail fungal infections, or onychomycosis, are typically caused by dermatophytes, yeasts, and non-dermatophyte molds, and can result in discoloration, thickening, and crumbling of the nails. Diabetic foot ulcers, a serious complication of diabetes, are often associated with bacterial colonization and infection, which can delay wound healing and lead to severe complications, including amputation (Baig*et al.,* 2022; Kalan *et al.,* 2019). To describe the microbial communities found on the toes, soles, and interdigital spaces, among other areas of the foot, this extensive study will make use of cutting-edge molecular tools, such as next-generation sequencing (Rosenthal *et al*., 2011; Oh *et al*., 2014). The objective is to build a thorough understanding of the microbial landscape and its possible consequences for foot health by examining the taxonomic composition, diversity, and functional potential of the foot microbiota. The study

will specifically utilize high-throughput sequencing of the 16S rRNA gene, a highly conserved region in prokaryotes, to identify and quantify the bacterial communities present on the foot (Zou *et al.,* 2020). Also in addition, metagenomic shotgun sequencing, which involves sequencing the collective genomes of all microorganisms in a sample, will be employed to gain insights into the functional potential of the foot microbiota, including their ability to produce enzymes, metabolites, and other bioactive compounds that may influence foot health and disease (Huang *et al.,* 2022; Pérez-Losada *et al.,* 2022; Zou *et al.,*2020).

Additionally, the study will examine how the foot microbiota is impacted by a number of variables, including age, gender, cleanliness habits, and environmental exposures. (Malone *et al*., 2020).For example, the study or research will look into how the microbial makeup and diversity of the foot are affected by frequent handwashing, using antimicrobial soaps, and using foot powders or lotions. They will also look at any possible variations in the foot microbiota between people who live in rural and urban settings, as well as people who live in various geographic locations with various climates. A comprehensive approach will provide insights into the factors that shape the microbial communities and potentially identify risk factors associated with foot-related disorders. For example, the study may reveal that certain hygiene practices or environmental exposures contribute to the overgrowth of pathogenic fungi or bacteria, increasing the risk of developing conditions like athlete's foot or diabetic foot ulcers.The study will also investigate the potential interactions between the foot microbiota and the immune system, as well as the role of microbial metabolites in modulating foot health (Kalan et al.,2016; McCarville *et al.,* 2020). The work will examine the production of antimicrobial peptides, cytokines, and other immune mediators by the host in response to the foot microbiota, as well as the ability of specific microbial species to modulate the immune response. Additionally, they will explore the potential of microbial metabolites, such as short-chain fatty acids and quorum-sensing molecules, to influence skin and nail health, as well as the pathogenesis of foot-related disorders (Pérez-Losada*et al.,* 2022). this information, specific therapies, like probiotics or prebiotics, may be developed to support a healthy foot microbiome and prevent or treat foot-related ailments. To restore a healthy microbial balance and lower the risk of foot infections and other disorders, the study may, for example, identify particular probiotic strains that can outcompete pathogenic fungi or bacteria, or prebiotic compounds that specifically promote the growth of beneficial

microbes. In addition to exploring the microbial composition and diversity, this study will address the potential transmission of microbes between individuals and the potential impact of footwear on the foot microbiota (Foulston*et al.*, 2018; Jneid et al., 2017). it will investigate the potential for microbial transfer through shared footwear, such as in fitness centers or locker rooms, and examine the role of footwear materials and design in influencing the foot microbiota. For instance, the study might show that some shoe designs, such boots or closed-toe shoes, foster the growth of specific microbial species by creating a warm, damp environment that raises the risk of infections or foot odor. On the other hand, breathable textiles like open-toed sandals might promote improved airflow and a more harmonious microbial ecology. This knowledge may have an impact on footwear design and cleanliness standards, which could ultimately lead to better foot health and wellbeing. Recommendations for appropriate footwear maintenance, such as routine cleaning and drying, or for the inclusion of antimicrobial materials or ventilation systems in footwear design to support a healthy foot microbiome, might be made in light of the study's findings.

Research Purpose

The human foot, often overlooked as a mere structural component for locomotion,harbors a complex and dynamic microbial ecosystem that plays a crucial role in our overall health and well-being. Despite its importance, the microbiota of the foot remains a relatively unexplored territory compared to other body sites, such as the gut or skin (Jneid*et al.*, 2017). The lack of understanding regarding the foot microbiota is a serious research issue that has to be addressed because it has been linked to a number of foot-related conditions and may have an effect on overall health. The absence of a thorough understanding of the makeup and diversity of the foot microbiota is one of the main research issues surrounding it. While previous studies have provided some insights into the microbial communities present on the foot (Jneid*et al*., 2017; Zou *et al.*, 2020; Tong *et al.*, 2020.), a more in-depth characterization is needed to fully grasp the complexity and functional potential of these communities. This knowledge gap hinders our ability to understand the role of the foot microbiota in maintaining foot health and preventing infections, as well as its potential contributions to overall well-being. The incomplete knowledge of the variables influencing the foot microbiota's structure and modulation represents another serious research challenge. The

composition and diversity of the foot microbiota can be influenced by a range of extrinsic and intrinsic factors, including footwear, hygiene practices, and environmental exposures, as well as genetic predisposition, age, and gender (Adamczyk*et al*.,2020). However, the specific impacts of these factors remain largely unexplored, hindering our ability to develop targeted interventions or preventive measures for foot-related disorders and other potential health implications. Furthermore, the potential interactions between the foot microbiota and the host immune system represent a significant research gap. While studies have explored the interactions between the gut microbiota and the immune system (Bay *et al.,* 2020), the role of the foot microbiota in modulating immune responses and its potential implications for foot health, disease, and overall well-being remain poorly understood (Bay *et al.,* 2020). Elucidating these interactions is crucial for developing targeted therapies, managing foot-related conditions, and potentially identifying novel therapeutic targets for systemic disorders influenced by the immune system. Potential microbe-to-person transfer and the effect of footwear on the microbiota of the foot present another important research challenge. There hasn't been much research done on the possibility of microbial transmission via shared shoes or contaminated surfaces, like those in fitness centers or locker rooms (Foulston*et al.,* 2018).Furthermore, little is known about how footwear ventilation, materials, and designs affect the microbial communities in the foot (Foulston*et al.*, 2018). Addressing these issues is essential for developing effective hygiene practices, footwear design guidelines, and potential interventions to promote a healthy foot microbiome.Moreover, the potential link between the foot microbiota and systemic health conditions, such as metabolic disorders, cardiovascular diseases, and autoimmune disorders, represents a significant research gap. It is still unknown how the foot microbiota affects general health and well-being, despite the gut microbiome being linked to a number of systemic illnesses (Adamczyk *et al.,* 2020). Examining this plausible association may reveal fresh perspectives on the complex interrelationships between the human microbiome and systemic illnesses, which could result in innovative treatment methods. Additionally, the potential role of the foot microbiota in wound healing and tissue regeneration represents a critical research problem. While the importance of the microbiota in wound healing has been recognized in other body sites (Adamczyk*et al.,* 2020), the specific contributions of the foot microbiota to this process remain poorly understood. Elucidating the mechanisms by which the foot microbiota

influences wound healing and tissue regeneration could pave the way for innovative therapies tailored for foot-related wounds, injuries, and other conditions involving impaired healing processes.Furthermore, the research problem extends to the potential impact of antimicrobial agents, such as antibiotics and antifungals, on the foot microbiota. While these agents are commonly used to treat foot-related infections, their effects on the overall microbial community and the potential consequences on foot health and disease progression are not well-understood. Investigating this aspect could lead to more judicious use of antimicrobial agents and the development of targeted approaches that preserve the beneficial components of the foot microbiota.The possible involvement of foot microbiota in the pathophysiology of inflammatory and autoimmune diseases is another field of research that merits further investigation. Emerging evidence suggests that dysbiosis, or an imbalance in the microbial communities, may contribute to the development and progression of various autoimmune and inflammatory disorders (Park *et al.*, 2019). However, the specific functions of the foot microbiota in various disorders remain mostly unclear, resulting in a significant research gap that may affect the treatment and prevention of disease. The foot microbiota poses a complex and multifaceted research problem that involves many different aspects. These include the lack of a thorough understanding of the composition and diversity of these microbial communities, the limited knowledge of the factors that shape and modulate these microbial communities, the potential interactions with the host immune system, the potential transmission of microbes and the impact of footwear, the potential link to systemic health conditions, the potential role of antimicrobial agents, the potential contribution to autoimmune and inflammatory conditions, and more. For the purpose of improving our knowledge of the foot microbiota and its consequences for foot health, general wellbeing, and the creation of focused interventions, preventive measures, and innovative therapeutic approaches, it is imperative that these research issues be addressed

Research Significance

Justifying the investigation of the foot microbiota is imperative as it addresses critical knowledge gaps, elucidating the role of microbial dysbiosis in foot-related disorders like athlete’s foot, toenail fungal infections, and diabetic foot ulcers. It could unravel links between the foot microbiota and systemic health conditions, as well as its interactions with

the immune system, potentially identifying novel therapeutic targets. Characterizing the foot microbiota's composition, diversity, and functional potential could pave the way for targeted interventions like probiotics, prebiotics, or antimicrobial agents to promote a healthy foot microbiome and prevent or manage foot-related disorders. The study will inform hygiene practices, footwear design, and judicious use of antimicrobials to preserve beneficial microbes. It may uncover mechanisms influencing wound healing, tissue regeneration, and impacts of factors like age, gender, and environmental exposures. This interdisciplinary collaboration fosters innovative thinking, methodologies, and technologies for investigating the foot microbiota's human health implications

Research questions

1. What is the composition and diversity of the foot microbiota in different populations?
2. How does the foot microbiota vary between individuals with and without certain foot conditions or diseases?
3. Are there specific factors, such as age, gender, or lifestyle, that influence the foot microbiota composition?

Limitation of Study

Potential bias in sampling might arise from the study's sample not being entirely representative of the total population. For example, the results could not apply to a larger population if the study only looks at a certain age range, sex or level of education.

The precision of prevalence estimations may be impacted by the sensitivity and specificity of the techniques used for fungi identification.

Definition of Key Terms

Foot Microbiota: The foot microbiome is a collection of bacteria, fungi and algae all living on the foot

Soccer Player: This a professional who plays soccer game

CHAPTER II

Literature Review

INTRODUCTION

Any and every part of the human body is covered by a large composition of microbial community ranging from bacteria, fungi, small protis and algae, called Microbiota. So also the foot as part of the body has its unique composition of microorganisms also known as the "microbiota of the foot." These organisms form a complex community known as the foot microbiota. In some cases whenever there's an alteration in the environmental factors around a microbiota, the harmless friendly microbe can easily turn into an infectious or pathogenic agent.

In the world of sports, footballers are often seen as athletes with exceptional skills and abilities. However, little attention has been paid to the hidden world of microorganisms that exist on their feet. The microbiota of the foot among footballers is a fascinating topic that deserves further exploration. In this article, we will delve into the different microorganisms involved, their distributions across the globe, and potential solutions to maintain foot health.
In recent years, there has been a growing interest in the field of microbiota and its impact on human health. Microbiota refers to the community of microorganisms that reside in and on our bodies, playing a crucial role in maintaining our overall well-being. While much research has focused on the gut microbiota, there is a fascinating untapped area within the realm of microbiota: the foot microbiota. This article aims to shed light on the foot microbiota in footballers, exploring its composition, functions, and potential implications for players' health and performance.

Since we are looking at the foot of athletes, three dimensions of the feet are involved: the nails, sole of the feet and the toes. This is classified in dermatology into three as captured as Tinea pedis, Tinea corporis and Tinea unguuim.

Some sporting facilities like wardrobe, pillowcases, gymnastic carpets, wrestling mats, saunas, swimming pools, etc. were studied in the recent 2020s, and the microbiota compositions recurrently found were *Trichophyton tonsurans, T. Mentagropytes and*

Microsporumgypseum. (Liang et al.2019, 2020A&B). They are also refered to dermatoprotofungi. Sports venues and corresponding equipment have become carriers or storehouses of pathogenic fungi. (Liang *et al*. 2019).

This work will help the gains of valuable insights into the intricate microbial ecosystems that exist on the feet of footballers. Origins of Foot Microbiota. The foot microbiota begins to establish shortly after birth and evolves throughout a person's life. Initial colonization occurs through contact with the mother's skin, the surrounding environment, and subsequent interactions with family members and other individuals. As footballers spend a significant amount of time in close contact with teammates and various surfaces, their foot microbiota may be influenced by the shared environment and interactions during training sessions and matches. Possible Infections and Treatment While foot microbiota play a vital role in maintaining skin health, imbalances or disruptions in this delicate ecosystem can lead to various infections. Common foot infections among footballers include athlete's foot (tinea pedis), fungal nail infections, and bacterial infections. These conditions can cause discomfort, pain, and even affect an athlete's performance. Prompt and appropriate treatment is essential to prevent the spread of infections and ensure the quick recovery of footballers. Care and Control of Spread To maintain foot health and prevent infections, proper care and control measures should be implemented. Footballers should practice good foot hygiene, including regular washing with mild soap and drying thoroughly, especially between the toes. Wearing clean and breathable socks made of natural fibers can also help prevent excessive moisture accumulation. Additionally, the use of appropriate footwear, regular inspection for any signs of infection, and avoiding sharing personal items are crucial preventive measures. For optimal care and control, footballers should consult healthcare professionals who specialize in foot-related conditions. Dermatophytes and non-dermatophytes were associated with the athlete's foot. The name tinea pedis should be reconsidered. The use of public sports facility may foster infection transmission.

Warm environment encourages the growth of dermatophytes particularly in the feet of athletes who consistently used occlusive footwears. Socks and sweating of the legs of athletes smears a great encouragement for the growth amongst players feet and trauma's their toenails and foot. (Caroline et al. 2019).

Tinea pedis is one of the most common superficial skin infections and represents a major public health problem globally. It is common among athletes especially soccer players. This cross-sectional prospective study was carried out to determine the degree of occurrence of tinea pedis and the associated risk factors among soccer players. (Ofonime and Barilee, 2019)

Footwear should be designed to avoid trauma and injury to the skin of the feet that can favor bacterial and fungal infections. Procedures and substances for sanitizing the interior of shoes are uncommon but are important aspects of primary prevention against foot infections and unpleasant odor (Gabriele,et al. 2015)

Tinea pedis, commonly known as athlete's foot, results from fungal infections on the skin of the feet caused by dermatophytes, including *Trichophyton rubrum*, *T mentagrophytes*, *T. interdigitale*, and *Epidermophytonfloccosum.* () This infection typically occurs through direct contact with the organism while walking barefoot in locker rooms, showers, and swimming complexes. Individuals with diabetes and those who wear occlusive shoes are at an increased risk of developing tinea pedis.

Tinea pedis typically presents with pruritic scales and erosions between the toes. Some patients may experience areas of hyperkeratosis with underlying erythema on the medial and lateral aspects and soles of the feet. Occasionally, patients with this condition may present with painful bullous lesions concurrently develop tinea corporis, onychomycosis, and tinea manuum.

Untreated tinea pedis can lead to cellulitis, pyoderma, and osteomyelitis, especially in patients with immunocompromised conditions, diabetes, or peripheral vascular disease. This topic explores the etiology and pathophysiology of tinea pedis, as well as highlights the critical roles of the interprofessional healthcare team in evaluating, managing, and preventing recurrence and complications of the condition.

UNDERSTANDING MICROBIOTA

Before delving into the foot microbiota specifically, it is important to understand what microbiota is and why it matters. Microbiota refers to the diverse collection of microorganisms, including bacteria, fungi, viruses, and archaea, that coexist with humans. These microorganisms form complex communities and play vital roles in various physiological processes, such as digestion, immunity, and metabolism. Disruptions in the balance of microbiota can lead to health issues, highlighting the significance of studying and understanding these microscopic players.

Microbiota refers to the community of microorganisms that reside on or within a specific environment, such as the human body. The human body is home to trillions of microorganisms, including bacteria, fungi, viruses, and other microbes. These microorganisms play a crucial role in maintaining overall health and preventing the colonization of harmful pathogens.

GLOBAL DISTRIBUTION

The distribution of foot microbiota among footballers is not limited to a specific region. It varies across the globe due to factors such as climate, hygiene practices, and cultural habits. In warmer climates, for instance, the prevalence of fungal infections tends to be higher due to increased moisture and heat. In contrast, bacterial infections may be more common in regions with poor sanitation practices.

FOOT MICROBIOTA: THE UNEXPLORED TERRITORY

While the gut microbiota has been extensively studied, the foot microbiota remains largely unexplored. The human foot, with its unique structure and exposure to various environments, offers a diverse habitat for microorganisms. Footballers, who spend a significant amount of time on their feet, provide an intriguing subject for studying foot

microbiota. Understanding the composition of the foot microbiota in footballers can offer valuable insights into the interplay between sports activities, foot health, and microbial communities. The foot, being in constant contact with various surfaces, provides an ideal environment for the growth and colonization of microorganisms. Footballers, who spend a significant amount of time on their feet, are particularly susceptible to foot-related issues. Understanding the microbiota of their feet is essential in preventing infections, odors, and other foot-related complications.

COMPOSITION OF FOOT MICROBIOTA IN FOOTBALLERS

Preliminary research suggests that the foot microbiota in footballers differs from that of the general population. The constant friction, pressure, and moisture experienced during training and matches create an environment conducive to the growth of specific microorganisms. Certain species of bacteria and fungi, such as Staphylococcus and Candida, have been found to be more prevalent in footballers' feet. These findings highlight the unique microbial signature associated with the sport and open up avenues for further investigation. This is shows the diversity of Foot Microbiota. The human foot is home to a vast array of microorganisms, comprising bacteria, fungi, viruses, and other microbes. The diversity of foot microbiota varies among individuals and can be influenced by factors such as genetics, hygiene practices, footwear, and environmental conditions. Several microorganisms are commonly found on the feet of footballers. Bacteria such as Staphylococcus, Streptococcus, and Corynebacterium are prevalent. Fungal species, including Candida and Trichophyton, are also frequently encountered. These microorganisms can lead to conditions like athlete's foot, toenail fungus, and bacterial infections. Understanding this diversity is crucial in comprehending the role of foot microbiota in the overall health and well-being of footballers.

FUNCTIONS OF FOOT MICROBIOTA

The foot microbiota is not merely a passive bystander but actively contributes to foot health and overall well-being. Studies suggest that the foot microbiota plays a role in preventing the growth of harmful pathogens by competing for resources and space. Additionally, the foot microbiota may be involved in modulating the immune response of footballers, potentially influencing their susceptibility to foot-related infections and injuries. Further research is needed to unravel the intricate mechanisms through which foot microbiota exerts its beneficial effects.

IMPLICATIONS FOR FOOTBALLERS' HEALTH AND PERFORMANCE

Understanding the foot microbiota in footballers has implications for both foot health and performance. Foot-related infections, such as athlete's foot, can be debilitating for players, affecting their ability to train and compete. By identifying specific microbial profiles associated with these infections, preventive measures can be developed to minimize their occurrence. Furthermore, the foot microbiota may play a role in foot odor, a common concern among footballers. Exploring strategies to manage foot odor through microbial modulation can enhance players' confidence and comfort on the field. Tinea pedis is one of the most common superficial skin infections and represents a major public health problem globally. It is common among athletes especially soccer players.

SOLUTIONS FOR FOOT HEALTH

Maintaining foot health is of utmost importance for footballers. Here are some potential solutions to prevent and manage foot-related issues:

1. Proper Hygiene Practices: Regularly washing and drying the feet, including between the toes, can help eliminate excess moisture and reduce the risk of infections.

2. Footwear Selection: Choosing appropriate footwear that allows proper ventilation and moisture control is crucial. Wearing clean and properly fitting socks can also help prevent foot issues.

3. Foot Care Routine: Implementing a foot care routine that includes moisturizing, exfoliating, and trimming nails can promote healthy feet and prevent the buildup of microorganisms.

4. Regular Check-ups: Footballers should consider regular check-ups with a podiatrist or a healthcare professional who specializes in foot health. This can help identify and address any potential issues before they escalate

CONCLUSIONS

Microbiota or flora of any surface are the possible foe of the same surface depending on the physical conditions they are exposed to. From the study we saw that the common microbiota compositions are the fungi which are dermatophytes and non-dermatophytes. Natural organismsasssociated with athletes' foot diseases are dermatophytes and non-dermatophytes. The use of public sports facility may foster infection transmission. (Ofonime and Barilee, 2019).The study of foot microbiota in footballers is a burgeoning field with immense potential. By unraveling the mysteries of these microscopic players, we can gain valuable insights into foot health, performance optimization, and preventive strategies. Future research should focus on elucidating the complex interactions between foot microbiota and football-related factors, paving the way for evidence-based interventions and personalized approaches. As we dive deeper into the world of foot microbiota, we embark on a journey to enhance the well-being and performance of footballers, one microscopic player at a time. The study of foot microbiota in footballers provides valuable insights into the diverse microbial communities that exist on their feet. Understanding the origins, possible infections, and treatment options associated with foot microbiota is essential

CHAPTER III

Materials and Methods

Introduction

Study area, sample collection procedure, selection of the participants, demography, data are all outlined in this section.

Study Area

The study was carried out in Nasarawa State, located in North Central Nigeria (Fig 1).Nasarawa State lies between longitude 8°32′N 8°18′E, is bordered to the east by Taraba and Plateau State, to the north by Kaduna State, to the south by Kogi and Benue State, and to the west by the Federal Capital Territory, having a total landmark of 26,256 km2 (10,137 sq mi) . A total of 300 Participants was used in this study within the age range of 18-35 years. The 300 participants were divided into three groups comprising of Nigerian soccer players from the city of Lafia, soccer players from different regions of the country playing in Lafia, Non-athletes comprising of office worker from the city of Lafia not engaged in regular physical activities.

Figure 3.1: Map of Nassarawa State https://www.researchgate.net/profile/Abubakar-Aliyu-12/publication/236618864/figure/fig3/AS:667078847639562@1536055399869/Map-of-Nasarawa-State-showing-the-two-towns-where-assessments-were-conducted.jpg (Accessed on 6th May, 2023).

Questionnaire

Structured questionnaire for the studied population was designed and written consent was obtained from individuals involved in the study. Demographic characteristics such as age, gender, race, occupation was considered prior to recruitment of participants.

Ethical Approval

Ethical clearance was obtained from the Ethical Committee of the Nasarawa State Ministry of Health, Lafia, Nasarawa State (NHREC Protocol No: 18/07/2018). Informed consent of the studied population was sought and assurance was given that information received will be of strict confidentiality as participation was also voluntary.

Sample Collection and transportation

Sample materials were obtained from the nail, sole and interdigital areas of the foot for a period of two weeks to allow for direct mycological and bacteriological examination and culture. Sterile swab sticks were be used to swab areas of the feet gently by making sure to cover sufficient area to capture representative sample. Upon swabbing, sample were taken to the laboratory for further analysis.

Statistical analysis

Data was analyzedusing Pearson chi-square testing method with SPSS version 20.0 and a *P*-value of 0.005 was considered significant.

Materials and Equipment used

Materials used during the course of this study include; spatula, cotton wool , petri dishes, swab sticks, conical flasks, spatula, aluminium foil paper, measuring cylinder, beakers, test tubes, aluminium foil, paper tape, marker, test tubes rack, inoculating loop, inoculating needle, distilled water and syringe needle.

The equipment used includes; autoclave, thermal cycler, incubator, refrigerator, weighing balance, Bunsen burner, spectrometer

Media and Reagents

The media and reagents used includes blood agar, McConkey agar, Eosin methylene blue agar ,Potatoe dextrose agar and distilled water

Preparation of Media.

Media	**Composition**	**Origin**
Blood agar	Heart Muscle,infusion,pancreatic digest of casein,yeastextract,sodiumchloride,agar	USA
McConkey agar	Peptone, sodium chloride, lactose, bile, salt mix, neutral red, crystal violet , agar-agar.	USA
Nutrient agar	Beef extract, yeast extract, peptone, sodium chloride.	USA
Sabouraud dextrose agar	Potatoe, dextrose and agar powder	USA

All media used were prepared according to manufacturer's instructions. Media were initially using a weighing balance and the appropriate quantities were dispensed in conical flasks while distilled water was added to make up the required volume. The media in the conical were homogenized on hot plate before they were sterilized in an autoclave at 121 for 15

minutes. The media were then allowed to cool, poured into sterile petri dishes to solidify and set for inoculation.

Inoculation

Upon getting to the laboratory, for bacterial isolation, serial dilution was carried out up till 10^7 and 0.1 mL of 10^4 and 10^6 dilutions was plated on blood agar, MacConkey agar and nutrient agar using the streak plate method and plates were incubated at 28°C for 24-48 hours for bacterial growth.

For fungi isolation, it was performed using the pour plate technique by plating 1 mL of sample onto Sabouraud dextrose agar (SDA) supplemented with chloramphenicol and plates were incubated at 37°C for 72 hours.

Bacteria DNA extraction

Genomic DNA was extracted using commercial kit (QiagenMiniprep 27104 Matrix Technologies Cooperation, USA) according to the manufacturers instruction and then stored at -80^{o}C. Purity and concentration of the DNA extract was determined using a spectrophotometer.

Polymerase Chain Reaction

The amplification of target DNA was carried out in a mix of 50 µL PCR mixture using a Simpli Amp thermal cycler for 35cycles. The mixture consisted of 1.3 µL template DNA, 5 µL of 10x PCR buffer, 0.5µL of 10× deoxy nucleotide tri phosphate, 1µL of forward and 1 µL of reverse primers, 1 µL of Taq DNA polymerase and sterile distilled water was used to adjust the mixture to 50 µL. The amplification consisted of an initial denaturation step of 3 minutes at 95^{o}C which was be followed by denaturation for 30 seconds at 94^{o}C, annealing at 60^{o}C for 30 seconds and elongation at 72^{o}C for 2 minutes.

Agarose Gel Electrophoresis

Two percent (2%) agarose gel was used to resolve DNA fragment. This was prepared by combining 2 g agarose in ten times concentration of tris-borate ethylene diamine

tetraacetate(10ml 10XTB-EDTA) buffer and 90 mL sterile distilled water in 250 mL beaker flask and heating in a microwave for 2 minutes until the agarose is dissolved. Exactly 0.7µL of ethidium bromide was added to the dissolved agarose solution with swirling to mix. The gel was then poured onto a mini horizontal gel electrophoresis tank and casting combs was inserted. The gel was allowed to set for 30 minutes. The casting combs were carefully removed after the agarose gel had solidified completely. One times concentration (1X) TBE buffer was added to the reservoir until it covered the agarose gel. Precisely 8µl of gel tracking dye (bromophenol blue) was added to 10µl of each sample with gentle mixing. The sample was loaded onto the wells of the gel at a concentration of 10 µl, the mini horizontal electrophoresis gel setup was covered, and electrodes connected. Electrophoresis was carried out at 100-200 mA for one hour. At the completion of electrophoresis, the gel was removed from the buffer and visualized under UV light and documented in a gel-doc system with CCD camera attached to it (Hero-Lab).

Sequencing

The 16s rRNA gene products of isolates was sequenced and products were subjected to cycle sequencing in both directions using universal primers. The sequencing will be done using the Sanger sequencing method. Nucleotide sequences classified using BLAST analysis and was edited using the software Chromas and then compared with published sequence in National Centre for Biotechnology Information (NCBI) database for determination of closest strain type.

Identification of fungi isolates

Fungal culture was confirmed by growing on Sabouraud dextrose agar for 48 hours at 37°C. It was then identified microscopically and macroscopically by placing the culture on a clean grease free microscopic slide, staining with lactophenol cotton blue and viewing under a light microscope at × 400 magnification. Fungi isolate was identified using Atlas of Fungi.

CHAPTER IV

Results

Demographic Study:

Demographic characteristics of the studied population are shown in Table 4.1. A total of 300 samples were collected by swabbing foot, nails and interdigital areas of volunteers that are footballers from playing in Lafia, outside Lafia and non athletes. A detailed information on their age, gender, race and level of education was also obtained.

Table 4.1: Demographic Study of Sampled Population

Parameters		Lafia athlete N=100	Non Lafia athlete N=100	Non athletes N=100
Age	18-24	50	57	35
	25-29	30	35	55
	30-35	20	8	10
Gender	Male	56	63	60
	Female	42	37	40
Race	Africans	100	100	100
	Caucasian	0	0	0
	Orientals	0	0	0
Level of Education	Primary school	15	21	20
	Secondary school	55	46	27
	University	30	33	53

Molecular Identification of Bacterial Isolates:

The bacteria isolates were identified using the 16Sr DNA partial gene sequencing and they were identified to share close similarity from the blast information (Table 4.2) as *Staphylococcus aureus, Micrococcus luteus, Staphylococcus haemolyticus* and *Bacillus licheniformis.* The gel from the agarose gel electrophoresis (Figure 4.1) showed the presence of DNA of the bacterial isolates

Table 4.2: Similarity Index of Bacteria Isolates Obtained from National Centre for Biotechnology Information (NCBI) Blast.

Isolate code	Related bacterial strain	Similarity (%)	Accession number
1	*Staphylococcus aureus* EDCC5398	99.14	CP053101.1
2	*Micrococcus luteus* NCTC 2665	99.23	KC005723
3	*Staphylococcus haemolyticus*ES1-263	100	FN393803
4	*Bacillus licheniformis* MV1	100	KJ190320.1

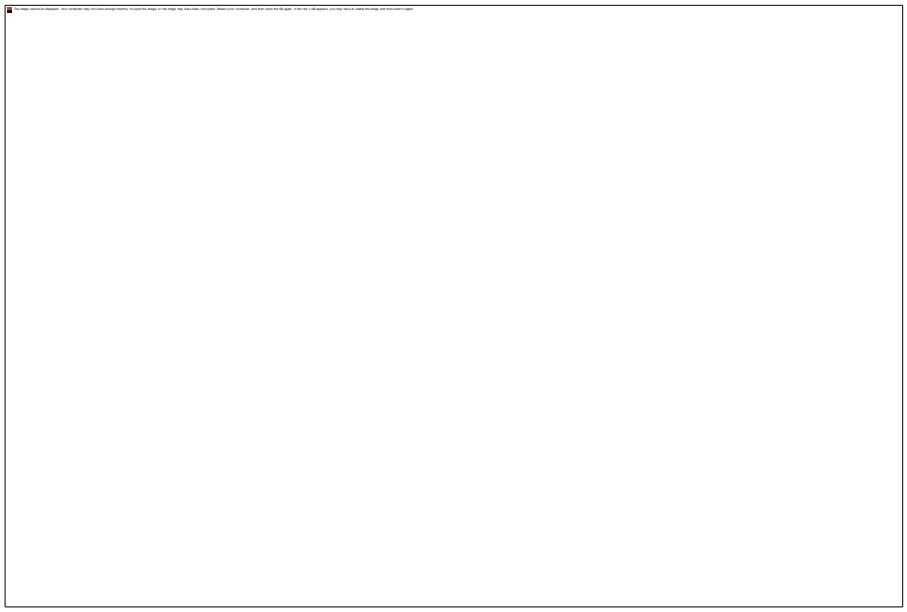

Fig 4.1: Gel Image Showing the Different Bands of DNA (Ladder DNA is 5kb, M1 represents isolate 1, M2 represents isolate 2, M3 represent isolate 3 and M4 represents isolate 4)

Microscopic Identification of Fungi Isolate:

The fungi isolates were identified using standard microbiological technique and confirmed to be*Aspergillus* sp., *Penicillium*sp., *Cladosporium* sp., *Candida* sp. and *Epidermophyton*sp. (Table 4.3).

Table 4.3: Microscopic Identification of Fungi isolates

Fungi				
		Microscopic appearance		
	Colour	Texture	Hyphae	Conidia
*Aspergillus*sp	Black	Smooth	Present and coloured	Present
*Penicillium*sp	Green	Granular	Septate	Present
*Cladosporium*sp	Yellowish green	Velvety	Symmetrically branched	Present and spherical
*Candida*sp	White	Spherical	Absent	Absent
*Epidermophyton*sp	Greenish brown	Flat	Present	Present

Demographic Study of the Frequency of Bacteria Isolates:

The distribution of bacteria isolates amongst the various demographic parameters is shown in Table 4.4. Age limit between 30-35 recorded the highest bacteria isolates while male foot had more bacteria isolates compared to female.

Table 4.4: Frequency of bacterial isolates with Respect to Age, Gender, Race and Level of Education

	Number of bacteria isolates		
Age limit	Lafia athletes	Non-Lafia athletes	Non athletes
18-24	4	3	1
25-29	3	5	1
30-35	5	5	3
Gender			
Male	10	9	4
Female	2	4	1
Race			
African	12	14	5
Caucasian	0	0	0
Orientals	0	0	0
Level of Education			
Primary school	6	5	4
Secondary school	5	5	1
University	1	3	0

Demographic Study of the Frequency of Fungi Isolates:

The distribution of fungi isolates amongst the various demographic parameters is shown in Table 4.5. Age limit between 30-35 recorded the highest bacteria isolates while male foot had more fungi isolates compared to female.

Table 4.5: Frequency of fungi isolates with Respect to Age, Gender, Race and Level of Education

		Number of fungi isolates	
Age limit	Lafia athletes	Non-Lafia athletes	Non athletes
18-24	3	4	0
25-29	6	7	2
30-35	12	7	3
Gender			
Male	20	12	4
Female	1	6	1
Race			
African	20	11	4
Caucasian	1	1	1
Orientals	0	0	0
Level of Education			
Primary school	15	12	3
Secondary school	4	5	1
University	2	1	1

Prevalence of Bacterial Isolates:

Staphylococcus aureus was the most prevalent bacteria for all three studied population. A prevalence rate of 60% was recorded with non athlete, which was followed by 58.3% for Lafia athletes and 46.1% for non Lafia athlete (Table 4.6). In contrast, *Bacillus licheniformis* was the least prevalent with non Lafia athletes recording the least (0%).

Table 4.6: Prevalence of Bacterial Isolate from Foot of Studied Population

Bacterial isolate	Lafia athlete N=100	Non Lafia athlete N=100	Non athletes N=100
Staphylococcus aureus	7(58.5%)	6(46.1%)	3(60%)
Micrococcus luteus	2(16.6%)	4(30.7%)	1(20%)
Staphylococcus haemolyticus	2(16.6%)	3(23.2%)	0(0%)
Bacillus licheniformis	1(8.3%)	0(0%)	1(20%)

Prevalence of Fungi Isolates:

Aspergillus spwas the most prevalent fungi for all three studied population. A prevalence rate of 40% was recorded with non athlete, which was followed by *Epidermophyton*spwhich recorded a prevalence rate of 33.3% for Lafia athletes and 33.3% for non Lafia athlete (Table 4.7). In contrast, *Epidermophyton*sp was the least prevalent with non Lafia athletes recording the least (0%).

Table 4.7: Prevalence of Fungi Isolate from Foot of Studied Population

Bacterial isolate	Lafia athlete N=100	Non Lafia athlete N=100	Non athletes N=100
Aspergillus sp	5(23.8%)	4(22.2%)	2(40%)
*Penicillium*sp	4(19.0%)	2(11.1%)	2(40%)
*Cladosporium*sp	2(9.6%)	3(16.6%)	0(0%)
*Candida*sp	3(14.1%)	3(16.6%)	1(20%)
*Epidermophyton*sp	7(33.3%)	6(33.5%)	0(0%)

Distribution of Bacteria Isolate Across Different Swab Areas

Staphylococcus aureus (100%) isolated from the interdigital area of the feet, *Bacillus licheniformis*(100%) isolated from the interdigital area and *Micrococcus luteus* (100%) isolated from the nails were the most prevalent bacteria in both Lafia athletes and non Lafia athletes (Table 4.8). In contrast, *Staphylococcus haemolyticus* (0%) recorded the least prevalence for all swabbed area for non athletes.

Table 4.8: Distribution of Bacterial Isolates in Different Areas of the Foot for Studied Population

Bacterial isolate	Area swabbed	Lafia athlete N=100	Non Lafia athlete N=100	Non athletes N=100
Staphylococcus aureus	Nail	1(14.2%)	0(0%)	0(0%)
	Sole	2(28.5%)	4(66.6%)	0(0%)
	Interdigital	4(57.1%)	2(33.3%)	3(100.0%)
Micrococcus luteus	Nail	0(0%)	0(0%)	1(100.0%)
	Sole	1(50,0%)	1(25.0%)	0(0%)
	Interdigital	1(50.0%)	3(75.0%)	0(0%)
Staphylococcus haemolyticus	Nail	0(0%)	0(0%)	0(0%)
	Sole	1(50.0%)	2(66.6%)	0(0%)
	Interdigital	1(50.0%)	1(33.3%)	0(0%)
Bacillus licheniformis	Nail	0(0%)	0(0%)	0(0%)
	Sole	0(0%	0(0%)	1(100.0%)
	Interdigital	1(100.0%)	0(0%)	0(0%)

Distribution of Fungi Isolate Across Different Swab Areas

Candida sp (66.6%) and *Epidermophyton*sp (57.1%) isolated from the sole of the feet, which was followed by *Cladosporium*sp (66.6%) isolated from interdigital areas were the most prevalent bacteria in both Lafia athletes and non Lafia athletes (Table 4.9). In contrast, *Cladosporium*sp (0%) and *Epidermophyton*sp (0%) were the least prevalent for all sampled area for non athlete.

Table 4.9: Distribution of Fungi Isolates in Different Areas of the Foot for Studied Population

Bacterial isolate	Area swabbed	Lafia athlete N=100	Non Lafia athlete N=100	Non athletes N=100
Aspergillus sp	Nail	1(20.0%)	1(25.0%)	0(0%)
	Sole	2(40.0%	1(25.0%)	1(50.0%)
	Interdigital	2(40.0%)	2(50.0%)	1(50.0%)
Penicilliumsp	Nail	0(0%)	0(0%)	1(50.0%)
	Sole	2(50.0%)	1(50.0%)	0(0%)
	Interdigital	2(50.0%)	1(50.0%)	1(50.0%)
Cladosporiumsp	Nail	0(0%)	0(0%)	0(0%)
	Sole	1(50.0%)	1(33.3%)	0(0%)
	Interdigital	1(50.0%)	2(66.6%)	0(0%)
Candida sp	Nail	0(0%)	0(0%)	0(0%)
	Sole	2(66.6%)	2(66.6%)	1(100%)
	Interdigital	1(33.3%)	1(33.3%)	0(0%)
Epidermophytonsp	Nail	2(28.5%)	2(33.3%)	0(0%)
	Sole	4(57.1%)	2(33.3%)	0(0%)
	Interdigital	1(14.2%)	2(33.3%)	0(0%)

CHAPTER V

Discussions

The feet represent one of the most distinct and diverse microbial environments on the human body. Like other areas of the body, the microbiome of the feet is influenced by factors such as skin thickness, anatomical characteristics (such as furrows, pockets, and skin creases), the density of sweat glands, skin pH, and the presence of oxygen.

The differences in skin pH, hormone, sebum and sweat production including lifestyle differences are believed to provide an explanation for the variability in the microbiome of the foot resulting from age and gender differences.

Foot fungal infections occur with varying frequencies in male individuals. These variations are largely influenced by social status and behaviour rather than biological factors. Men often do not seek healthcare regularly, and when they do, it is often because the problem has already progressed. There is a slight predominance of young individuals participating in Lafia soccer teams (Table 1). However, the age limitations for participation in this study impact this specific data.

The bacteria isolates identified using the 16Sr DNA partial gene sequencing were *Staphylococcus aureus, Micrococcus luteus, Staphylococcus haemolyticus* and *Bacillus licheniformis* (Table 4.2) while the fungi isolated in this study were *Aspergillus* sp., *Penicillium*sp., *Cladosporium* sp., *Candida* sp. and *Epidermophyton*sp. (Table 4.3). This study is in agreement with the works of Ross *et al*. (2017) who reported that the normal healthy skin of the foot is inhabited by bacteria like *Corynebacteriaceae, Micrococcaceae, Propionibacteriaceae, Actinobacteria, Clostridiales, Lactobacillaceae, Streptococcaceae, Enterobacteriaceae, Moravellaceae, Neisseriaceae, Pastereullaceae*, and *Proteobacteria*. They also reported that common fungi on the soles of the examined foot were also *Candida albicans*. These results are confirmed by the studies by Costello *et al*. (2009), who showed that the surface of foot skin is largely colonized by bacteria belonging to the *Staphylococcus* genus.

A higher occurrence of both bacterial (Table 4.4) and fungal isolates (Table 4.5) was observed between the ages of 30-35. The importance of isolation of these microorganisms from apparently healthy relatively elderly footballers may lie in the sharing of beds and towels among other footballers leading transmission of such organisms in the community with public health sequalae. Non athletes recorded lower number of bacterial and fungal isolated compared with athletes. This could be attributed to a better hygiene practice and non- involvement in strenuous exercise which could have resulted to profuse sweating in areas around the feet allowing for colonization of microorganisms.

Gender has been a major issue in the distribution of bacteria and fungi in the foot. In this study, it was observed that bacterial (Table 4.4) and fungal (Table 4.5) were more isolated from male than the female. This could be as a result of hygiene as female footballers have a better hygiene practice than the male.

In Nigeria, soccer players represent a relatively diverse racial mix (Table 4.4). The notion that ethnic background impacts the likelihood of developing fungal and bacterial infections remains a topic of significant controversy. Race has also been linked to unique discoveries, such as melanonychiastriata, which is exclusively predominant in black individuals. This study had showed that more bacterial and fungi were isolated from the African race than any other race.

The level of education amongst athletes and non athletes also have an impact on the number of bacterial and fungal isolates. It was observed that in the present study, most microorganisms were isolated from most athletes with primary school education. Their low level of education may also have resulted in these athletes not practicing good hygiene which can lead to the proliferation of microorganisms.

The frequency of *Staphylococcus aureus* was highest compared to other bacterial in soccer players and non-athletes (Table 4.6), but the non-athlete's category issue was more serious (60%) because of inadequate foot ventilation throughout the workday. This could lead to the development of bacterial diseases acquired through interdigital maceration from perspiration and occlusion from shoes and stockings. The low relatively reduced prevalence of *Staphylococcus aureus* in athletes may be as a result of regular stocking and shoe changes as well as appropriate health care provider

education.These findings corroborate work done by Steglinska*at al*. (2019) who also reported high prevalence of *Staphylococcus aureus* in the foot skin.

In the present study, *Aspergillus*sp (40%) recorded the highest prevalence (Table 4.7) and this finding agrees with reports by Steglinska*et al*. (2019) who also reported the prevalence of *Aspergillus* sp. Non athletes recorded a higher prevalence of fungi than athletes and this could have been as a result of excessively sweating during the day and bad hygiene practice. The use of textile with biocides that have antimicrobial and hygienic qualities is a significant way to prevent the growth of fungi and bacteria on the skin of the feet (Fratini*et al*., 2016; Haaseet*et al*., 2017). In the textile sector, these materials are used to make tights, socks, mattresses, and in soles, among other products. (Scharschmidt&Fischbach, 2013)

The athletes from both Lafia and non Lafia had more bacterial when different areas of the feet were swabbed compared to non athletes. *Staphylococcus aureus* (100%) and *Bacillus licheniformis*(100%) isolated from the interdigital area of the feet and *Micrococcus luteus* (100%) isolated from the nails were the most prevalent bacteria in both Lafia athletes and non Lafia athletes (Table 4.8). In contrast, *Staphylococcus haemolyticus* (0%) recorded the least prevalence for all swabbed area for non athletes. The interdigital area of the foot harbored more bacterial than any other part. This is possible due to the constant dampness between digital spaces aided in the mycosis's development (Purim*et al*., 2005).

Candida sp (66.6%) and *Epidermophyton*sp (57.1%) isolated from the sole of the feet, which was followed by *Cladosporium*sp (66.6%) isolated from interdigital areas were the most prevalent bacteria in both Lafia athletes and non Lafia athletes (Table 4.9). In contrast, *Cladosporium*sp (0%) and *Epidermophyton*sp (0%) were the least prevalent for all sampled area for non athlete. In the Lafia soccer players, the high prevalence of *Candida*sp as may have been attributed to possible skin pH changes and maceration and sweating. Emotional stress from the league play offs and Nigeria League Championship could also have contributed to reduced organic defenses and immunity problems.

Fungus was least isolated in the non athletes in the nail area. This could have been as a result of the toughness and dry nature of the nails thereby preventing fungus from proliferating such area.

CHAPTER VI

Conclusion and Recommendations

Athlete and non athlete foot was colonized mainly by genera of *Staphylococcus, Micrococcus, and Aspergillus, Penicillium, Cladosporium, Candida and Epidermophyton sp*. Age and gender, as well as race and level of education were factors that influenced the number and biodiversity of human foot skin microorganisms, The number of bacteria and fungi isolated in age limit 30-35 were higher than any other group with men harboring more microorganisms. Likewise, microorganisms were isolated in African than other races.

Staphylococcus aureus was the most prevalent bacteria in both athletes and non athletes. Likewise, *Aspergillus*sp was the most prevalent fungi for both athletes and non athletes. It can be concluded that these two microorganisms are the most prevalent microorganisms in foot.

The bacterial distribution indicated that *Bacillus licehniformis* was the most prevalent in the interdigital area for Lafia athletes while *Staphylococcus aureus* was the most prevalent in the sole with Non Lafia athletes. It can be concluded that Athletes harbour more bacteria in various part of the foot compared to non athletes. Sports activities increase the risk of getting skin and nail mycosis.

Recommendation: Based on the study conducted, the following can be recommended

I. Use of biocidal socks and insoles with antimicrobial properties by non athletes should be encouraged
II. Athletes and non athletes should maintain good hygiene practices
III. Older athletes should go for regular feet examination to prevent harbouring infectious fungi due to weak immune system.

Limitation of study:

I. Traditional culturing method for fungi was not employed
II. Equipments and athlete fabrics were not swabbed as these could serve as formites
III. Sampling of participants could have been done before and after exercise

Appendix

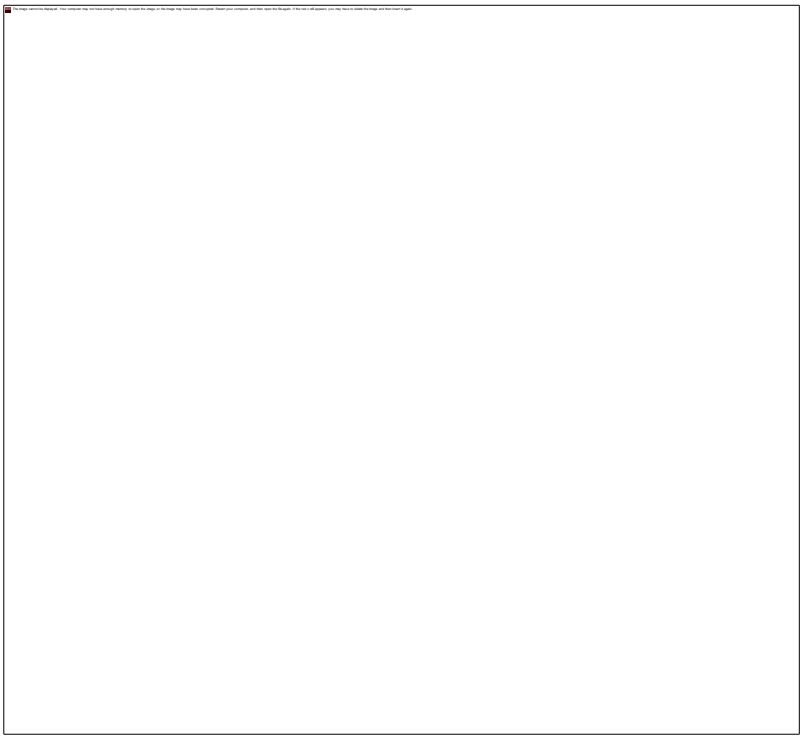

Plate 1: *Aspergillus*sp growing on Sabouraud dextrose agar after 48 hours

Plate 2: *Staphylococcusaureus* growing on Nutrient agar after 24 hours

Plate 3: *Micrococcus luteus* growing on Nutrient agar after 24 hours

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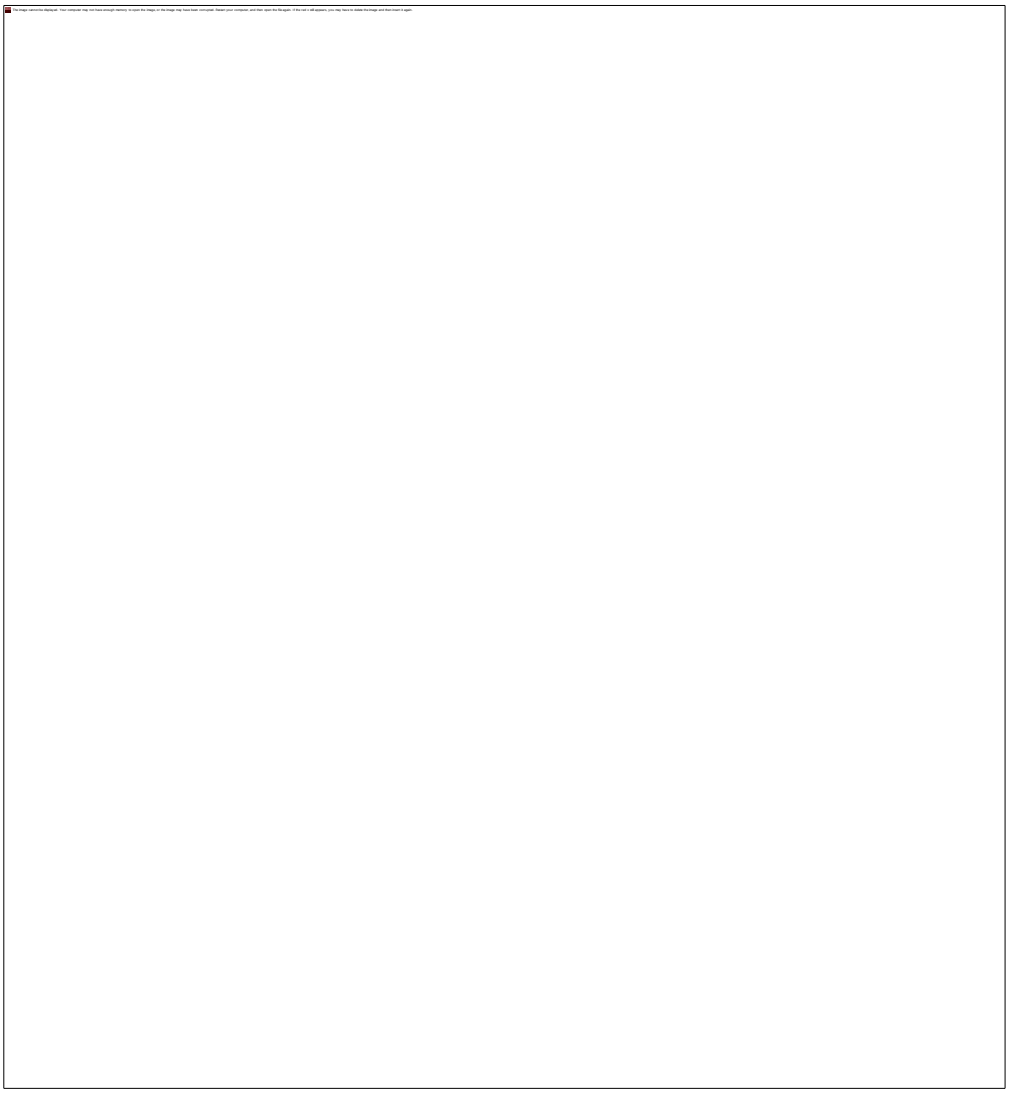

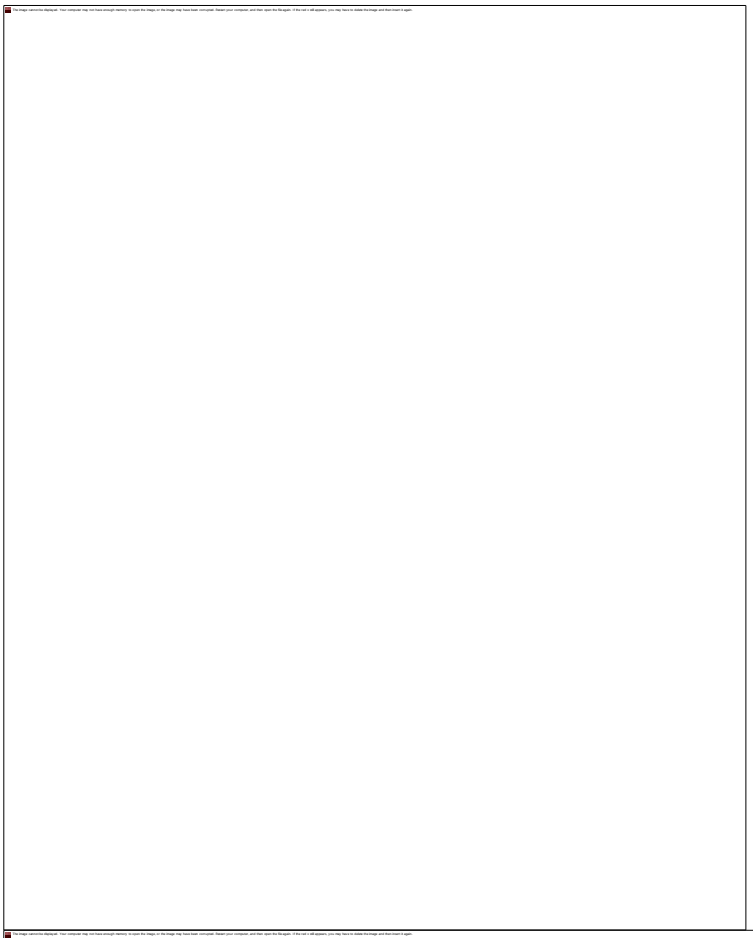

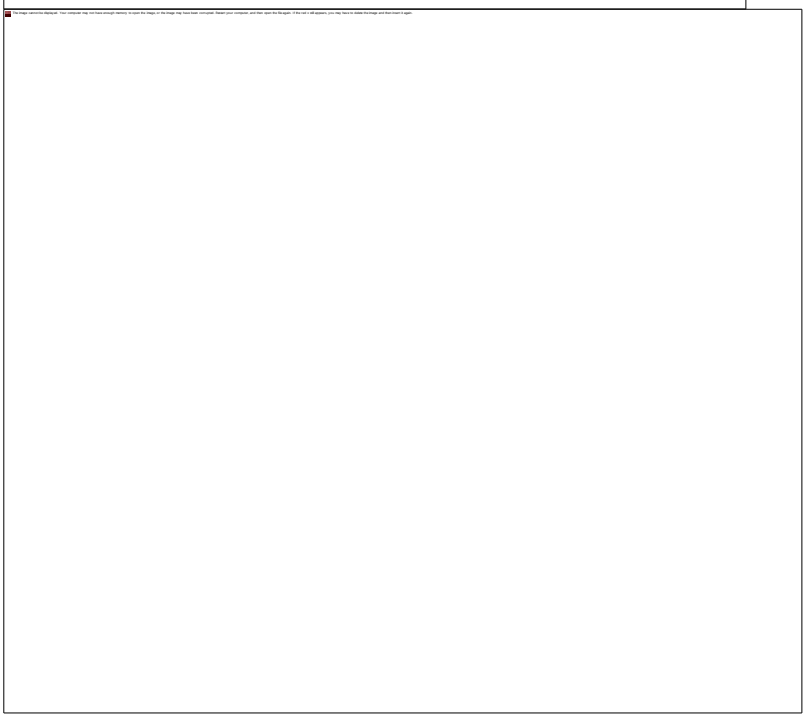

TOCHUKWU ANSELEM UJU

KOMBOS 9 APARTMENT GIRNE KKTC

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Ujurex65@gmail.com

Date of Birth: 28 Dec 2001

Nationality: Nigeria

Marital Status Single

PROFILE

A meticulous, focused and hardworking microbiologist who is more than able to assist staff and clients in the design, execution and evaluation of research projects. Tochukwu has a keen interest in professional development towards employment in the field of advanced microbiological research. He can accurately follow oral and written instructions, and is guaranteed to make a professional researcher's job easier and more efficient. • Dedicated in research and laboratory activities and procedures. • Resourceful and passionate educator with adoptable and approachable style. Multitalented and consistently rewarded for success in planning and operational improvement experience in policy development and staff management procedures, positively impacting overall morals and productivity. Experience in laboratory research with over one year of experience in Biotechnology advanced laboratory Sheda Abuja, excellent reputation for resolving problems.

EMPLOYMENT HISTORY

2022 till date

Hungry house fast food limited .

Turkish republic of northern Cyprus.

Manager

ANDY WORLD CONSTRUCTIONS

CATALKOY GIRNE KKTC

Maintenance manager

Feb 2017- Nov 2017

Biotechnology Advanced Laboratory, Abuja, Nigeria

Laboratory assistant • Planned and carried out trials • Collected specimens/samples from a variety of locations • Recorded, analysed and interpreted data • Ensured accurate recording of data in accordance to guidelines • Kept (and still keeping) up to date with scientific and research developments • Exhibited and observed high aseptic technique; health and safety standards • Grow and maintained microbial cultures • Wrote research papers, reports and reviews • Sterilized, disinfected and fumigated laboratory equipment and facilities • Maintained and calibrated buffers and analytical equipment • Encapsulated silver nano particles • Encapsulated gold nanoparticues • Mushroom cultivation and culturing • Harvesting and culturing of prodigiosin • Antibiotics examiations

Sept 2019- July 2020

Twins College, MayodassaJalingo.

Mathematics Teacher

Sept 2019- July 2020

Ministry of youth and sports, Jalingo,

Planning Officer

EDUCATION

2021 Oct – June 2024 M.Sc. Medical microbiology and clinical microbiology

Near East University.

Turkish Republic of Northern Cyprus.

Oct 18th 2014- June 22nd 2019 B.Sc. (Hons) Microbiology,

Federal University Lafia.Nasarawa state Nigeria.

2020-2020

world health organisation's E-learning I P C E-learning programme: infection prevention and control.

2009-2013 God's Time Comprehensive College Onyigbo River state. WAEC

2007-2009 Junior Secondary School Jiwa Abuja JSSCE

2003-2007 L.E.A Primary school Jiwa Abuja. FSLC

SKILLS

Research, • First aid / C P R • Problem resolving • Computer literate • Relationship development • Team management • Team work • College preparation • Common core standards • Technology integration • Strong research, organizational and writing skills. • Ability to work without or with minimum supervision, result-oriented and adaptable. • Responds quickly to messages; online (emails, social media) and offline • Good communication and interpersonal skills. • Ability to undertake focused research and present result to variety of audience. • Strong adherence to aseptic techniques. • Keeping accurate records of experiments and investigations. • Determined, resourceful and target-driven. • Existing computer skills with Microsoft Office, and statistical software. • Proficiency in smartphones and communications technology • Good orator and public speaker. • Ability to adjust work assignments or schedules in order to meet changing work priorities. • A good team player, member and follower. • Good leadership qualities. • Marketing • Business relationship

HOBBIES

Research,

Playing football,

Reading

Traveling

LANGUAGES

English, Igbo, Turkish

REFERENCES

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