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Microbiology and antimicrobial effects of kombucha, a short overview

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ABSTRACT

Kombucha is a beverage usually prepared with black or green tea containing sucrose, and a synbiotic culture of bacteria and yeasts (SCOBY). This paper aims at offering an overview on kombucha microbiota, as well as on its nutritional composition, and antimicrobial effects. The microbiota of kombucha includes acetic acid bacteria (*Acetobacter*, *Gluconobacter*, *Gluconacetobacter*, *Komagataeibacter*), lactic acid bacteria (*Lactobacillus*, *Lactiplantibacillus*, *Lacticaseibacillus*) and yeasts (*Brettanomyces*, *Candida*, *Saccharomyces*, *Zygosaccharomyces*), depending on raw materials, starter cultures, and fermentation temperature. The second topic of this review is the production path and kombucha composition, with a synopsis from a quali-quantitative point of view of the most important compounds. Finally, the review examines the antimicrobial potential, focusing on both Gram-positive and Gram-negative bacteria.

An open question is on the probiotic status of kombucha; this review offers a contribution to this debate, suggesting for this beverage the status of post-biotic.

1. Introduction

Kombucha, also defined as fermented tea, is a beverage usually prepared with black or green tea containing sucrose and a synbiotic culture of bacteria and yeasts (SCOBY), which varies between fermentations (Kruk et al., 2021). Generally, kombucha is composed of two phases, that is a floating biofilm layer and a sour liquid (Kruk et al., 2021).

SCOBY consists of acetic acid bacteria (*Komagataeibacter*, *Gluconobacter*, *Acetobacter* species) (AAB), lactic acid bacteria (Lactobacillaceae, *Lactococcus*) (LAB), bifidobacteria, and yeasts (*Schizosaccharomyces pombe*, *Saccharomycodes ludwigii*, *Kloeckera apiculata*, *Saccharomyces cerevisiae*, *Zygosaccharomyces bailii*, *Torulaspora delbrueckii*, *Brettanomyces bruxellensis*) (Kruk et al., 2021; Villarreal-Soto et al., 2019); however, ther is a debate on the distinction between species essential for kombucha production and contaminant/not essential microorganisms (Harrison & Curtin, 2021). According to Coton et al. (2017), the viable count of bacteria and yeasts is at 6–7 log CFU/mL.

Some authors report a probiotic potential for kombucha, due to its high levels of LAB and bifidobacteria (Coton et al., 2017; Pei et al., 2020). However, the use of the term probiotic for kombucha has a big issue due to the high level of non-living microorganisms as a consquence of a long fermentation processes and pasteurisation of commercial kombucha; therefore, it is more suitable to refer to kombucha as a postbiotic, which is defined by ISAPP (The International Scientific Association of Probiotics and Prebiotics) as “non-living microorganisms and/or their components that provide health benefits to the host” (Antolak et al., 2021). In addition, according to Hill et al. (2014) traditional fermented foods cannot be simply labeled as “probiotics”; the main requirement for a claim of “probiotic food” is the isolation and indentification of strains with health-promoting effects.

There is an increasing number of papers focusing on kombucha, and an evaluation of the most important keywords and topics through VosViewer software reveals some areas of interest. The first one is on the chemistry, antioxidant activity, and effects on metabolism of kombucha (purple circles); a second area is on microbiology (green, blue, and yellow circles) with some topics covered (microbial consortia, end-products of fermentations, approaches for microorganisms’ identification and characterization, use of starter cultures or natural fermentations), while the third area is on controlled studies to demonstrate the health effects of kombucha (Fig. 1).

Thus, this figure suggests that kombucha should be described and studied at different levels; therefore, the main aim of this review is to offer a synopsis on the existing knowledge on kombucha, with a focus on

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some specific topics.

a) Kombucha production, and microbiota, with a qualitative description at species-level of the most important microorganisms.
b) Nutritional composition of kombucha, reporting both major and minor ingredients.
c) Potential benefits of kombucha, with a special emphasis on its antimicrobial effects towards a wide range of pathogens.

Finally, this review wants to contribute to the open debate on the use of the term probiotic of kombucha, offering the alternative definition of post-biotic.

2. Kombucha production and fermentation

The main materials required for the production are SCOBY and a liquid part of kombucha (back-slopping), tea or dried herb leaves, table sugar as sucrose source, and water, as summarized in Fig. 2; both SCOBY and the liquid part constitute the starter culture (Jayabalan et al., 2014).

Briefly, kombucha fermentation is generally as follows. Tea or dried herb leaves (1.5–10 g/L) are added to the tap water at 74–100 °C for 3–15 min; then, leaves are filtered and 5%–10% sucrose is added. SCOBY (7–40 g/L) and/or 10%–20% kombucha beverage is added to the infused tea containing sucrose in the glass jar, and cooled to room temperature (25 °C). The fermentation process begins by covering the matrix with a sterile cotton cloth, used as a protection from the surrounding environment (insects, dust, etc.) during the production; the process is conducted in contact with oxygen (Cetojevic-Simin et al., 2008; Fu et al., 2014; Gaggìa et al., 2018; Jayabalan et al., 2014; Kitwetcharoen et al., 2023; Malbaša et al., 2011; Martínez-Leal et al., 2020; Villarreal-Soto et al., 2019; Vitas et al., 2020; Vohra et al., 2019). The temperature required for fermentation is 24–28 °C (Gaggìa et al., 2018; Tu et al., 2019; Yıkmış & Tuğgüm, 2019; Ziska & Agustina, 2019). Green and black tea are generally used, but other leaves could be added, for example, rooibos (Gaggìa et al., 2018), winter savory tea (Cetojevic-Simin et al., 2008), African mustard leaves (Rahmani et al., 2019), peppermint, stinging nettle, wild thyme, elderberry and quince (Vitas et al., 2020), soy whey (Tu et al., 2019), purple basil (Yıkmış & Tuğgüm, 2019), yerba mate, lavender, oregano and fennel (Ramírez Tapias et al., 2022), lemon balm, thyme, sage and peppermint tea (Velicanski et al., 2013), mint, linden, sage (Kayisoglu & Coskun, 2020), olive leaves (Lazzaroli et al., 2023), nettles leaves and banana peels (Pure & Pure, 2016), reishi mushroom (Sknepnek et al., 2018).

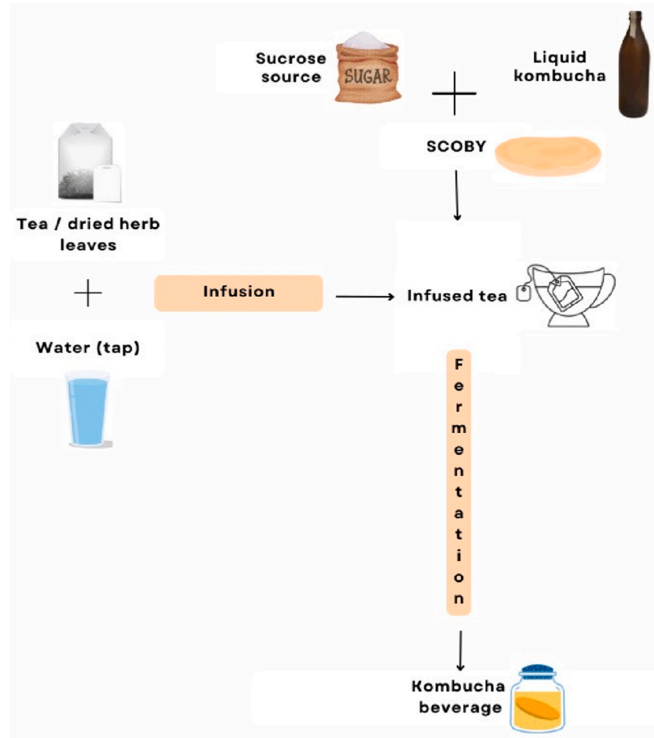

Fig. 2. Kombucha production process.

The metabolic transformation that enables the formation of

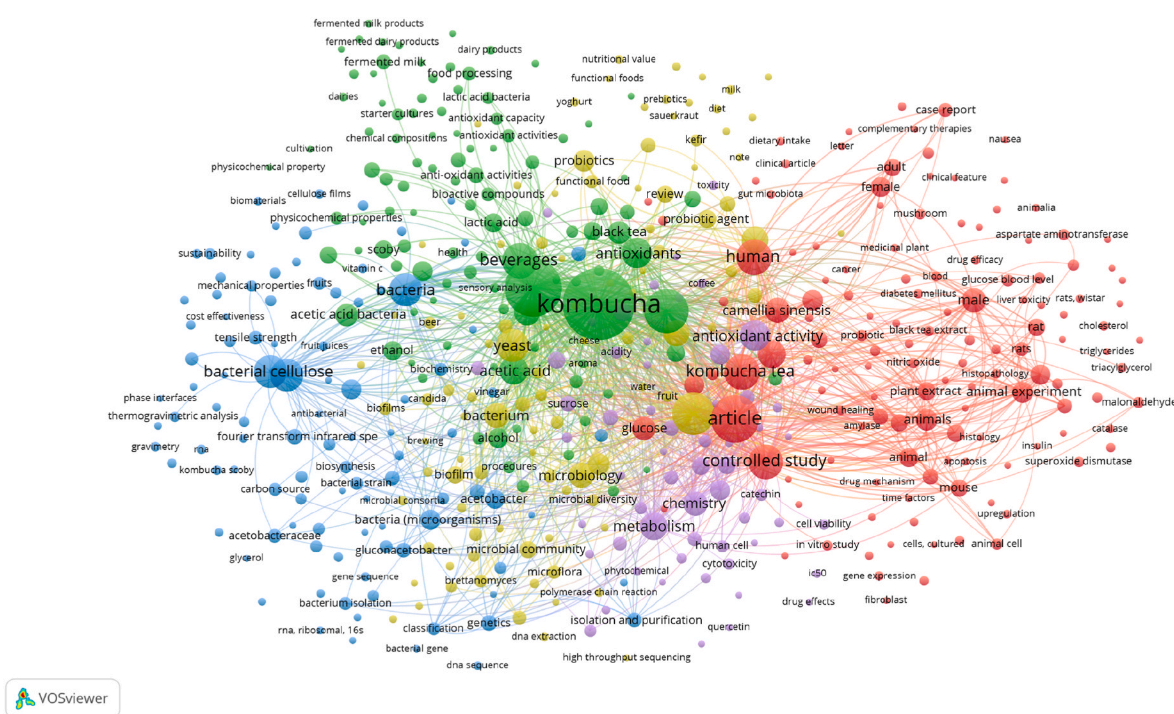

Fig. 1. Kombucha literature analysed through VosViewer tool.

kombucha is not limited to a simple fermentation (Tran et al., 2020). Fermentation processes frequently observed in kombucha production can be classified as lactic acid fermentation, alcoholic fermentation by yeasts, and acetic acid fermentation (oxidation of carbohydrates and alcohols by acetic acid bacteria) (Kruk et al., 2021). Sucrose at a concentration of 5%–20% is the primary carbon source (Martínez Leal et al., 2018), and is hydrolysed to glucose and fructose via invertase enzyme. This step explains the symbiosis observed in kombucha due to the inability of AAB to metabolise monosaccharides to produce organic acids (Neffe-Skocińska et al., 2017). As the system is in contact with oxygen, AAB produce acetic and gluconic acids (Chakravorty et al., 2016; Martínez Leal et al., 2018). Then, they convert gluconic acid into glucuronic acid, which has various health benefits (Lee, Jo, et al., 2021; Villarreal-Soto et al., 2019).

Finally, LAB either produce lactic acid by utilising glucose via the Embden-Meyerhof-Parnas pathway or lactic acid, ethanol, and carbon dioxide via the pentose phosphate pathway (Antolak et al., 2021).

3. Nutritional and chemical composition

Kombucha contains various enzymes (phytase, α-glycosidase, tannase), organic acids (acetic, gluconic, formic, glucuronic, lactic, oxalic, tartaric, malic, and citric acids), vitamins B_1, B_2, B_6, B_{12} and C, ethanol, polyphenols (gallic acid derivatives), copper, iron, manganese, zinc, nickel, F^-, CI^-, Br^-, I^-, NO_3^-, HPO_4^-, SO_4^- anions (Kaewkod et al., 2019; Mousavi et al., 2020; Villarreal-Soto et al., 2019). The most important polyphenols are theaflavin, thearubigin, and caffeine; a key-compound is also d-saccharic acid-1,4-lactone (DSL), whose concentration depends on the raw material (Chakravorty et al., 2016). Enzymes such as phytase, α-glycosidase, and tannase, which are active during the fermentation of kombucha, are crucial for the degradation of complex polyphenols into small phenolic compounds (Kaewkod et al., 2019), thus increasing the bioavailability of tea polyphenols (Tamer et al., 2021).

Generally, the bioavailability of polyphenols increases as a result of the conjugation of glucuronic acid with tea polyphenols (Martínez Leal et al., 2018).

Various health protective effects of glucuronic acid (GlcUA) and DSL have been reported (Lee, Jo, et al., 2021). DSL has hypocholesterolaemic, hepatoprotective, and antihyperglycaemic effects (Emiljanowicz & Malinowska-Pańczyk, 2020; Özdemir & Çon, 2017), while GlcUA is a precursor of vitamin C, and has several functions (toxin dextoxification, increase of the bioavailability of phenolic compounds by taking part in glucuronidation, and reduction of oxidative damage). In addition, vitamin C, polyphenols, and lactic acid in kombucha, together with GlcUA, play a role in reducing gastric cancer proliferation (Kitwetcharoen et al., 2023). An overview of kombucha composition is in Table 1.

4. Microbial community and dominant species of kombucha

There is not a single formula that describes the microbiota of kombucha, because it depends mainly on the starter cultures used in fermentation, but also on the raw materials (plants and other ingredients), the amount of sucrose, the fermentation temperature, and the duration of the process (Diez-Ozaeta & Astiazaran, 2022). It is worth mentioning that kombucha fermentation takes place mainly in the presence of AAB and yeast, although variations in bacteria or yeasts species are observed (Chakravorty et al., 2016), while LAB presence is not a *sine qua non conditio*, although they constitute an important part of the microbiota of kombucha (Coton et al., 2017; Nguyen, Dong, et al., 2015).

As reported in the introduction, the microbiota of SCOBY is a driver for the composition of the microbiota of kombucha. In a study examining the microbial content of five different SCOBYs, *Gluconacetobacter* was the predominant genus; in addition, low levels of *Acetobacter* were

Table 1
Chemical composition of kombucha.

Compound		Amount
Vitamins	Vitamin C	1.51 mg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		25–30 mg/L, and 8–10 mg/L (Malbaša et al., 2011)[b]
		~0.25–1.00 mg/100 mL (Lončar et al., 2006)[c]
		0.40–1.20 mg/L (Vitas et al., 2018)[d]
		0.02 mg/100 g (Phung et al., 2023)[e]
		0.14–6.95 mg/mL (Klawpiyapamornkun et al., 2023)[f]
		0.60–0.70 g/L (Kaewkod et al., 2019)[ww]
		1.55 g/L (Ivanišová et al., 2019)[qq]
	Thiamine	0.74 mg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		0.05 mg/100 g (Phung et al., 2023)[e]
	Riboflavin	8–10 mg/100 mL (Malbaša et al., 2011)[b]
		ND (Phung et al., 2023)[e]
	Niacin	0.07 mg/100 g (Phung et al., 2023)[e]
	Pyridoxine	0.52 mg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		0.01 mg/100 g (Phung et al., 2023)[e]
	Folic acid	0.01 mg/100 g (Phung et al., 2023)[e]
	Cyanocobalamin	0.84 mg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		ND (Phung et al., 2023)[e]
Minerals	Manganese	31.24 mg/kg (Phung et al., 2023)[e]
		0.07 g/100 g (Jayabalan et al., 2010)[g]
		0.462 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		1.57 mg/L (Ivanišová et al., 2019)[qq]
	Phosphorus	63.78 mg/kg (Phung et al., 2023)[e]
		0.02 g/100 g (Jayabalan et al., 2010)[g]
	Magnesium	77.80 mg/kg (Phung et al., 2023)[e]
		0.40 g/100 g (Jayabalan et al., 2010)[g]
	Potassium	991.95 mg/kg (Phung et al., 2023)[e]
		0.17 g/100 g (Jayabalan et al., 2010)[g]
	Sodium	16.96 mg/kg (Phung et al., 2023)[e]
		0.30 g/100 g (Jayabalan et al., 2010)[g]
	Calcium	72.30 mg/kg (Phung et al., 2023)[e]
		0.03 g/100 g (Jayabalan et al., 2010)[g]
	Iron	7.60 mg/kg (Phung et al., 2023)[e]
		0.05 g/100 g (Jayabalan et al., 2010)[g]
		0.353 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		0.31 mg/L (Ivanišová et al., 2019)[qq]
	Nitrogen	1.4 g/kg (Phung et al., 2023)[e]
	Nickel	0.346 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		0.42 mg/L (Ivanišová et al., 2019)[qq]
	Copper	20.85 mg/kg (Phung et al., 2023)[e]
		0.237 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		0.14 mg/L (Ivanišová et al., 2019)[qq]
	Zinc	71.75 mg/kg (Phung et al., 2023)[e]
		0.09 g/100 g (Jayabalan et al., 2010)[g]
		0.154 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		0.53 mg/L (Ivanišová et al., 2019)[qq]
	Chlorine	0.04 g/100 g (Jayabalan et al., 2010)[g]
	Sulphur	0.12 g/100 g (Jayabalan et al., 2010)[g]
	Lead	0.005 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		0.12 mg/L (Ivanišová et al., 2019)[qq]
	Cobalt	0.004 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		0.23 mg/L (Ivanišová et al., 2019)[qq]
	Chromium	0.001 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		ND (Ivanišová et al., 2019)[qq]
	Cadmium	0.00 μg/mL (Bauer-Petrovska & Petrushevska-Tozi, 2000)[a]
		ND (Ivanišová et al., 2019)[qq]

(*continued on next page*)

Table 1 (*continued*)

Compound		Amount
Polyphenols	Total	206.0–320.1 mg/L (Jakubczyk et al., 2020)[h]
	Isorhamnetin	156.38 μg/mL (Bhattacharya et al., 2016)[s]
	Catechin	0.05–2.00 mg/L (Gaggìa et al., 2018)[i]
		0.3–1.5 μg/mL (Yang et al., 2022)[y]
		68.17 μg/mL (Bhattacharya et al., 2016)[s]
	(−)-epicatechin	1.3–11.6 μg/mL (Yang et al., 2022)[y]
		0.05–50.0 mg/L (Gaggìa et al., 2018)[i]
		~10.0–250.0 mg/L (Zhou et al., 2022)[w]
	(−)-epicatechin gallate	4.7–32.1 μg/mL (Yang et al., 2022)[y]
		0.05–1.0 mg/L (Gaggìa et al., 2018)[i]
		~2.5–225.0 mg/L (Zhou et al., 2022)[w]
	(−)-epigallocatechin	0.1–80.0 mg/L (Gaggìa et al., 2018)[i]
	(−)-epigallocatechin gallate	7.0–51.1 μg/mL (Yang et al., 2022)[y]
		12.5–50.0 mg/L (Gaggìa et al., 2018)[i]
		20.24 μg/mL (La Torre et al., 2021)[q]
		~200.0–600.0 mg/L (Zhou et al., 2022)[w]
	(+)-gallocatechin	0.1–5.0 mg/L (Gaggìa et al., 2018)[i]
		~40.0–120.0 mg/L (Zhou et al., 2022)[w]
	Gallocatechin gallate	~10.0–20.0 mg/L (Zhou et al., 2022)[w]
	Vitexin	1.91 μg/mL (Ivanišová et al., 2019)[u]
	Rutin	13.35 μg/mL (Ivanišová et al., 2019)[u]
	Syringic acid	4.51 μg/mL (Ivanišová et al., 2019)[u]
	Gallic acid	30.23 μg/mL (Ivanišová et al., 2019)[u]
		~35.0–80.0 mg/L (Zhou et al., 2022)[w]
	Ferulic acid	0.33 μg/mL (Ivanišová et al., 2019)[u]
		2.97 μg/mL (La Torre et al., 2021)[q]
	Ellagic acid	1.93 μg/mL (Ivanišová et al., 2019)[u]
		~4.0–11.0 mg/L (Zhou et al., 2022)[w]
	p-Coumaric acid	0.79 μg/mL (Ivanišová et al., 2019)[u]
	Protocatechuic acid	2.11 μg/mL (Ivanišová et al., 2019)[u]
	Chlorogenic acid	14.86 μg/mL (Ivanišová et al., 2019)[u]
		29.60 μg/mL (La Torre et al., 2021)[q]
	Quercetin	ND (La Torre et al., 2021)[q]
	Quercitrin	~3.0–9.0 mg/L (Zhou et al., 2022)[w]
	Myricetin	~1.25–2.0 mg/L (Zhou et al., 2022)[w]
	Astragalin	~5.0–20.0 mg/L (Zhou et al., 2022)[w]
Alcohol		0.15%–0.40% (Alderson et al., 2021)[j]
		2.0%–3.0% (Jakubczyk et al., 2020)[h]
		0.4% (Ivanišová et al., 2019)[qq]
	Ethanol	0.09%–0.99% (v/v) (Phung et al., 2023)[e]
		1.14–5.83 mg/mL (Gaggìa et al., 2018)[i]
		0.59%–0.84% (v/v) (Akbarirad et al., 2017)[k]
		1.00–4.00 g/L (Tanticharakunsiri et al., 2021)[x]
		0.93–4.4 g/L (Velicanski et al., 2013)[xx]
		0.00%–1.30% (Yang et al., 2022)[y]
		0.14 g/L (Chakravorty et al., 2016)[z]
		1.04%–1.01% (Coton et al., 2017)[o]
		3.28 mmol/L (Tan et al., 2020)[p]
Sugars	Glucose	22.93 g/100 g (Phung et al., 2023)[e]
		15.12–18.10 mg/mL (Gaggìa et al., 2018)[i]
		~1.00–2.00 g/L (Lončar et al., 2006)[c]
		4.60 mmol/L (Tan et al., 2020)[p]
		9.35 g/L (Ivanišová et al., 2019)[qq]
	Fructose	18.87 g/100 g (Phung et al., 2023)[e]
		5.50–8.83 mg/mL (Gaggìa et al., 2018)[i]
		~0.75–3.20 g/L (Lončar et al., 2006)[c]
		21.01 mmol/L (Tan et al., 2020)[p]
		1.41 g/L (Ivanišová et al., 2019)[qq]
	Sucrose	10.80 g/100 g (Phung et al., 2023)[e]

Table 1 (*continued*)

Compound		Amount
		26.13–33.65 mg/mL (Gaggìa et al., 2018)[i]
		7.5–9.5 g/100 mL (Jakubczyk et al., 2020)[h]
		2.3–7.2 g/100 mL (Akbarirad et al., 2017)[k]
		~22.5–32.5 g/L (Lončar et al., 2006)[c]
		11.51 mmol/L (Tan et al., 2020)[p]
		17.81 g/L (Ivanišová et al., 2019)[qq]
Organic acids	Acetic acid	20.90%–46.06% (Phung et al., 2023)[e]
		4.34–6.70 mg/mL (Abou-Taleb et al., 2017)[l]
		4.89–9.18 mg/mL (Gaggìa et al., 2018)[i]
		9071.02–9147.40 mg/L (Jakubczyk et al., 2020)[h]
		3.4–3.8 g/100 mL (Akbarirad et al., 2017)[k]
		16.71–78.28 mg/mL (Klawpiyapamornkun et al., 2023)[f]
		~6.0–14.0 g/L (Wang et al., 2022)[m]
		0.32–2.25 g/L (Utoiu et al., 2018)[n]
		12.53 g/L (Chakravorty et al., 2016)[z]
		8.17–15.72 mmol/L (Coton et al., 2017)[o]
		0.33 mmol/L (Tan et al., 2020)[p]
		12.53 mg/mL (Bhattacharya et al., 2013)[r]
		5.77 g/L (Tu et al., 2019)[t]
		10.42–11.15 g/L (Kaewkod et al., 2019)[ww]
		1.55 g/L (Ivanišová et al., 2019)[qq]
		1131.8–2755.8 mg/L (Shahbazi et al., 2018)[zz]
	Citric acid	590.00 mg/100 g (Phung et al., 2023)[e]
		~0.5–1.0 g/L (Wang et al., 2022)[m]
		1.07 g/L (Tu et al., 2019)[t]
		0.05 g/L (Ivanišová et al., 2019)[qq]
		39.22–471.58 mg/L (Shahbazi et al., 2018)[zz]
	Formic acid	ND (Phung et al., 2023)[e]
		0.78 g/L (Tu et al., 2019)[t]
	Gluconic acid	6.93–15.35 mg/mL (Klawpiyapamornkun et al., 2023)[f]
		0.94–2.55 g/L (Utoiu et al., 2018)[n]
		6.38 g/L (Chakravorty et al., 2016)[z]
		0.15–0.20 mmol/L (Coton et al., 2017)[o]
		6.59 mmol/L (Tan et al., 2020)[p]
		6.38 mg/mL (Bhattacharya et al., 2013)[r]
		41.42–70.11 g/L (Kaewkod et al., 2019)[ww]
	Glucuronic acid	1.96–3.23 mg/mL (Gaggìa et al., 2018)[i]
		ND (Klawpiyapamornkun et al., 2023)[f]
		0.05 mmol/L (Coton et al., 2017)[o]
		2.30 g/L (Tu et al., 2019)[t]
		0.07–1.58 g/L (Kaewkod et al., 2019)[ww]
		118.92–1158.2 mg/L (Shahbazi et al., 2018)[zz]
	DSL (D-Saccharic acid 1,4-lactone)	0.44–1.26 mg/mL (Klawpiyapamornkun et al., 2023)[f]
		1.32 g/L (Chakravorty et al., 2016)[z]
		1.34 mg/mL (Bhattacharya et al., 2013)[r]
		3.44–5.23 g/L (Kaewkod et al., 2019)[ww]
	Lactic acid	~0.2–0.3 g/L (Wang et al., 2022)[m]
		0.37–0.72 g/L (Utoiu et al., 2018)[n]
		15.37–10.46 mmol/L (Coton et al., 2017)[o]

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Table 1 (*continued*)

Compound		Amount
		90.81–269.83 mg/L (Shahbazi et al., 2018)[zz]
	Oxalic acid	∼0.05–0.2 g/L (Wang et al., 2022)[m]
		8.4–24.8 mg/L (Shahbazi et al., 2018)[zz]
	Tartaric acid	∼0.1–0.2 g/L (Wang et al., 2022)[m]
		0.23 g/L (Ivanišová et al., 2019)[qq]
		16.8–73.4 mg/L (Shahbazi et al., 2018)[zz]
	Pyruvic acid	∼0.05–0.1 g/L (Wang et al., 2022)[m]
	Malic acid	∼1.8–3.0 g/L (Wang et al., 2022)[m]
		0.13 mmol/L (Tan et al., 2020)[p]
		89.0–312.0 mg/L (Shahbazi et al., 2018)[zz]
	α-ketoglutaric acid	∼0.1–0.5 g/L (Wang et al., 2022)[m]
	Succinic acid	∼0.2–0.3 g/L (Wang et al., 2022)[m]
		3.05 g/L (Kaewkod et al., 2019)[ww]
	Citric acid	∼0.5–0.1 g/L (Wang et al., 2022)[m]
		ND – 0.04 g/L (Utoiu et al., 2018)[n]
	Propionic acid	0.16–0.42 g/L (Utoiu et al., 2018)[n]
	Butyric acid	0.28–1.06 g/L (Utoiu et al., 2018)[n]
Caffeine		100.72 μg/mL (Ivanišová et al., 2019)[u]
		39.00 μg/mL (Miranda et al., 2016)[v]
		15.1–112.6 μg/mL (Yang et al., 2022)[y]
		0.713 g/L (Chakravorty et al., 2016)[z]
		356.25 μg/mL (La Torre et al., 2021)[q]
		∼80.0–175.0 mg/L (Zhou et al., 2022)[w]
Amino acids	Isoleucine	35.2 mg/g (Jayabalan et al., 2010)[g]
	Leucine	35.9 mg/g (Jayabalan et al., 2010)[g]
	Lysine	48.0 mg/g (Jayabalan et al., 2010)[g]
	Methionine	11.3 mg/g (Jayabalan et al., 2010)[g]
	Phenylalanine	22.3 mg/g (Jayabalan et al., 2010)[g]
	Threonine	13.2 mg/g (Jayabalan et al., 2010)[g]
	Valine	22.3 mg/g (Jayabalan et al., 2010)[g]
	Tryptophan	12.3 mg/g (Jayabalan et al., 2010)[g]
	Alanine	41.9 mg/g (Jayabalan et al., 2010)[g]
	Arginine	30.8 mg/g (Jayabalan et al., 2010)[g]
	Aspartic acid	42.0 mg/g (Jayabalan et al., 2010)[g]
	Cysteine	15.2 mg/g (Jayabalan et al., 2010)[g]
	Glutamic acid	42.3 mg/g (Jayabalan et al., 2010)[g]
	Glycine	17.2 mg/g (Jayabalan et al., 2010)[g]
	Histidine	10.6 mg/g (Jayabalan et al., 2010)[g]
	Proline	35.2 mg/g (Jayabalan et al., 2010)[g]
	Serine	22.2 mg/g (Jayabalan et al., 2010)[g]
	Tyrosine	18.6 mg/g (Jayabalan et al., 2010)[g]
Enzymes	Mn-SOD	+ (Tanticharakunsiri et al., 2021)[x]
	Catalase	+ (Tanticharakunsiri et al., 2021)[x]
	GRe	+ (Tanticharakunsiri et al., 2021)[x]

Table footnotes.

[a] Black tea kombucha, 6–15 days of fermentation.
[b] Black tea kombuchas, 10th day of fermentation.
[c] Black tea kombuchas, 10th day of fermentation.
[d] Yarrow kombuchas, 7th day of fermentation.
[e] Black tea kombuchas with and without different amounts of pineapple peel and seed, 14th day of fermentation.
[f] Green tea kombuchas with and without Indian gooseberry supplement, 21st day of fermentation.
[g] Dried tea fungus, 14th day of fermentation of black tea.
[h] White, green, black and red tea kombuchas, 14th day of fermentation.
[i] Green tea, black tea and rooibos tea kombuchas, 14th day of fermentation.
[j] Black tea, kawakawa (*Piper excelsum*) leaves, hops and black pepper kombuchas, 7th day of fermentation.
[k] Pomegranate, red grape, sour cherry and apple juice kombuchas, 14th day of fermentation.
[l] Black tea, rice and barley kombuchas, 8th and 10th day of fermentation.
[m] Black and green tea kombuchas, 15th day of fermentation.
[n] Green tea kombuchas with and without pollen, 13th day of fermentation.
[o] Green and black tea kombuchas, 8th day of fermentation.
[p] Black tea with soursop juice kombucha, 14th day of fermentation.
[r] Black tea kombucha, 14th day of fermentation.
[s] Black tea kombucha, 14th day of fermentation.
[t] Black tea with soy whey kombucha, 7th day of fermentation.
[u] Black tea kombucha, 7th day of fermentation.
[v] Black tea kombucha, 14th day of fermentation.
[y] Commercial kombuchas of black tea, green tea, or both, and/various flavoring ingredients, unknown fermentation day.
[z] Black tea kombucha, 14th day of fermentation.
[q] Black tea kombucha, 30th day of fermentation.
[w] Green and black tea kombuchas, 15th day of fermentation.
[x] Mint and oolong tea kombuchas, 14th day of fermentation.
[xx] Kombucha from medicinal herbs belonging to Lamiaceae family: lemon balm, thyme, peppermint and sage, 5–12 days of fermentation.
[ww] Green tea, oolong tea, and black tea kombuchas, 15th day of fermentation.
[qq] Black tea kombucha, 7th day of fermentation.
[zz] Green tea with cinnamon, cardamom, and Shirazi thyme kombuchas, 16th day of fermentation.

found, while *Lactobacillus* could be recovered at high frequencies. *Komagataeibacter*, *Acetobacter, Gluconobacter,* and *Gluconacetobacter* were the most important AAB, with a major role of *K. intermedius, K. rhaeticus, K. saccharivorans, K. hansenii, A. xylinum, A. aceti, A. pasteurians*, *A. tropicalis*, and *G. oxydans* at species level (Table 2) (Arıkan et al., 2020; De Filippis et al., 2018; Gaggìa et al., 2018; Reva et al., 2015).

LAB are very important for the production of DSL (Nguyen, Nguyen, et al., 2015), mainly lactobacilli and lactococci, as shown in Table 2 (De Filippis et al., 2018; Lee, Jo, et al., 2021).

Yeasts biota includes *Brettanomyces, Hanseniaspora, Saccharomyces, Schizosaccharomyces, Dekkera, Zygosaccharomyces, Pichia, Candida,* and *Lachancea* (Chakravorty et al., 2016; Landis et al., 2022; Marsh et al., 2014; Tran et al., 2021), with a high recovery of *B. bruxellensis, H. valbyensis, S. cerevisiae, Schizo. pombe, D. anomala,* and *Z. bailii* (Table 2).

The strong differences in kombucha microbiota probably depend on the different approaches or protocols used, as well as on the different kinds of kombucha and sampling time. However, some useful information could be gained from Marsh et al. (2014), who used a metagenomic approach to analyse the microbiota of kombucha. They identified five main bacterial phyla, including Actinobacteria, Bacteroidetes, *Deinococcus-Thermus*, Firmicutes, and Proteobacteria. Focusing on the data after 10 days, the genus mainly represented in all samples was *Gluconacetobacter*, with lower recovery frequencies of lactobacilli (Fig. 3). The same trend was found for biofilm, with just one sample difference. Yeast biota was mainly represented by *Zygosaccharomyces* spp. (79%–99%).

The importance of AAB and their dominance was highlighted also by Kaashyap et al. (2021), who found that the genus mostly represented was *Acetobacter* spp., followed by *Komagataeibacter*, and *Gluconobacter*.

From a quantitative point of view, the levels of the different groups are highly variable, depending on the raw material, as well as on the methodologies used by the researchers to perform experiments. Neverthless it was possible to find some details from various bibliographic references and build a violin plot (Fig. 4). This graph is a powerful tool for the visualization of data from both small-sized and high-sized samples, and enables the reader to understand whether data distribution follows a normal trend, or if it is unimodal, or multimodal. The plot highlights the high variability of AAB levels (5.5–8.5 log CFU/mL in green tea and 4.5–8.5 log CFU/mL in black tea kombucha); a certain degree of variability was also found for yeasts (6.0–8.0 log CFU/mL), and for LAB in green tea kombucha (5.8–8.0 log CFU/mL), while the variability was lower for LAB in black tea kombucha (5.5–6.5 log CFU/mL).

5. Probiotic microorganisms from kombucha

Kombucha has several health-promoting effects, including antioxidant, antitumor, anti-inflammatory, antihypertensive, antidiabetic, hypocholesteremic, and hepatoprotective properties, as well as the ability to modulate gut microbiota (Diez-Ozaeta & Astiazaran, 2022; Moreira et al., 2022; Permatasari et al., 2022), but it is controversial

Table 2
Microbiota of kombucha.

GENUS	SPECIES	TYPE OF KOMBUCHA	REFERENCES
ACETIC ACID BACTERIA			
Acetobacter	spp.	Green and black tea, biofilm	(De Filippis et al., 2018; Fabricio et al., 2022; Góes-Neto et al., 2021; Marsh et al., 2014; Watawana et al., 2016)
	indonesiensis	Black and green tea	Tran et al. (2022)
	xylinum	Black tea	(Al-Mohammadi et al., 2021; Sievers et al., 1995)
	aceti	Black tea	(Al-Mohammadi et al., 2021; Sievers et al., 1995)
	pasteurianus	Green and black tea	(Al-Mohammadi et al., 2021; Landis et al., 2022; Sievers et al., 1995)
	lovaniensis	Green tea	Coton et al. (2017)
	okinawensis	Black and green tea	Coton et al. (2017)
	peroxydans	Green tea	Coton et al. (2017)
	syzygii	Green tea	Coton et al. (2017)
	tropicalis	Green and black tea	Coton et al. (2017)
		Green tea	Landis et al. (2022)
	senegalensis	Green tea	Landis et al. (2022)
	pomorum	Green tea	Landis et al. (2022)
	musti	Green tea	Landis et al. (2022)
	nitrogenifigens	No data available (reported as only "kombucha")	Dutta and Gachhui (2006)
	papayae	Black tea	Tran et al. (2021)
Gluconobacter	spp.	Black tea	(Chakravorty et al., 2016; Fabricio et al., 2022; Reva et al., 2015)
	entanii	Rooibos, green tea	Gaggìa et al. (2018)
	oxydans	Black tea, green tea, lemon verbena, mallow, wild rose, peppermint	(Grassi et al., 2022; Lee, Jo, et al., 2021; Podolich et al., 2017; Reva et al., 2015; Villarreal-Soto et al., 2020)
Gluconacetobacter	spp.	Green and black tea, biofilm,	(Arıkan et al., 2020; De Filippis et al., 2018; Fabricio et al., 2022; Góes-Neto et al., 2021; Landis et al., 2022; Marsh et al., 2014; Villarreal-Soto et al., 2020; Watawana et al., 2016)
	saccharivorans	Green and black tea	De Filippis et al. (2018)
	xylinus	Green and black tea	De Filippis et al. (2018)
	europaeus	Green and black tea	Coton et al. (2017)
	hansenii	Black tea	Coton et al. (2017)
	intermedius	Green and black tea	Coton et al. (2017)
	liquefaciens	Black tea	Coton et al. (2017)
	xylinus	Green tea	Coton et al. (2017)
	takamatsuzukensis	Black tea	Tran et al. (2021)
	diazotrophicus	Black tea	Reva et al. (2015)
	entanii	Black tea	Reva et al. (2015)
	cerinus	Black tea	Coton et al. (2017)
	oxydans	Green and black tea	(Coton et al., 2017; Landis et al., 2022)
Komagataeibacter	spp.	Rooibos, green tea, black tea	(Arıkan et al., 2020; Chakravorty et al., 2016; Fabricio et al., 2022; Gaggìa et al., 2018; Góes-Neto et al., 2021; Podolich et al., 2017)
	intermedius	Rooibos, green tea, black tea	(Gaggìa et al., 2018; Landis et al., 2022; Reva et al., 2015; Villarreal-Soto et al., 2020)
	rhaeticus	Rooibos, green and black tea	(Arıkan et al., 2020; Gaggìa et al., 2018; Góes-Neto et al., 2021; Landis et al., 2022; Lee, Barh, et al., 2021; Semjonovs et al., 2017; Villarreal-Soto et al., 2020)
	saccharivorans	Rooibos, green tea, black tea, lemon, verbena, mallow, wild rose, peppermint	(Gaggìa et al., 2018; Góes-Neto et al., 2021; Grassi et al., 2022; Landis et al., 2022; Mukadam et al., 2016)
	xylinus	Green and black tea	(Landis et al., 2022; Reva et al., 2015; Villarreal-Soto et al., 2020)
	hansenii	Green tea and black tea	(Góes-Neto et al., 2021; Landis et al., 2022; Lee et al., 2021a, 2021b; Semjonovs et al., 2017)
	swingsii	Green tea	Landis et al. (2022)
	europaeus	Green and black tea	(Landis et al., 2022; Villarreal-Soto et al., 2020)
	medellinensis	Green tea	Landis et al. (2022)
	cocois	Green tea	Landis et al. (2022)
	diospyri	Green tea	Landis et al. (2022)
	nataicola	Green and black tea	(Landis et al., 2022; Reva et al., 2015)

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Table 2 (*continued*)

GENUS	SPECIES	TYPE OF KOMBUCHA	REFERENCES
	oboediens	Black tea	Lee, Barh, et al. (2021)
Novacetimonas	*hansenii*	Green tea, lemon verbena, mallow, wild rose, peppermint	Grassi et al. (2022)
Tanticharoemia	*sakaeratensis*	Green tea	Coton et al. (2017)
LACTIC ACID BACTERIA			
Enterococcus	*faecium*	Green tea	Landis et al. (2022)
Lactobacillus	spp.	Black tea, biofilm	(Chakravorty et al., 2016; Lee, Jo, et al., 2021; Marsh et al., 2014; Watawana et al., 2016)
	delbrueckii	Black tea	Lee, Jo, et al. (2021)
	acidophilus	Black tea	Al-Mohammadi et al. (2021)
Lacticaseibacillus	*casei*	Black tea	Lee, Jo, et al. (2021)
Lactiplantibacillus	*plantarum*	Green tea	Landis et al. (2022)
Ligilactobacillus		Black tea	Fabricio et al. (2022)
Limosilactobacillus	*fermentum*	Black tea	Al-Mohammadi et al. (2021)
Lactococcus	spp.	Green, black tea, biofilm	Marsh et al., 2014; De Filippis et al., 2018; Watawana et al., 2016
Liquorilactobacillus	spp.	Black tea	Fabricio et al. (2022)
	ghanensis	Green tea	Landis et al. (2022)
	nagelii	Green and black tea	(Coton et al., 2017; Landis et al., 2022)
	satsumensis	Green tea	Coton et al. (2017)
Leuconostoc	spp.	Biofilm	Watawana et al. (2016)
Oenococcus	*oeni*	Green and black tea	(Coton et al., 2017; Lee, Jo, et al., 2021)
Sporolactobacillus	*shoreae*	Black tea	(Lee, Jo, et al., 2021)
Streptococcus	spp.	Green and black tea	De Filippis et al. (2018)
Weissella	spp.	Black tea	Chakravorty et al. (2016)
OTHER BACTERIA			
Acidomonas	*methanolica*	Green tea	Landis et al. (2022)
Acidiphilium	spp.	Black tea	Góes-Neto et al. (2021)
Bifidobacterium	spp.	Black tea and biofilm	Chakravorty et al., 2016; Watawana et al., 2016
	bifidum	Black tea	(Lee, Jo, et al., 2021)
	longum	Black tea	(Lee, Jo, et al., 2021)
Burkholderia	spp.	Black tea	(Góes-Neto et al., 2021; Reva et al., 2015)
Collinsella	spp.	Black tea	Chakravorty et al. (2016)
Corynebacterium	spp.	Green and black tea	De Filippis et al. (2018)
Enterobacter	spp.	Black tea	Chakravorty et al. (2016)
Herbaspirillum	spp.	Black tea	Reva et al. (2015)
	putei	Black tea	Reva et al. (2015)
Halomonas	spp.	Black tea	Reva et al. (2015)
	phocaea	Black tea	Reva et al. (2015)
Propionibacterium	spp.	Green and black tea	De Filippis et al. (2018)
Pseudomonas	spp.	Black tea	(Góes-Neto et al., 2021; Lee, Barh, et al., 2021)
Ralstonia	*pickettii*	Black tea	(Lee, Jo, et al., 2021)
Shewanella	*algae*	Black tea	Reva et al. (2015)
	haliotis	Black tea	Reva et al. (2015)
Zymomonas	spp.	Black tea	Fabricio et al. (2022)
YEASTS			
Brettanomyces/ Dekkera	spp.	Black tea, biofilm	Góes-Neto et al., 2021; Marsh et al., 2014; Watawana et al., 2016; Fabricio et al., 2022
	anomala	Green and black tea, lemon verbena, mallow, wild rose, peppermint	Grassi et al., 2022; Coton et al., 2017; Podolich et al., 2017; Reva et al., 2015
	bruxellensis	Black tea, rooibos	(Coton et al., 2017; Gaggìa et al., 2018; Landis et al., 2022; Tran et al., 2022)
	naardenensis	Green and black tea	Landis et al. (2022)
Candida	spp.	Black tea	(Góes-Neto et al., 2021; Reva et al., 2015)
	boidinii	Green and black tea	Coton et al. (2017)
	parapsilosis	Black tea	Chakravorty et al. (2016)
	stellata	Black tea	Teoh et al. (2004)
	stellimalicola	Black tea	Chakravorty et al. (2016)
	tropicalis	Black tea	Chakravorty et al. (2016)
Debaryomyces	*hansenii*	Black tea	Chakravorty et al. (2016)
Eremothecium	*cymbalariae*	Black tea	Chakravorty et al. (2016)
	ashbyii	Black tea	Chakravorty et al. (2016)
Hanseniaspora	spp.	Black tea	Fabricio et al. (2022)
	meyeri	Black tea	Chakravorty et al. (2016)
	uvarum	Black tea	Chakravorty et al. (2016)
	valbyensis	Green and black tea	Coton et al., 2017; Tran et al., 2021, 2022
	vineae	Black tea	Chakravorty et al. (2016)
Kazachstania	spp.	Black tea	Marsh et al. (2014)
	exigua	Black tea	Chakravorty et al. (2016)
	telluris	Black tea	Chakravorty et al. (2016)
Kluyveromyces	*marxianus*	Black tea	Chakravorty et al. (2016)
Lachancea	spp.	Black tea	Góes-Neto et al. (2021)
	fermentati	Black tea or other unspecified matrices	Chakravorty et al. (2016)

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Table 2 (*continued*)

GENUS	SPECIES	TYPE OF KOMBUCHA	REFERENCES
	kluyveri	Black tea	Chakravorty et al. (2016)
	thermotolerans	Black tea	Chakravorty et al. (2016)
Leucosporidiella	spp.	Black tea kombucha biofilm	Marsh et al. (2014)
Merimbla	*ingelheimense*	Black tea	Chakravorty et al. (2016)
Meyerozyma	*caribbica*	Black tea	Chakravorty et al. (2016)
	guilliermondii	Black tea	Chakravorty et al. (2016)
Pichia	spp.	Black tea and biofilm	Watawana et al. (2016)
	occidentalis	Black tea	Reva et al. (2015)
	cecembensis	Black tea	Reva et al. (2015)
	fermentans	Black tea	Reva et al. (2015)
	membranifaciens	Green and Black tea	(Coton et al., 2017; Landis et al., 2022)
	mexicana	Black tea	Chakravorty et al. (2016)
	kudriavzevii	Black tea	Tsilo et al. (2021)
Rhodotorula	*mucilaginosa*	Black tea	Teoh et al. (2004)
Saccharomyces	*cerevisiae*	Green and black tea	(Al-Mohammadi et al., 2021; Chakravorty et al., 2016; Coton et al., 2017; Fabricio et al., 2022; Góes-Neto et al., 2021; Landis et al., 2022; Tran et al., 2021, 2022)
	uvarum	Black tea	Coton et al. (2017)
Saccharomycopsis	*fibuligera*	Black tea	Chakravorty et al. (2016)
Saccharomycodes	*ludwigii*	Green tea	Landis et al. (2022)
Schizosaccharomyces	*pombe*	Green and Black tea	(Al-Mohammadi et al., 2021; Góes-Neto et al., 2021; Landis et al., 2022; Teoh et al., 2004; Villarreal-Soto et al., 2020)
Sporopachydermia	*lactativora*	Black tea	Chakravorty et al. (2016)
Starmera	*amethionina*	Black tea	Chakravorty et al. (2016)
	caribaea	Black tea	Chakravorty et al. (2016)
Torulospora	*delbreuckii*	Black tea	Teoh et al. (2004)
	microellipsoides	Green tea	Coton et al. (2017)
Yarrowia	*lipolytica*	Black tea	Reva et al. (2015)
Zygosaccharomyces	spp.	Green and black tea, biofilm, lemon verbena, mallow, wild rose, peppermint Black tea	(Arıkan et al., 2020; Grassi et al., 2022; Marsh et al., 2014; Watawana et al., 2016)
	bailii	Green and black tea	(Arıkan et al., 2020; Landis et al., 2022; Mukadam et al., 2016; Podolich et al., 2017; Teoh et al., 2004)
	mellis	Green tea	Landis et al. (2022)
	parabailii		Gaggìa et al., 2018; Landis et al., 2022
	rouxii	Green tea	Landis et al. (2022)
Zygotorulaspora	*florentina*	Black and green tea	Coton et al. (2017)
Zygowilliopsis	*californica*	Black tea	Chakravorty et al. (2016)

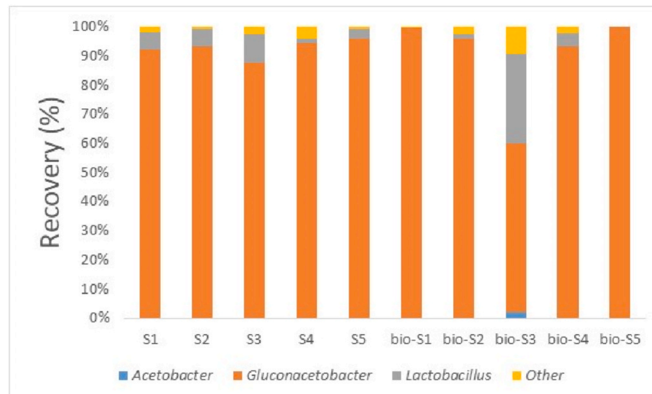

Fig. 3. Bacterial biota of kombucha. Data from Marsh et al. (2014).
S1, S2, S3, S4 and S5, kombucha samples from Country 1, Country 2, Country 3, Country 4 and Country 5.
bio-S1, bio-S2, bio-S3, bio-S4 and bio-S5, SCOBY from Country 1, Country 2, Country 3, Country 4 and Country 5.

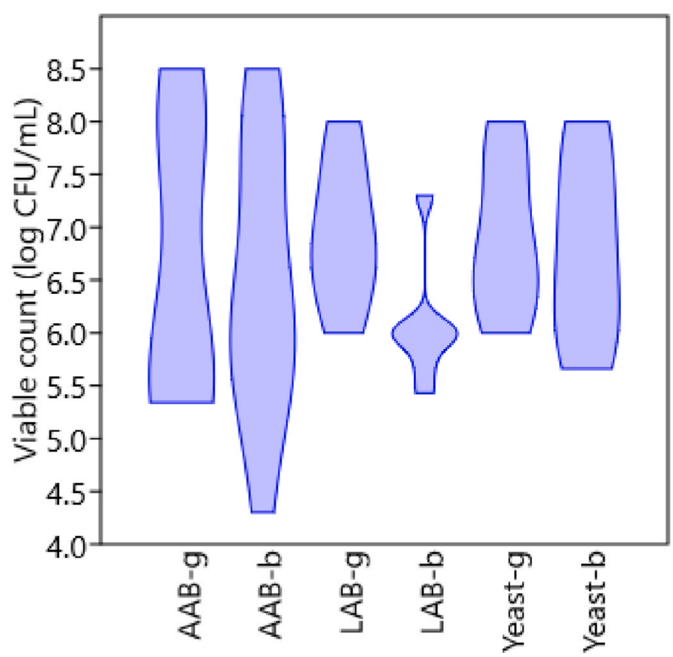

Fig. 4. Violin plot on the viable count of some microbial groups; AAB-b and AAB-g, acetic acid bacteria from black or green tea kombucha; LAB-b and LAB-g, lactic acid bacteria from black or green tea kombucha; Yeast-b and Yeast-g, yeasts in kombucha from green or black tea. Data from various bibliographic sources.

whether it is a probiotic drink or not.

According to the guidelines and amendment on probiotic definition, fermented foods with unknown or not characterized microbial consortia cannot be labeled as "probiotic" (Hill et al., 2014), although many recent papers and reviews on kombucha use this definition (Selvaraj & Gurumurthy, 2023; Vargas et al., 2021). Due to the high biodiversity of kombucha, it is reasonable that potential probiotic strains could be isolated, identified, and characterized. However, according to the requirements set by different Regulatory Agencies (at least in EU), the use of the term "probiotic" is misleading and incorrect.

Possible probiotic strains could be isolated in kombucha from the species *Lacticaseibacillus casei*, *Lb. delbrueckii*, *Lactiplantibacillus plantarum*, *Lb. acidophilus*, *S. cerevisiae*, *Schizo. pombe*, *G. oxydans*, *Bif. bifidum*, and *Bif. longum*, among others, as shown in Table 2.

Bogdan et al. (2018) isolated a strain of *Pediococcus pentosaceus*, able to survive the harsh conditions of gut, to produce bacteriocins, as well as to adhere to intestinal cell lines (Utoiu et al., 2018), to exert antioxidant and antimicrobial activities (Diguță et al., 2020).

Pei et al. (2020) isolated and characterized a strain of *Lpb. plantarum* producing a bacteriocin, which increased cell membrane permeability, causing potassium ion release, and inhibits the formation of biofilms.

Potential probiotic strains were also found among AAB; Wang et al. (2014) identified a strain exerting hepatoprotective effects and identified it as *Gluconacetobacter* sp.; moreover, they also identified the compound responsible of this health-promoting effect, that is DSL.

6. Antimicrobial properties of kombucha

Due to the presence of various organic acids, high polyphenol content and LAB, the importance of kombucha as a natural antimicrobial source is increasing and has therefore been widely studied in recent years (Kaewkod et al., 2019). Pei et al. (2020) reported that SGL10 bacteriocin produced by *Lpb. plantarum* SLG10 isolated from kombucha acts on Gram positive and Gram negative bacteria. Another study has shown the antimicrobial effects of kombucha prepared using green, oolong, and black tea on *Escherichia coli*, *E. coli* O157:H7 DMST 12743, *Shigella dysenteriae* DMST 1511, *Salmonella* Typhi DMST 22842, and *Vibrio cholerae* (Kaewkod et al., 2019).

In general, essential oils' antimicrobial activity is attributed to several small terpenoid and phenolic compounds (such as thymol, carvacrol, eugenol) (Battikh et al., 2013). Bhattacharya et al. (2016, 2018) compared the antimicrobial effects of polyphenol content of black tea and kombucha on enterotoxigenic *E. coli*, *V. cholerae*, *Sh. flexneri*, and *Salmonella* Typhimurium. They found that the antimicrobial effect was related to some key-compounds (isorhamnetin, and catechin) able to cause an increase in membrane permeability.

In another study, unfermented tea and acetic acid were used as control, and kombucha was found to have antimicrobial effects on *Staphylococcus aureus*, *Sh. sonnei*, *E. coli*, *Aeromonas hydrophila*, *Yersinia enterolitica*, *Pseudomonas aeruginosa*, *Enterobacter cloacae*, *Staph. epidermidis*, *Campylobacter jejuni*, *Salmonella* Enteritidis, *Salmonella* Typhimurium, *Bacillus cereus*, *Helicobacter pylori*, and *Listeria monocytogenes*; only *Z. bailii* was not affected (Sreeramulu et al., 2000).

Battikh et al. (2012) evaluate the antimicrobial activity of kombucha produced from thyme, lemon verbena, rosemary, fennel, and peppermint, and black tea. *Staph. epidermidis*, *Staph. aureus*, *Micrococcus lysodeikticus*, *E. coli*, *Ps. aeruginosa*, *Salmonella* Typhimurium, and *L. monocytogenes* were found to be sensitive to black tea, lemon verbena, and peppermint kombucha.

Greenwalt et al. (1998) reported that kombucha prepared with different amounts of green and black tea showed antimicrobial effects against *Staph. aureus*, *E. coli*, *Salmonella* Typhimurium, *B. cereus*, *Agrobacterium tumefaciens*, even at the lowest amount of tea. In contrast, no effect was observed against *Candida albicans*.

Diguță et al. (2020) showed that two probiotic strains belonging to the specie *P. pentosaceus* and *P. acidiliactici* had high inhibitory activity against pathogenic bacteria such as *Salmonella* Typhimurium, *L. monocytogenes*, *L. ivanovii*, *B. cereus*, *Proteus hauseri*, and methicillin-resistant *Staph. aureus*.

7. Conclusions

Kombucha represents a high source of biodiversity, and is a promising raw material for the isolation and characterization of functional microorganisms; in addition, it is also a source of bioactive compounds, with health-promoting effects and antimicrobial properties towards a wide variety of pathogens (*Salmonella* sp., *L. monocytogenes*, *Staphylococcus* spp., *C. albicans*, among others).

The microbiota of kombucha is composed of five main bacterial phyla (Actinobacteria, Bacteroidetes, Deinococcus-Thermus, Firmicutes, and Proteobacteria), and AAB, mainly *Gluconacetobacter*, *Acetobacter*, *Komagataeibacter*, and *Gluconobacter*, represent the most important group, while LAB are usually recovered at low frequencies. Yeast biota is also characterized by a high degree of biodiversity and *Zygosaccharomyces* is the most important genus.

There is still a debate on the "probiotic status" of kombucha, but according to authors' experience postbiotic definition could be more suitable.

Due to the complex biota of SCOBY, and the interactions occurring among the different taxa there living, kombucha could be a valuable model system to understand the importance of biodiversity to design new processes and products, thus improving fermentation paths and procedures.

This paper has contributed to the debate on the potentialities and microbiology of kombucha and has pointed out future perspectives and open questions.

Author contribution

All authors conceived the research; Antonio Bevilacqua, and Hayrunisa Içen performed literature search; Antonio Bevilacqua, performed statistics; Antonio Bevilacqua and Hayrunisa Içen wrote the first draft of the paper; Maria Rosaria Corbo, Milena Sinigaglia, and Burcu Irem Omurtag Korkmaz revised the manuscript; Maria Rosaria Corbo, and Milena Sinigaglia funded the research.

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Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

Data will be made available on request.

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