Identification And Isolation Of Microorganisms From Human Skin (Mouth, Armpit And Nose)

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Abstract: Large numbers of microorganisms live on and in the various components of the normal skin. Depending on the body location and the amount of skin moisture, the number of skin bacteria may range from only about 1000 organisms per square centimeter on the back to more than 10 million in the mouth, nose, groin and armpit, where moisture is more plentiful. A study of the carriage of microorganisms in mouth, armpits and nose was carried out on students of Science Laboratory Technology, Federal Polytechnic Offa, Kwara State, Nigeria. The mouth, armpits and nose were swabbed and the microbiological analyses were carried out on the swab samples. The total bacterial counts of sample A (mouth) ranged from 8.0×10^4 to 4.9×10^6 Cfu/g. The total bacterial counts of sample B (armpit) ranged from 9.9×10^4 to 6.2×10^6 Cfu/g. The total bacterial counts of sample C (nose) ranged from 5.2×10^4 to 3.2×10^6 Cfu/g. Sample B (armpit) had the highest bacterial count of 6.2×10^6 Cfu/g while sample C (nose) had the least bacterial count of 3.2×10^6 Cfu/g. The organisms isolated include Staphylococcus epidermidis, Lactobacillus specie, Staphylococcus aureus, Corynebacterium specie, Streptococcus pyogenes and Actinobacteria specie. The result of this finding defines mouth, armpit and nose as a reservoir for bacterial pathogens. All of the bacteria isolated were opportunistic pathogens, and their presence in the body could stress the immune system. When the immune system is compromised, the body's ability to fight infection is impaired and it becomes more susceptible to disease. Personal hygiene can go a long way to prevent diseases; among these are hand-washing, daily bathing and proper care of the different parts of the body.

I. INTRODUCTION

Large numbers of microorganisms live on and in the various components of the normal skin. The number of microorganisms increases after a hot shower because of increased flow of secretion from the skin glands where many reside (Nester *et al.,* 2004). In humans, the formation of body odors is mainly caused by skin glands excretions and bacterial activity (Lundstrom and Olsson, 2020).

Respiratory tract infections are one of the important causes of morbidity and mortality worldwide (Roth and James, 2018). The human nose, perpetually exposed to the environmental flora, is prone to get colonized with a variety of microbial agents. Bacterial pathogens such as *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Haemophilus influenzae*, *Neisseria meningitidis*, and *Staphylococcus aureus* often colonize the human upper respiratory tract. The

pathogens get easily transmitted from colonized/infected individuals to healthy population via respiratory droplets or oropharyngeal secretions. Asymptomatic colonization by potential pathogens like *Streptococcus pneumoniae*, *Streptococcus pyogenes*, *Haemophilus influenzae*, and *Neisseria meningitidis* may lead to invasive infections and serious complications. The carrier rates of these pathogens vary depending upon socioeconomic status, environmental conditions, age, and antimicrobial therapy of the population (Masuda *et al.,* 2020).

The axilla, a skin region around the armpit usually differs from other regions of the body with respect to the presence, identity and number of sweat glands. The axillary region is of particular interest, as it contains dense aggregations of eccrine, apocrine, and sebaceous glands that nurture diverse communities of microbiota which plays an important role in generating individual odour (Taylor *et al.,* 2019). Between the

different types of skin glands, the human body odor is primarily the result of the apocrine sweat glands, which secrete the majority of chemical compounds needed for the skin flora to metabolize it (Lundstrom and Olsson, 2020). This happens mostly in the axillary (armpit) region, although the gland can also be found in the areola, anogenital region, and around the navel (Turkington and Dover, 2017). In humans the armpit regions seem more important than the genital region for body odor which may be related to human bipedalism. The genital and armpit regions also contain springy hairs which retains sweat and causes body odors (Claus, 2017). Body odor is influenced by the actions of the skin flora, including members of *Corynebacterium*, which manufacture enzymes called lipase, as it contains dense aggregations of eccrine, apocrine, and sebaceous glands that nurture diverse communities of microbiota knownt to play an important role in generating body odor (Taylor *et al.*, 2019).

II. MATERIALS AND METHODS

Sources of collection of samples: Armpit, nose and mouth swabs of students from Science Laboratory Technology, Federal Polytechnic Offa, Kwara State, were collected using sterile swab sticks moistened with 1.0 ml of sterile normal saline and were rubbed vigorously with rotation over the armpits, nose and mouth of participants. The samples were collected into sterile container and sample swabs were taken to Microbiology Laboratory of the Department of Science Technology for immediate analysis in order to maintain the viability of the organisms to be isolated.

PREPARATION OF MEDIA

The media used in the research were Nutrient Agar (NA). Nutrient Agar (NA) was prepared according to the manufacturer's instructions i.e. 14g of powdered Nutrient Agar (NA) was measured into a clean conical flask and dissolved with 500ml of sterile distilled water and shaken gently. The conical flask was gently warmed in hot plate to completely dissolve the medium and the mouth was blocked with cotton wool, wrapped with aluminium foil. The medium was sterilized in an autoclave at $121^{o}C$ for 15minutes at 15pascal.

Preparation Of Serial Dilution: The sample was dipped into the first tube containing 9ml of distilled water placed in the test tube rack. 1ml of the stock was collected using a needle and syringe from the first test tube into the second test tube up to the ninth test tube respectively i.e. 10^{-1}, 10^{-2}, 10^{-3}, 10^{-4}, 10^{-5}, 10^{-6}, 10^{-7}, 10^{-8}, 10^{-9} respectively. 10^{-4} and 10^{-5} were used as the dilution factor and 1ml was taken from each factor into a sterilized petri dish in duplicate.

ISOLATION OF BACTERIA:

The method used for isolation of bacteria was pour plate. Serial 10^{-1} fold (decimal) dilutions of sample suspension up to 10^{-9} where made i.e. the sample was dipped was dipped in 10ml of sterile distilled water. It was agitated for 2 minutes. This form 10^{-1} dilution, from this dilution, 1ml of the Aliquot

using needle and syringe was transferred into fresh 9ml of distilled water in sterile test-tube. Subsequent were made up to 10^{-9}.

ENUMERATION OF COLONIES

After the incubation period, the numbers of bacteria colonies counted using a colony counter. The number of spores on a plate was multiplied by the dilution factor to give the plate count per ml of the sample.

SUB-CULTURING

After the incubation period of 24 hours, the petri-dishes were brought out and were observed for growth of bacteria. With the aid of sterile wire loop, a small portion was picked and streaked onto a freshly prepared solidified prepare culture media (i.e. nutrient agar) to get a pure culture.

III. RESULTS

BACTERIAL COUNT OF THE SAMPLES

The total bacterial counts are from the mouth, armpit and nose of some of the students of Science Laboratory Technology, Federal Polytechnic Offa, Kwara State is shown in Table 1 The total bacterial counts of sample A (mouth) ranged from 8.0×10^4 to 4.9×10^6Cfu/g. The total bacterial counts of sample B (armpit) ranged from 9.9×10^4 to 6.2×10^6Cfu/g. The total bacterial counts of sample C (nose) ranged from 5.2×10^4 to 3.2×10^6Cfu/g (Table 1).

SAMPLE	DILUTION SERIES	PLATE 1	PLATE 2	MEAN	Cfu/ml
A	10^{-3}	86	74	80	8.0×10^5
	10^{-4}	52	45	49	4.9×10^6
B	10^{-3}	92	106	99	9.9×10^5
	10^{-4}	78	46	62	6.2×10^6
C	10^{-3}	58	46	52	5.2×10^5
	10^{-4}	28	36	32	3.2×10^6

KEY:
Sample A = Mouth
Sample B = Armpit
Sample C = Nose
Table 1: Bacterial Count Of The Samples (Cfu/ml)

IV. CULTURAL CHARACTERISTICS OF THE BACTERIAL ISOLATES FROM SAMPLE A (MOUTH)

The cultural characteristics of the bacteria isolates from sample A (mouth) are shown in Table 2. The isolate A1 on the agar plate showed medium to irregular shape, they were creamy with flat elevation and surface appearances which are rough. The isolate A2 on the agar plate showed big to irregular shape, they are creamy with flat elevation and surface appearances which are rough.

Morphology	Isolate A1	Isolate A2
Size	Medium	Big
Shape	Irregular	Irregular
Surface	Rough	Rough
Edge	Rhizoid	Undulate
Elevation	Flat	Flat
Pigmentation	Creamy	Creamy
Optical	Translucent	Translucent
Consistency	Viscid	Viscid

KEY:

Sample A = Mouth

Table 2: Cultural Characteristics Of The Bacteria Isolates From Sample A Cultural Characteristics Of The Bacterial Isolates From Sample B (Armpit)

The cultural characteristics of the bacteria isolates from sample B (Armpit) are shown in Table .3. The isolate B1 on the agar plate showed big to irregular shape, they are creamy with flat elevation and surface appearances which are rough. The isolate B2 on the agar plate showed small to regular shape, they are creamy with flat elevation with surface appearances which are smooth

Morphology	Isolate B1	Isolate B2
Size	Big	Small
Shape	Irregular	Regular
Surface	Rough	Smooth
Edge	Entire	Undulate
Elevation	Flat	Flat
Pigmentation	Creamy	Creamy
Optical	Translucent	Translucent
Consistency	Viscid	Viscid

KEY:

Sample B = Armpit

Table 3: Cultural Characteristics Of The Bacteria Isolates From Sample B

V. CULTURAL CHARACTERISTICS OF THE BACTERIAL ISOLATES FROM SAMPLE C (NOSE)

The cultural characteristics of the bacteria isolates from sample C (nose) are shown in Table 4. The isolate C1 on the agar plate showed big to irregular shape, they are creamy with flat elevation and surface appearances which are smooth. The isolate C2 on the agar plate showed big to irregular shape, they are creamy with flat elevation with surface appearances which are smooth. The isolate C3 on the agar plate showed small to regular shape, they are creamy with flat elevation and surface appearances which are rough.

Morphology	Isolate C1	Isolate C2	Isolate C3
Size	Big	Big	Small
Shape	Irregular	Irregular	Regular
Surface	Smooth	Smooth	Rough
Edge	Undulate	Entire	Rhizoid
Elevation	Flat	Flat	Flat
Pigmentation	Creamy	Creamy	Creamy
Optical	Opaque	Translucent	Translucent
Consistency	Viscid	Viscid	Viscid

KEY:

Sample C = Nose

Table 4: Cultural Characteristics Of The Bacteria Isolates From Sample C

VI. DISCUSSION

This study investigated the populations and distribution of bacteria in the mouth, armpits and nose of some students of Science Laboratory Technology, Federal Polytechnic Offa, Kwara State. The research findings have shown that bacteria were detected in the mouth, armpits and nose of the students investigated.

The total bacterial counts of sample A (mouth) ranged from 8.0×10^4 to 4.9×10^6 Cfu/g. The total bacterial counts of sample B (armpit) ranged from 9.9×10^4 to 6.2×10^6 Cfu/g. The total bacterial counts of sample C (nose) ranged from 5.2×10^4 to 3.2×10^6 Cfu/g (Table 1). Sample B (armpit) had the highest bacterial count of 6.2×10^6 Cfu/g while sample C (nose) had the least bacterial count of 3.2×10^6 Cfu/g (table 1).

Diverse species of bacteria were isolated from the mouth, armpits and nose of some students of Federal Polytechnic Offa, Kwara State. *Lactobacillus* specie and *Staphylococcus aureus* were isolated from Sample A (mouth). *Staphylococcus epidermidis, Corynebacterium* specie and *Staphylococcus aureus* were isolated from Sample B (armpit). *Streptococcus pyogenes* and *Actinobacteria* specie were isolated from sample C (nose). This agrees with the findings of Roseline *et al.* (2020) who isolated *Staphylococcus aureus, Corynebacterium* specie, *Streptococcus pyogenes* and *Actinobacteria* from the human skin of some of the students of Lagos State University, Nigeria. This also collaborates with the finding of Bolognia *et al.* (2018) who isolated *Streptococcus pyogenes, Staphylococcus aureus,* and *Corynebacterium* specie from the human armpit and mouth analyzed. Kadhem *et al.* (2016) in a study conducted on the human nose and mouth, isolated *Staphylococcus aureus, Corynebacterium* specie, *Streptococcus pyogenes* and *Actinobacteria.*

In this study, *Staphylococcus* species was the most predominant organism isolated. *Staphylococcus epidermidis,* although a normal flora of the skin, skin glands, anterior nares, and mucous membranes of humans and animals, is an opportunistic pathogen for humans that can cause urinary tract infections, wound infections, endocarditis, and septicemia. Due to contamination, it is probably the most common species found in laboratory tests (Queck and Otto, 2018). *S. epidermidis* is also a major concern for people with catheters or other surgical implants because it is known to cause biofilms that grow on these devices (Salyers and Whitt, 2020).

The isolated bacteria from this study have many health implications. *S. aureus* is known to cause illnesses ranging from pimples and boils to pneumonia and meningitis, a scenario supported by the high population of colony isolates. From the study of Karabay *et al.* (2017), most of the organisms isolated were skin flora, 16.7% of the samples were positive for pathogens known to be associated with nosocomial transmission, such as *S. aureus* (Karabay *et al.,* 2017). Roseline *et al.* (2020) reported that mouth, armpit and nose harbor pathogenic bacteria. The pathogenesis of *S. epidermidis* in the armpit associated infections mostly relies on the potential of the bacterium to adhere to the armpit

surface. Human skin has become veritable reservoirs of pathogens. Gholamreza *et al.* reported that *S. epidermidis* was the most commonly cultured microorganism isolated from armpit. *S. epidermidis* has emerged as major causative agents of nosocomial infections (Karabay *et al.,* 2017).

Among the microbial isolates identified from the mouth, armpit and nose are of public health concern is *Staphylococcus aureus*. The micro-organism is a pathogenic bacterium responsible for severe health problems such as chronic infections and vomiting in humans (Jay *et al.,* 2016). *Staphylococcus aureus* is a known commensal on human skin, but it is an opportunistic pathogen causing a wide range of infections among which are furuncles (boils), carbuncles, impetigo, epidermal necrosis, osteomyelitis, staphylococcal food poisoning and toxic shock syndrome. *Streptococcus* species from the nose is reported to cause endocarditis and other systemic infections. Although the bacterium exists as a normal flora, it may turn into an opportunistic pathogen and cause serious complications.

VII. CONCLUSION

The study reveals that the mouth, armpits and nose harbor bacteria. Bacteria associated with the surface of the mouth, armpit and nose include *Staphylococcus epidermidis, Lactobacillus* specie, *Staphylococcus aureus, Corynebacterium* specie, *Streptococcus pyogenes* and *Actinobacteria* specie. These bacteria cause infection. The result of this finding defines mouth, armpit and nose as a reservoir for bacterial pathogens. The armpits are more likely to harbor bacterial pathogens. It is therefore advised that hygienic practices be adopted by all.

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