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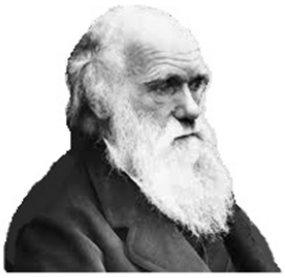

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Microbial Quality, Proximate, and Mineral Composition of Different Species of Freshwater Snails: A Comparative Study on *Achatina fulica* (Bowdich, 1822), *Lanistes libycus* (Morelet, 1848), and *Pomacea canaliculate* (Lamarck, 1822)

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ABSTRACT

This study presents a thorough investigation into the microbial and mineral composition of freshwater snails, specifically *Achatina fulica, Lanistes libycus,* and *Pomacea canaliculata*, employing standard microbiological methods. Microbial assessments revealed significant variation in heterotrophic bacteria counts across the species. For *Achatina fulica*, counts ranged from 5.0×10^7 cfu/g to 4.45×10^9 cfu/g. In *Lanistes libycus*, the counts varied from 3.6×10^5 cfu/g to 2.02×10^7 cfu/g, while *Pomacea canaliculata* exhibited counts from 7.95×10^5 cfu/g to 2.78×10^6 cfu/g. Vibrio counts demonstrated diversity, with *Achatina fulica* showing a range from 1.35×10^3 CFU/g to 1.78×10^4 cfu/g, *Lanistes libycus* ranging from 4.05×10^3 cfu/g to 7.1×10^3 cfu/g, and *Pomacea canaliculata* presenting counts between 1.4×10^3 cfu/g and 8.5×10^3 CFU/g. *Staphylococcus* counts varied among the species: *Achatina fulica* had counts ranging from 2.95×10^4 cfu/g to 2.51×10^5 cfu/g, *Lanistes libycus* ranged from 9.05×10^3 cfu/g to 5.7×10^4 cfu/g, and *Pomacea canaliculata* exhibited counts between 9.0×10^2 cfu/g and 1.98×10^4 cfu/g. Coliform counts also demonstrated a wide range, with the highest counts observed in Achatina fulica (from 7.6×10^4 cfu/g to 2.18×10^6 cfu/g), *Lanistes libycus* ranging from 4.469×10^4 cfu/g to 8.356×10^5 cfu/g, and *Pomacea canaliculata* showing counts between 3.05×10^4 cfu/g and 1.95×10^5 cfu/g. Morphological and biochemical characterization identified thirteen genera of bacteria, including 19.2% *Staphylococcus,* 4.3% *Micrococcus,* 8.5% *Bacillus,* 6.2% *Corynebacterium,* 11.3% *Escherichia coli,* 5.0% *Klebsiella,* 10.6% *Pseudomonas,* 9.2% *Vibrio,* 5.0 *Serratia,* 7.1% *Enterobacter,* 3.6% *Salmonella,* 4.3% *Citrobacter,* and 5.7% *Proteus*. The proximate composition analysis revealed variations in ash content, moisture content, lipid content, crude protein, and carbohydrate levels among

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the species. The mineral analysis included measurements of phosphorus, calcium, and potassium content across the different snail species. These findings enhance our understanding of the microbial ecology, nutritional richness, and mineral composition of freshwater snails. This research lays a foundation for future investigations into the ecological significance of these snails and their potential applications in human nutrition, highlighting their importance in both ecological conservation and dietary considerations.

***Keywords*:** Fresh water snail, Microbial quality, Vibrio species, Proximate and Mineral composition, *Achatina fulica, Lanistes libycus, Pomacea canaliculata*

1. INTRODUCTION

Freshwater ecosystems support a diverse array of life forms that are essential to the health of our planet (Irfan & Alatawi, 2019). While many organisms within these ecosystems receive scholarly attention, freshwater snails are frequently overlooked despite their significant ecological roles. As members of the gastropod mollusk family, these snails have successfully adapted to various freshwater habitats, including rivers, lakes, ponds, and streams (Min et al., 2022).

As vital components of these ecosystems, freshwater snails profoundly influence both biotic and abiotic elements. Their ecological relevance is underscored by their participation in the complex interactions between terrestrial and aquatic systems. Freshwater snails engage with microbial communities, facilitate mineral cycling, and accumulate heavy metals, which can have considerable implications for both the snails and the overall health of the ecosystem, including human populations. The shells of freshwater snails are primarily composed of calcium carbonate ($CaCO_3$) and other minerals such as magnesium carbonate ($MgCO_3$) (Parveen et al., 2020). The mineral composition of snail shells reflects the availability of these minerals in their habitats and can vary in response to environmental stressors such as changes in water quality or temperature (Nkansah et al., 2021). Snails may adjust their shell mineralogy to cope with stress, potentially affecting their fitness and reproductive success (Horton et al., 2019).

In Nigeria, freshwater snails are commonly utilized as a protein-rich alternative in traditional cuisine, as noted by Nkansah et al. (2021) and Pissia et al. (2021). The global recognition of snail meat's nutritional value stems from its high protein content, which includes essential amino acids beneficial for human health (Pissia et al., 2021). The practice of snail farming has gained importance in agriculture, particularly in Nigeria, Africa's most populous nation, where farmers specialize in snail production to meet growing demand.

However, assessing heavy metal levels in snail tissues is crucial, especially in regions like Nigeria where snails are consumed, as these metals can pose significant health risks to humans. Freshwater ecosystems are rich in microorganisms, including bacteria, viruses, fungi, and protists, which are integral to nutrient cycling, organic matter decomposition, and maintaining water quality (Gupta et al., 2016).

Many freshwater snail species function as filter feeders, consuming suspended particles such as algae, bacteria, and detritus (Scherer et al., 2017). This feeding behavior exerts a top-down effect on microbial populations, altering their composition and abundance within their habitats (Scherer et al., 2017).

Examining the microbial community within snails can serve as an indicator of water quality, with shifts in microbial diversity and specific taxa reflecting changes in water chemistry, pollution levels, or other stressors (Horton et al., 2019).

Freshwater snails harbor diverse microorganisms both internally and externally, displaying considerable variability that can differ among species and environmental conditions. Some microbial communities form mutualistic relationships with snails, assisting in digestion or detoxification. Within the snail's digestive tract, these microorganisms play a crucial role in breaking down complex plant materials and cellulose, allowing snails to extract nutrients from their food (Chen et al., 2021). The microbial communities within snails can significantly influence their health and behavior, and snails can transfer these microorganisms to their environments through excretions, potentially impacting the microbial composition of the surrounding ecosystem. This study aims to investigate the microbial, proximate, and mineral composition of various freshwater snail species, contributing to our understanding of their ecological roles and nutritional value.

2. MATERIALS AND METHODS

2. 1. Area of Study/ sample collection

Sixty (60) snail samples of three different species (*Achatina fulica*, *Laniste libycus* and *Pomacea canaliculata*) were sourced randomly from different snail sellers within Obio-Akpor, and Port Harcourt City Local Government Areas of Rivers State and were transported in a sterilized bag to the Microbiology laboratory for analysis.

2. 2. Processing of Samples

All snail meat samples studied were removed from their shell (deshelled) after through washing of the shell with deionized water using a sterile knife, weighted using sterile foil and weighed balance and used for serial dilution.

2. 3. Serial Dilution of Samples

25g of each dissected snail meat sample was weighed into a stomacher bag containing 225 ml of sterile diluent (peptone water), homogenized in a stomacher for 2mins to obtain the stock solution. Ten-fold serial dilution was performed on the samples. 1ml of the aliquot was pipetted into a test-tube containing 9 ml sterile 0.1% peptone water to make 10^{-1} to 10^{-6}. Using a sterile 1ml pipette (syringe), 1 ml of each of the dilution were inoculated on the different agar plates for enumeration and culture.

2. 4. Microbial Analysis

1 ml of diluted sample from the different dilutions were plated onto the solidified Plate Count Agar (PCA), Thiosulfate citrate bile salt (TCBS), Mannitol Salt agar(MSA) and MacConkey agar(MAC) spread on the surfaces of the media using a sterile glass rod. The plates were then incubated at 37 °C for 24hours. Colonies observed were enumerated for total heterotrophic bacteria count, total vibrio count, total staphylococcus count and total coliform count then sub-cultured on nutrient agar plates to purify and stored on agar slants.

2. 5. Purification and storage of Isolates

Streak plating technique was done on nutrient agar plates using for all isolates obtained from the various selective media. Distinct colonies from the differential agar plates were picked and streaked on the solidified nutrient agar medium and incubated for 24 hrs at 37 °C to purify. Purified distinct colony were then picked and introduced into already prepared nutrient agar slants and stored in refrigerator until reuse.

2. 6. Examination of bacteria

All the isolates were identified morphologically with reference to their growth characteristics on appropriate culture media. Materials, reagents, protocols and identification according to (Cheesebrough, 2000) were used to identify distinct colonies on the bacteriological media of sub-cultured isolates.

2. 7. Physiochemical Analysis

Proximate analysis was done on representative samples of the raw snail meat as described by AOAC (1990). The dried sample was ground into powder in an electric blender. 2 grams of the samples were taken for analysis where the moisture, ash and protein, crude fiber were analyzed by the methods described by AOAC (1990). The protein was determined by the Micro-kjeldahl method. Fat content was determined by Bligh and Dyer method.

The mineral content was determined by dissolving the ash obtained from the sample in standard flask with distilled de-ionized water. A few drops of concentrated hydrochloric acid were added. The mixture was warmed and evaporated on Bochy water bath and filtered using a filter paper. The aliquots were taken for estimates of calcium, phosphorus, iron, sodium and potassium following the methods of AOAC (1990)

2. 8. Statistical analyses

Analysis of variance (ANOVA) was used to compare means at $p < 0.05$. This analyses were performed to visualize the association between the microbial loads of the flesh samples of the different snail species using SPSS (Statistical Package for the Social Sciences), also known as IBM SPSS Statistics, is a software package used for the analysis of statistical data.

3. RESULTS AND DISCUSSION

3. 1. Total Heterotrophic Bacteria Counts of Different Snail Species (*Achatina Fulica, Lanistes libycus* and *Pomacea canaliculata*) Studied

The total heterotrophic bacteria count obtained for the different snail species - *Achatina fulica*, *Lanistes libycus*, and *Pomacea canaliculata* - are presented in Figure 1. For *Achatina fulica*, the heterotrophic bacteria count ranged from 5.0×10^7 to 4.45×10^9 cfu/g. In the case of *Lanistes libycus*, the range was from 3.6×10^5 to 2.02×10^7 cfu/g. The counts for *Pomacea canaliculata* varied between a high of 2.78×10^6 cfu/g and a low of 7.95×10^5 cfu/g.

These results highlight the variations in microbial load across the different species, with *Achatina fulica* exhibiting the highest range of heterotrophic bacterial counts, followed by *Lanistes libycus*, while *Pomacea canaliculata* showed relatively lower counts. A comparison

of the viable microbial counts for all species, as depicted in Figure 1, reflects these differences in bacterial contamination levels.

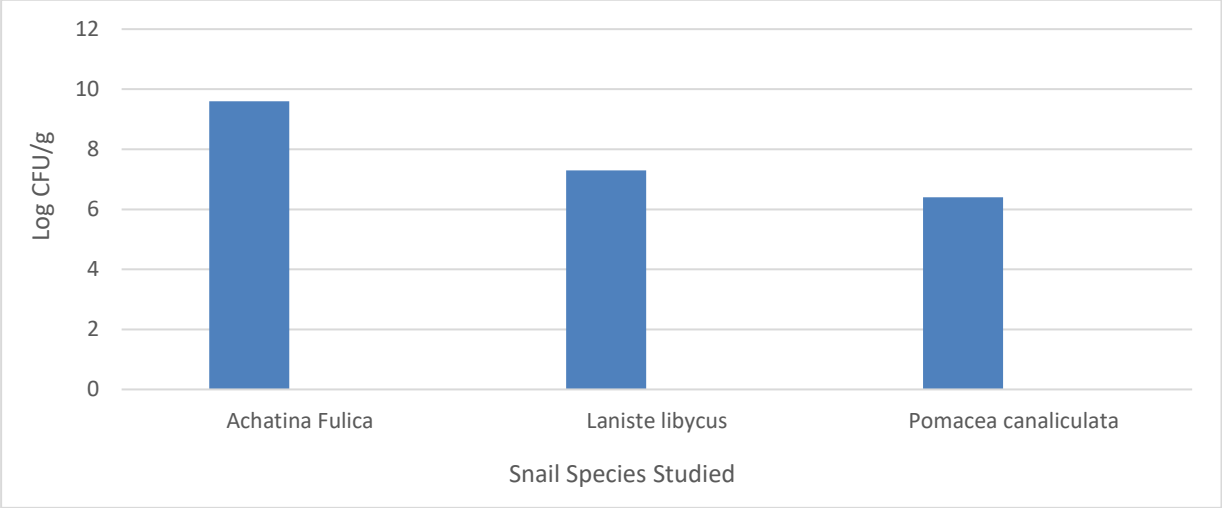

Fig. 1. Mean Total Heterotrophic Bacteria Count Obtained from different Snail Species Studied.

3. 2. Total Vibrio Counts of Different Snail Species (*Achatina Fulica, Lanistes libycus* and *Pomacea canaliculata*) Studied

The *Vibrio* counts obtained for the three snail species - *Achatina fulica*, *Lanistes libycus*, and *Pomacea canaliculata* - are detailed in Figure 2. For *Achatina fulica*, the *Vibrio* counts ranged from 1.35×10^3 CFU/g to 1.78×10^4 CFU/g. The counts for *Lanistes libycus* varied between 4.05×10^3 CFU/g and 7.1×10^3 CFU/g. For *Pomacea canaliculata*, the *Vibrio* counts ranged from 1.4×10^3 CFU/g to 8.5×10^3 CFU/g.

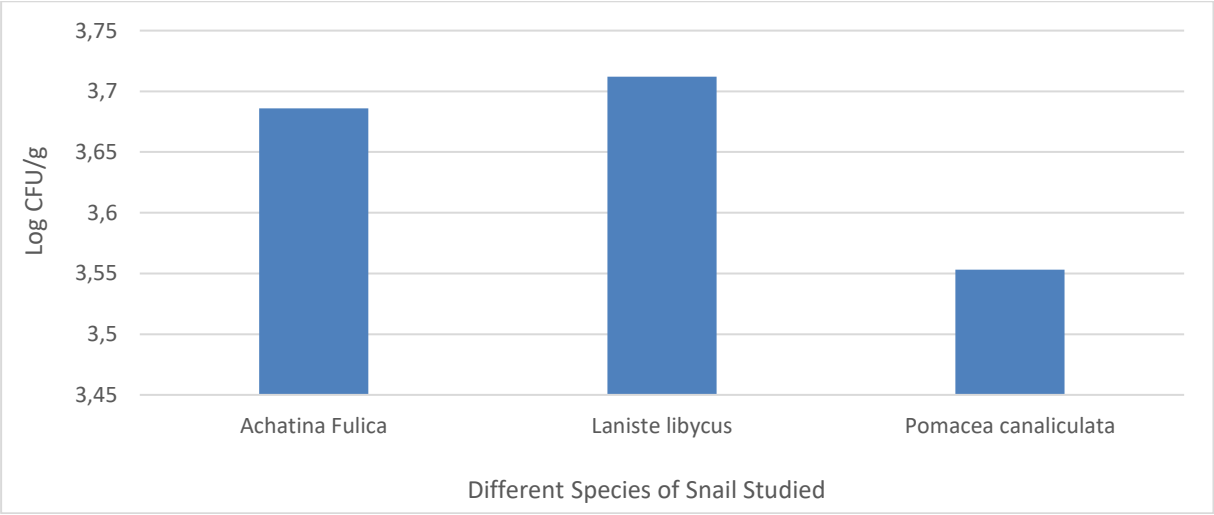

Fig. 2. Mean Vibrio Counts Obtained from different Snail Species Studied.

These results, as illustrated in Figure 2, indicate variability in *Vibrio* contamination among the different snail species, with *Achatina fulica* exhibiting the highest range of counts, followed by *Pomacea canaliculata* and *Lanistes libycus*. The distribution of *Vibrio* bacteria across these species reflects potential differences in their habitats and environmental conditions that may influence microbial contamination levels.

3. 3. Total Staphylococcus Counts of Different Snail Species (*Achatina Fulica, Lanistes libycus* and *Pomacea canaliculata*) Studied

The *Staphylococcus* counts obtained for the three snail species - *Achatina fulica*, *Lanistes libycus*, and *Pomacea canaliculata* - are presented in Figure 3. For *Achatina fulica*, the *Staphylococcus* counts ranged from 2.95×10^4 to 2.51×10^5 CFU/g. In the case of *Lanistes libycus*, the counts ranged from 9.05×10^3 to 5.7×10^4 CFU/g. For *Pomacea canaliculata*, the *Staphylococcus* counts ranged from 9.0×10^2 CFU/g to 1.98×10^4 CFU/g. These results, as depicted in Figure 3, reveal differences in *Staphylococcus* contamination levels among the species, with *Achatina fulica* showing the highest counts, followed by *Lanistes libycus*, while *Pomacea canaliculata* exhibited the lowest range. The variation in *Staphylococcus* counts could be influenced by factors such as handling practices, rearing conditions, and environmental contamination.

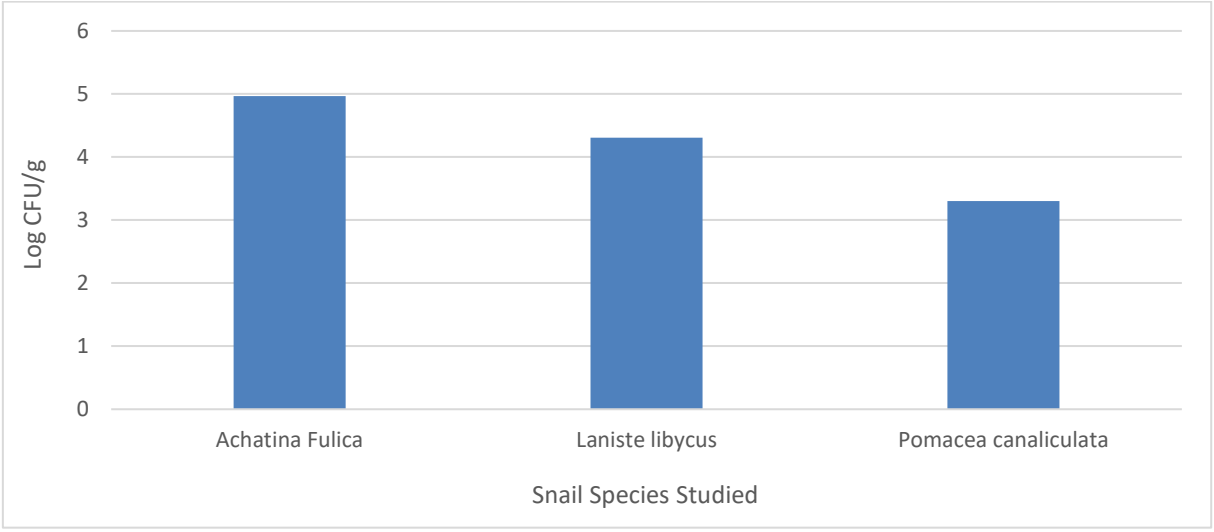

Fig. 3. Mean Staphylococcus Counts Obtained from different Snail Species Studies.

3. 4. Total Coliform Counts of Different Snail Species (*Achatina Fulica, Lanistes libycus* and *Pomacea canaliculata*) Studied

The coliform counts obtained for the three snail species - *Achatina fulica*, *Lanistes libycus*, and *Pomacea canaliculata* - are displayed in Figure 4. For *Achatina fulica*, the coliform counts ranged from 7.6×10^4 to 2.18×10^6 CFU/g. The counts for *Lanistes libycus* varied between 3.05×10^4 CFU/g and 1.8×10^5 CFU/g. For *Pomacea canaliculata*, the coliform counts ranged from 6.0×10^3 CFU/g to 1.58×10^4 CFU/g. These results, as shown in Figure 4, highlight differences in coliform contamination levels across the species. *Achatina fulica* exhibited the

highest coliform counts, followed by *Lanistes libycus*, while *Pomacea canaliculata* had the lowest range. The variation in coliform levels may be associated with factors such as habitat conditions, hygiene practices during handling, and rearing practices that influence the extent of fecal contamination.

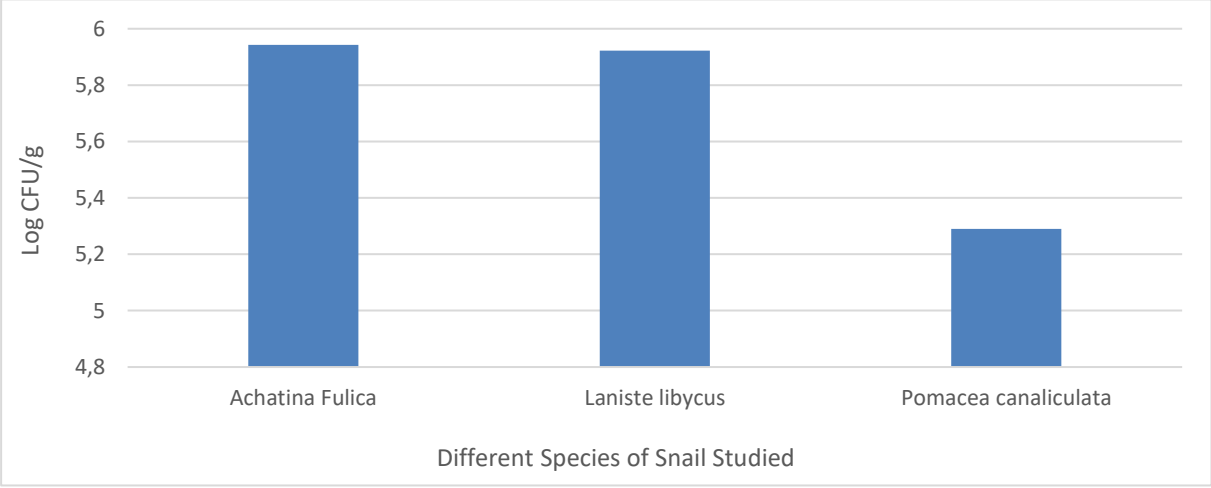

Fig. 4. Mean Total Coliform Counts Among different Snail Species Studied.

Table 1. Frequency of Occurrence of Bacteria Isolated from Different Species of Snail.

Bacteria genera	***Achatina fulica*** **n (%)**	***Lanistes libyeus*** **n (%)**	***Pomacea canaliculata*** **n (%)**	**Total N (%)**
Micrococcus spp.	1 (1.7)	3 (6.9)	2 (5.0)	6 (4.3)
Staphylococcus spp.	9 (15.5)	9 (20.9)	9 (22.5)	27 (19.2)
Bacillus spp.	5 (8.6)	2 (4.7)	5 (12.5)	12 (8.5)
Corynebacterium spp.	4 (6.9)	2 (4.7)	3 (7.5)	9 (6.2)
Escherichia coli	7 (12.1)	4 (9.3)	5 (12.5)	16 (11.3)
Klebsiella spp.	3 (5.2)	2 (4.7)	2 (5.0)	7 (5.0)
Pseudomonas spp.	4 (6.9)	5 (11.6)	6 (15.0)	15 (10.6)
Vibrio spp.	8 (13.7)	3 (6.9)	2 (5.0)	13 (9.2)
Serratia spp.	3 (5.2)	3 (6.9)	1 (2.5)	7 (5.0)
Enterobacter spp.	4 (6.9)	4 (9.3)	2 (5.0)	10 (7.1)

Salmonella spp.	3 (5.2)	2 (4.7)	0	5 (3.6)
Citrobacter spp.	3 (5.2)	2 (4.7)	1 (2.5)	6 (4.3)
Proteus spp.	4 (6.9)	2 (4.7)	2 (5.0)	8 (5.7)
Total	58 (100)	43 (100)	40	141 (100)

Table 2. Proximate and Mineral Composition of *Achatina fulica* and *Pomacea canaliculata* Studied.

Sample Code	Ash (%)	Moisture Content (%)	Lipid (%)	Crude Protein (%)	Crude Fibre (%)	Carbohydrate (%)	Phosphorus (mg/Kg)	Calcium (mg/Kg)	Potassium (mg/Kg)
Achatina fulica	19.11	1.08	1.15	8.70	0.93	62.03	1.41	27.98	0.82
Pomacea canaliculata	18.39	2.36	1.45	4.91	1.09	71.80	13.67	27.89	3.66
Lanistes libycus	16.2	1.47	1.64	3.78	1.24	56.42	6.62	23.11	2.54

4. DISCUSSION

Snails are widely consumed as a protein source around the world. Beyond providing protein, they are also considered rich in essential minerals such as iron, calcium, and phosphorus, and are reported to contain nearly all the amino acids required by humans. However, the bacteriological quality of snail meat can be compromised by poor farming practices and inadequate personal hygiene during handling. This study aimed to investigate the microbial contamination, proximate composition, and mineral content of three freshwater snail species: *Achatina fulica*, *Lanistes libycus*, and *Pomacea canaliculata*. The total heterotrophic bacterial count (THBC) is commonly used to assess the quality, shelf life, and potential post-harvest contamination of food products (Mouafo et al., 2020).

The results revealed that meat from all three snail species was significantly contaminated, with THBCs ranging from 5.0×10^7 to 4.45×10^9 cfu/g for *Achatina fulica*, 3.6×10^5 to 2.02×10^7 cfu/g for *Lanistes libycus*, and 7.95×10^5 to 2.78×10^6 cfu/g for *Pomacea canaliculata*, as illustrated in Figure 1. The high heterotrophic counts observed across all species indicated a statistically significant difference in the mean THBCs among the three snail species ($p < 0.05$). These findings are consistent with previous studies reporting high bacterial loads in snails. For instance, Temelli et al. (2006) recorded a THBC of 6.85 Log cfu/g in *Helix aspersa*, while

Adegoke et al. (2010) observed 8.16 Log cfu/g in *A. fulica*. Similarly, Ebenso et al. (2012) reported THBCs ranging from 7.39 to 8.19 Log cfu/g.Nyoagbe et al. (2016) reported heterotrophic bacterial counts of 7.87 Log cfu/g for *Achatina achatina* and 7.01 Log cfu/g for *Achatina marginata*. In this study, the total heterotrophic bacterial counts across all snail samples ranged from 3.6×10^5 to 4.45×10^9 cfu/g among the three species examined. The highest counts were found in *Achatina fulica*, followed by *Lanistes libycus* and *Pomacea canaliculata*.

All snail samples, regardless of species, exhibited heterotrophic bacterial counts exceeding the recommended level of 5.7 Log cfu/g, as specified by the European Commission (EC, 2005). Although these counts indicate microbial contamination above the recommended safety threshold, it does not necessarily imply that the snails are unsuitable for human consumption. This is because the snail meat would typically undergo various treatments, such as heating, which could significantly reduce the bacterial load before consumption.The *Vibrio* counts obtained for the snail samples varied across species, with *Achatina fulica* ranging from 1.35×10^3 to 1.78×10^4 cfu/g, *Lanistes libycus* from 4.05×10^3 to 7.1×10^3 cfu/g, and *Pomacea canaliculata* from 3.85×10^3 to 8.5×10^3 cfu/g, as illustrated in Figure 2, which shows the mean Log_{10} cfu/g values.Freshwater snails can serve as carriers or reservoirs for *Vibrio* species, potentially transmitting these bacteria to other organisms, including humans, through direct contact, consumption of contaminated water, or ingestion of snail meat or related products. The detection of *Vibrio* spp. in these freshwater snails suggests suboptimal water quality, as these bacteria typically flourish in warm, nutrient-rich conditions. This finding may signal underlying water pollution issues, emphasizing the need for enhanced water management practices to preserve a healthy aquatic ecosystem.

The *Staphylococcus* counts observed in the snail samples varied across species, with *Achatina fulica* ranging from 2.95×10^4 to 2.51×10^5 cfu/g, *Lanistes libycus* from 9.05×10^3 to 5.7×10^4 cfu/g, and *Pomacea canaliculata* from 9.0×10^2 to 1.98×10^4 cfu/g, as shown in Figure 3, which presents the mean Log10 cfu/g values. The frequent handling of snails during rearing may contribute to contamination with *Staphylococcus* spp., as suggested by Adagbada et al. (2011) and Bukola et al. (2011), who also detected *Staphylococcus aureus* in snail meat. Temelli et al. (2006) found 3.96 Log cfu/g of *Staphylococcus* spp. in snail meat. Among the species analyzed, *Lanistes libycus* exhibited the highest *Staphylococcus* count, while *Pomacea canaliculata* had the lowest. These differences could be attributed to variations in feeding practices during rearing, as observed by Barimah (2013) in snails reared in Ghana. All raw snail samples had *Staphylococcus* levels exceeding the acceptable limit of 2 Log cfu/g set by the European Commission (EC, 2005). Although *Staphylococcus* spp. are heat-sensitive and can be reduced by cooking, the presence of heat-stable enterotoxins (Brooks et al., 2004) poses a risk of foodborne intoxication, as noted by Diasso (2018).

The coliform counts also indicated contamination, with *Achatina fulica* ranging from 7.6×104 to 2.18×10^6 cfu/g, *Lanistes libycus* from 4.4×10^4 to 8.35×10^5 cfu/g, and *Pomacea canaliculata* from 3.05×10^4 to 1.95×10^5 cfu/g, as shown in Figure 4. These counts surpassed the recommended limits, indicating potential health risks. High coliform levels may reflect fecal contamination in the snails' habitat, potentially due to inadequate removal of feces and dead snails during rearing, creating a favorable environment for pathogenic growth (Ekundayo and Fagade, 2005; Nyoagbe et al., 2016). The findings align with those of Daminabo and Kpornmon (2023), who reported heterotrophic counts ranging from 3.7×10^6 to 8.7×10^6 cfu/g, and coliform counts from 0.6×10^4 to 4.6×10^4 cfu/g. Similarly, Egwu et al. (2021) observed total heterotrophic counts between 2.1×10^5 and 8.1×10^5 cfu/g, *Staphylococcus* counts ranging from 8.0×10^4 to

1.01×10^6 cfu/g, and coliform counts of 1.0×10^5 to 1.1×10^6 cfu/g. Adebayo-Tayo reported higher total heterotrophic counts, ranging from 4.0×10^7 to 1.42×10^8 cfu/g, and coliform counts from 2.21×10^7 to 6.4×10^7 cfu/g.

Contamination sources in snails may include environmental factors such as exposure to air, dust, and insects, rearing conditions, and the quality of feed and water used. Studies by Danilova and Danilova (2019) identified exposed pens, cleaning practices, and proximity to roadways as major contributors to microbial contamination. Additionally, variations in microbial counts may be influenced by temperature, handling practices, and storage conditions in markets. The microbial levels observed in this study exceeded the safety limits recommended by regulatory bodies such as the World Health Organization (WHO), which advises that total bacterial counts should not exceed 5×10^5 cfu/g. The counts were also higher than the standards set by the International Commission on Microbiological Specifications for Foods (ICMSF, 1982) and the U.S. Food and Drug Administration (USFDA, 1991), which recommend limits of 1×10^5 cfu/g for bacteria and fungi, and 1×10^2 cfu/g for coliforms.

A total of thirteen bacterial genera were isolated from all the snail samples analyzed, including *Staphylococcus*, *Micrococcus*, *Bacillus*, *Corynebacterium*, *Escherichia coli*, *Klebsiella*, *Pseudomonas*, *Vibrio*, *Serratia*, *Enterobacter*, *Salmonella*, *Citrobacter*, and *Proteus*. However, the distribution and diversity of these bacteria varied across the snail species studied (Table 1). The overall frequency of occurrence of the bacterial isolates was as follows: *Staphylococcus* (19.2%), *Micrococcus* (4.3%), *Bacillus* spp. (8.5%), *Corynebacterium* spp. (6.2%), *Escherichia coli* (11.3%), *Klebsiella* spp. (5.0%), *Pseudomonas* spp. (15.0%), *Vibrio* (9.2%), *Serratia* spp. (5.0%), *Enterobacter* spp. (7.1%), *Salmonella* (3.6%), *Citrobacter* spp. (4.3%), and *Proteus* spp. (5.7%). These findings are consistent with previous reports by Adebayo-Tayo et al. (2011) and Daminabo and Kpornmon (2023), who identified similar bacterial species in snail samples.

The proximate composition of *Lanistes libycus*, *Achatina fulica*, and *Pomacea canaliculata* is summarized in Table 2. The ash content was 16.2%, 19.11%, and 18.39%, respectively, while moisture content was highest in *Pomacea canaliculata* (2.36%) compared to *Achatina fulica* (1.08%) and *Lanistes libycus* (1.47%). *Achatina fulica* exhibited the highest protein content (8.70%), followed by *Pomacea canaliculata* (4.91%) and *Lanistes libycus* (3.78%). The crude fiber content was 0.93%, 1.09%, and 1.24%, while carbohydrate levels were 56.42%, 62.03%, and 71.80% for *Lanistes libycus*, *Achatina fulica*, and *Pomacea canaliculata*, respectively. These variations may be due to differences in rearing conditions, feed quality, and mineral intake from soil and food sources, as indicated by Fagbuaro (2015). The results align with studies by Fagbuaro et al. (2006) and Marcel et al. (2020), although slightly lower than the values reported by Adebayo-Tayo et al. (2011) for snails from the Niger Delta creek in Nigeria.

Regarding mineral content, *Achatina fulica*, *Pomacea canaliculata*, and *Lanistes libycus* exhibited the following levels of phosphorus, calcium, and potassium: 1.41 mg/kg, 27.98 mg/kg, 0.82 mg/kg for *Achatina fulica*; 13.67 mg/kg, 27.89 mg/kg, 3.66 mg/kg for *Pomacea canaliculata*; and 6.62 mg/kg, 23.11 mg/kg, 2.5 mg/kg for *Lanistes libycus* (Table 2). These values were higher than those reported by Adebayo-Tayo et al. (2011), who found potassium, calcium, and phosphorus levels of 0.412%, 0.198% 0.198% and 0.314%. respectively. The observed differences in mineral content across species may be due to their distinct dietary needs, habitats, life stages, and health factors. The presence of essential minerals such as calcium, potassium, and phosphorus in freshwater snails makes them valuable sources of

nutrients that contribute to protein synthesis, nucleic acid formation, and other cellular functions. These minerals are crucial for healthy growth, muscle and nerve function, and metabolism, highlighting the potential nutritional benefits of incorporating snails into human and animal diets, particularly for growing individuals.

5. CONCLUSION

The investigation into the microbial, mineral, and nutritional composition of *Achatina fulica*, *Lanistes libycus*, and *Pomacea canaliculata* has yielded comprehensive insights into both the ecological and nutritional aspects of these freshwater snail species. The findings reveal that while these snails possess significant nutritional benefits, including valuable protein content and essential minerals like calcium, potassium, and phosphorus, they also harbor diverse microbial communities, some of which exceed recommended safety thresholds for human consumption.

The presence of potentially pathogenic microorganisms underscores the need for thorough safety assessments, including proper handling, processing, and cooking methods to mitigate health risks. These findings indicate the potential of freshwater snails as a dietary protein source, provided stringent safety measures are observed. This study establishes a foundation for future research into the ecological and nutritional roles of freshwater snails. It emphasizes the need for continued investigations into their environmental significance, the impacts of habitat conditions on their microbial quality, and their potential contributions to sustainable food systems. The results are also valuable for ecological conservation efforts and public health considerations, offering insights that could guide both dietary strategies and environmental management practices.

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References

[1] Adebayo-Tayo, B.C., Onilude, A.A. & Etuk F.I. (2011). Studies on Microbiological, Proximate Mineral and Heavy Metal Composition of Freshwater Snails from Niger Delta Creek in Nigeria. *AU J.T.* 14(4) (2011) 290-298

[2] Chen, L., Li, S., Xiao, Q. *et al.* Composition and diversity of gut microbiota in *Pomacea canaliculate* in sexes and between developmental stages. *BMC Microbiol* 21(4) (2021) 200

[3] Abuoa, F.. Proximate analysis and mineral contents of two Giant African snails consumed in Ivory Coast. *Tropical Science, England.* 35 (1995) 220-222

[4] AOAC, (Association of Official Analytical Chemists). Official Methods of Analysis, 15th Ed. Association of Official Analytical Chemists, Washington DC. (1990)

[5] Diasso D. Aliments de rue prépares et vendus à « ciel ouvert. *Food Nutr.* 14(5) (2018) 2-10

[6] Ekundayo E.O., Fagade S.O. Microbial flora associated with soils of edible snail farms in Southern Nigeria. *Niger. J. Soil Sci.* 15 (2005) 7565-7580

[7] Nyoagbe L.A., Appiah V., Nketsia-Tabiri J., Larbi D., Adjei I. Evaluation of African giant snails (Achatina and Archachatina) obtained from markets (wild) and breeding farms. *Afr. J. Food Sci. Res.* 10(7) (2016) 94-104

[8] Barimah M.N.Y. University of Ghana; Ghana. Microbiological Quality of Edible Land Snails from Selected Markets in Ghana. Master Thesis. (2013) p. 110

[9] European Commission Regulation (EC) 2073/2005 Microbiological criteria for foodstuffs. *Off. J. Eur. Union.* (2005) 338: 1-26

[10] Brooks G.F., Butel J.S., Morse S.A. In: Jawetz, Melnick & Adelberg's Medical Microbiology. 23rd Edition. Brooks G.F., Butel J.S., Morse S.A., editors. Vol. 223. McGraw-Hill Companies; New York. The staphylococci; (2004) 225-227

[11] Bukola C.A., Abiodun A.O., Florence I.E. Studies on microbiological, proximate mineral and heavy metal composition of freshwater snails from Niger Delta Creek in Nigeria. Technical Report. *AU J.T.* 14(4) (2011) 290-298

[12] Adagbada A.O., Orok A.B., Adesida S.A. The prevalence and antibiotic susceptibility pattern of Entero-pathogens isolated from land sails eaten in Cross-River and Akwa-Ibom States South-Southern Nigeria. *Asian J. Pharmaceut. Health Sci.* 1(3) (2011) 123-127

[13] Temelli S., Dokuzlu C., Kurtulus C., Sen M. Determination of microbiological contamination sources during frozen snail meat processing stages. *Food Control.* 17 (2016) 22-29

[14] European Commission Regulation (EC) 2073/2005 Microbiological criteria for foodstuffs. *Off. J. Eur. Union.* 2005; 338: 1-26

[15] Mouafo H.T., Baomog A.M.B., Adjele J.J.B., Sokamte A.T., Mbawala A., Ndjouenkeu R. Microbial profile of fresh beef sold in the markets of Ngaoundéré Cameroon, and antiadhesive activity of a biosurfactant against selected bacterial pathogens. *J. Food Qual.* (2020) 1-10

[16] Danilova I., Danilova T. The influence of the environment on microbiological parameters of snails' meat. *Ukr. J. Ecol.* 9(3) (2019) 37–40.

[17] Temelli S., Dokuzlu C., Kurtulus C., Sen M. Determination of microbiological contamination sources during frozen snail meat processing stages. *Food Control.* 17(2006) 22-29

[18] Ebenso I., Ekwere A., Akpan B., Okon B., Inyang U., Ebenso G. Occurrence of Salmonella, Vibro and E. coli in edible land snails in Niger Delta, Nigeria. *J. Microbiol. Biotechnol. Food Sci.* 2(2) (2012) 610-618

[19] Nyoagbe L.A., Appiah V., Nketsia-Tabiri J., Larbi D., Adjei I. Evaluation of African giant snails (*Achatina* and *Archachatina*) obtained from markets (wild) and breeding farms. *Afr. J. Food Sci. Res.* 10(7) (2016) 94-104

[20] Adegoke A.A., Adebayo-Tayo C.B., Inyang U.C., Aiyegoro A.O., Komolfe O.A. Snails as meat source; epidemiological and nutritive perspective. *J. Microbiol. Antimicrob.* 2(1) (2010) 1-5

[21] Ejidike, B.N., Oyekunle, S.K.. Survival and growth performance of African land snail Juvenile reared on different soil types. *J. Molluscan Res.* 5 (2019) 25-30

[22] Fagbuaro, S.S.,Carcass characteristics, proximate composition and mineral analysis of African giant snail (Archachantina marginata). *ECORFAN J. Mexico* 6 (14) (2015) 1162-1169

[23] Marcel, K.N., Rosemonde, Y.A., Patricia, K.A., Alexandre, Z.B.F.G., Ambroise, A.N., Ernest, A.K.. Evaluation of the nutritional potential of snail (Achatina spp.) meat in Rat. *Eur. Sci. J.* 16 (12) (2020) 111-121

[24] Fagbuaro, O., Oso, J.A., Edward, J.B., Ogunleye, R.F. Nutritional status of four species of giant land snails in Nigeria. J. Zhejiang Univ. Sci. B. Sep. 7 (9) (2006) 686–689.

[25] Daminabo V. & Kpormon L.B. . Evaluation of Bacteriological Quality and Proximate Composition of African Giant Snail (Archachatina Marginata) Sold in Port Harcourt, *Nigeria. African Journal of Advanced Sciences & Technology Research,* 11(1) (2023)1-11.

[26] Egwu, O. C., Jennifer, U. O., Goretti, A. C. M., Uchechukwu, O. & Marksydney, E. U. Toxic Elements and Microbial Loads in African Giant Land Snail (Archachatina margenata) reared with Waste Contaminated Soil. Applied Research in Scince and Technology, 1(1) (2021) 26-35.

[27] Gupta A, Gupta R, Singh RL. Microbes and Environment. Principles and Applications of Environmental Biotechnology for a Sustainable Future. 15 (2016) 43–84.

[28] Horton DJ, Theis KR, Uzarski DG, Learman DR. Microbial community structure and microbial networks correspond to nutrient gradients within coastal wetlands of the Laurentian Great Lakes. *FEMS Microbiol Ecol.* (2019) 95(4): fiz033

[29] International Commission of Microbiological Specification for Food (ICMSF). Microorganisms in foods. Vol. 1: Their significance and methods of enumeration. 2nd ed., F.S. Thatcher and D.S. Clark (eds.). University of Toronto Press, Toronto, ON, Canada, 9 (1982) 19-30.

[30] Irfan, S. and Alatawi, A. Aquatic Ecosystem and Biodiversity: A Review. *Open Journal of Ecology*, 9 (2019) 1-13

[31] Min, F.; Wang, J.; Liu, X.; Yuan, Y.; Guo, Y.; Zhu, K.; Chai, Z.; Zhang, Y.; Li, S. Environmental Factors Affecting Freshwater Snail Intermediate Hosts in Shenzhen and Adjacent Region, South China. *Trop. Med. Infect. Dis.* 7 (2022) 426

[32] Nkansah MA, Agyei EA, Opoku F. Mineral and proximate composition of the meat and shell of three snail species. *Heliyon* (2021), 7(10): e08149

[33] Parveen S, Chakraborty A, Chanda DK, Pramanik S, Barik A, Aditya G. Microstructure Analysis and Chemical and Mechanical Characterization of the Shells of Three Freshwater Snails. *ACS Omega* 5(40) (2020) 25757-25771

[34] Pissia, M.A., Matsakidou A. & Kiosseoglou, V. Raw materials from snails for food preparation. *Future Foods* 3 (2021) 100034

[35] Scherer C, Brennholt N, Reifferscheid G, Wagner M. Feeding type and development drive the ingestion of micro plastics by freshwater invertebrates. *Sci Rep.* 7(1) (2017) 17006

[36] United States Food and Drug Administration (USFDA) Sanitation of shellfish growing areas. Seafood safety. F.E. Ahmed (ed.). National Academic Press, Washington, DC, USA. (1991)

[37] WHO/FAO. Codex alimentarius commission. Food additives and contaminants. Joint FAO/WHO Food Standards Programme, ALINORM 10/12A. (2001)