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Original Research Article

Microbiota and phytochemical composition of locally- and industrially-produced vinegar

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Abstract

Purpose: *To determine the microbiota and phytochemical compounds present in locally and industrially produced vinegar.*

Methods: *Isolated microbiota from the locally and industrially produced vinegar were identified using next-generation sequencing methods. The phytochemical content was evaluated using standard methods. The FTIR spectroscopic and GC-MS spectrometric analyses were conducted to identify the functional groups and constituents of vinegar samples.*

Results: *Acetobacter species were found in all vinegar samples except Vin D (Bragg raw unfiltered apple cider vinegar), representing the industrially produced vinegar. The presence of Fusobacterium necrophorum and Legionella species showed the need for pasteurization to prevent transmission of infectious organisms. Phytochemical analysis of the samples indicated the presence of flavonoids in all vinegar samples, while FTIR revealed the presence of functional groups such as alcohol, carboxylic acid, alkenes, amines and cyclic alkenes. The GC-MS showed the presence of acetic acid as well as other organic acids, alcohols and ketones in all the samples.*

Conclusion: *The vinegar samples contain acetic acid bacteria and flavonoids, with no substantial variation in phytochemical content of the local and industrial vinegar samples. The identified metabolites may contribute to the nutritional quality of vinegar.*

Keywords: *Next-generation sequencing, Microbial contamination, Acetobacter, Gas chromatography-mass spectrometry, Acetic acid, Flavonoids*

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INTRODUCTION

Vinegar is an edible liquid made from agricultural raw materials containing starch and sugars or both. It is produced through a two-stage fermentation procedure involving both sequences of alcoholic and acetic fermentation, and it must contain a specific amount of acetic acid [1]. Traditionally, it has been considered a wholesome and unprocessed cuisine and is frequently used in many food applications [2]. Vinegar is traditionally produced by employing

fruit-based juices including grape, coconut, rice, apple, plum, potato and tomato as basic ingredients [3]. It is prevalent in dietary substances that include sugar or in products with fermentation that contain alcohol. Various species of acetic acid bacteria (AAB) have been extracted from different types of vinegar, such as classic varieties like balsamic, white wine, red wine, spirit, rice wine, cider and industrial vinegar.

Production of industrial vinegar proceeds from an aerated submerged culture. Manufacturing of vinegar normally requires alcoholic fermentation, where simple sugars in raw material are transformed into alcohol by yeasts. During the final fermentation process known as acetic fermentation, the alcohol produced is oxidized by AAB to form acetic acid [4,5]. The conventional method enhances the formation of fragrance and taste through gradual formation of fruits, vegetables and other plant-based meals, which are rich in several phytochemicals [6]. Consumption of these foods has tremendous health benefits. Microbes involved in the fermentations include yeast, moulds, AAB, and lactic acid bacteria (LAB). The yeast facilitates alcoholic fermentation while the AAB is required for acetic acid production [7].

Although several bacteria generate acetic acid, species of *Acetobacter* (*Gluconoacetobacter*) are utilized to improve the quality and functionality of the product, usually the aerobic bacterium *A. species* at 27 - 37 °C [8]. Other species typically recovered from vinegar fermentations include *Acetobacter polyoxogenes*, *Gluconacetobacter intermedius*, *Acetobacter pasterianus*, *Gluconacetobacter hansenii*, *Gluconacetobacter oboediens*, and *Gluconacetobacter xylinus* [9]. The metabolic activities of these microorganisms determine the aroma, acidity and flavour of the vinegar sample. Today, there is an increased demand for vinegar made by conventional techniques (surface culture production) due to high antioxidant activity and bioactive components [1-3].

Fruit vinegars in general are incorporated in human diets due to their numerous useful compounds such as organic acids, polyphenols, melanoidin and tetramethylpyrazine [10]. There are locally manufactured vinegars in Nigerian markets, which may not meet international standard requirements for vinegar due to poor quality assurance procedures. More worrisome is that many consumers do not pay attention to the potential pathogenic risks associated with poor-quality locally produced vinegar.

There is a need, therefore, to assess the phytochemical composition of both locally and industrially produced vinegar to ascertain conformity with the required standards. Furthermore, understanding the microbiota of vinegar helps in optimizing fermentation conditions for high turnover, discovery of potential novel strains for industrial applications and consistent quality. This study, therefore, investigated the microbiota and phytochemical contents of some locally and industrially produced vinegar samples.

EXPERIMENTAL

Vinegar samples

Locally and industrially produced vinegar samples were obtained from Chychy Gilgal Limited Laboratory and Consultant Services, Ichida, Nigeria. The vinegar samples were designated Vin A to Vin D depending on the basic ingredients employed for indigenous fermentation. Vin A is composed of a blend of lemon, lime, orange and grape peels. Vin B was comprised of a blend of red apples and greens with peels. Vin C consisted of a blend of jackfruit, pineapple, and pawpaw with peel and oranges, while Vin D contained Bragg raw unfiltered apple cider vinegar with mother and served as the control.

DNA isolation and sequencing

The DNA from genomes was obtained from the vinegar samples using DNeasy Toolkit (Qiagen), executed on a QIAcube computerized extraction device. Genomic DNA was synthesised for amplicon sequencing of the next generation, utilising a two-stage PCR technique to create amplicons equipped with Illumina sequencing adapters and individualized barcodes. Specifically, gDNA was PCR amplified using primers CS1 515F (“Parada”) and CS2 806R(“Apprill”) encoding the V4 regions within microbial SSU rRNA genes employing a 2-stage TAS technique. Stage one PCR amplifications were done in 10 µL operations in 96-well plates, using MyTaq HS 2X master mix. The PCR conditions followed the sequence: 95 °C/5 min, 28 cycles of 95 °C/30 s, 55 °C/45 s and then 72 °C/30 s. Stage two PCR amplification was done in 10 µL reactions in 96-well plates [11]. A master mix for complete plate was made utilizing the MyTaq HS 2X master mix. Each well received a unique primer pair (a 10-base barcode from the AccessArray Barcode Library for Illumina). The cycling conditions include an initial denaturation at 95 °C/5 min, 8 cycles of 95 °C/30 s, 60 °C/30 s and 72 °C/30 s. A final

elongation phase was performed at 72 °C for 7 min. The pooled sample library underwent an AMPure XP cleaning procedure (0.6X, vol/vol; Agencourt, Beckmann-Coulter) to exclude fragments shorter than 300 bp. The pooled library, with a 20 % phiX spike-in, was loaded onto an Illumina MiniSeq mid-output flow cell (2 x 153 paired-end reads). To achieve a more balanced distribution of reads, the amplicons (before purification) were re-pooled based on the allocation of readings per barcode. The re-pooled library was cleaned again using the AMPure XP procedure described earlier. Demultiplexing of measurements was carried out on the instrument.

Phytochemical analysis

The presence or absence of metabolites such as carbohydrates, tannins, saponins, flavonoids, alkaloids, and quinones was determined using standard methods [12].

Fourier-transform infrared analysis

The FT-IR spectrum of each of the fermented vinegars was determined with FTIR-4500 (Agilent Technologies, USA). Each sample was put on the diamond crystal and the spectrum was subsequently captured using Diamond ATR accessory.

GC-MS analysis

The vinegar sample (2 mL) was mixed with methanol (4 mL) in a capped test tube and sonicated at 70 °C for 30 min in an ultrasonic bath. The organic layer was dried with Na_2SO_4 and condensed to 2 mL under vacuum for GC-MS analysis. The mass spectrometer (MS) was auto-tuned to perfluorotributylamine, and the GC-MS analysis was performed in Scan mode to ensure the determination of all target components. An Agilent 7820A GC coupled with a 5975C inert MS (with a triple-axis detector) and an electron-impact source (Agilent Technologies, USA) was used. The stationary phase was an HP-5 capillary column coated with 5 % phenyl methyl siloxane (30 m length x 0.32 mm diameter x 0.25 µm film thickness; Agilent Technologies, USA). Helium was used as the carrier gas at a constant flow of 1.4871 mL/min, with an initial nominal pressure of 1.4902 psi and an average velocity of 44.22 cm/s. The sample (1 µL) was injected in splitless mode at 300 °C. The purge flow to the split vent was 15 mL/min at 0.75 min, with a total flow of 16.654 mL/min, and the gas-saving mode was turned off. The oven temperature was set to 40 °C for 1 min, then ramped up at 12 °C/min to 300 °C (held for 10 min). The total run time was 32.667 min, with a 5 min solvent delay.

The MS operated in electron-impact ionization mode at 70 eV, with an ion source, a quadrupole and a transfer line temperature of 230, 150 and 280 °C respectively. Ions were acquired in scan mode, scanning from m/z 45 to 550 amu at a scan rate of 2.0 s/scan. The mass spectrometer shows the spectrum that was used to identify the compounds present as well as their amount in the sample. The % area was equivalent to the concentration of the component in the sample [13].

Data analysis

Data was analyzed using GraphPad Prism version 5 (GraphPad Software, San Diego, CA, USA) and presented in frequency and percentages using bar charts.

RESULTS

Microbiota of vinegar samples

The vinegar samples were analyzed for microorganisms present and their relative abundance. The result showed the relative abundance of the microbiota in the vinegar samples (Figures 1 - 3). Only *Acetobacter pasteurianus* was recovered from Vin A, while 3 phyla, 3 classes, 3 orders, 4 families and 4 genera of bacteria were recovered from Vin B (Figure 1). In Vin C (Figure 2), 4 phyla, 6 classes, 7 orders, 6 families and 7 genera were recovered, while 3 phyla, 4 classes, 4 orders, 4 families and 4 genera of bacteria were recovered from Vin D (Figure 3). *Acetobacter sp* was found in all the samples except Vin D (industrially produced vinegar).

Qualitative phytochemical constituents

Phytochemical analysis revealed the absence of alkaloids, tannins, saponins and quinones in the vinegar samples. However, carbohydrates and flavonoids were detected in all samples tested.

FTIR spectra of vinegar samples

The FTIR analysis showed the presence of alcohol (O-H), carboxylic acid (COOH), alkenes (C=C), conjugated alkenes (C=C-C=C), amine (N-H), cyclic alkenes (C=C), fluoro-compound (C-F), or aromatic amine (C-N) in the vinegar samples (Table 1).

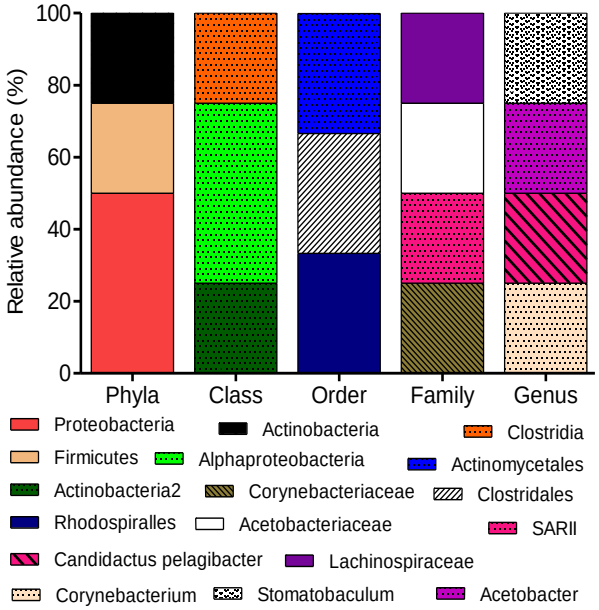

Figure 1: Relative abundance of the microbiota in Vin B. *(Acetobacter* recovered were *A. pastorianus, A. tropicalis and A. oryzoeni; Corynebacterium* recovered were *C. falsenii, C. jeikeinum and C. bovis; Stomatobaculum* appeared as an uncultured bacterium)

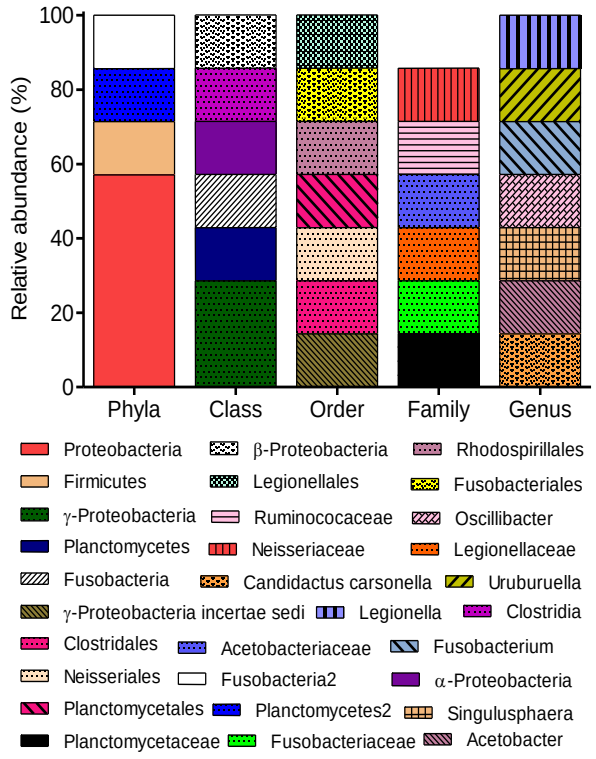

Figure 2: Relative abundance of the microbiota of Vin C. *(Acetobacter* recovered were *A. pastorianus, A. ghanensis, A. tropicalis* and *A. oryzoeni; Fusobacterium* recovered were *F. necrophorum; Uruburuella* recovered were *U. testudines and U. suis;* Others appeared as an uncultured bacterium)

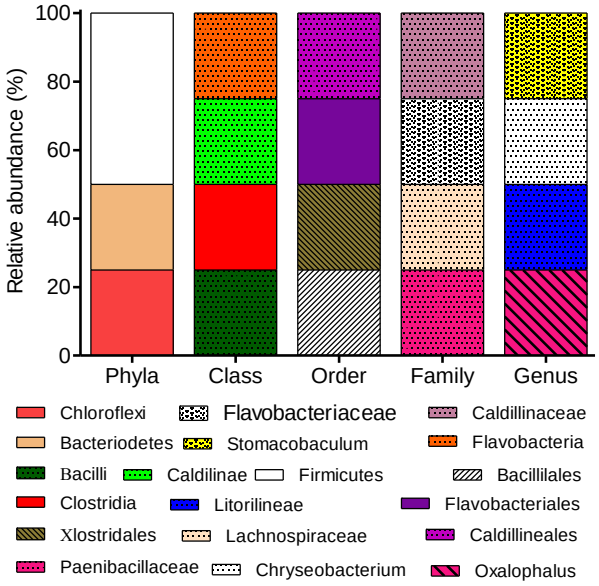

Figure 3: Relative abundance of the microbiota of Vin D. *(Chryseobacterium* recovered was *C. pallidum.* Others appeared as an uncultured bacterium)

GC-MS spectrometry of vinegar samples

The GC-MS spectrum of Vin A, Vin B, in C, and Vin D showed 121, 131, 157 and 116 peaks respectively. Compounds with high relative abundance (~ 1 %) in the vinegar samples were identified (Tables 2 - 5). The prevalent compounds present in the vinegar were acetic acid and 2,3 butanediol. The industrially produced vinegar (Vin D) which served as control contained the highest acetic acid content (35.802 %), followed by the locally produced apple cider vinegar (Vin B; 21.06 %), with the lowest concentration (3.90 %) obtained from Vin A. Highest concentration of 2,3-butanediol was found in Vin B (6.11 %), while the lowest was obtained in Vin A with a relative abundance of (2.48 %).

DISCUSSION

This study evaluated the microbiota content and phytochemical compounds in locally and industrially produced vinegar samples. Next-generation sequencing identified both culturable and non-culturable microbial populations in the vinegar samples. Vin A had only *Acetobacter pasteurianus*. Vin B contained multiple *Acetobacter* species and other bacteria, with some non-culturable bacteria. Vin C included *Acetobacter* species, *Fusobacterium necrophorum*, and non-culturable bacteria. Vin D contained *Chryseobacterium pallidum* and non-culturable bacteria.

Table 1: FTIR spectral characteristics of vinegar samples

Sample	Absorption (cm^{-1})	Functional group	Class	Appearance
Vin A	3242.8	O-H str	Alcohol	s, b
		O-H str	carboxylic acid	s, b
	1636.3	C=C str	Alkene	m
		C=C str	Conjugated alkene	m
		N-H bend	Amine	m
		C=C str	Cyclic alkene	m
Vin B	3246.3	O-H str	Alcohol	s, b
		O-H str	Carboxylic acid	s, b
	1636.3	C=C str	Alkene	m
		C=C str	Conjugated alkene	m
		N-H bend	Amine	m
		C=C str	Cyclic alkene	m
	1397.8	O-H bend	Carboxylic acid	m
		O-H bend	Alcohol	s
		S=O str	Sulphate	s
		C-F str	Fluoro compound	s
	1274.7	C-F str	Fluoro compound	s
		C-N str	Aromatic amine	s
		C-O str	Aromatic ester	s
		C-O str	Alkyl aryl ether	s
Vin C	3261.4	O-H str	Alcohol	s, b
		O-H str	Carboxylic acid	s, b
	1636.3	C=C str	Alkene	m
		C=C str	Conjugated alkene	m
		N-H bend	Amine	m
		C=C str	cyclic alkene	m
Vin D	3257.7	O-H str	Alcohol	s, b
		O-H str	Carboxylic acid	s, b
	1636.3	C=C str	Alkene	m
		C=C str	Conjugated alkene	m
		N-H bend	Amine	m
		C=C str	Cyclic alkene	m
	1386.6	C-F str	Fluoro compound	s
		O-H bend	Phenol	m
		S=O str	Sulfonyl chloride	s
		O-H bend	Alcohol	m
		S=O str	Sulphate	s
	1247.8	C-F str	Fluoro compound	s
		C-O str	Alkyl aryl ether	s
		C-N str	Amine	m

Stretching (str), bending (bend), strong (s), medium (m), broad (b)

Table 2: Compounds identified from the GC-MS of Vin A

RT (min)	Area (%)	MW (g/mol)	Formula	Library ID
4.2765	3.900	60.1	CH_3CO_2H	Acetic acid
4.6692	2.484	90.1	$C_4H_{10}O_2$	2,3-Butanediol
13.2167	5.299	186.3	$C_{11}H_{22}O_2$	Butanoic acid, 3-methyl-, hexyl ester
13.3495	1.966	24.3	$C_{11}H_{22}O_5$	Butyl 2-(2-(2-methoxy ethoxy) ethoxy) acetate
13.8808	2.516	210.4	$C_{14}H_{26}O$	9-Tetradecenal, (Z)-
14.1’523	2.921	228.4	$C_{14}H_{28}O_2$	Tetra decanoic acid
14.3948	1.431	342.3	$C_{12}H_{22}O_{11}$	Maltose
14.5739	3.430	182.2	$C_6H_{14}O_6$	Galactitol
15.6423	2.475	254.4	$C_{16}H_{32}O_2$	Palmitoleic acid
15.8906	6.487	256.4	$C_{16}H_{32}O_2$	n-Hexadecanoic acid
16.1909	1.473	294.6	$C_{12}H_{42}$	10-Heneicosene (c,t)
16.7396	1.242	294.5	$C_{19}H_{36}O_2$	9-Octadecenoic acid (Z)-, methyl ester
17.2247	9.464	282.5	$C_{18}H_{34}O_2$	9-Octadecenoic acid, (E)-
17.3749	2.317	284.5	$C_{18}H_{36}O_2$	Octadecanoic acid
17.9178	1.042	338.6	$C_{22}H_{42}O_2$	Erucic acid
18.6281	4.533	310.5	$C_{20}H_{38}O_2$	cis-13-Eicosenoic acid
19.968	4.872	338.6	$C_{22}H_{42}O_2$	Erucic acid

Retention time (RT), molecular weight (MW)

Table 3: Compounds identified from the GC-MS of Vin B

RT (min)	Area (%)	MW (g/mol)	Formula	Library ID
3.5721	1.6999	102.2	$C_6H_{14}O$	Butane, 2-ethoxy-
3.6991	1.166	101.2	$C_7H_{13}NS$	Thiazole, 4,5-dihydro-2-methyl-
4.0746	21.0163	60.5	CH_3CO_2H	Acetic acid
4.1669	2.4521	266.3	$C_{11}H_{22}O_7$	2,5,8,11,14-Pentaoxahexadecan-16-ol
4.4846	6.1188	90.1	$C_4H_{10}O_2$	2,3-Butanediol
4.5655	0.9747	116.2	$C_6H_{12}O_2$	Oxirane, ((1-methyl ethoxy) methyl)
4.7098	2.8414	116.2	$C_7H_{16}O$	2-Pentanol, 2,4-dimethyl-
5.2874	1.2624	98.1	$C_5H_6O_2$	1,2-Cyclopentanedione
8.3772	1.0214	146.1	$C_6H_{10}O_4$	Dianhydromannitol
12.1657	1.862	194.2	$C_7H_{14}O_6$	3-Methylmannoside
14.0485	2.7968	228.4	$C_{14}H_{28}O_2$	Tetradecanoic acid
15.7927	11.3199	256.4	$C_{16}H_{32}O_2$	n-Hexadecanoic acid
17.1498	9.3465	285.5	$C_{18}H_{34}O_2$	Oleic Acid
17.3058	3.2574	284.5	$C_{18}H_{36}O_2$	Octadecanoic acid
18.5532	2.292	310.5	$C_{20}H_{38}O_2$	cis-13-Eicosenoic acid
19.8873	1.416	338.4	$C_{22}H_{42}O_2$	Erucic acid
22.9136	2.4621	222.5	$C_{12}H_{22}Si_2$	1,2-Bis(trimethylsilyl)benzene

Retention time (RT), molecular weight (MW)

Table 4: Compounds identified from the GC-MS of Vin C

RT (min)	Area (%)	MW (g/mol)	Formula	Library ID
3.8896	10.1027	60.1	CH_3CO_2H	Acetic acid
4.0397	1.7965	130.2	$C_8H_{18}O$	Di-sec-Butyl ether
4.1264	1.3408	90.1	$C_4H_{10}O_2$	1,2-Butanediol
4.3285	5.9602	90.1	$C_4H_{10}O_2$	2,3-Butanediol
4.6115	1.7391	116.2	$C_6H_{12}O_2$	2-Pentanone, 4-hydroxy-4-methyl-
8.3597	1.2218	146.1	$C_6H_{10}O_4$	Dianhydromannitol
14.031	1.1026	228.4	$C_{14}H_{28}O_2$	Tetradecanoic acid
14.1696	1.7317	266.5	$C_{19}H_{38}$	1-Nonadecene
15.7925	10.4581	256.4	$C_{16}H_{32}O_2$	n-Hexadecanoic acid
17.1785	6.1542	282.5	$C_{18}H_{34}O_2$	9-Octadecenoic acid, (E)-
17.3114	5.2268	284.5	$C_{18}H_{36}O_2$	Octadecanoic acid
18.553	1.3851	310.5	$C_{29}H_{38}O_2$	cis-13-Eicosenoic acid
24.0165	1.161	150.2	$C_{10}H_{14}O$	Thymol, TBDMS derivative
24.467	1.6984	426.7	$C_{30}H_{50}O$	Tirucallol
24.8712	2.1974	414.7	$C_{29}H_{50}O$	.γ.-Sitosterol
25.1946	2.0405	426.7	$C_{30}H_{50}O$	9,19-Cyclolanost-24-en-3-ol, (3β)

Retention time (RT), molecular weight (MW)

Table 5: Compounds identified from the GC-MS of Vin D

RT (min)	Area (%)	MW (g/mol)	Formula	Library ID
4.2246	35.802	60.1	CH_3CO_2H	Acetic acid
4.3748	1.7221	88.1	$C_4H_8O_2$	Acetoin
4.6	4.8267	90.1	$C_4H_{10}O_2$	2,3-Butanediol
4.8311	13.6809	102.1	$C_5H_{10}O_2$	Oxirane, (methoxymethyl)-
5.5934	2.2158	192.2	$C_8H_{20}N_2O_3$	Methenamine, 1,1-dimethoxy-N, N-dimethyl-
7.9439	1.6491	119.2	$C_{11}H_{11}O_2S$	Ethoxy(methoxy)methyl silane
10.179	1.5786	144.2	$C_7H_{12}O_3$	trans-4-Hydroxycyclohexanecarboxylic acid
23.1503	5.2011	222.4	$C_{12}H_{22}Si_2$	1,2-Bis(trimethylsilyl)benzene

Retention time (RT), molecular weight (MW)

Acetobacter pasteurianus was found in Vin A, B, and C, aligning with previous studies, while Vin D lacked *Acetobacter* [14]. The phylum, Proteobacteria was most abundant in Vin B while Vin D had no known acetic acid bacteria, and showed high acetic acid content, possibly due to unidentified bacteria. The results also identified the prevalence of acetic acid bacteria, especially from the *Acetobacter* genus, which is crucial for vinegar production. *Acetobacter* strains are found in alcohol-rich environments, confirming their presence in vinegar [15]. Other bacteria such as *Urubururella* and *Litorilinea* were detected, though not previously recorded in vinegar. The absence of *Acetobacter* in industrial vinegar samples might have resulted from extensive

pasteurization [15]. Further analysis is needed to determine the vinegar-producing potential of the identified organisms. The presence of pathogenic organisms like *Legionella* and *Fusobacterium necrophorum* underscores the need for pasteurization and purification to prevent diseases [10]. Understanding the microbial composition of vinegar and ensuring proper pasteurization and purification is essential for safe consumption and commercial production. Further research is needed to evaluate the vinegar-producing capabilities of the newly identified microorganisms in this study. The phytochemical assay showed that carbohydrates and flavonoids were present in the vinegar samples, while saponins, tannins, quinones and alkaloids were absent. A previous study on pineapple vinegar also identified the presence of carbohydrates and flavonoids, supporting the nutritional and medicinal values of vinegar [16]. Flavonoids and other phytochemicals like glycosides and tannins from fruits and vegetables may play key roles in disease amelioration [10]. Fermentation by microbiota is known to generate enzymes, polyphenols and organic acids which possess anti-inflammatory, antioxidant and other probiotic potential [1-5]. The FTIR spectroscopy of vinegar samples (Vin A, B, C, D) revealed O-H stretching at specific wave numbers, indicating the presence of alcohol and carboxylic acid. The spectrum of Vin B showed both stretching and bending vibrations, while Vin D had only alcohol bending vibrations which confirmed alcoholic and acetous fermentation. Carboxylic acid (acetic acid) is a key vinegar component. Alkenes and amines were identified at 1636 cm^{-1}. Similar compounds were detected in Vin A and C while Vin B and D contained additional compounds such as sulphates and phenols, which support microbial survival. Compounds such as sulphate, fluoro-compound, aromatic ester and alkyl aryl ether were also found in both samples, while phenol was found only in Vin D. Sulphate is an ester of sulphuric acid, and it is usually found in toothpaste, antacids and foods. It is an inert anion activated by nature to ester derivatives, which are vulnerable to reduction to sulphites [17]. Many anaerobic organisms exploit these processes for metabolic needs or the manufacture of sulphur compounds necessary for survival [17]. Therefore, the presence of sulphates supports the survival of microbiota present in vinegar samples. Previous studies revealed that the amine groups originated from biogenic amine generated by microbial decarboxylation of amino acids contained in vinegar [18]. Nutritional and medicinal benefits of vinegar are attributed to these bioactive components such as organic acids, phenolic compounds and amino acids which are generated from raw materials [8]. The GC-MS analysis also identified *n*-hexadecanoic acid (6.4 %), butanoic acid (5.2 %) and 9-octadecanoic acid (9.46 %) in Vin A; acetic acid (21 %), *n*-hexadecanoic acid (11 %) and oleic acid (9 %) in Vin B; acetic acid (10 %) and *n*-hexadecanoic acid (10 %) in Vin C and acetic acid (35 %), oxirane (13 %) and 2,3-butanediol (4.8 %) in Vin D.

Presence of some aromatic compounds in the vinegar samples may contribute to their flavours and sensory characteristics while the amino acids, organic acids, sugars, polyphenols, and melanoidins contents may be responsible for their nutritional, anti-inflammatory, antimicrobial, antifatigue and antitumor properties [1-6,10]. Presence of pentanol in Vin B indicated high acetic fermentation while the presence of acetic acid in all samples showed high vinegar quality. Medicinal, chemical and organoleptic qualities of vinegar also depend on raw materials and fermentation techniques which have been reported in a previous study [19]. This study revealed the presence of aromatic compounds in different vinegar samples, emphasizing the influence of raw materials and production methods on vinegar composition and quality.

CONCLUSION

Microbial population in the vinegar samples is diverse, with *Acetobacter spp* present in the locally-produced vinegar. Both locally and industrially produced vinegar samples share compound similarities, with acetic acid confirming that they were vinegar. Industrial vinegar contains higher acetic acid levels than locally produced vinegar. The presence of pathogenic *Legionella* and *Fusobacterium* in local vinegar may be of public health concern requiring pasteurization and purification for safe consumption.

DECLARATIONS

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Ethical approval

Not required.

Availability of data and materials

The datasets used and/or analyzed during the current study are available from the corresponding author on reasonable request.

Use of Artificial intelligence/Large language models

We declare also that we did not use Generative artificial intelligence (AI) and AI-assisted technologies in writing the manuscript.

Conflict of interest

No conflict of interest is associated with this work.

Contribution of authors

We declare that this work was done by the author(s) named in this article, and all liabilities pertaining to claims relating to the content of this article will be borne by the authors.

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