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IDENTIFICATION OF MICROBIOTA CAUSING BROMHIDROSIS IN THE AXILLARY

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ABSTRACT

Bromhidrosis is a clinical condition defined by an uncomfortable or unpleasant body odor. Since the apocrine glands are only active during puberty, most bromhidrosis occurs in the apocrine glands in the armpit and occurs when apocrine gland secretions approach the skin's surface, where they undergo various biochemical reactions caused by the presence of microbiota in the axillary skin, resulting in odor in the axilla. This research aims to identify microbiota species in the axilla that can cause bromhidrosis. A laboratory experimental research design with purposive sampling is used in this study. In this study, 60 samples were collected from students aged 15 to 18 years old at a high school in Medan, and the samples were analyzed at the University of North Sumatra Hospital's Microbiology Laboratory. All samples were taken from the right axillary skin swab, a Gram stain was performed, and the identified microbiota isolates were identified. The results of skin smear culture revealed a Gram-positive cocci group in 59 samples (98.3%) and a Gram-positive bacilli group in only one sample (1.7%). The microbiota responsible for bromhidrosis was identified as Staphylococcus hominis spp. hominins (30.4%), Staphylococcus epidermidis (27.8%), Staphylococcus aureus (16.5%), Kocuria kristinae and Staphylococcus haemolyticus (6.3%), Staphylococcus lugdunensis and Staphylococcus saprophyticus. The most common microbiota that causes bromhidrosis in the axilla is Staphylococcis hominis spp. Hominis, Staphylococcus epidermidis, and Staphylococcus aureus.

Keywords: body odor; bromhidrosis; microbiome; staphylococcus

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INTRODUCTION

Body odor is not a life-threatening condition, but its presence can disrupt social relationships between individuals. In the medical world, body odor has several terms such as bromhidrosis or osmidrosis, which are defined as clinical conditions characterized by abnormal and unpleasant body odor (Mogilnicka et al., 2020). The classification of sweat glands into eccrine glands and apocrine glands also divides bromhidrosis based on the type of sweat glands found in humans, namely eccrine bromhidrosis and apocrine bromhidrosis (Baker, 2019).

The division of bromhidrosis types makes it easier to see the area where bromhidrosis occurs and the age group where bromhidrosis appears. Eccrine bromhidrosis often occurs on the soles of the feet and occurs in all age groups. While apocrine bromhidrosis often occurs in the axilla and will only appear after puberty because the apocrine glands are only active after puberty (Wohlrab et al., 2023). Body odor is not produced by the secretion of eccrine or apocrine glands. The odor that appears is caused by several factors such as in the eccrine glands where the odorous volatile metabolites occur due to the softening of keratin due to the action of eccrine gland secretion (Di Cicco et al., 2023).

Certain types of food, medications, and metabolic disorders cause eccrine bromhidrosis. In apocrine bromhidrosis, the odor is also caused by several factors, but the type of microbiota that inhabits the axilla plays an important role in the occurrence of odor (Patel et al., 2019). Each microbiota has its mechanism for changing the odorless secretions of apocrine glands into foul-smelling ones (Townsend & Kalan, 2023). Corynebacteria, Propionibacteria, and Staphylococci are the most common skin microbiota. However, each microbiota has its preferred area type such as the dry area on the upper buttocks, the sebaceous area on the forehead, and the moist area on the axilla and navel (Carmona-Cruz et al., 2022). The moist axillary area is an area dominated by Corynebacterium, Propionibacterium, Micrococcus, and Staphylococcus microbiota (Zhu et al., 2023). Previous research conducted on 24 healthy men to determine the type of axillary odor experienced, whether it was type C (cumin-like, spicy) or type M (milky, skin-based), found that microbiota from the genera Anaerococcus, Corynebacterium, Staphylococcus, Moraxella and Peptoniphilus were found in abundance in both types C and M (Okamoto et al., 2018).

Of the five genera, the most dominant genera are Corynebacterium, Staphylococcus, and Anaerococcus, this seems to reaffirm that Corynebacterium and Staphylococcus are the genera that most often cause axillary odor (Mondal et al., 2023). Previous research on 12 men and women also found Corynebacterium, Staphylococcus, and Propionibacterium as microbiota that cause body odor (Kim et al., 2021). This research is also in line with what was found by other studies where the results stated that Staphylococcus, Propionibacterium, and Corynebacterium were most commonly found in the axillae of adolescents and children (Gehrke et al., 2023).

Previous research also involved 24 men and women aged 25 to 50 years, of Caucasian descent in Geneva, Switzerland stated that Staphylococcus epidermidis had a weak correlation with bromhidrosis while Staphylococcus hominis and Corynebacterium tuberculostearicum had a close relationship with bromhidrosis (Amelia et al., 2023). Furthermore, previous studies have shown that Staphylococcus epidermidis is found in the axillae of children and adolescents, Staphylococcus hominis is found in the neck of children but not in adolescents, and Corynebacterium pseudogenitalium and Corynebacterium tuberculosteriacum are found in the axillae of adolescents (Severn et al., 2022).

The study involved 30 children and adolescents, both male and female, divided into 2 large groups, namely a group of children aged 5-9 years and a group of adolescents aged 15-18 years in the Philippines by collecting samples from several parts of the body such as the neck, axilla, and head (Schäfer et al., 2020). Previous researchers conducted a study on 23 adolescents aged 11-17 years diagnosed with bromhidrosis in Russia and found that Corynebacterium tuberculostearicum and Staphylococcus hominis dominated the microbiota species found in the axilla, with about 82.6% of the microbiota in the axilla dominated by the genus Corynebacterium and Staphylococcus (Lam et al., 2018). Therefore, this study aims to identify the species of microbiota in the axilla that cause bromhidrosis.

METHOD

The study was an experimental laboratory that aimed to identify the microbiota in the axilla that causes bromhidrosis. The sample in this study involved 60 high school students selected using purposive sampling. Inclusion criteria: 1) aged 15-18 years; 2) complaining of axillary odor; and 3) willing to follow the research procedure by signing an informed consent. Exclusion criteria: 1) suffering from skin disease in the axillary area; 2) using deodorant-antiperspirant in the 48 hours before the examination; 3) bathing using antibacterial soap in the 48 hours before the examination; and 4) consuming antibiotics in the last 1 month. Bromhidrosis was measured using a questionnaire, Skin microbiota was measured using gram staining, and Corynebacterium species and Staphylococcus species were measured using Vitec-2 compact. The research data were collected and tabulated. Respondent characteristics data, gram staining examination data, and identification results data are displayed in tabular form. Data were analyzed using descriptive. The study has received approval from the Health Research Ethics Commission, University of North Sumatra (No.1214/KEP/USU/2021).

RESULTS

Table 1 shows that students who complained about the underarm odor they experienced were dominated by male students, 31 people (51.7%), followed by female students, 29 people (48.3%). The most dominant ethnic group is the Javanese with 18 people (30%), followed by the Mandailing ethnic group with 16 people (26.7%), the Minang ethnic group with 10 people (16.7%), the Batak Toba ethnic group with 7 people (11.7%), the Karo ethnic group with 3 people (5%), the Acehnese ethnic group with 2 people (3.3%) and followed by the Ambonese, Betawi, Indian, and Nias ethnic groups with 1 person each (1.7%).

Table 1.
Respondent characteristics (n=60)

Respondent characteristics	f	%
Gender		
Male	31	51,7
Female	29	48,3
Ethnic		
Java	18	30,0
Mandailing	16	26,7
Minang	10	16,7
Batak toba	7	11,7
Karo	3	5,0
Aceh	2	3,3
Ambon	1	1,7
Betawi	1	1,7
India	1	1,7
Nias	1	1,7

Table 2 shows that the Gram staining of the Gram-positive Coccus group was found in 59 people (98.3%) and the Gram-positive Bacil group was found in 1 person (1.7%).

Table 2.
Gram stain distribution

Gram stain	f	%
Gram-positive Coccus	59	98,3
Gram-positive Bacillus	1	1,7

Table 3 shows that the cause of bromhidrosis in respondents was dominated by Staphylococcus hominis spp hominins, totaling 24 people (30.4%), then Staphylococcus epidermidis totaling 22 people (27.8%), Staphylococcus aureus totaling 13 people (16.5%), Staphylococcus haemolyticus and Kocuria kristinae, each totaling 5 people (6.3%), Staphylococcus saprophyticus totaling 2 people (2.5%), Aerococcus viridans, Micrococcus luteus, Staphylococcus lentus, Staphylococcus pseudointermedius, Staphylococcus sciuri and Turicella otitidis, each totaling 1 person (1.3%).

Table 3.
Microbiota species causing bromhidrosis

Bacteria	f	%
Staphylococcus hominis spp hominis	24	30,4
Staphylococcus epidermidis	22	27,8
Staphylococcus aureus	13	16,5
Kocuria kristinae	5	6,3
Staphylococcus haemolyticus	5	6,3
Staphylococcus lugdunensis	2	2,5
Staphylococcus saprophyticus	2	2,5
Aerococcus viridans	1	1,3
Micrococcus luteus	1	1,3
Staphylococcus lentus	1	1,3
Staphylococcus pseudointermedius	1	1,3
Staphylococcus sciuri	1	1,3
Turicella otitidis	1	1,3

DISCUSSION

In this study, it was found that subjects who had complaints of bromhidrosis did not have a significant difference between male and female subjects, where male subjects numbered 51.7% (n=31) while female subjects numbered 48.3% (n=29). In the Philippines, based on an extensive survey conducted, it was identified that bromhidrosis is indeed a significant problem, especially in the social and psychological fields of children and adolescents (Lam et al., 2018). Research in Indonesia mostly focuses on body odor and personal hygiene of adolescents, making it difficult to see the psychological and social impacts of body odor on adolescents (Garbett et al., 2023).

Gram staining is one of several differential staining techniques. The Gram staining technique is the most important and most widely used technique to determine the morphology of the preparation and to determine whether the bacterial culture is included in the Gram-positive and Gram-negative groups (Vijayakumar et al., 2023). The difference between Gram-positive and Gram-negative is based on the differences in cell wall structure between the two types of bacteria (Hardiansyah et al., 2020). Gram-positive will retain the purple color of crystal violet fluid because they have cell walls containing thick peptidoglycan. On the other hand, the Gram-negative cell wall is rich in high lipid content so that when stained, Gram-negative will retain the pink color of the safranin used (Vijayakumar et al., 2023). In this study, it was found that the samples in Gram staining were dominated by Gram-positive cocci in as many as 59 samples (98.3%). These results are not much different from what previous research has shown that moist skin areas such as the axillae are dominated by microbiota from the Staphylococcus and Corynebacteria groups, which are groups of Gram-positive cocci and bacilli (Smythe & Wilkinson, 2023).

The results of this study are also in line with the results obtained in previous research in the Philippines involving 30 children and adolescents aged 15-18 years with samples obtained from the neck, axilla, and head dominated by Gram-positive, both Gram-positive cocci and Gram-positive bacilli (Singh et al., 2023). This study also obtained the same results as in previous studies with the results that coccus and Gram-positive bacilli were the most dominant microbiota (Cao et al., 021). The results of this study are also in line with what was reported that the dominance of Gram-positive bacteria on human skin consists of the genera Staphylococcus spp., Corynebacterium spp., Enhydrobacter spp., Micrococcus spp., Cutibacterium spp., and Veillonella spp. (Boxberger et al., 2021).

There are 3 genera of microbiota found in axillary skin swab cultures including Staphylococcus, Micrococcus, and Aerococcus. In this study, Staphylococcus hominis spp hominis (30.4%) was found to be the most dominant species causing bromhidrosis, followed by Staphylococcus epidermidis (27.8%) and Staphylococcus aureus (16.5%). The results of this study are in line with previous studies which reported that Staphylococcus epidermidis was the most commonly found species in the axillae of children and adolescents in the Philippines (Siciliano et al., 2023). The results of this study are also in line with previous research findings that stated that Staphylococcus hominis has a strong correlation with bromhidrosis, but the study also stated that Staphylococcus epidermidis has a weak correlation with bromhidrosis (Khairani et al., 2023).

The results of this study are also in line with previous studies involving 23 adolescents diagnosed with bromhidrosis in Russia reporting that 39.5% of microbiota causing bromhidrosis came from the Staphylococcus group where the largest species of the group was Staphylococcus hominis (79.2%) followed by Staphylococcus epidermidis (14.8%) and Staphylococcus aureus (9.2%) (Lam et al., 2018). Another study that is in line with this study is a previous study conducted on 53 research subjects that obtained results for the Staphylococcus spp. group (61%) (Thomson et al., 2022).

The microbiota causing bromhidrosis in this study was dominated by the Staphylococcus group. As is known, Staphylococcus can ferment fatty acids and glycerol into 3M2H which then releases several fatty acids such as short-chain fatty acids, propionic acid, and acetic acid which when on the skin surface are directly bound to the ASOB 1 and ASOB 2 enzymes which produce an unpleasant odor (Liu et al., 2024). Staphylococcus epidermidis is assisted by lactic acid and glycerol to make pyruvate capable of degrading amino acids such as leucine, valine, and isoleucine to produce long-chain transaminase amino acids, isovaleric acid, and branched-chain fatty acids which emit a sour odor in the axilla (Frank et al., 2021).

In Staphylococcus hominins, the transport of the compound Cys-Gly-3M3SH occurs by the di/tri peptide transporter PepTSh across the membrane along with the movement of protons. The dipeptidase enzyme then cuts the terminal glycine residue from S-Cys-Gly-3M3SH to produce Cys-(S)-3M3SH (Rudden et al., 2020). Thiols released from Cys-(S)-3M3SH by the enzyme C-S-lyase also release ammonia, pyruvate, and 3M3SH thioalcohol which are odorous and volatile. Ammonia, pyruvate and 3M3SH then diffuse or are carried out of the cell, causing odor in the axilla. The journey of Cys-Gly-3M3SH to produce 3M3SH thioalcohol (Rudden et al., 2020).

CONCLUSION

There was no significant difference based on gender in subjects who complained of body odor in this study. Gram staining was dominated by Gram-positive cocci of 98.3%. There were 3 genera of microbiota found in axillary skin swab cultures including Staphylococcus, Micrococcus, and Aerococcus. The species causing bromhidrosis in this study were dominated by Staphylococcus hominis spp hominis (30.4%), followed by Staphylococcus epidermidis (27.8%) and Staphylococcus aureus (16.5%).

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