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Research Article

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Nutritional and Microbial evaluation of Composite jam from apple *(Malus domestica* Borkh), Pineapple (*Ananas comosus*) and Watermelon (*Citrullus lanatus*)

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Abstract

Jam production serves as an effective strategy for ensuring the year-round availability of seasonal fruits and reducing post-harvest losses. This study aimed at developing acceptable jam formulations using blends of apple, pineapple, and watermelon. Fresh fruits were washed, peeled, and pulped, after which single-fruit and mixed-fruit formulations were prepared using standard jam-processing techniques. Sensory evaluation was carried out using a nine-point hedonic scale. Proximate and mineral compositions were determined using standard AOAC methods. Microbial load was assessed by plating on appropriate media, while bacterial isolates were identified using molecular techniques. Antibiotic susceptibility patterns of the isolates were evaluated using the disc diffusion method. The sensory evaluation showed clear variations in quality among samples, with mixed-fruit formulations outperforming single-fruit jams. The Apple–Pineapple–Watermelon Jam (APWJ) achieved the highest overall acceptability score of 9.80±0.13. Microbial counts of the jam samples ranged up to 4×10^3 CFU/g. All samples harbored bacteria identified as *Enterococcus faecium, Staphylococcus aureus, Bacillus cereus, Bacillus subtilis* and *Escherichia coli*. Gram positive isolates were generally highly susceptible to the antibiotics tested, while *E. coli* exhibited moderate variation in response. The proximate composition of the blended fruits and their jams ranged between 9.88–86.45% (moisture), 0.00–2.10% (ash), 0.33–1.69% (crude fat), 0.21–1.01% (crude fibre), 0.56–6.92% (protein), and 11.00–87.00% (carbohydrate). Composite jams (APJ and APWJ) contained higher mineral values across most parameters. Mineral contents of blended fruits, mixed formulations, and single-fruit jams ranged from 0.33–0.64 mg/100 g (iron), 4.54–25.40 mg/100 g (sodium), 8.41–60.33 mg/100 g (potassium), 1.02–1.93 mg/100 g (calcium), and 0.97–2.81 mg/100 g (magnesium), indicating that these products meaningfully contribute to dietary mineral intake.

The findings demonstrate that composite fruit jams are nutritionally superior, microbiologically safe, and sensory-acceptable value-added products. Their production provides a promising avenue for reducing fruit wastage, extending shelf life, and supplying affordable nutritious foods year-round. This study supports the attainment of SDG 2 (Zero Hunger) and SDG 12 (Responsible Consumption and Production).

Keywords: Apple Jam; Pineapple jam; Watermelon jam; Composite, Nutritional properties; Sensory analysis.

Introduction

Fresh fruits consumption is very crucial to human health as they contain vitamins, minerals, sugars and beneficial organic compounds (Slavin and Lloyed, 2012; Aili *et al*., 2021), but fruits of all kind are not available year round because they are known to be highly perishable due to their high moisture content and readily available nutrients which support the viability of spoilage microorganisms (Arah *et al*., 2016; Mafe *et al*., 2024). Most fruits are abundant during their season but become scarce during their off seasons. Unless fruits are handled properly during their seasons, they result in large economic losses to farmers and vendors. The loss of fruits yearly has contributed to the increased poverty rate and malnutrition in so many developing countries. According to FAO (2011), food/fruit waste and loss is a decrease in the quantity of edible food within food systems and this means that any food that was cultivated for human consumption, but not consumed regardless of its alternative use, is considered food loss or waste. The increasing human population coupled with the advancement of mechanized farming, fruit production has increased, as has fruit waste, according to FAO (2022) approximately 40 –60 % of food produced for human consumption is either lost or wasted each year globally. Fruit loss due to heavy harvest and over availability are very critical challenges (Kor *et al*., 2022; Amol *et al*., 2023). Each year, Nigeria wastes and loses over 39% of its total food production mostly fruits, ranking the country 96th out of 113 on the Global Food Security Index (World Bank, 2020). It is important to have a wide variety of fresh or processed fruits throughout the year if poverty and malnutrition are to be tackled effectively especially in underdeveloped and developing countries like Nigeria. To check wastage in fruits, many conventional and modern biotechnological methods have been used, such as pickling (Ayeni *et al*., 2019), canning, pasteurization, irradiation, addition of preservative coatings or chemicals and jam production (Larousee and Brown, 1997; Shephard, 2001; Kor *et al*., 2022; Rajabhuvaneswari *et al*., 2022). Jam production has been one of the methods used in the preservation of fruits, especially the ones with high glycemic index. Jam is a mixture of fruit boiled with sugar and allowed to congeal (Dianne, 2011). Fruits such as lemon, apple, cranberries, bananas, pineapple, and orange have been used for producing jam. Jam is often spread on bread, biscuit and ice cream. Jam is a type of fruit preservation which can be canned, sealed for long term storage. Jam making involves the disruption of the fruit's tissues followed by heating with addition of water and sugar to activate its pectin before being put into containers. The sugar and the fruits used in producing jam vary according to the type of fruit and its ripeness, when the temperature of the mixture reaches 104^0C the acid and the pectin react with sugar (Awolu *et al.*, 2017). Normally, jam preparation requires the addition of commercial or natural pectin as a gelling agent (Awolu *et al*., 2016). The uses of ingredients and how the jams are prepared determine the type of jam produced. Jams are one of the most popular products because of their low cost, availability and organoleptic properties (Eke and Owuno, 2013). In this study, apple, pineapple and watermelon fruits being the most nutritious fruits among the health-conscious individuals were processed into Jam and their nutritional and microbial properties were evaluated.

Materials and Methods

Sample Preparation and Collection

Fresh watermelon (*Citrullus lanatus*), red apple (*Malus domestica*), and pineapple (*Ananas comosus*) fruits were procured from *Waso* market within Ogbomoso metropolis and were conveyed to the laboratory in sterile polythene bags. The samples were sorted and washed with sterile distilled water to remove adhering soil and debris, after which the samples were peeled manually with sterile stainless steel knife and sliced after the removal of the seeds.

Preparation of the Jam

Two hundred gram of each sample was blended separately for 4minutes using a sterilized electric blender and kept in sterile transparent jars at room temperature (±28 ^{o}C). Sugar (50g), lime juice (10ml), and salt (0.05g) were added to each of the pulp to enhance gel formation and the mixture was left at room temperature (±28 ^{o}C) for 20minutes, then, subsequently cooked slowly with infrequent stirring for 15 minutes to enhance homogenization of the mixture. The jam was poured into a sterilized jar and allowed to cool at a room temperature (±28 ^{o}C) for further analysis.

Organoleptic test of the jam samples

The sensory evaluation of the jam samples along with bread serving as a carrier were evaluated by 20-membered trained panelists using 9-point hedonic scale of 9 (like extremely) to 1 (dislike extremely) for appearance, taste, texture, and overall acceptability.

Microbial Evaluation of the Jam Samples

One gram of each sample was measured into 9 mL of sterilized peptone water and homogenized; the mixture was subjected to ten-fold serial dilution. 0.5 mL aliquot was drawn from the 10^{-4} and 10^{-6} diluents and then introduced into sterile petri dishes containing sterilized Nutrient Agar, Mckonckey Agar, Eosine methylene blue agar, *Salmonella-shigella* agar and Potato Dextrose Agar respectively which were incubated for 24 hours at 37 °C. Subculture of the isolates was done to acquire the pure culture which was stored in slant bottles. The microbial load of the produced jam samples was determined at the interval of three, six and nine days. Plate counting was done to know the microbial load of the samples.

Molecular Characterization of isolates

Genomic DNA Extraction

The genomic DNA extraction of the isolates was done using the modified method of Oladipo *et al*. (2013). In this process, the selected isolates were grown overnight in nutrient broth. The cells in the broth were pelleted by centrifugation at 4000 rpm for 10 min. The pellets were then washed twice with TE buffer (10-mM Tris-Cl, 1-mM EDTA, pH 8.0). The genomic DNA of the isolated strains was extracted using the guanidium thiocyanate–N-lauroylsarcosine denaturing method. The quantity and the purity of the total DNA were verified using agarose gel electrophoresis, and the DNA was stored at − 20°C until needed (Drancourt *et al.,* 2000).

16SrRNA Amplification of the Isolates DNA

The method of Drancourt *et al*. (2000) was also employed for 16S rRNA amplification. The PCR assays were performed in an automated temperature cycling device (Test Kit, China), using 5µl of extracted DNA, 25-µl NzyTaq 2× Green Master Mix (Genaxxon Bioscience, Germany) and 2µl of each primer in a total volume of 50µl. The amplification cycling program consisted of a 5-min initial denaturation at 94°C, followed by 35 cycles of a 2-min denaturation at 94°C, a 1-min annealing at 51°C, and a 2-min extension at 72°C, with a final extension at 72°C for 5 min as reported by Plessa *et al.,* (2017). The amplified fragments were verified by electrophoresis on 1% (w/v) agarose gels stained with 0.5 µg/mL ethidium bromide. Fragment sizes were verified as positive for the universal 16S rRNA gene. These were then r sequenced using an automatic sequencer. The raw

sequences were manually base-called using the Bio Edit software and nBLAST searches were performed using the GenBank Internet server (http://www.ncbi.nlm.nih.gov) for comparison with other strains deposited in the public databases to identify the species of each isolate. Sequences that showed more than 98% similarity were considered as belonging to the same taxonomy unit.

Antibiotics Susceptibility Test

Antibiotics Susceptibility Test is a laboratory test used to determine the sensitivity of bacteria to specific antibiotics. The antibacterial susceptibility testing was carried out using disc diffusion assay (Baker, 1998; Cheesebrough, 2002). Sterilized nutrient broth was inoculated differently in sterile super bottles with each organism aseptically and incubated at 37^0C for three hours and a control which allows slight turbidity to be differentiated. Pure isolates of bacteria were tested against selected antibiotics. Inoculums were swabbed unto diagnostic sensitivity test agar (DSTA) under aseptic condition and commercially obtained antibiotics multidisc were carefully placed unto the surface of the swabbed plates using a sterile forceps and incubated at 37^0C for 24 hours. All plates were prepared in duplicate, after 24 hours the zones of inhibition were measured. Antibiotic susceptibility Test by the CDS (calibrated Dichotomous Sensitivity) method was used for standard interpretation of zone of inhibition. Annular Radius: ≥6mm = Susceptibility, ≤6mm = Resistance (Bell *et al.,* 2009)

Proximate Evaluation of the Samples

Determination of moisture content

The percentage of moisture content of the samples was determined by oven method as described by Bukar *et al*. (2019). Exactly 50 mL of the samples were dried in the oven for 24 hours at 100 ºC. The percentage moisture content was calculated by the following formula:

$$\%Moisture\ Content = \frac{Wt\ of\ sample + dish\ before\ drying - Wt\ of\ sample + dish\ after\ drying}{Wt\ of\ sample\ taken}\ x\ 100$$

Determination of fat content

The fat content of the samples was determined using the method of Oladipo *et al*. (2022a). Briefly, 5 g of sample was mixed with 0.88 mL of ammonia solution and 10 mL of 95 % ethanol and mixed well. 25 mL of diethyl ether was added to the mixture and shaken vigorously for 1 minute. This was then followed by addition of 25 mL of petroleum ether and shaken vigorously to mix well. The mixture was then left to stand for an hour to allow aqueous and organic phase to separate. The fat extract (organic phase) was collected, and the solvent was removed by distillation. The fat in the flask was dried in the oven at 100 ºC for 30 minutes and the solvent was removed completely. The flasks were then cooled in a desiccator and were weighed for their mass of fat. The percentage fat was calculated by the following formula:

$$Ether\ extract = \frac{weight\ of\ flask + extract - tare\ weight\ of\ flask}{Weight\ of\ Sample} x100$$

Determination of crude fiber

The crude fiber of the samples was determined according to the procedure reported by Oladipo *et al*. (2022b). It was determined as the fraction remaining after digestion with standard sulphuric acid and sodium hydroxide. Exactly 2mL of the sample was hydrolyzed in a beaker containing 299 mL of 1.25 % of sulphuric acid and then boiled for 30 minutes. The mixture was filtered under vacuum and the residue was washed with hot distilled water 3 times and then boiled again for 30 minutes with 200 mL of 1.25 % of sodium hydroxide and filtered again. The digested sample was washed with hydrochloric acid to neutralize sodium hydroxide and then with hot distilled water for 3 times. The residue was taken into a crucible, dried at 100 ºC for 2 hours in an oven; the sample was cooled in a desiccator and then weighed. The sample in the crucible was incinerated at 500 ºC for 5 hours until all carbonaceous matter was burnt. Finally, the crucible containing the ash was cooled in the desiccator and weighed.

$$\%\text{Crude fibre} = \frac{\text{Dry wt. of residue before ashing} - \text{weight of residue after ashing}}{\textit{weight of sample}} \; x\ 100$$

Determination of crude protein content of the samples

The crude proteins were determined by the macro Kjeldahl method as described by Oladipo *et al*. (2014). 50ml of the sample was introduced into a Kjeldahl digestion flask together with 10g of copper sulphate and sodium sulphate in the ratio of 5:1. 25 mL of concentrated sulphuric acid was added to the digestion flask and the digestion was carried out in the fume cupboard until frothing ceased. A clear and light blue coloration was observed. The digest was cooled and diluted up to the mark with distilled water in 100 mL volumetric flask. 10 mL of the diluted mixture was poured into the distillation apparatus and 18 mL of 40% of sodium hydroxide was added. 25 mL of 2% boric acid was added into the receiving conical flask and two drops of bromocresol green, and methyl red mixed indicator was added. The distillation continued until boric acid solution turned from pink to yellowish green. After the distillation, the solution in the conical flask was titrated against 0.1N hydrochloric acid until the end point was reached. The protein was calculated as:

$$\%N = \frac{14 \times VA \times 0.1 \times w}{1000} \; x\ 100$$

VA = volume of acid used, w= weight of sample, %crude protein = %N x 6.25

Determination of ash content of the samples

The ash content of the samples was determined by direct heating method as described by Oladipo *et al*. (2020). Briefly, 50mL of each of the samples were weighed in dried glass crucibles separately. The samples were then incinerated to ash in a muffle furnace for 3 hours at 550 ºC. The crucibles were then removed, cooled in desiccator and the weight of the ash was determined. The percentage ash content was calculated by the following formula

$$\%\text{Ash} = \frac{\text{wt.of crucible} + \text{ash} - \text{wt.of crucible}}{\textit{wt of sample}}$$

Determination of carbohydrate content

The carbohydrate content of the samples was determined by different methods as described by Oladipo *et al*. (2014). The total carbohydrate content was calculated by subtracting the sum of the percentages of moisture, ash, crude protein, crude fiber and fat from 100 %. The carbohydrate content was calculated using the following formula:

$$\%Carbohydrate = 100 - (\%moisture + \%Ash + \%Crude\ protein + \%Crude\ fat + \%Crude\ fiber)$$

Mineral Composition of the Jam samples

The mineral content of the samples was determined using the AOAC method with slight modifications. Approximately 1 g of each sample was weighed into a 100 mL round bottom flask, and 5 mL of perchloric acid was added and heated over an electric heater in a fume chamber until the solution became colorless. The solutions were diluted with distilled water to 10 mL mark, and the diluted samples were set aside for further studies. The Ca, Zn, Mg, K, Na, and Fe contents were analyzed using an atomic absorption spectrophotometer (AAS).

Data analysis

The obtained data underwent one-way analysis of variance (ANOVA). The results were expressed as the mean values ± standard deviation (SD) of duplicate measurements. The Fishers least significant difference (LSD) test helped to resolve the differences between mean values. The level of statistical significance was set at $P < 0.05$ (95% confidence Interval).

Results and Discussion

The process for producing the apple (*Malus domestica* Borkh), pineapple (*Ananas comosus*), and watermelon (*Citrullus lanatus*) jams is presented in Figure 1. Each jam sample displayed a distinct colour that reflected the natural pigments of the fruits used. The watermelon jam appeared reddish, while the pineapple jam developed a light brown colour. The apple jam showed a yellowish tone, consistent with its natural fruit pulp. The composite jam made from apple and pineapple had a brownish-yellow appearance, whereas the blend of apple, pineapple, and watermelon produced a darker brown colour, likely due to the combined effects of heating and mixed fruit pigments. These observations agree with earlier reports. Oni *et al.* (2021) described watermelon and pineapple jams with reddish and brownish hues, while Iftikhar *et al*. (2009) reported a pale yellow colour for apple jam. The colour variations found in this study therefore align with documented characteristics of fruit-based jams.

The organoleptic evaluation of the jam samples revealed clear variations in sensory quality, with the mixed-fruit formulations generally performing better than the single-fruit jams. The Apple–Pineapple–Watermelon jam (APWJ) recorded the highest overall acceptability score of 9.80±0.13, indicating that combining the three fruits produced the most appealing sensory experience. APWJ also obtained a high taste score of 9.20±0.15, ranking second in this category.

Across the individual parameters, Watermelon jam (WJ) achieved the highest taste rating (9.70±0.15), suggesting that it possessed the most favourable flavour profile among the single-fruit variants. In contrast, Apple jam (AJ) consistently received the lowest scores in all attributes, including the least acceptable taste (7.30±0.21), the lowest texture rating (8.10±0.31), and the minimum overall acceptability (8.70±0.26), indicating the need for formulation improvement. The Apple–Pineapple jam (APJ) produced the best texture score (9.80±0.37), reflecting superior consistency and mouthfeel. For appearance, Pineapple jam (PJ) ranked highest (8.50±0.22), while Apple jam (AJ) again had the lowest score (7.40±0.22). Overall, these results suggest that multi-fruit jams, particularly APWJ, offer enhanced sensory qualities and greater consumer appeal when compared with single-fruit jams, especially apple-based formulations (Figure 2). These findings align with previous research. Oni *et al*. (2021) reported similar sensory outcomes in pineapple, watermelon, and banana jams, where pineapple jam received the highest acceptability score (8.90±1.59) due to its pleasant taste. Likewise, Olugbenga *et al.* (2018) observed that pineapple jam exhibited the best acceptability in comparable fruit blends. Adegbanke (2025) also documented favourable sensory scores in multi-

fruit blends, with apple-based mixed jam achieving an overall acceptability of 7.65±0.81. Together, these reports support the conclusion that blending fruits enhances sensory attributes and consumer preference.

A total of 7 organisms were isolated from all the jam samples. Molecular identification of the isolates was carried out by extraction of the DNA and subsequent amplification of the DNA. The PCR products (amplified DNA) were purified, sequenced, and aligned using BLAST with the published sequences of the 16SrRNA genes of other strains deposited in NCBI databases. According to the BLAST results, the isolates had 100% similarities with *Enterococcus faecium strain*, *Staphylococcus aureus* strain, *Bacillus cereus* strain, *Bacillus subtilis* strain and *Escherichia coli strain* as shown in Table 1.

The phylogenetic analysis of the isolates is shown in Figures 3 and 4. The molecular identification of the isolates revealed a perfect match between each sample and its closest reference strain in the GenBank database. *Enterococcus faecium* PQ657463 showed 100 percent sequence homology with *Enterococcus faecium* strain N21-03014, as previously described by McCracken *et al*. (2025). Similarly, *Escherichia coli* PQ657466 and *Escherichia coli* PQ657465 both aligned completely with *Escherichia coli* strain JCM20135, reported by Kato and Ohkuma (2025), confirming their identity with high confidence. *Staphylococcus aureus* PX427492 and PX427495 each displayed 100 percent homology with *Staphylococcus aureus* strain ARN2, consistent with the findings of Ali (2020). *Bacillus cereus* PX427493 also showed complete similarity with Bacillus cereus strain NCDO1769 (Ash *et al*., 1991). In addition, *Bacillus subtilis* PX427494 exhibited 100 percent homology with *Bacillus subtilis* strain SP1, as reported by Richts *et al*. (2020). The sequence alignment across all isolates indicates that the molecular characterization was accurate and reliable, providing strong confirmation of the species identities.

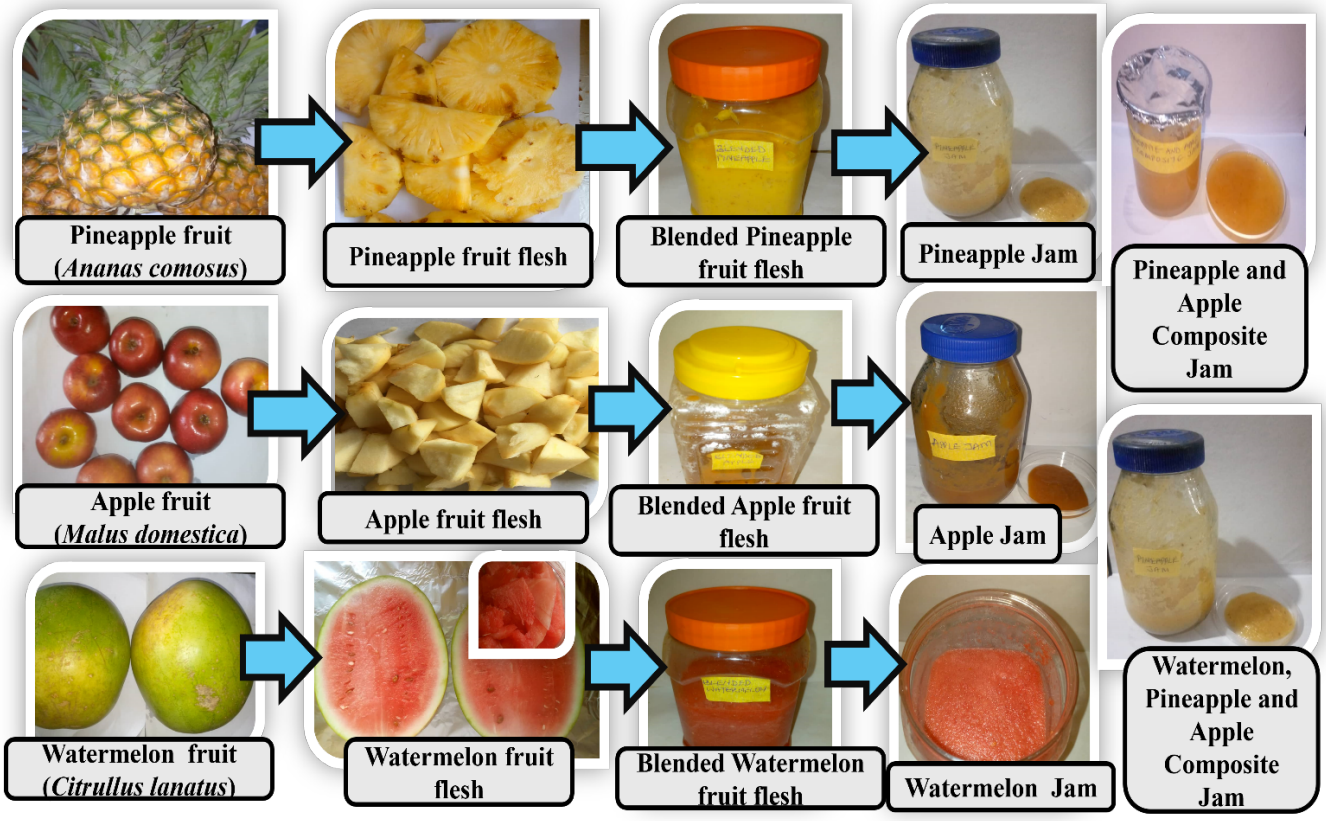

Figure 1: Production of apple, pineapple and watermelon jam

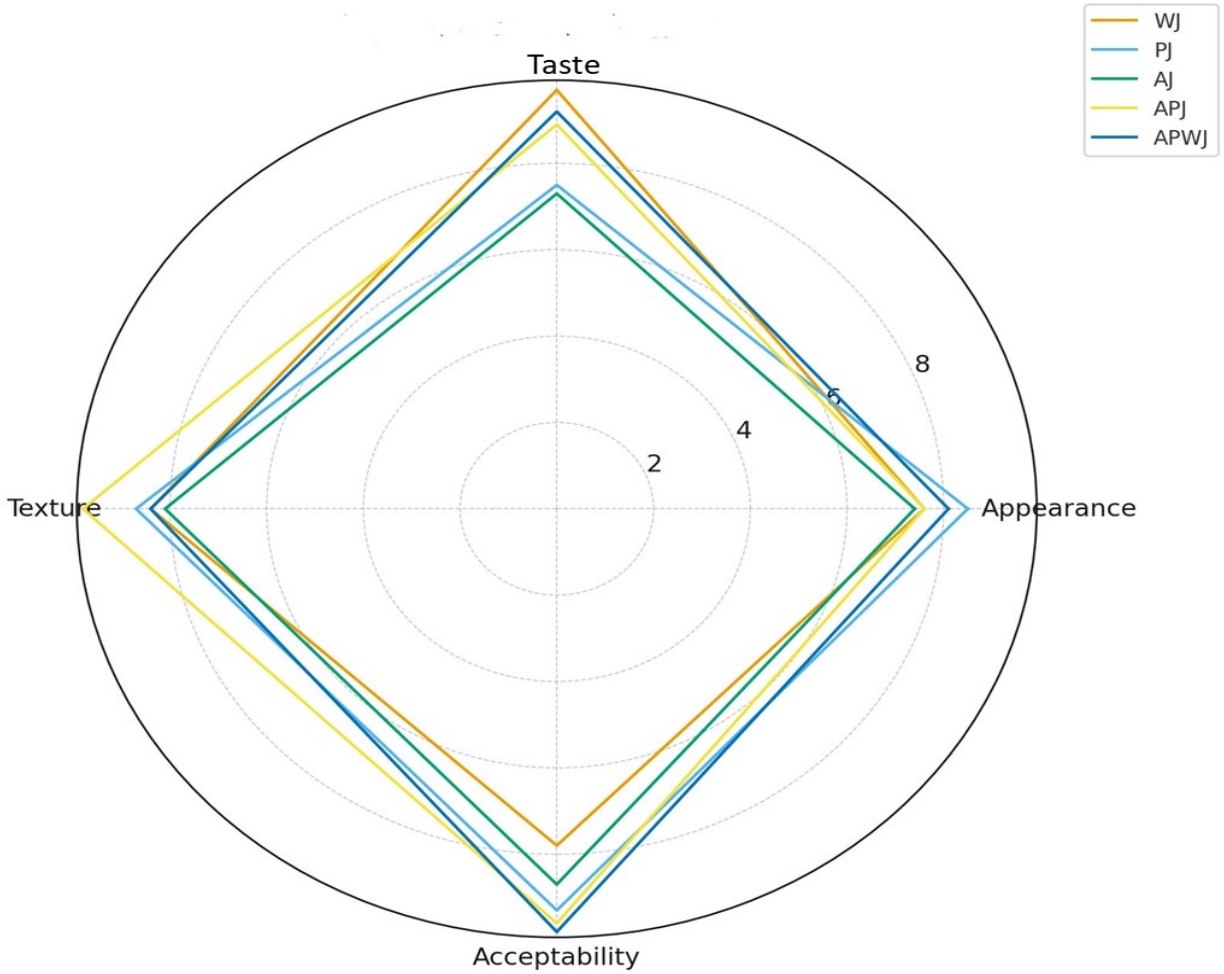

Figure 2: Organoleptic test for all the Jam samples
Key: WJ (Watermelon jam), PJ (pineapple jam), AJ (apple jam), APJ (Apple and pineapple jam), APWJ (Apple, pineapple and watermelon jam).

Table 1: Molecular Characterization of the selected isolates

Source	Sample code	% identification	Identified isolates	Accession number
watermelon jam	NWJ	100	*Enterococcus faecium*	PQ657463
Apple jam	NAJ	100	*Escherichia coli*	PQ657466
Pineapple jam	PJ	100	*Escherichia coli*	PQ657465
Apple, pineapple and watermelon jam	APWJ	100	*Staphylococcus aureus*	PX427492
Apple and pineapple jam	APJ	100	*Bacillus cereus*	PX427493
Watermelon Jam	WJ	100	*Bacillus substilis*	PX427494
Pineapple jam	NPJ	100	*Staphylococcus aureus*	PX427495

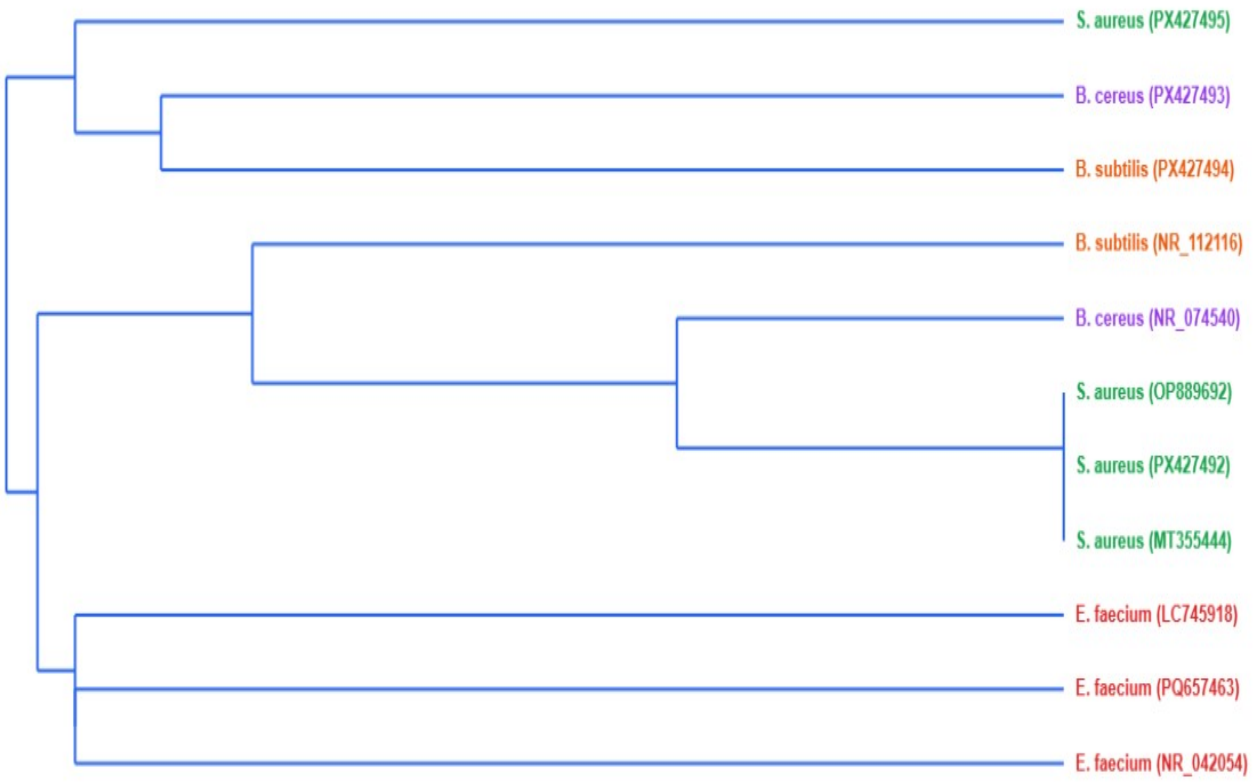

Figure 3: The phylogenetic tree showing the relationship between *S. aureus* (PX427495), *S. aureus* (PX427492), *B. cereus* (PX427493), *Bacillus subtilis* (PX427494), *Enterococcus faecium* (PQ657463) and other closely related species.

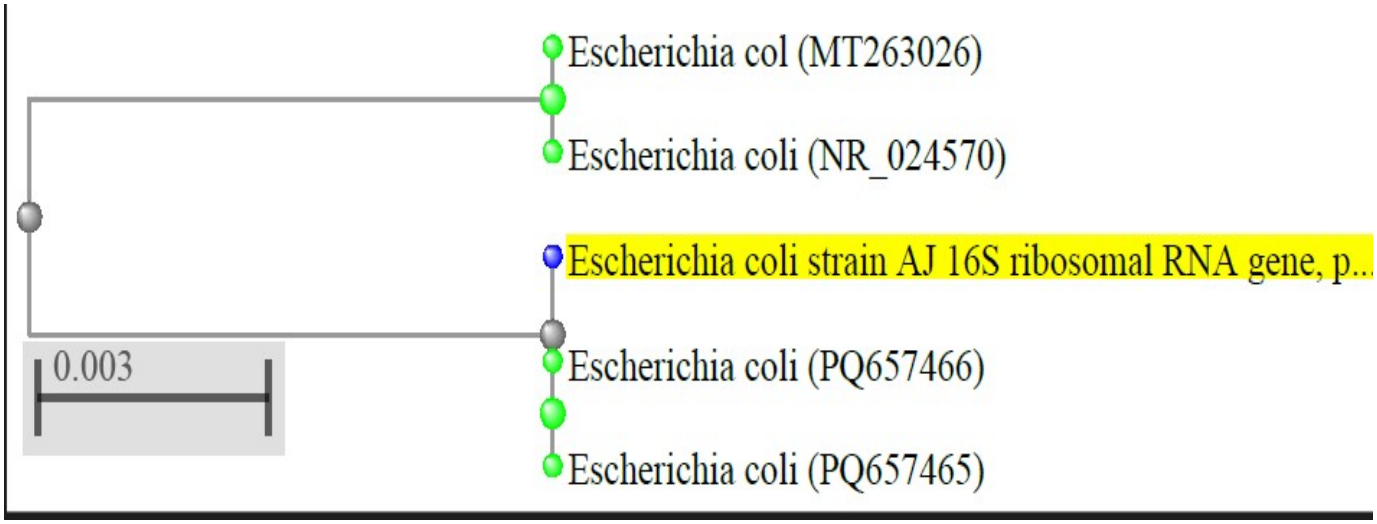

Figure 4: The phylogenetic tree showing the relationship between *E. coli* (PQ657466), and *E. coli* (PQ657465) and other closely related species.

Table 2 shows the microbial load of the jam samples produced. It was observed that, there was no growth on Salmonella shigella and Maconckey agar. The highest colony forming unit of 4.0 x 10^3 was noted for apple and pineapple jam on nutrient agar. Adegbanke (2025) reported highest total bacteria count of 1 x 10^3 CFU/g. Oni *et al*. (2021) also reported highest total fungi count of 1.08 x 10^3CFU/g for pineapple blend jam. According to the International Commission of Microbiology Specifications of Foods (ICMSF, 2005) all the microbial load of the samples were below the acceptable limits of $>10^5$.

Table 3 shows the microbial load of the jam samples on days 1, 3, and 6 after production. Across all samples, the microbial count increased progressively with storage time, indicating gradual microbial proliferation as the days advanced. Although the counts remained within the 10^3 CFU/g range throughout the six-day period, the consistent upward trend suggests that the jams experienced natural microbial build-up during storage. This pattern agrees with the findings of Eke-Ejiofor *et al*. (2019), who reported similar increases in the bacterial load of stored jam samples. In their study, the bacterial count rose from 1.0 × 10^6 CFU/g on day 1 to 7.2 × 10^6 CFU/g by day 7, confirming that microbial growth tends to intensify with longer storage durations regardless of fruit type or formulation.

The Gram positive isolates generally showed high susceptibility to the antibiotics tested, with only a few specific resistances observed. *Enterococcus faecium* NWJ displayed resistance to cefoxitin, which aligns with the intrinsic low susceptibility of Enterococcus species to cephalosporins. *Staphylococcus aureus* APWJ was resistant to amoxicillin, a pattern commonly associated with beta-lactamase production, while *Staphylococcus aureus* NPJ and the *Bacillus subtilis* WJ remained fully susceptible to all tested antibiotics. *Bacillus cereus* demonstrated resistance to erythromycin and clarithromycin, a finding consistent with its known variability in macrolide susceptibility due to both intrinsic and acquired resistance genes (Table 4). The susceptibility pattern suggests that most Gram positive isolates in the study do not harbour multidrug resistance signatures. The susceptibility patterns observed show strong agreement with previously published findings. The resistance of *Enterococcus faecium* NWJ to cefoxitin corresponds with reports that Enterococcus species are intrinsically resistant to most cephalosporins due to their low-affinity penicillin-binding proteins (Hollenbeck and Rice, 2012). The amoxicillin resistance detected in one *Staphylococcus aureus* APWJ isolate also mirrors earlier work in foodborne *S. aureus*, where beta-lactamase-mediated resistance to penicillins is frequently documented (Kadariya et al., 2014). Resistance of *Bacillus cereus* to macrolides such as erythromycin and clarithromycin has similarly been described by Bottone (2010), who noted that *B. cereus* often carries erm genes that confer macrolide-lincosamide resistance.

The Gram negative *Escherichia coli* isolates exhibited moderate variations in their antibiotic response. *Escherichia coli* NAJ showed resistance to ofloxacin only, while *E. coli* PJ was resistant to pefloxacin and ciprofloxacin. Despite these few resistances, both isolates remained susceptible to key therapeutic agents, suggesting that broad-spectrum resistance mechanisms such as extended-spectrum beta-lactamase (ESBL) or carbapenemase production are unlikely in these samples (Table 5). Fluoroquinolone resistance in *Escherichia coli*, such as resistance to ofloxacin and pefloxacin, has been widely reported in food and environmental isolates and is often attributed to mutations in gyrA or plasmid-mediated qnr genes (Jacoby *et al*., 2014; Redgrave *et al*., 2014). Despite the observed resistance to a few antibiotics, both *E. coli* isolates remained susceptible to ceftazidime, imipenem, and ampicillin, a pattern consistent with earlier reports that *E. coli* from fruit-based products and food processing environments rarely show ESBL or carbapenemase activity (Adegoke *et al*., 2020; Campos *et al*., 2022). The absence of multidrug resistance in these isolates aligns with similar findings from studies on microbial contamination of jam, juice, and other processed fruit commodities, which typically harbor low-risk Gram negative bacteria (Eke-Ejiofor *et al*., 2019).

The proximate composition of the blended fruit samples and their corresponding jams is shown in Table 6. Moisture content varied widely among the samples, with the highest values recorded for blended watermelon (BW) and the apple–pineapple–watermelon composite jam (APWJ), both at 86.45%. In contrast, apple jam (AJ) had the lowest moisture content at 9.88%, reflecting its higher concentration of soluble solids. Ash content ranged from 0.00% in blended apple (BA); likely due to extremely low mineral residue and detection of up to 2.10% in pineapple jam (PJ), indicating the highest mineral concentration. Crude fat values were generally low across samples, typical of fruit-based products; pineapple jam (PJ) had the highest crude fat content at 1.69%, while apple jam (AJ) recorded the lowest at 0.33%. Crude fiber was highest in the apple–pineapple composite jam (APJ) and watermelon jam (WJ), both at 1.01%, whereas blended watermelon (BW) and the composite jam (APWJ) showed the least fiber at 0.21%. Protein content peaked in the apple–pineapple composite jam (APJ) at 6.92%, while the lowest value (0.56%) was observed in both blended watermelon (BW) and APWJ. Carbohydrate content was highest in apple jam (AJ) at 87.0%, consistent with its low moisture level, and lowest in BW and APWJ, both at 11.0%.

These findings align with previous studies. Ho *et al*. (2020) reported low fat (0.55%), protein (0.39%), ash (0.27%) and moderate fiber (1.95%) in *Averrhoa bilimbi* jam, similar to the low macronutrient levels observed in most of the samples in this study. Cornelia and Galyuoni (2022) also documented moisture contents of 15.61–19.79%, ash contents of 2.40–7.55%, proteins of 1.00–1.54%, fats of 2.56–3.00%, fibers of 3.00–7.90%, and carbohydrates of 66.54–70.70% for pineapple and pumpkin pulp blend jams; these values compare favorably with the current results, although variations reflect differences in fruit type and formulation.

The nutritional profile of the fruit jams in this study is consistent with established standards for fruit preserves. According to the Codex Alimentarius Commission (CAC, 2024), jams should contain high soluble solids typically 60 to 65% to inhibit microbial growth and ensure shelf stability. Samples such as AJ, with 87.0% carbohydrate and only 9.88% moisture, meet this requirement and are expected to exhibit low water activity (aw < 0.85), which supports microbial safety. The FDA (2021) further stipulates that fruit preserves must be prepared from wholesome fruit ingredients and processed to achieve safe moisture solid balance; the composition observed in this study falls within these regulatory expectations. The ash and protein contents also confirm that essential minerals and nutrients are retained, contributing positively to the nutritional value of the jam products. Collectively, the proximate characteristics of the blends and jams demonstrate compliance with food quality, nutritional, and preservation standards, indicating that the products are both safe and suitable for human consumption.

The mineral composition of the blended fruits, single-fruit jams, and composite jam samples is shown in Table 7. The results show clear variations across samples, reflecting differences in the intrinsic mineral profiles of the fruits used and the synergistic effects of blending. Among the samples, apple and pineapple composite jam (APJ) recorded the highest levels of iron (0.64 mg/100 g), sodium (25.40 mg/100 g), and potassium (60.33 mg/100 g). For calcium, the blended pineapple (BP) sample showed the highest value at 1.93 mg/100 g, while the apple, pineapple, and watermelon composite jam (APWJ) had the highest magnesium content at 2.81 mg/100 g. In contrast, the lowest mineral contents were observed in various samples: APWJ had the lowest iron content (0.33 mg/100 g), apple jam (AJ) had the lowest sodium (4.54 mg/100 g) and magnesium (0.97 mg/100 g), while blended pineapple (BP) recorded the lowest potassium (8.41 mg/100 g) and watermelon jam (WJ) had the lowest calcium (1.02 mg/100 g).

The composite jams (APJ and APWJ) contained higher mineral values for most parameters, likely due to the combined nutrient contributions of different fruits, which enhanced mineral density. This suggests that blending fruits can improve

micronutrient retention during processing, making composite jams more nutritionally rich than single-fruit jams. The mineral values recorded in this study align with the natural mineral composition of the respective fruits and indicate that the processing methods used preserved substantial micronutrients. These minerals play important physiological roles: iron for oxygen transport, sodium and potassium for fluid and electrolyte balance, calcium for bone structure, and magnesium for enzymatic reactions and energy metabolism (Singh *et al*., 2018).

The results of this study are consistent with earlier reports. Usman *et al*. (2015) documented mineral contents of pineapple–orange–sourplum composite jam as follows: 0.40–0.85 g/100 g potassium, 6.3×10^{-3}– 8.9×10^{-3} g/100 g iron, 0.62–1.25 g/100 g magnesium, 9.6×10^{-3}–1.99 g/100 g phosphorus, and 1.80–3.00 g/100 g calcium. Their findings similarly demonstrated that composite jams tend to retain and even enhance mineral profiles due to fruit combinations. The mineral levels observed in this study fall within expected ranges for fruit-based products and highlight the nutritional viability of the jams for human consumption.

Table 2: Microbial load of the jam samples

Samples	TBC (CFU/ml)	TSSC (CFU/ml)	TCC (CFU/ml)
AJ	3×10^3	-	-
PJ	2×10^3	-	-
WJ	3×10^3	-	-
APJ	4×10^3	-	-
APWJ	2×10^3	-	-

Key**:** TBC (Total bacterial count), TSSC (Total *Salmollena Shigella* Count), TCC (Total coliform count), AJ (Apple jam), PJ (pineapple jam), WJ (watermelon jam), APJ (Apple and pineapple jam), APWJ (Apple, pineapple and watermelon jam).

Table 3: Shelf life of the sample

Samples	Day 1	Day 3	Day 6
AJ	3×10^3	7×10^3	12×10^3
PJ	2×10^3	7×10^3	12×10^3
WJ	3×10^3	5×10^3	11×10^3
APJ	4×10^3	6×10^3	12×10^3
APWJ	2×10^3	7×10^3	13×10^3

Key: AJ (Apple jam), PJ (pineapple jam), WJ (watermelon jam), APJ (Apple and pineapple jam), APWJ (Apple, pineapple and watermelon jam).

Table 4: Antibiotic Susceptibility pattern of Gram-positive isolates

Organism	OX	E	FOX	CLR	Z	AMX	R	AMP	Phenotypic Resistance Pattern
E. faecium NWJ	S	S	R	S	S	S	S	S	FOX
S. aureus APWJ	S	S	S	S	S	R	S	S	AMX
B. cereus APJ	S	R	S	R	S	S	S	S	E, CLR
B. substilis WJ	S	S	S	S	S	S	S	S	-
S. aureus NPJ	S	S	S	S	S	S	S	S	-

Key: OX- Oxacillin=1µg, E-Erythromycin=30µg, FOX- Cefoxitin=30µg, CLR-Clarithromycin=15µg, Z-Azithromycin=5µg, AMX- Amoxicillin=25µg, R– Roxithromycin =5µg, AMP- Ampicillin=10µg, R= Resistant, S = Sensitive.

Table 5: Antibiotic Susceptibility pattern of Gram-negative isolates

Organism	PEF	CAZ	CPX	OFX	IPM	AMX	CPX	AMP	Phenotypic Resistance Pattern
E. coli NAJ	S	S	S	R	S	R	S	S	OFX
E. coli PJ	R	S	R	S	S	S	S	S	PEF, CPX

Keys: PEF- Pefloxacin=30µg, CAZ- Ceftazidime=30µg, CPX-Ciprofloxacin=10µg, OFX- Ofloxacin=5µg, IPM-Imipenem =10µg, AMX- Amoxicillin=25µg, CPX- Ciprofloxacin =30µg, AMP- Ampicillin=10µg, R= Resistant, S = Sensitive.

Table 6: Proximate Profile of the Jam and blended Fruit Samples

Sample	Moisture	Ash	Crude fat	Crude fiber	Protein	Carbohydrate
BA	18.51 ± 0.01^{d}	0.00 ± 0.00^{e}	1.29 ± 0.01^{b}	0.26 ± 0.01^{d}	1.01 ± 0.01^{e}	78.00 ± 0.00^{c}
BP	34.50 ± 0.00^{c}	1.60 ± 0.00^{b}	0.85 ± 0.01^{c}	0.51 ± 0.00^{c}	1.49 ± 0.00^{d}	61.00 ± 0.00^{e}
BW	86.45 ± 0.01^{a}	0.50 ± 0.00^{d}	0.42 ± 0.00^{d}	0.21 ± 0.00^{e}	0.56 ± 0.00^{f}	11.00 ± 0.00^{f}
AJ	9.88 ± 0.01^{f}	0.07 ± 0.06^{e}	0.33 ± 0.00^{e}	0.44 ± 0.01^{c}	1.75 ± 0.00^{c}	87.00 ± 0.00^{b}
PJ	18.62 ± 0.00^{d}	2.10 ± 0.00^{a}	1.69 ± 0.00^{a}	0.53 ± 0.00^{b}	1.66 ± 0.01^{d}	75.00 ± 0.00^{c}
WJ	22.00 ± 0.01^{d}	0.20 ± 0.00^{e}	1.09 ± 0.01^{b}	1.01 ± 0.01^{a}	5.09 ± 0.01^{b}	70.00 ± 0.00^{d}
APJ	16.00 ± 0.00^{e}	1.00 ± 0.00^{c}	1.31 ± 0.00^{b}	1.01 ± 0.01^{a}	6.92 ± 0.00^{a}	73.00 ± 0.00^{cd}
APWJ	86.45 ± 0.01^{a}	0.50 ± 0.00^{d}	0.42 ± 0.00^{d}	0.21 ± 0.00^{e}	0.56 ± 0.00^{f}	11.00 ± 0.00^{f}

Values are Mean± SEM. Mean values with the same alphabet as superscript on the same column are not significantly different from one another ($p < .05$).
Key: BP = Blended pineapple, BA = Blended apple, BW = Blended watermelon, APJ = Apple and Pineapple composite jam, APWJ = Apple, pineapple and Watermelon composite jam, AJ = Apple jam, PJ = Pineapple jam, WJ = Watermelon jam.

Table 7: Mineral Composition of the Jam and blended Fruit Samples

Samples	Iron mg/100	Sodium mg/100	Potassium mg/100	Calcium mg/100	Magnesium mg/100
BP	0.41	9.29	8.41	1.93	1.96
BA	0.47	9.55	8.61	1.11	1.28
BW	0.44	8.62	8.49	1.06	1.71
AJ	0.62	4.54	8.93	1.10	0.97
PJ	0.44	9.66	8.58	1.06	1.93
WJ	0.41	5.35	8.69	1.02	1.44
APJ	0.64	25.40	60.33	1.33	2.61
APWJ	0.33	18.28	59.53	1.77	2.81

Key: BP = Blended pineapple, BA = Blended apple, BW = Blended watermelon, APJ = Apple and Pineapple composite jam, APWJ = Apple, pineapple and Watermelon composite jam, AJ = Apple jam, PJ = Pineapple jam, WJ = Watermelon jam.

Conclusion

This research successfully showed that composite jams produced from apple (*Malus domestica*), pineapple (*Ananas comosus*), and watermelon (*Citrullus lanatus*) fruits are nutritionally adequate, safe, and organoleptically acceptable for human consumption. The composite jam formulation (apple, pineapple, and watermelon) achieved the highest overall acceptability value of 9.80±0.13, indicating superior sensory attributes compared to single-fruit varieties. Proximate analysis revealed that the jam samples contained appropriate carbohydrate (11.0-87.0%), protein (0.56-6.92%), moisture (9.88-86.45%), and mineral contents that align with established food safety standards and ensure microbiological stability through reduced water activity. The microbiological evaluation confirmed that all samples maintained acceptable microbial loads below the ICMSF threshold of $>10^5$ CFU/ml, with isolated organisms showing limited antibiotic resistance patterns that pose minimal food safety concerns. The mineral composition analysis demonstrated that these jams serve as valuable sources of essential micronutrients including iron (0.33-6.04 mg/100g), potassium (8.41-60.33 mg/100g), and magnesium (0.97-2.81 mg/100g), thereby contributing to dietary mineral intake. These findings conclusively establish that composite fruit jams represent a viable value-addition strategy for extending fruit shelf life, reducing post-harvest losses, and providing nutritious food products year-round without compromising safety or quality standards. This research contributes to achieving SDG 2 (Zero Hunger) and SDG 12 (Responsible Consumption and Production)

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