Research Progress on the Composition and Interaction of Microbes in Kombucha

Aqi Cao [1, a], Weihua Qiu [2, *]

[1] Colloge of Biology Science, China Agriculture University, Beijing, China

[2] Institute of Process Engineering, Chinese Academy of Sciences, Beijing, China

* Corresponding Author Email: whqiu@mail.ipe.ac.cn, [a] cbser@foxmail.com

Abstract. Kombucha, a fermented beverage produced by a symbiotic culture system of bacteria and yeast (SCOBY), is rich in bioactive compounds, thereby exhibiting various health benefits. In recent years, kombucha has gained global popularity as a healthy fermented beverage, leading to an upsurge in worldwide research interest. The diversity of microbial communities and the interactions between microorganisms play a vital role in the formation of unique flavor and health benefits of kombucha. At present, they have aroused widespread research interest worldwide. This review systematically summarizes recent achievements in research on the microbial composition and interactions in kombucha fermentation. Firstly, the progress obtained on the microbial species identification and the characteristics of their composition of kombucha were summarized. Then, the current researches on the interactions of the native microorganisms in Kombucha SCOBY were presented, as well as the interactions between additional microorganisms and native microorganisms. Finally, the dynamic changes observed during kombucha fermentation, including microbial species composition and key active substances such as organic acids and polyphenols, were reviewed. This article aims to provide valuable reference for using targeted microbial regulation to enhance the fermentation efficiency, and optimize product quality and efficacy of kombucha.

Keywords: Kombucha, symbiotic cultures of bacteria and yeast, fermented beverage, microbial community.

1. Introduction

Kombucha is a fermented beverage that originated in China over 2,000 years ago. It was first used as medicine and spread to Japan in 414 AD. With the expansion of trade, it later spread to Russia and Eastern Europe. This ancient Chinese traditional health drink is known for its slightly sweet and slightly sour taste [1]. Kombucha is a non-alcoholic or low-alcohol functional beverage that employs symbiotic cultures of bacteria and yeast (SCOBY) to ferment the sweetened green or black tea [2]. During the fermentation, a diverse range of microorganisms work together to produce a variety of nutrients that benefit for human health, including polyphenols, organic acids, vitamins, amino acids, and minerals. The presence of these substances imparts kombucha with distinct functionalities such as antioxidative properties, antibacterial attributes, anti-inflammatory characteristics, antidiabetic potentiality as well as therapeutic efficacy in addressing stomach ulcers and high cholesterol levels. Furthermore, it can enhance the effect of hepatic detoxification, strengthen immunity, as well as other efficiencies [3]. Currently, kombucha has achieved widespread industrialization and commercialization [4]. Due to its distinctive flavor profile and health-oriented concept, the market size of kombucha has been expanded world widely in recent years. In 2019, the global market size reached $1.85 billion USD, with projections indicating it will reach $10.45 billion USD by 2027, thereby generating significant economic benefits [5]. The strong health effects and substantial economic advantages of kombucha made it received considerable attentions over the world.

Currently, various microorganisms have been identified from the SCOBY and liquid of kombucha, predominantly bacteria and yeasts. The bacterial community consists of acetic acid bacteria (AAB, e.g., *Acetobacter* spp., *Gluconacetobacter* spp., *Gluconobacter* spp., *Komagataeibacter* spp., and *Tanticharoenia* spp.) as well as lactic acid bacteria (LAB, e.g., *Lactobacillus* spp. and *Lactococcus* spp.) [6]. Yeast populations exhibit remarkable diversity, mainly include *Candida* spp.,

Zygosaccharomyces spp., *Brettanomyces* spp., *Hanseniaspora* spp., *Saccharomyces* spp., and *Lanchancea* spp., *Schizosaccharomyces* spp. [3]. The microbial composition of kombucha is influenced by various factors including the selection of raw materials, geographical location, environmental conditions, and fermentation parameters [5, 7].

The fermentation process of kombucha involves intricate interactions among microorganisms, resulting in the release of intermediate and secondary metabolites that contribute to the quality and efficacy of kombucha. During this process, yeasts play crucial roles in the production of invertase, which convert disaccharides into glucose and fructose. Yeast undergoes metabolic decomposition to generate ethanol, while AAB oxidize ethanol to produce acetic acid and gluconic acid. Additionally, *Komagataeibacter* spp. (including *Gluconacetobacter* spp. and *Acetobacter* spp.) as the dominant bacterial genus is also responsible for the production of bacterial cellulose production [8].

Research on microorganisms in kombucha is crucial for achieving large-scale production, ensuring optimal health benefits, and preventing the formation of harmful substances. This paper presents a review of the composition and interactions of microorganisms in kombucha, as well as their impact on material changes during fermentation. These progresses are valuable for increasing the yield of functional ingredients, enhancing production efficiency, and expanding large-scale manufacturing.

2. Species of microorganisms in kombucha

The composition of microorganisms in kombucha is significantly influenced by the source of the culture medium, fermentation conditions, processing techniques, and substrate type, which makes the specific identification of microorganisms in kombucha a challenge [7]. However, the dominant microbial composition in the kombucha remains relatively stable. The microbial species in kombucha can be isolated and identified by culture methods, however, these techniques only capture a small fraction of the microorganisms present in kombucha. Therefore, relying solely on culture methods is insufficient for accurately determining the microbial species [9]. As technologies developed, especial high-throughput sequencing analyses, microbes in kombucha achieved comprehensively recognition. Marsh et al. [10] conducted high-throughput sequencing analyses of bacterial and fungal populations in the SCOBY and liquid of kombucha. By using 16sRNA sequencing technique, five phyla were identified, which were *Actinobacteria*, *Bacteroidetes*, *Deinococcus-Thermus*, *Firmicutes* and *Proteobacteria*. Among these phyla, *Proteobacteria* was found to be the most abundant and included *Acetobacter* and *Gluconacetobacter*. *Gluconacetobacter* accounted for over 85% of all sample readings and emerged as the predominant bacteria genus in all samples. Additionally, an obvious presence of lactic acid bacteria in SCOBY of kombucha such as *Lactobacillus* and *Lactococcus* were observed. In terms of yeast, *Zygosaccharomyces* was identified as the dominant genus accounting for approximately 95%. Based on the 16S rRNA and high-throughput internal transcription sequencing analysis Pradhan et al. [11] found that *Komagataeibacter rhaeticus* was the predominant bacterial species in kombucha, followed by *Gluconacetobacter* sp., which was constituting 93% and 6% of the total population, respectively. Meanwhile, acetate bacteria (AAB) was dominant in kombucha [10, 12].

Fully understanding the diversity of microorganisms in kombuca is crucial for better guiding industrial production. Recently, high-throughput sequencing analysis are widely utilized in the researches of kombucha species identification. Due to the influence of various factors on the types of microorganisms in kombucha, a large number of new microorganisms are constantly being reported, as been summarized in Table 1 [3, 13-15].

Table 1. The main microbial species in kombucha

Sort	Species	
Yeast [3, 13-16]	*Brettanomyces anomalus*	*Lachacea thermotolerans*
	B. bruxellensis	*Lodderomyces elongisporus*
	B. custersii	*Medusomyces gisevii*
	B. lambicus	*Pichia membranaefaciens*
	B. naardenensis	*P.fermantans*
	Candida albicans	*Saccharomycodes ludwigii*
	C. stellata	*Saccharomyces cerevisiae*
	C. crusei	*Schizosaccharomyces pombe*
	C. parapsilosis	*Torulaspora delbrueckii*
	Kloeckera apiculata	*Zygosaccharomyces bailii*
	Kluyveromyces africanus	*Z. rouxii*
acetic acid bacteria [3, 13-15]	*Acetobacter xylinum*	*Komagataeibacter europaeus*
	A. xylinoides	*K. xylinus*
	A. aceti	*K. saccharivorans*
	A. pasteurianus	*K. intermedius*
	A. musti	*K. hansenii*
	A. indonesiensis	*K. rhaeticus.*
	A. nitrogenifigens	*Gluconobacter oxydans*
	A. syszygii	*G. potus*
	A. tropicalis	*G. entanii*
	A. pomorum	*Gluconacetobacter kombuchae*
	A. okinawensis	*G. saccharivorans*
	A. senegalensis	*G. hansenii*
	A.papayae	*G. xylinus*
lactic acid bacteria [3, 13-15, 17]	*Lactobacillus casei*	*Leuconostoc* sp.
	Lactococcus faecium.	*Bifidobacterium sp.*
	Lactobacillus plantarum	*Lactobacillus nagelii*
	Lactobacillus rhamnosus	*L. mali*
	Pediococcus pentosaceus	*P. acidiliactici*
Others [3, 13-15]	*Actinobacteria*	*Deinococcus-Thermus*
	Bacteroidetes	*Firmicutes*
	Proteobacteria	

3. The microbial interactions in the fermentation of Kombucha

The fermentation process of kombucha is highly intricate, involving a complex interaction of diverse microorganisms that mutually influence each other to yield the distinctive flavor and efficacy. On the other hand, various microorganisms can be added to the starter of kombucha to improve the fermentation efficiency of kombucha.

3.1. Interaction of microorganisms in the kombucha

The microbial composition of SCOBY kombucha differs from the variations in metabolic processes, environmental conditions, and resulting products. Under the symbiotic relationship between different microorganisms in kombucha, the species and composition of microorganism in the fermentation process undergo dynamic changes. It also found that symbiosis does not imply mutual benefit but rather denotes the ability to achieve stable coexistence, perhaps there exist undefined interactions between them [18].

Currently, the interaction between different microbes in kombucha aroused strong interest all over the world. The primary approach for investigating the interaction is to isolate the dominant microbes from kombucha and employ microbial dynamics to examine the difference in cell abundance, metabolites, and growth rates when they coexist or exist individually. The yeast, AAB (Acetic Acid Bacteria), and LAB (Lactic Acid Bacteria) constitute the dominant populations in kombucha, and their interplay significantly impacts the fermentation process. Meng et al conducted the Spearman correlation analysis on the quantities of yeast and AAB in the microbial communities during various stages of fermentation, revealing a positive correlation and a symbiotic relationship between *Komagataeibacter*, *Dekkera*, and *Pichia* throughout the fermentation process, while, *Komagataeibacter* demonstrating a negative correlation with other fungi [19]. The metabolic activity of yeasts in the kombucha would significantly influence the chemical composition of the product, while bacterial species have a secondary impact on the composition of organic acids. Acetic acid bacteria lack effective sucrose hydrolysis capabilities. Therefore, in kombucha fermentation process, usually yeast with high invertase activity would first break down sucrose into glucose and fructose, which would be consumed by AAB for ethanol production. Then the ethanol would be oxidized by AAB to generate acetic acid and gluconic acid. AAB could also induce a metabolic shift in *Saccharobacteria cerevisiae*, leading the enhancement of invertase activity and fermentation capacity. It is generally assumed that there is a symbiotic relationship between yeast and AAB, and the diverse strategies involving sucrose utilization can be used to explain the undiscovered microbial interactions [20].

Bacteria cellulose is another major products in kombucha. Many researches indicated that only specific combinations of microorganisms can mutually stimulate the formation of cellulose membranes. The experimental results of Landis et al. [16] showed that when fermented with a combination of *K. rhaeticus*, *B. bruxellensis*, and *Z. bisporus*, *B. bruxellensis* and *K. rhaeticus* could successfully reconstructe the pH and biofilm formation characteristics of kombucha fermentation, while *Z. bisporus* failed to induce bacterial cellulose membrane production. This study once again emphasized the metabolic interaction between yeast and AAB.

3.2. Interactions between additional and native microorganisms in kombucha

The advancement of kombucha research has stimulated interest in novel resources which capable of providing carbon and nitrogen sources for kombucha fermentation, which besides modifying the fermentation efficiency, generating more advantageous and health-promoting bioactive beverages [21]. To optimize substrate utilization, enhance ingredient efficacy, and minimize the production of detrimental compounds, a multitude of microorganisms was added to the starter of kombucha to facilitate yeast-mediated sugar metabolism [22]. Venegas et al. [23] reported that the fermentation capacity would be enhanced by added *Saccharomyces eubayanus* into the SCOBY culture compared to the fermentation with SCOBY alone. The co-culture of *S. eubayanus* with SCOBY exhibited a higher ethanol concentration compared to that fermented with SCOBY only, and yielded increased acetic acid production during co-fermentation conditions. Meanwhile, the biodiversity of the SCOBY during fermentation depends on the specific strain of used *S. eubayanus*. Lactic acid bacteria are commonly used as probiotics to improve gut microbiome ecology and enhance immune function. To enhance the antioxidant and antibacterial properties of kombucha, strains of *Lacticaseibacillus casei* and *Lactiplantibacillus plantarum* can be added [24]. During the process of kombucha fermentation, it's been observed that the presence of LAB significantly boosts the production of D-saccharic acid, 1,4-lactone (DSL), and glucuronic acid, especially, DSL has been proved as a potent inhibitor of β-glucosidase and plays a crucial role in cancer prevention [25].

4. Dynamic changes of chemical components during kombucha fermentation

4.1. The variation of organic acids

The fermentation process of kombucha produces various organic acids, such as acetic acid, citric acid, tartaric acid, malic acid, and succinic acid. The levels of these organic acids are consistent with the total acidity and pH values and show an increasing trend. Notably, acetic acid is the primary organic acid in kombucha [26]. During the process of kombucha fermentation, AAB oxidized ethanol to produce acetic acid and the accumulation of acetic acid results in the decrease of pH, which is not conducive to the growth of yeast [17]. Furthermore, AAB have the ability to convert glucose into glucuronic acid and gluconic acid, which can be further oxidized by AAB to produce 2-ketogluconic acid and 2,5-diketogluconic acid. As for fungal in kombucha, only *Brettanomyces bruxellensis* is correlated negatively with ethanol but positively with acetic acid due to its ability to produce high concentrations of acetic acid from glucose and ethanol under aerobic conditions. In terms of bacteria, *Komagataeibacter europaeus*, *Komagataeibacter xylinus*, and *Komagataeibacter rhaeticus* are positively associated with organic acids [27]. *Gluconacetobacter* and *Komagataeibacter* are types of bacteria that can produce cellulose. They also play a role in the oxidation reaction of glucose dehydrogenase. This reaction creates glucose and glucuronic acid. Citric acid is typically synthesized by yeast during kombucha fermentation.

4.2. The variation of polyphenols during the fermentation of kombucha

The beneficial effects of polyphenols on human health have been extensively investigated, such as alleviating inflammation and arthritis, preventing cancer, and enhancing the immune system, which might attribute to its antioxidant activity mediated by the presence of polyphenols [28]. Although the biotransformation pathway of tea polyphenols during kombucha fermentation has not been specified, there were evidences suggesting that microorganisms could catalyze the hydrolysis of various phenolic compounds through ring cleavage, hydrolysis, demethylation, reduction, decarboxylation, and isomerization [29]. Shi et al reported that in the kombucha fermented by *Z. bailii* and *G. xylinus* the concentration of low molecular weight phenols was significantly enhanced, while a community consisting of *Z. bailii*, *D. hansenii*, and *L. plantarum* could effectively enhance cellular metabolic activity to sustain polyphenol biotransformation, consequently increase the content of polyphenol [30]. Zhou et al. [31] discovered that the fermentation of tea residue could significantly enhance the antioxidant activity (up to 3.25-fold) and polyphenol concentration (5.68-fold) of kombucha, thus providing valuable insights for the production of polyphenol-enriched kombucha beverages.

5. Conclusion and perspective

Kombucha, a health-oriented fermented beverage, has gained worldwide popularity and possesses substantial economic value. Presently, extensive researches are concentrated on deciphering the complicated symbiotic relationships among diverse microorganisms and their influence on the functional compounds found in its metabolites. With the development of advanced technologies such as high-throughput screening, isolation culture, and metaproteomic sequencing methods, more and more comprehensive understanding of the complex microbial community in kombucha and its correlation with beverage flavor profiles and health benefits have achieved. In the future, further investigation should be focus on improving the production mode of kombucha by deciphering the mechanisms underlying these microbial interactions, enhancing production efficiency and health-promoting properties, as well as ensuring commercial viability. Furthermore, in addition to traditional kombucha fermented from tea infusion, extensive research should be conducted by using novel raw materials such as Chinese herbs, medicinal and edible plants, fruits, and vegetables to develop functional kombucha beverages that with enhanced health benefits. Therefore, it is necessary to investigate the new requirements for novel kombucha fermentation, including studies on microbial composition (e.g., the addition of specific microorganisms) and interactions between active

compounds from new materials and kombucha-associated microorganisms. Additionally, the stability and persistence of the microbial composition in SCOBY as the starter culture for kombucha remain unknown, which will affect the productivity, stability, and safety of kombucha. Therefore, future research in this area needs to be strengthened. In conclusion, a comprehensive understanding of the diversity of the microbial community in kombucha and the precise regulation of microbial composition using the most advanced genome and fermentation technologies will open up new approaches for the research and industrial applications of kombucha.

References

[1] Soares MG, de Lima M, Reolon Schmidt VC. (2021) Technological aspects of kombucha, its applications and the symbiotic culture (SCOBY), and extraction of compounds of interest: A literature review. Trends in food science & technology. 110: 539-550. https://doi.org/10.1016/j.tifs.2021.02.017.

[2] Antolak H, Piechota D, Kucharska A. (2021) Kombucha tea—a double power of bioactive compounds from tea and symbiotic culture of bacteria and yeasts (SCOBY). Antioxidants. 10: 1541. https://doi.org/10.3390/antiox10101541.

[3] Kim H, Hur S, Lim J et al. (2023) Enhancement of the phenolic compounds and antioxidant activities of Kombucha prepared using specific bacterial and yeast. Food bioscience. 56: 103431. https://doi.org/10.1016/j.fbio.2023.103431.

[4] He XY, Zhu YY, Cheng FY, Liu TT, Ruan H. (2023). Research progress on fermentation technology of kombucha. Modern food. 29: 55-58. https://doi.org/10.16736/j.cnki.cn41-1434/ts.2023.05.015.

[5] Grassi A, Cristani C, Palla M et al. (2022) Storage time and temperature affect microbial dynamics of yeasts and acetic acid bacteria in a kombucha beverage. International journal of food microbiology. 382: 109934. https://doi.org/10.1016/j.ijfoodmicro.2022.109934.

[6] Morales D. (2020) Biological activities of kombucha beverages: The need of clinical evidence. Trends in food science & technology. 105: 323-333. https://doi.org/10.1016/j.tifs.2020.09.025.

[7] Chong AQ, Lau SW, Chin NL, Talib RA, Basha RK. (2023) Fermented beverage benefits: a comprehensive review and comparison of kombucha and kefir microbiome. Microorganisms. 11: 1344. https://doi.org/10.3390/microorganisms11051344.

[8] Subbiahdoss G, Osmen S, Reimhult E. (2022) Cellulosic biofilm formation of Komagataeibacter in kombucha at oil-water interfaces. Biofilm. 4: 100071. https://doi.org/10.1016/j.bioflm.2022.100071.

[9] Kaashyap M, Cohen M, Mantri N. (2021) Microbial diversity and characteristics of kombucha as revealed by metagenomic and physicochemical analysis. Nutrients. 13: 4446. https://doi.org/10.3390/nu13124446.

[10] Marsh AJ, O'Sullivan O, Hill C, Ross RP, Cotter PD. (2014) Sequence-based analysis of the bacterial and fungal compositions of multiple kombucha (tea fungus) samples. Food microbiology. 38: 171-178. https://doi.org/10.1016/j.fm.2013.09.003.

[11] Pradhan S, Prabhakar MR, Parvathy KRK et al. (2023) Metagenomic and physicochemical analysis of Kombucha beverage produced from tea waste. Journal of food science and technology-mysore. 60: 1088-1096. https://doi.org/10.1007/s13197-022-05476-3.

[12] Li S, Wang S, Wang L et al. (2023) Unraveling symbiotic microbial communities, metabolomics and volatilomics profiles of kombucha from diverse regions in China. Food research international. 174: 113652. https://doi.org/10.1016/j.foodres.2023.113652

[13] Içen H, Corbo MR, Sinigaglia M, Korkmaz BIO, Bevilacqua A. (2023) Microbiology and antimicrobial effects of kombucha, a short overview. Food bioscience. 56: 103270. https://doi.org/10.1016/j.fbio.2023.103270.

[14] Liang S, Granato D, Zou C et al. (2021) Processing technologies for manufacturing tea beverages: From traditional to advanced hybrid processes. Trends in food science & technology. 118: 431-446. https://doi.org/10.1016/j.tifs.2021.10.016.

[15] Wang B, Rutherfurd-Markwick K, Zhang XX, Mutukumira AN. (2022) Kombucha: production and microbiological research. Foods. 11: 3456. https://doi.org/10.3390/foods11213456.

[16] Landis EA, Fogarty E, Edwards JC et al. (2022) Microbial diversity and interaction specificity in kombucha tea fermentations. mSystems. 7: e0015722. https://doi.org/10.1128/msystems.00157-22.

[17] Diguță CF, Nițoi GD, Matei F, Luță G, Cornea CP. (2020) The biotechnological potential of Pediococcus spp. isolated from kombucha microbial consortium. Foods. 9: 1780. https://doi.org/10.3390/foods9121780.

[18] May A, Narayanan S, Alcock J, Varsani A, Maley C, Aktipis A. (2019) Kombucha: a novel model system for cooperation and conflict in a complex multi-species microbial ecosystem. Peerj. 7: e7565. https://doi.org/10.7717/peerj.7565.

[19] Meng YC, Wang XJ, Li YH, Chen J, Chen XL. (2024) Microbial interactions and dynamic changes of volatile flavor compounds during the fermentation of traditional kombucha. Food Chemistry. 430: 137060, https://doi.org/10.1016/j.foodchem.2023.137060.

[20] Subbiahdoss G, Osmen S, Reimhult E. (2022) Cellulosic biofilm formation of Komagataeibacter in kombucha at oil-water interfaces. Biofilm. 4: 100071. https://doi.org/10.1016/j.bioflm.2022.100071.

[21] Su J, Tan Q, Tang Q, Tong Z, Yang M. (2023) Research progress on alternative kombucha substrate transformation and the resulting active components. Frontiers in microbiology. 14: 1254014. https://doi.org/10.3389/fmicb.2023.1254014.

[22] Sanwal N, Gupta A, Bareen MA, Sharma N, Sahu JK. (2023) Kombucha fermentation: recent trends in process dynamics, functional bioactivities, toxicity management, and potential applications. Food chemistry advances. 3: 100421. https://doi.org/10.1016/j.focha.2023.100421.

[23] Venegas CA, Saona LA, Urbina K, Quintrel P, Peña TA, Mardones W, Cubillos FA. (2023) Addition of Saccharomyces eubayanus to scoby fermentations modulates the chemical and volatile compound profiles in kombucha. Food microbiology. 116: 104357. https://doi.org/10.1016/j.fm.2023.104357.

[24] Nguyen NK, Dong NT, Nguyen HT, Le PH. (2015) Lactic acid bacteria: promising supplements for enhancing the biological activities of kombucha. Springerplus. 4: 91. https://doi.org/10.1186/s40064-015-0872-3.

[25] Taha M, Uddin N, Ali M, Anouar EH, Rahim F, Khan G, Farooq RK, Gollapalli M, Iqbal N, Farooq M, Khan KM. (2020) Inhibition potential of phenyl linked benzimidazole-triazolothiadiazole modular hybrids against β-glucuronidase and their interactions thereof. International journal of biological macromolecules. 161: 355-363. https://doi.org/10.1016/j.ijbiomac.2020.06.006.

[26] Wang S, Li CW, Wang Y, Wang S, Zou YP, Sun Z, Yuan L. (2023) Changes on physiochemical properties and volatile compounds of Chinese kombucha during fermentation. Food bioscience. 55: 103029. https://doi.org/10.1016/j.fbio.2023.103029.

[27] Yao L, Zhang J, Lu J, Chen D, Song S, Wang H, Sun M, Feng T. (2023) Revealing the influence of microbiota on the flavor of kombucha during natural fermentation process by metagenomic and GC-MS analysis. Food research international. 169: 112909. https://doi.org/10.1016/j.foodres.2023.112909.

[28] Ahmed RF, Hikal MS, Abou-Taleb KA. (2020) Biological, chemical and antioxidant activities of different types kombucha. Annals of Agricultural Sciences. 65: 35-41. https://doi.org/10.1016/j.aoas.2020.04.001.

[29] Marhuenda-Muñoz M, Laveriano-Santos EP, Tresserra-Rimbau A, Lamuela-Raventós RM, Martínez-Huélamo M, Vallverdú-Queralt A. (2019) Microbial phenolic metabolites: which molecules actually have an effect on human health? Nutrients. 11: 2725. https://doi.org/10.3390/nu11112725

[30] Shi S, Wei Y, Lin X, Liang H, Zhang S, Chen Y, Dong L, Ji C. (2023) Microbial metabolic transformation and antioxidant activity evaluation of polyphenols in kombucha. Food bioscience. 51: 102287. https://doi.org/10.1016/j.fbio.2022.102287.

[31] Zhou DD, Saimaiti A, Luo M, Huang SY, Xiong RG, Shang A, Gan RY, Li HB. (2022) Fermentation with tea residues enhances antioxidant activities and polyphenol contents in kombucha beverages. Antioxidants. 11: 155. https://doi.org/10.3390/antiox11010155.