

Study on the function and mechanism of lactic acid bacteria in the brewing process of Baijiu

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Abstract: As the main dominant functional microorganism in the brewing process of Chinese Baijiu, lactic acid bacteria influences and determines the composition of microbial community structure, function, and enzyme profile in the Baijiu brewing process to a certain extent. Based on the important position and functional role of lactic acid bacteria in Chinese Baijiu and the progress of microbial analysis and detection technology, the research on lactic acid bacteria has become more and more in-depth in recent years. This paper reviews the research progress of lactic acid bacteria in the Chinese Baijiu brewing process in recent years, and lactic acid bacteria on the functional role and mechanism of lactic acid bacteria in Baijiu brewing process, aiming to provide theoretical reference for the research of lactic acid bacteria in Baijiu brewing process.

Keywords: lactic acid bacteria; Baijiu; functional mechanism; functional contribution

1. Introduction

Baijiu as the national liquor of China^[1] and one of the top six distilled fermented grains in the world, its brewing process has a deep history of thousands of years and it is a cultural treasure of China. There are many different types of Chinese *Baijiu*, which can be divided into twelve types of flavor depending on the brewing raw materials and production processes, with the main flavor being: Maotai-flavor, Luzhou-flavor, Fen-flavor, and Rice-flavor. Unlike the other five major distilled fermented grains in the world, *Baijiu* can contain hundreds of flavor substances in just one aroma type due to its special brewing process, so it has a mellow taste, harmonious aroma, long-lasting fragrance, and long finish.

At present, the domestic *Baijiu* market is mainly dominated by Maotai-flavor *Baijiu* and Luzhou-flavor *Baijiu*, whose brewing process is an open production operation, multi-strain co-solid fermentation production process, and its brewing process has two main carriers: one is the *Daqu*, and the other is the fermented grains. As a fermenting agent, saccharifying agent and aromatizing agent in the production of *Baijiu*, *Daqu* is formed by the natural fermentation of wheat as the main raw material with peas and *Daqu* as auxiliary grains, which provides rich microbial communities and enzymatic systems for *Baijiu* fermentation^[2]. Therefore, the importance of the *Daqu* to *Baijiu* is self-evident, and its quality is one of the key factors affecting the quality and flavor of *Baijiu*^[3, 4] fermented grains is a brewing system formed by fermenting sorghum as the main raw material and mixing it with *Daqu* and other auxiliary ingredients in a sealed cellar, which is the main solid carrier of fermentation in the cellar during the brewing process. Microorganisms from the raw grains, environment, *Daqu* and cellar mud carry out complex metabolic activities in the fermented grains, decomposing and metabolizing starch, protein and other organic *Daqu*s in the fermented grains into small molecules such as reducing sugars and amino acids, which are then transformed into alcohols, esters, organic acids and other flavor substances through the metabolic activities of microorganisms, thus forming the unique flavor of *Baijiu*. The structure and metabolic activities of microbial flora have an important impact on the quality of *Baijiu*. Lactic acid bacteria is the absolute dominant microorganism in both the *Daqu* and the fermented grains, so it is crucial for the production and brewing of *Baijiu*.

Lactic acid bacteria is one of the most widely distributed bacteria in nature, and it is a kind of bacteria without spores or bacilli that can metabolize fermentable sugar to produce lactic acid. It belongs to facultative anaerobic bacteria and is the main high-abundance dominant functional bacterial microorganism in the process of *Baijiu* brewing, which exists in a large number in *Daqu* and fermented grains^[5]. Lactic acid metabolized by lactic acid bacteria is one of the four major organic acids in *Baijiu*. Lactic acid can not only reduce or remove the dry, spicy and bitter taste of *Baijiu*, but also increase the

mellow feeling of *Baijiu* and improve the taste and quality of *Baijiu*. It is also an important precursor for the synthesis of ethyl lactate and other flavor substances in *Baijiu*. Lactic acid bacteria can inhibit the growth, reproduction and ethanol production of *Pichia*, and *Pichia* and lactic acid bacteria are important biological factors affecting the difference of higher alcohol metabolism in *Baijiu* brewing. In addition, in the process of *Baijiu* fermentation, *Lactobacillus* will affect the synthesis of ethyl carbamate. Lactic acid bacteria can also participate in Maillard reaction in *Baijiu* brewing, which is beneficial to the production of pyrazine and other flavor substances with baking taste in *Baijiu*. Therefore, the presence of lactic acid bacteria is crucial for the renewal and evolution of the microbial community structure of *Baijiu* brewing and the accumulation of flavor substances in *Baijiu*. Therefore, an in-depth study of *Lactobacillus* in the *Baijiu* brewing process is of great scientific value, not only to elucidate the functional role of *Lactobacillus* in various stages of *Baijiu* brewing, but also to analyze the influence and contribution of *Lactobacillus* to the structure and function of the microbial communities in *Baijiu* brewing, and to help analyze the functional mechanism of the interaction between *Lactobacillus* and the microbial communities in the *Baijiu* brewing and fermentation process.

The key to *Baijiu* brewing lies in the co-fermentation mode of microbial mixes, and lactic acid bacteria, as the absolute dominant microorganisms and functional microorganisms in the *Baijiu* brewing process, deserve our in-depth research and attention. This paper reviews the research progress of lactic acid bacteria in the brewing process of *Baijiu* in recent years and elucidates the functional role of lactic acid bacteria in the brewing process of *Baijiu*, aiming to provide a theoretical reference for the study of lactic acid bacteria in the brewing process of *Baijiu*, which will be beneficial to the improvement of the quality and quantity of *Baijiu* by regulating the brewing microbial communities in the actual production process of *Baijiu*.

2. Overview of Chinese *Baijiu* brewing

2.1 Overview of *Baijiu* and brewing process

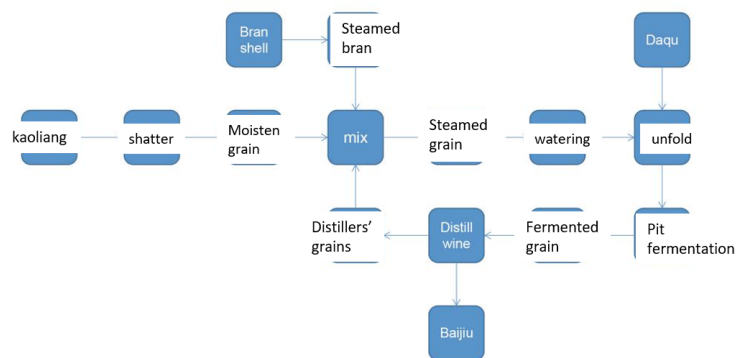


Figure 1: *Baijiu* brewing process flow chart

With a long history and unique technology, Chinese *Baijiu* is a distilled spirit with unique national characteristics in China, and is known as one of the six major distilled fermented grains in the world, along with whiskey, vodka, brandy, rum and gin. According to the differences in the types of saccharifying ferments, production processes and natural environment, different flavor *Baijius* have their own characteristics and typical styles. At present, there are 12 flavor types of *Baijiu* in China, including the four basic flavor types of Luzhou-flavor, Maotai-flavor, Fen-flavor and Rice-flavor, as well as the derived dual-flavor, medicinal-flavor, phoenix-flavor, special-flavor, sesame-flavor, black bean-flavor, dry-flavor and rich-flavor. Chinese *Baijiu* belongs to fermented food, which takes *Daqu* as saccharifying and fermenting aroma-producing agent and fermentation starter, and then mixes it into fermentation raw materials, and then transfers it to a cellar to ferment it into fermented grains. Finally, the fermented grains are distilled to get *Baijiu*, and then blended and stored, and finally an alcoholic beverage-*Baijiu* is formed. Fermentation mainly depends on the metabolic function of microbial population. *Baijiu* fermentation process is a fermentation process under the open bilateral solid mixed bacteria system, which mainly relies on microbial sources obtained in the open fermentation process, and its fermentation and brewing process flow is shown in Figure 1. The uniqueness of *Baijiu* fermentation lies in its special fermentation process. The open fermentation process of *Baijiu* endows it with the ability to network and screen microorganisms from raw materials and environment in every

link of the fermentation process, and finally retain beneficial microbial groups suitable for *Baijiu* brewing and *Daqu* and fermented grains fermentation. The microbial source of *Baijiu* fermentation is mainly provided by *Daqu*, followed by microorganisms from fermentation raw materials and air, and microorganisms incidental to fermentation and production operation. With the fermentation of *Daqu* and fermented grains, the environmental conditions and physical and chemical factors of *Baijiu* brewing will also change accordingly, so that the microorganisms from the air, raw materials, fermentation and production operation can be cultivated and domesticated into functional microbial groups suitable for *Baijiu* brewing system, and then *Baijiu* can be produced in the fermentation process of *Daqu* and fermented grains.

2.2 Overview of the maceration and *Baijiu* fermented grains

Daqu, is a micro-ecological product made from wheat as the main raw material and peas, *Daqu*, millet and other auxiliary materials through open bilateral solid-state fermentation, which is used for saccharification and fermentation of raw materials in the process of brewing *Baijiu* and is rich in microbial flora, enzymes and flavor substances. It can contribute to the flavor composition of *Baijiu*. Due to the difference of fermentation process, *Daqu* is mainly divided into high-temperature *Daqu*, medium-temperature *Daqu* and low-temperature *Daqu*, of which high-temperature *Daqu* is mainly used in the production of Maotai-flavor *Baijiu*, while medium-temperature and medium-temperature *Daqu* are mainly used in the production of Luzhou-flavor *Baijiu* and low-temperature *Daqu* is mainly used in the production of Fen-flavor *Baijiu*. The process flow diagram of the production and fermentation of *Daqu* is shown in Figure 2.

Fermented grains are the main part of cellar fermentation in the process of *Baijiu* fermentation, which are mainly divided into single-grain brewing and multi-grain brewing. Single-grain brewing fermented grains are fermented with sorghum as the main raw material, while multi-grain brewing fermented grains are fermented with sorghum, wheat, rice, corn and glutinous rice as the main raw materials, with chaff shells and other auxiliary materials. Fermented grains are also carriers of pit mud, *Daqu* and various microorganisms in the environment during *Baijiu* brewing. The microorganisms in fermented grains can transform macromolecular fermented grains such as polysaccharides, cellulose and protein into various flavor substances in *Baijiu*. Therefore, the microbial community structure and metabolic activities in fermented grains have an important influence on the quality of *Baijiu*.

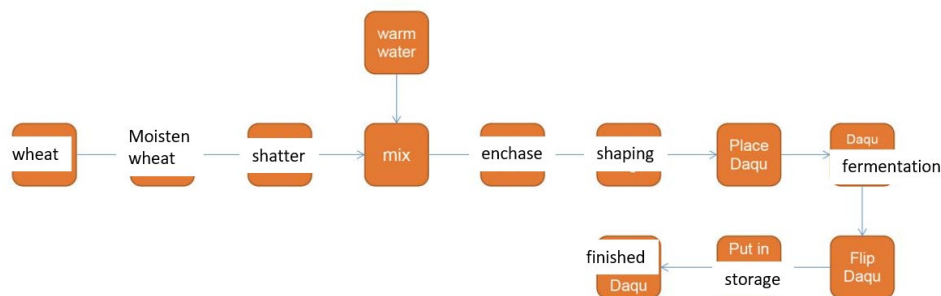


Figure 2: *Daqu* production process flow chart

The fermentation system of the *Daqu* and fermented grains is a complex multi-species open fermentation system, which is a multi-species common fermentation process through the interactions of many microorganisms and their respective life activities and metabolic activities. There are not only a large number of bacteria, but also many fungi, molds and yeasts in the fermentation process of the *Daqu* and fermented grains. Among them, yeast not only produces alcohol (ethanol)^[6] It can also produce polyols and esters such as ethyl acetate and many other flavor compounds^[7] *Bacillus* and *Aspergillus* are capable of producing various saccharifying enzymes such as amylase, pectinase, protease and cellulase for saccharification and fermentation (Guo & Jia, 2018).^[8-11] , *Bacillus* is also implicated in the production of pyrazine flavor substances in *Baijiu*, providing substrates for the growth of other microorganisms. *Lactobacillus* can regulate the microecological environment of the *Daqu* by producing organic acids, competing for nutrients, and producing bacteriocins, which in turn affect the growth and reproduction of other microorganisms, thus regulating the structure of other microbial communities during the fermentation of the *Daqu* and fermented grains.

3. Distribution and classification of lactic acid bacteria in the brewing process of Chinese Baijiu

3.1 Overview and classification of lactic acid bacteria

Lactic acid bacteria is a generic term for a group of Gram-positive bacteria that consume reducing sugars during fermentation and produce lactic acid, rather than the standard taxonomic name for bacteria. Lactic acid bacteria are catalase-negative, non-motile or rarely motile, non-budding, oxygen-tolerant, grow under anaerobic or partly anaerobic conditions, and can carry out homo- and hetero-lactic acid fermentation. Lactic acid bacteria are mainly present in the fermentation process of the fermented grains of *Baijiu* and *Daqu* during the brewing process of *Baijiu*. The existing research reports found that lactic acid bacteria in *Baijiu*-making mainly included *Weissella*, *Lactobacillus*, *Leuconostoc*, *Bifidobacterium*, *Streptococcus*, *Lactococcus*, *Pediococcus*, *Enterococcus*, *Aerococcus*, *Streptococcus*, g__ unclassified _f__ *Leuconostocaceae*, g__ unclassified _f__ *lactobacillus*, etc. Among them, *Weissella*, *Lactobacillus* and *Leuconostoc* are the main dominant lactic acid bacteria in *Daqu* and fermented grains. In addition, *Lactobacillus* and *Bifidobacterium* are also the most commonly used and common beneficial lactic acid bacteria in fermented food industry.

3.2 Distribution of lactic acid bacteria in the brewing process of Baijiu

Table 1: Distribution of lactic acid bacteria in the brewing process of Baijiu

<i>Baijiu</i> flavor type	Fermentation stage	lactic acid bacteria research results
Maotai-flavor type	<i>Daqu</i> ,fermented grains	Song et al. ^[12] revealed that the lactic acid bacteria group during fermentation was the dominant microorganism by amplicon sequencing technique, including <i>Lactobacillus</i> , <i>Pediococcus</i> , <i>Leuconostoc</i> , <i>Weissella</i> , and <i>Enterococcus</i> ; where <i>Lactobacillus</i> was the dominant lactic acid bacteria classification. wang et al. ^[13] found that lactic acid bacteria are the main bacteria in the fermentation process of <i>Daqu</i> , mainly including <i>Lactobacillus</i> , <i>Pediococcus</i> , and <i>Weissella</i> .
Luzhou-flavor	<i>Daqu</i>	Zhang et al. ^[14] <i>Lactobacillus</i> , <i>Weissella</i> , <i>Leuconostoc</i> , and <i>Pediococcus</i> were found in Luzhou-flavor <i>Daqu</i> by PCR-DGGE technique, and <i>Lactobacillus</i> accounted for 30.95% of all identified bacteria and dominated in the <i>Daqu</i> samples.Zhu et al. ^[15] found that <i>Weissella</i> and <i>Lactobacillus</i> were the main bacterial genera in <i>Daqu</i> .
Fen-Flavor	fermented grains	Wang et al. ^[16] The samples were followed through the fermentation process by amplicon sequencing technique, and the results showed that the microbial structure was complex at 0 days of fermentation, and the lactic acid flora became the dominant microorganism after 5 days of fermentation, where <i>Lactobacillus</i> and <i>Pediococcus</i> were the dominant lactic acid bacteria classification from 5 to 15 days of fermentation, and <i>Lactobacillus</i> became the dominant lactic acid bacteria classification at 15 days of fermentation.Huang et al. et al. ^[17] found the existence of lactic acid bacteria such as <i>Lactobacillus</i> and <i>Leuconostoc</i> in fen-flavor fermented grains, and the relative abundance of <i>lactobacillus</i> was more than 79%.
dry-flavor (Laobaigan-flavor)	fermented grains	Wang et al. ^[18] found that the lactic acid bacteria group became the dominant microorganism after 4 days of fermented grains fermentation, among which <i>Lactobacillus</i> was the dominant lactic acid bacteria.
dual-flavor (Maotai - Luzhou - flavor)	fermented grains	Liu et al. ^[19] found that <i>Lactobacillus</i> and <i>Lactococcus</i> dominated the bacterial community during the brewing of Bai Yunbian <i>Baijiu</i> .

In the early research on the microorganisms in *Baijiu* brewing, the traditional culturable method was mainly used to isolate and identify the microorganisms. However, since only about 1% of the microorganisms in the brewing process can be cultured and analyzed by traditional culturable methods,

the use of traditional culturable methods to investigate the structure of the microbial flora in the brewing process is very limited, and it does not provide a comprehensive and accurate picture of the microbial flora in the brewing process. It does not reflect the distribution of the microbial flora in the brewing process. At present, the detection technology for microorganisms in the brewing process of *Baijiu* is gradually maturing, from the traditional culturable method to PCR-DGGE detection technology, and nowadays, the use of modern molecular biology technologies such as high-throughput sequencing technology, macro-genomics technology and macro-transcriptomics technology has made people's research and understanding of microorganisms in *Baijiu* brewing more and more in-depth. Due to the mature use of microbial detection techniques, a more comprehensive and clear understanding of the distribution of lactic acid bacteria in the brewing process of *Baijiu* has been achieved.

4. Contribution of lactic acid bacteria in the brewing process of Chinese Baijiu

4.1 Functional contribution of lactic acid bacteria in the brewing process of Baijiu

The functional pathway of lactic acid production by lactic acid bacteria in the process of *Baijiu* brewing mainly exists in 3 main carbohydrate fermentation pathways: (1) homo-lactic acid fermentation: glucose through the glycolytic pathway generates pyruvate, which is reduced to lactic acid under the action of lactate dehydrogenase, 1 molecule of glucose generates 2 molecules of lactic acid; (2) hetero-lactic acid fermentation: glucose through the pentose phosphate pathway generated into 5-phosphate ribulose, through 3-phosphoglyceraldehyde, pyruvate, and finally reduced to lactic acid, 1 molecule of glucose generates 1 molecule of lactic acid and 1 molecule of ethanol, the conversion of lactic acid to sugar is 50%; (3) Bifid fermentation pathway: 1 molecule of glucose through the hexose phosphate dehydrogenase pathway generates 1 molecule of lactic acid and 1.5 molecules of acetic acid, the conversion of lactic acid to sugar is 50%. In the metabolism of lactobacillus, sugars are first degraded to pyruvate, and by metabolizing pyruvate thus forming lactate and other metabolites, while the production of different compounds during sugar metabolism by Lactobacillus is the result of the action of four enzymes, which include lactate dehydrogenase, pyruvate formate lyase, pyruvate dehydrogenase and α -acetyl lactate synthase.

During the fermentation process of *Baijiu*, organic acids such as lactic acid and acetic acid produced by lactic acid bacteria can maintain the acidic environment of *Baijiu* brewing, which is conducive to the starch saccharification and ethanol fermentation in the *Daqu* and fermented grains. Lactic acid bacteria can also produce amylase and protease^[20], which is helpful for saccharification and protein degradation of macromolecular raw materials in *Daqu* and fermented grains during *Baijiu* brewing, thus providing nutrients necessary for the growth of other microorganisms in *Daqu*. Therefore, lactic acid bacteria have an indispensable functional role in the brewing of *Baijiu*. Liu et al.^[21] For the first time, Lactobacillus was found to have the highest transcript abundance in the methyl cycle pathway in a Luzhou-flavor *Baijiu* brewing system, playing a key role in the cyclic supply of methionine lucidly. Lu et al.^[22] revealed that five kinds of lactic acid bacteria, *Acetobacter pasteurianus*, *Lactobacillus buchneri*, *Lactobacillus reuteri*, *Lactobacillus fermentum* and *Lactobacillus brevis*, participated in the formation of acetoin. Wu et al.^[23] used macrogenomics to reveal that various lactic acid bacteria such as Lactobacillus can be involved in the anabolism of flavor components such as lactic acid, acetic acid, lactic acid acetyl, glutamic acid, proline, and alanine. Song et al.^[12] combined with macro-transcriptomics techniques revealed that Lactobacillus plays a dominant role in pyruvate metabolism in late fermentation showing high *Idh* gene transcriptional activity and is the main contributing microorganism for lactate accumulation. Francesca et al.^[24] revealed by macro-transcriptomic techniques that lactic acid bacteria such as *Streptococcus* and *Lactobacillus* can be involved in protein hydrolysis. Wang et al.^[25] found that lactic acid bacteria and *Pichia* are the key microorganisms secreting glucoamylase in *Daqu*, including three glycosidases and two glycosyltransferases, especially the glucoamylase secreted by Lactobacillus and *Rhizobia* is the most abundant. In addition, these glycosidases-secreting microorganisms have low activity in *Baijiu* brewing, which provides a profound insight into the key microbial flora with saccharifying function in *Baijiu* brewing.

4.2 Contribution of lactic acid bacteria to the flavor of Baijiu during the brewing of Baijiu

Lactic acid bacteria can produce organic acids such as lactic acid and acetic acid by metabolizing pyruvic acid in the raw material material of the *Daqu* and fermented grains during the brewing process of *Baijiu*^[26, 27] Lactic acid not only reduces or removes the dryness, spiciness and bitterness of *Baijiu*,

increases the fullness of *Baijiu*, and enhances its mellowness, but it is also a precursor substance of esters such as ethyl acetate and ethyl lactate, methyl lactate, propyl lactate and butyl lactate, which are the main flavor substances in *Baijiu*, and the esters can bring floral and fruity flavor to *Baijiu*, thus increasing the flavor hierarchy of *Baijiu*. Lactic acid bacteria also have the functions of amino acid production and polysaccharide metabolism in *Baijiu* brewing, which are beneficial to the production of reducing sugar and amino acid, and reducing sugar such as amino acid and glucose can further promote the production of higher alcohols, sugar aldehydes, pyrazines and furans in *Baijiu* brewing. Therefore, lactic acid bacteria are closely related to aldehydes, phenols, furans and pyrazines in *Baijiu* and some higher alcohols and nitrogen-containing flavors in *Daqu*. Lactic acid bacteria also participate in the glycolysis of starch and other polysaccharides during the fermentation of Luzhou-flavor *Baijiu*, and at the same time, they also have the potential to metabolize *Baijiu* flavor precursors such as butyric acid and propionic acid.

In addition, Lactic acid bacteria can inhibit the growth, reproduction and ethanol production of *Pichia*, and *Pichia*, and lactic acid bacteria are important biological factors that affect the metabolic differences of higher alcohol flavor substances such as phenylethanol, isoamyl alcohol and isobutanol during *Baijiu* brewing. In addition, in the process of *Baijiu* fermentation, lactobacillus and Bacillus will affect the synthesis of ester flavors such as ethyl carbamate, ethyl palmitate, ethyl linoleate and ethyl oleate. Huang et al.^[28] evaluated the correlation between microorganisms and potential metabolic function by analyzing the characteristics of microbial composition and metabolites during *Baijiu* fermentation, found that the level of metabolic flavor was positively correlated with bacterial community during *Baijiu* brewing, and determined the potential of yeast and lactic acid bacteria to reduce substrate and produce flavor substances during *Baijiu* fermentation. Wu et al.^[23] used metagenomics technology to reveal that many kinds of lactic acid bacteria, such as Lactobacillus, can participate in the anabolism of flavor components such as lactic acid, acetic acid, lactic acid acetyl, glutamic acid, proline and alanine.

Therefore, lactic acid bacteria are very important for the formation of flavor substances in white *Baijiu*. Lactic acid bacteria can also use sugars to produce aldehydes such as acetaldehyde (fruity and almond-scented), 3- hydroxy -2- butanone and 2, 3- butanedione (creamy-scented) and other flavor substances^[29]. It can be concluded that lactic acid bacteria contribute to the formation of flavor substances in *Baijiu* brewing.

4.3 Contribution of lactic acid bacteria to the formation of the microbial communities structure of *Baijiu* brewing in Chinese *Baijiu* brewing

In the process of *Baijiu* brewing, *Candida* can regulate ethyl lactate in *Daqu* through its influence on lactic acid bacteria^[30]. Lactic acid bacteria can promote Acetobacter and Gluconobacter to oxidize ethanol into acetic acid through alcohol dehydrogenase and aldehyde dehydrogenase^[31], and acetic acid is a precursor of ethyl acetate, the main flavor substance in *Baijiu*. The co-culture of lactobacillus and *Pichia* can significantly improve the yield of ethyl lactate in *Baijiu* fermentation. Lactic acid produced by lactic acid bacteria metabolism can promote the production of propionic acid by brewing microorganisms. Butyric acid bacteria can use lactic acid produced by lactic acid bacteria as carbon source to produce butyric acid, and lactic acid bacteria can also produce ethyl lactate through esterification with ester-producing yeast. Lactic acid bacteria can also maintain the acidic brewing environment of *Baijiu* through various organic acids such as lactic acid and acetic acid produced by metabolism^[32], and then screen and eliminate not acid-resistant brewing microorganisms, thus helping to regulate and maintain the balance relationship between microbial community structures in the *Baijiu* fermentation system. Lactic acid bacteria can also produce hydrogen peroxide and bacteriocin-like polypeptides, such as lactobacillin and bifidobacterium, which have antagonistic effects on *Shigella*, *Staphylococcus* and *Salmonella*, and eliminate pathogenic microorganisms in the *Baijiu* fermentation system. In addition, lactic acid bacteria have fast reproduction and high abundance in the process of *Baijiu* fermentation, which can gain a favorable competitive position through huge group advantages, which is also an aspect of antibacterial mechanism for brewing microorganisms. Thus, it is evident that Lactobacillus has an important role in contributing to the composition of the microecology of *Baijiu* brewing. At the same time, the relative abundance of lactic acid bacteria is in an absolute dominant position in *Daqu* bacterial microorganisms. According to Ma et al.'s report, lactic acid bacteria exist as high-importance biomarkers to distinguish different fermentation stages of *Daqu*, and they also play an important role in the co-occurrence network of *Daqu* microbial correlation, which is also an important biological factor that affects and promotes the succession of *Daqu* microbial community structure during *Daqu* fermentation.^[33] This shows that lactic acid bacteria play an indispensable role in the

process of *Baijiu* brewing and the fermentation of *Daqu* and fermented grains and play an important role in fermentation.

5. Conclusion and Outlook

This paper summarized the important functions and functions of lactic acid bacteria in China *Baijiu*-making, and explained the indispensable position of lactic acid bacteria in *Baijiu*-making. In order to provide theoretical reference for future researchers who study the functional mechanism of lactic acid bacteria in China *Baijiu* fermentation.

The main body of China *Baijiu* brewing mainly depends on the microbial community in the process of *Baijiu* fermentation. The microbial community in the process of *Baijiu* brewing can use its own functions to produce flavor compounds such as alcohols, aldehydes, acids, esters, ketones, phenols, alkanes, alkenes, pyrazines and furans necessary for *Baijiu* through life metabolism activities, thus bringing unique *Baijiu* body and taste to China *Baijiu*. Therefore, it is very important to study the microbial community and its functional contribution in the process of *Baijiu* fermentation for analyzing the functional mechanism of China *Baijiu*-making microbial community. Lactic acid bacteria, as the main dominant microorganisms with high abundance and important functional microorganisms in the process of *Baijiu* brewing, need us to deeply understand and study its functions and functions. The study of lactic acid bacteria is beneficial to regulate the content of lactic acid in *Baijiu*, and the content of lactic acid is very important to the taste of *Baijiu*. Too much lactic acid will lead to the sour taste of *Baijiu*, while too little lactic acid will lead to the uncoordinated taste of *Baijiu*. At the same time, lactic acid can further react with other metabolites in *Baijiu* fermentation system to synthesize a variety of *Baijiu* flavor substances, such as ethyl lactate and other ester flavors. Therefore, it is very important to study lactic acid bacteria in the process of *Baijiu* brewing for regulating the taste of *Baijiu* and improving the quality of *Baijiu*.

With the development of modern molecular biology technology, we have a deep understanding of the composition of microbial community structure in the process of *Baijiu* brewing, but the understanding of the functional mechanism and action mechanism of microorganisms is not in-depth and comprehensive, and the functional mechanism of more detailed microbial genera and species is even less studied, which remains to be studied by us. Therefore, the research on lactic acid bacteria should further understand the functions of various lactic acid bacteria genera. Such as *Weissella*, *Lactobacillus*, *Leuconostoc*, *Bifidobacterium*, *Streptococcus*, *Lactococcus*, *Pediococcus*, the detailed functional mechanism of lactic acid bacteria at the level of *Enterococcus* and other genera, on this basis, it is necessary to further study the influence of lactic acid bacteria on the microbial flora of *Baijiu* brewing and its contribution to the brewing function of *Baijiu* fermentation system. In order to provide more accurate reference for the functional research and mechanism of lactic acid bacteria in *Baijiu* brewing, and also provide theoretical reference for improving *Baijiu* quality by regulating lactic acid bacteria and other *Baijiu* functional microorganisms.

In addition to studying the functional mechanism of lactic acid bacteria, it is necessary to further study the influence of lactic acid bacteria on the microbial community structure and succession, microecological environment factors, volatile flavor group metabolism and microbial flora function in *Daqu* and fermented grains during *Baijiu* brewing, which is beneficial to our in-depth analysis of microbial community interaction during *Baijiu* brewing and to improve the quality of *Baijiu* by regulating the microbial community structure in *Daqu* and fermented grains.

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