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Microbiological assessment of unwashed female hair among students of Federal University Wukari, North-East, Nigeria

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ABSTRACT

Microbes are cosmopolitan in distribution. In humans they can exist as either normal flora or as pathogens. The scalp and hair are parts of the human body that may house them, and their load largely depends on hygiene practices. This study investigates the microbial load and microbial diversity in unwashed hair among female students of Federal University Wukari. Hair samples were collected from 200 healthy female student donors across 100 to 400 levels using sterilized scissors, ensuring at least 1 cm of hair growth, and excluding those with scalp conditions or chemical treatments. The samples were labeled and transported to the Microbiology Laboratory at Federal University Wukari for analysis. The samples were analyzed using standard microbiological procedures. The Total Aerobic Plate Count (TAPC) range is between 1.1×10^6 - 8.0×10^6 cfu/g. There was no fungal growth in all the samples cultured. The bacterial isolates include *Escherichia coli*, *Staphylococcus aureus*, *Staphylococcus saprophyticus*, *Staphylococcus epidermidis*, and *Bacillus* spp., with *E. coli* being the most prevalent (28.6%), followed by *S. saprophyticus* (23.8%) and *S. aureus* (19.0%), while *S. epidermidis* and *Bacillus* spp. accounted for 14.3% each. The distribution of bacterial isolates varied across academic levels, with *E. coli* and *S. aureus* predominantly found in 100-level students. Poor hair hygiene can facilitate the transmission of pathogenic bacteria. These findings emphasize the need for improved personal hygiene awareness to minimize bacterial contamination. Public health interventions should focus on promoting regular hair washing, avoiding the sharing of hair tools, and maintaining a clean environment to reduce potential health risks associated with bacterial colonization.

Keywords: Female, Hair, Microbial examination, Personal hygiene, Public health, Student

INTRODUCTION

The ubiquity of microorganisms is usually connected to their larger surface area-to-volume ratio. Virtually all existing ecosystems on earth have their autochthonous (resident) and allochthonous (transient) microbial flora. One of such important complex ecosystems is the human body surface. Cells of the resident flora by far outnumber a person's own cells 10 to 1, whereas transient flora colonize humans for hours to weeks

but do not establish themselves permanently. Healthy people normally live an interdependent life with most of the microorganisms that colonize the nonsterile sites of the body, such as the mouth, skin, nose, throat, large intestine, and vagina (Sunarti, 2022).

The resident flora at each body site includes several different types of microorganisms. Some sites are normally colonized by several diverse kinds of different types of microorganisms. Factors such as diet, antibiotic use, sanitary conditions, air pollution, and hygienic habits are the primary influencers of the species composition of man's resident flora. Should there be any temporary disturbance (for example, by washing the skin or using antibiotics), the resident flora usually reestablishes itself promptly. Similarly, rather than causing disease, the resident flora often protects the body against human pathogens (Xu *et al.,* 2024).

The most common bacteria of the skin flora are the Gram-positive, catalase-positive cocci of the genera *Staphylococcus* and *Micrococcus*. Although *S. aureus* can occasionally be found on the skin, it is more commonly found in the nose in those people that carry it in their normal flora (Fayisa and Tuli, 2023).

The human scalp is one such dynamic and important ecosystem that hosts a diverse community of microorganisms, including bacteria, fungi, and yeasts. These microorganisms, collectively known as scalp microflora, coexist in a delicate balance that plays a vital role in maintaining the health of both the scalp and hair (Bhattacharya *et al.,* 2023). The scalp's rich supply of sebaceous glands provides an environment that supports the growth of both beneficial and potentially harmful microbes. This microbial balance is essential for overall scalp health, as disruptions can lead to common disorders such as dandruff, seborrheic dermatitis, and infections (Xu *et al.,* 2024). The scalp microbiome is primarily composed of bacteria and fungi, with each group playing a role in maintaining or disrupting scalp health (Shah *et al.,* 2024). *Staphylococcus epidermidis* is a common beneficial species that helps protect the scalp by preventing the colonization of harmful pathogens. However, *Staphylococcus aureus*, another bacterial species found on the scalp, can cause infections when it overgrows, leading to conditions such as folliculitis, an inflammation of the hair follicles that results in redness, swelling, and pus-filled bumps (Severn and Horswill, 2023). *Cutibacterium acnes* (formerly *Propionibacterium acnes*) contributes to scalp health but can cause scalp acne when it becomes trapped in hair follicles (Lousada *et al.,* 2021).

Fungal species, particularly those of the *Malassezia* genus, are also abundant on the scalp. In small amounts, *Malassezia* is harmless, but when it multiplies excessively, it leads to dandruff and seborrheic dermatitis. Additionally, other fungal species such as *Trichophyton* and *Microsporum* can cause scalp ringworm (tinea capitis), a contagious fungal infection that results in itchy, scaly patches and hair loss (Warsi *et al.,* 2025).

Hair and the scalp are natural reservoirs for microorganisms, many of which are part of the normal microbiota. However, when hygiene practices are neglected, the accumulation of sebum, sweat, and environmental debris on hair can increase microbial load, many of which might be opportunistic pathogens posing potential health risks. Due to hectic schedules owing to academic obligations and lack of awareness among female students, there is a possibility of irregular hair washing, increases the risk of

microbial contamination. Despite these risks, there is limited research on the microbial profile of unwashed hair, particularly among female students. Most existing studies focus on scalp-related conditions or clinical infections, leaving a gap in understanding how microbial contamination varies with hair hygiene practices in everyday settings. Understanding the microbial profile of unwashed hair is essential for addressing potential health risks and promoting good hygiene practices. Therefore, the aim of this study was to examine the microbial load of unwashed hair among female students in Federal University Wukari, Taraba State.

MATERIALS AND METHODS

Ethical Approval and Informed Consent

Ethical approval was sought from the Taraba State Ministry of Health, Jalingo, through the Directorate of Students Affairs, Federal University Wukari, and was granted by the appropriate authority before sample collection. Similarly, consent of the participants was sought as well after clearly explaining the purpose of the research.

Sample Collection and Preparation

Before samples were collected, the media (Nutrient Agar and Sabouraud Dextrose Agar) used were prepared in the laboratory according to the manufacturer's instructions. Using clean scissors, a strand of hair approximately 0.5 cm in diameter was cut off as close to the scalp as possible, ensuring that at least 1 cm of hair growth is present. Hair samples derived from the distal parts (usually representing 10–30% of the total hair length, away from the scalp) (Kerk *et al.,* 2018). The collected samples were labeled and placed into a Ziploc bag and transported to the Microbiology Laboratory Federal University Wukari for microbiological analysis. Two hundred (200) samples were collected across the 100 to 400 levels labeled as 100 A, 100 B, 200 A, 200 B, 300 A, 300 B, 400 A and 400 B (25 samples for each category). Sample size was determined using the formula;

$n = z^2 * p * (1 - p) / d^2$

(where, 'n' = sample size, 'z' = z-score corresponding to the desired confidence level, 'p' = estimated prevalence, and 'd' is the desired margin of error).

Samples of hair shafts were cut using sterilized scissors and chopped into pieces of 5 mm length with the scissors before use (Watanabe *et al.,* 2019). Six test tubes labeled T1 to T6 clearly containing 9 mL of sterile normal saline were set. Then using a sterile pipette, 1 mL of the original sample solution was transferred into the first test tube (T1) and vortexed appropriately. One (1) mL was transferred from T1 to the second test tube (T2), and subsequent dilutions were made till 10^{-6} (Kenaw *et al.,* 2024). One (1) ml of the sixth (10^{-6}) dilution for each sample was evenly spread on nutrient agar (NA) and Sabouraud dextrose agar (SDA) and then incubated at 37^{o}C for 24 hours and 35 ^{o}C for 48 hours for total bacterial fungal count, respectively.

Bacterial Characterization

A distinct colony of bacteria was sub-cultured onto a freshly prepared nutrient agar and incubated at 37 ^{o}C for 24 hours to obtain a pure bacterial colony for further bacterial characterization. The bacterial isolates were then characterized using cultural Gram staining and biochemical tests, mainly coagulase, catalase, oxidase, citrate, indole, triple

sugar iron, and Voges-Proskauer tests (Cheesebrough, 2006; Naureen *et al.,* 2022). Bacteria were identified based on their colony characteristics, including shape, color, texture, size, elevation, margin, and surface appearance, as well as their cultural and biochemical properties (Ogodo *et al.,* 2022).

Fungi Characterization and Identification

Fungi were characterized and identified based on their morphological structure of hyphae (septate or non-septate), colony morphology (texture, color, and growth pattern), size, and cultural characteristics such as colony shape, pigmentation, and growth rate using the Lactophenol Cotton Blue Staining technique described by Cheesebrough (2006).

RESULTS

The mean total aerobic plate count (MTAPC) is presented in Table 1; the results show variations in bacterial load across different samples. The bacterial count ranges from 1.1 × 10^6 cfu/g to 8 × 10^6 cfu/g. Sample 100 A has the highest bacteria load, 8 × 10^6 cfu/g, while the lowest bacterial count is observed in Sample 400 B, 1.1 × 10^6 cfu/g.

Table 1: Total aerobic plate count

Sample (Level)	Mean total aerobic plate count (cfu/g) A	B
100	8.0 x 10^6	6.0 x 10^6
200	4.0 x 10^6	2.9 x 10^6
300	6.0 x 10^6	1.9 x 10^6
400	1.1 x 10^6	4.4 x 10^6

Table 2 presents the frequency and percentage of occurrence of the identified bacterial isolates. A total of 21 bacterial isolates were recovered, with *Escherichia coli* being the most prevalent at 6 (28.6%), followed by *Staphylococcus saprophyticus* at 5 (23.8%). *Staphylococcus aureus* accounted for 4 (19.0%), while both *Staphylococcus epidermidis* and *Bacillus* spp. had an equal occurrence of 3 (14.3%) each.

Table 2: Frequency and percentage of occurrence of bacteria isolates

Isolates	Frequency	Percentage (%)
Escherichia coli	6	28.6
Staphylococcus aureus	4	19.0
Staphylococcus saprophyticus	5	23.8
Staphylococcus epidermidis	3	14.3
Bacillus spp	3	14.3
Total	21	100

Based on colonial morphology and biochemical characterization of bacterial isolates, five bacterial species: *Escherichia coli, Staphylococcus aureus, Staphylococcus saprophyticus, Staphylococcus epidermidis*, and *Bacillus* spp. were identified.

The distribution of bacterial isolates across different academic levels is shown in Figure 1. *Escherichia coli* was detected in 100-level (2 isolates) and 200-level (2 isolates) students, with a lower presence in 400-level (1 isolate) and the control group (1 isolate). *Staphylococcus aureus* was found in 100-level (2 isolates) and 400-level (2 isolates) students but was absent in 200-level, 300-level, and the control group. *Staphylococcus saprophyticus* was most prevalent in 200-level students (4 isolates) and detected in 300-level students (1 isolate). *Staphylococcus epidermidis* was isolated from 200, 300, and 400 level students (1 isolate each). *Bacillus* spp. was found exclusively in 300 level students (3 isolates) and was absent in other groups.

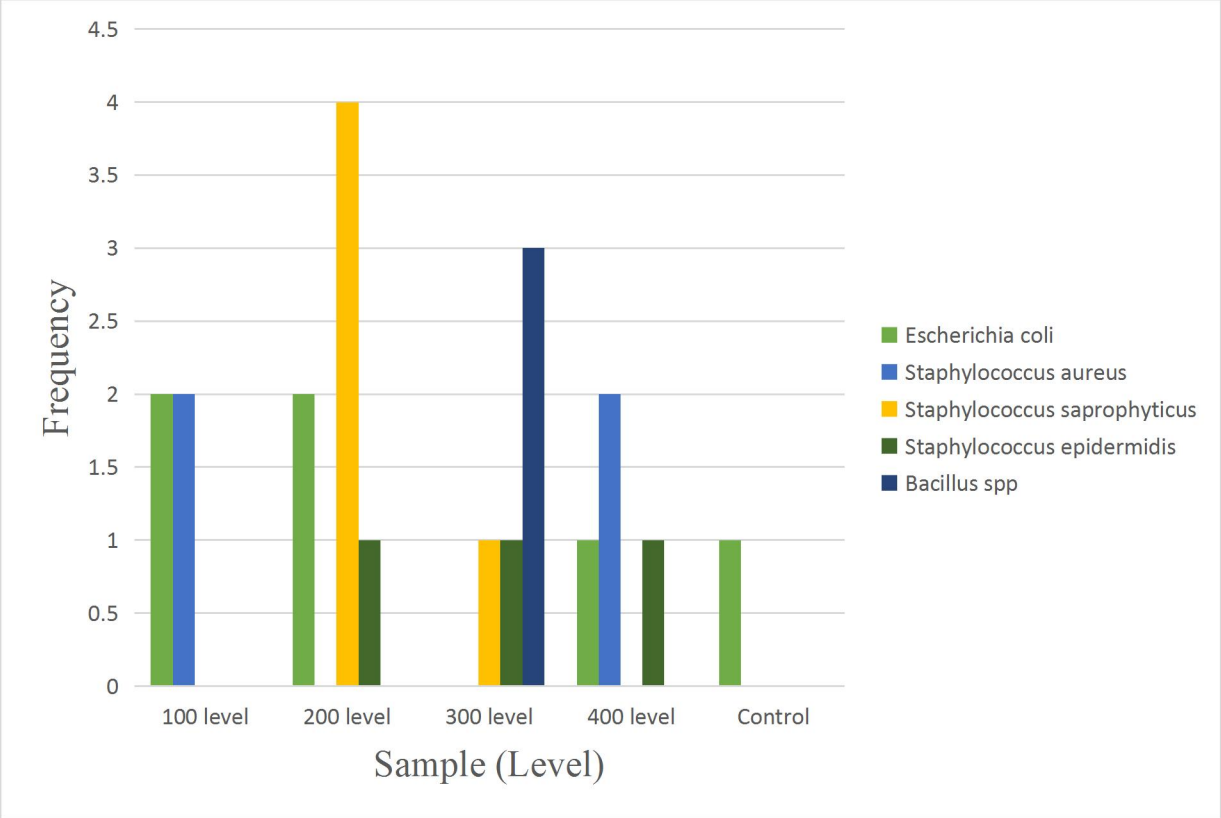

Figure 1: Occurrence of bacteria isolates according to level of study

Across all the samples, no growth was observed on the SDA media.

DISCUSSION

The microbial examination of unwashed hair among female students at Federal University Wukari revealed different bacterial loads across different samples. Sample 100 level A has the highest bacteria loads while the lowest bacterial count is observed in sample 400 B. The higher bacterial load in 100-level students compared to 400-level students can be attributed to differences in hygiene awareness, lifestyle, and environmental exposure. Unlike the first-year students, senior students are not only more familiar with proper hair care routines but also with the operations of the institution, making the latter prioritize academic activities above routine personal

hygiene. Younger students may share hair tools like combs and headscarves, increasing the risk of bacterial transmission.

The bacteria identified in this study include *Escherichia coli, Staphylococcus aureus, Staphylococcus saprophyticus, Staphylococcus epidermidis*, and *Bacillus* spp. These findings align with previous research on bacterial presence in human hair. For instance, similar to Yamada *et al.* (2024), this study identified *Staphylococcus* spp. in hair samples, confirming the common occurrence of this genus in human hair under different conditions. Likewise, Severn and Horswill (2023) also reported *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *Escherichia coli* among the hair of female students. Bhattacharya *et al.* (2023) isolated *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *Escherichia coli* from instruments used in female hairdressers' salons, which are also present in the current study. This similarity suggests that bacterial contamination in human hair may also stem from shared hair tools and equipment. However, the findings in this study are not in agreement with those of Kerk *et al.* (2018), who isolated *Leuconostoc mesenteroides* subsp. *cremoris*, *Kocuria rosea*, *Staphylococcus haemolyticus*, *Kocuria kristinae*, *Stenotrophomonas maltophilia*, and *Micrococcus luteus/lylae* from hair.

Escherichia coli (28.6%) was the predominant bacteria isolate. This does not align with the findings of Yamada *et al.* (2024), who reported *Staphylococcus* spp. as the predominant bacteria in hair. This high occurrence of *Escherichia coli* suggests possible contamination from hand-to-hair contact or exposure to unclean surfaces. One of the primary sources is hand-to-hair contact, especially if individuals do not practice proper hand hygiene. *E. coli* is commonly found in the human gastrointestinal tract, and improper handwashing after using the toilet can lead to its transfer from hands to hair (Townsend and Kalan, 2023). Students frequently touch shared objects such as door handles, desks, mobile phones, and bathroom facilities, which may harbor *E. coli* if proper cleaning is not maintained. According to Watkins and David (2021), the presence of *E. coli* in unwashed hair poses significant health risks, particularly due to its association with gastrointestinal infections, urinary tract infections (UTIs), and skin infections. One of the major concerns is the risk of fecal-oral transmission, where bacteria from contaminated hands or hair can be transferred to the mouth, leading to infections such as diarrhea, food poisoning, and gastroenteritis. If students touch their hair and then eat without washing their hands, they may introduce *E. coli* into their digestive system, increasing the risk of illness.

Staphylococcus saprophyticus (23.8%) was the second most frequent isolate, found in 5 samples. The presence of *Staphylococcus saprophyticus* in unwashed hair among female students can be attributed to several factors. This bacterium is part of the normal flora of human skin, scalp, and mucous membranes (Shah *et al.,* 2024). When hair is not washed regularly, natural oils (sebum), sweat, and dead skin cells accumulate, creating a moist and nutrient-rich environment that promotes bacterial growth. While it is generally less pathogenic than *Staphylococcus aureus*, it can lead to hair and scalp infections such as folliculitis, dermatitis, and minor skin abscesses (Lin *et al.,* 2021). The presence of *Staphylococcus saprophyticus* in unwashed hair among female students suggests poor hygiene practices and potential exposure to environmental contaminants. Given its role in UTIs and skin infections, maintaining proper hair and personal hygiene

is crucial in reducing health risks and preventing bacterial transmission in university settings.

Owing to its opportunistic pathogenic activities, the presence of *Staphylococcus aureus* in unwashed hair among female students is particularly concerning (Polak-Witka *et al.,* 2020). While *S. aureus* is naturally found on human skin, in the nasal passages, and in hair, poor hygiene and unclean environments can promote its overgrowth and increase the risk of infection. The presence of *S. aureus* in unwashed hair poses significant health risks, particularly in individuals with weakened immune systems or underlying skin conditions. One of the most common concerns is the development of skin and scalp infections, such as folliculitis, boils, and impetigo. These infections occur when *S. aureus* enters hair follicles or broken skin, leading to redness, swelling, pus formation, and discomfort (Ito and Amagai, 2022). A major concern is the risk of antibiotic resistance, particularly with strains such as methicillin-resistant *Staphylococcus aureus* (MRSA). MRSA infections are difficult to treat because they do not respond to common antibiotics, making prevention even more critical (Naureen *et al.,* 2022). *Staphylococcus epidermidis* is a common bacterium found on human skin, including the scalp (Lin *et al.,* 2021). In unwashed hair, especially among female students, it can accumulate due to sweat, oil, and environmental exposure. Poor hair hygiene creates a favorable environment for bacterial growth, leading to potential scalp issues such as folliculitis or dandruff. While *S. epidermidis* is generally harmless, excessive buildup can contribute to unpleasant odors, greasy hair, and, in rare cases, opportunistic infections, especially in individuals with weakened immunity (Addissouky, 2025).

Bacillus species are a group of bacteria commonly found in soil, air, water, and on human skin and hair. These bacteria are spore-forming, allowing them to survive harsh conditions, including heat and dryness (Kenaw *et al.,* 2024). The presence of *Bacillus* species in unwashed hair can be attributed to exposure to dust, sweat, and environmental contaminants. Poor hair hygiene can contribute to increased bacterial presence. Frequent hand-to-hair contact can transfer *Bacillus* spp. from contaminated surfaces, such as desks, books, and doorknobs.

The fungal culture yielded no growth. The absence of fungal growth in all samples could be attributed to unconducive conditions for fungal proliferation, possibly due to effective sterilization, inhibitory environmental factors, or the absence of fungal spores in the sample source. Additionally, the presence of antifungal agents or competition from other microorganisms could have suppressed fungal growth, preventing spores from germinating (Su *et al.,* 2023).

CONCLUSION

This study revealed variations in bacterial load across different academic levels, with 100-level students having the highest bacterial count and 400-level students the lowest with no fungi growth. The most prevalent bacterial isolate was *Escherichia coli*, followed by *Staphylococcus saprophyticus*, *Staphylococcus aureus*, *Staphylococcus epidermidis*, and *Bacillus* spp. Poor hair hygiene can facilitate the transmission of pathogenic bacteria like *Escherichia coli* and *Staphylococcus aureus*, increasing the risk of scalp infections and potential systemic infections. The findings suggest that personal hygiene practices, environmental exposure, and hair care habits may influence bacterial presence in unwashed hair. Regular hair hygiene and awareness of bacterial contamination are essential for reducing public health risks.

CONFLICTS OF INTEREST

The authors declare no conflicts of interest

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