

Comparative Study of Black *Daqu* Blocks and Normal *Daqu* in *Strong-Flavor Daqu*

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Abstract: Due to the heterogeneity of solid-state fermentation, black *Daqu* blocks often form in the cross-sections of *strong-flavor Daqu*. These black blocks exhibit microbial communities and physicochemical properties significantly different from normal *Daqu*. This study aims to investigate the impact of black blocks on the quality of *Daqu* by comparing the microbial diversity, enzymatic properties, and physicochemical indicators of black blocks and normal *Daqu*, and by conducting correlation analyses to uncover the underlying mechanisms. The results showed that the microbial diversity in normal *Daqu* was higher than that in black blocks. Normal *Daqu* was rich in yeast species, including *Dipodascaceae sp.*, *Candida tropicalis*, and *Wickerhamomyces anomalus*, as well as bacteria dominated by lactic acid bacteria and *Bacillus* species, such as *Enterococcus faecalis*, *Weissella confusa*, *Bacillus licheniformis*, and *Bacillus amyloliquefaciens*. Normal *Daqu* exhibited superior acidity and fermentation capacity. In contrast, the fungal community in black blocks was predominantly composed of *Thermomyces lanuginosus*, *Wallemia mellicola*, and *Aspergillus chevalieri*. while the bacterial community was dominated by *Staphylococcus gallinarum*. Black blocks demonstrated stronger saccharification and liquefaction abilities. Correlation analysis indicated that the primary microorganisms in normal *Daqu* were significantly associated with acidity and fermentation capacity. whereas the dominant microbial groups in black blocks were correlated with moisture, saccharification, and liquefaction abilities. This study highlights the quality differences between black blocks and normal *Daqu* in *strong-flavor Daqu*, providing theoretical insights for optimizing *Daqu* production.

Keywords: *Strong-flavor Daqu*; Black *Daqu* Blocks; Microbial Communities; Physicochemical Properties.

1. Introduction

strong-flavor Daqu is typically produced from fermented raw materials such as wheat and peas, harboring abundant microbial resources. Its manufacturing employs a solid-state fermentation process, where complex microbial communities generate diverse enzymes and flavor precursors [1]. During production, significant gradients in temperature, oxygen supply, and moisture distribution exist within the *Daqu* bricks [2]. These gradients lead to the formation of intricate internal structures after high-temperature fermentation, resulting in marked variations in microbial distribution and physicochemical properties across different regions of the *Daqu* [3]. Due to these internal environmental disparities, color differences—most notably the formation of blackened blocks—often appear on cross-sections of *Daqu*. These differentially colored sections exhibit distinct microbial compositions and functional characteristics.

Existing studies confirm that variations in *Daqu* color correspond to significant differences in microbial composition, enzymatic properties, and physicochemical parameters. Deng *et al.* [4] utilized amplicon sequencing to analyze microbial communities in high-temperature *Daqu*, revealing that *white Daqu* exhibits higher abundances of *Kroppenstedtia* and *Bacillus*, whereas *black Daqu* is enriched with *Thermoactinomyces* and *Thermomyces*. *Red Daqu* demonstrates greater prevalence of *Saccharopolyspora* and *Thermomyces*. Pang *et al.* [5] determined that *white Daqu* displays higher liquefying capacity, while *black Daqu* exhibits superior saccharifying and esterification capacities.

Currently, the mechanisms underlying blackened *Daqu* block formation in *strong-flavor Daqu* and its impact on quality remain unclear. Comparative analysis of

physicochemical properties and microbial communities between blackened blocks and normal *Daqu* will advance understanding of their formation mechanisms and potential effects on fermentation quality. This study systematically compares the physicochemical characteristics and microbial community structures of blackened *Daqu* blocks and normal *Daqu* to identify critical factors influencing quality.

2. Materials and Methods

2.1. Materials and Reagents

2.1.1. Samples

Daqu samples after fermentation were collected at three different time points from a Luzhou-flavor liquor enterprise in Yibin, China. At each time point, one *Daqu* sample with black qu block cross-sections (B1, B2, B3) and one normal *Daqu* sample (W1, W2, W3) were respectively collected. For normal *Daqu* (see the *Daqu* on the left side of Figure 1), it was directly crushed and placed into sterile bags. For black qu blocks, they were scooped out from the cross-sections using sterile spoons (the red-circled area in the *Daqu* on the right side of Figure 1), crushed, and placed into sterile bags. The prepared qu powder was divided into two parts, stored at 4°C (for physicochemical and enzymatic property analysis) and -20°C (for DNA extraction), respectively.

2.1.2. Reagents

Reagents used included sodium hydroxide, potassium hydrogen phthalate, glucose, ethylenediaminetetraacetic acid disodium salt, snailase, lysozyme, cetyltrimethylammonium bromide, sodium dodecyl sulfate, Tris-buffered phenol, chloroform, sulfuric acid, hydrochloric acid, glacial acetic acid, mercury iodide, potassium iodide, potassium sodium tartrate, ammonium chloride, glucose, copper sulfate,

potassium dihydrogen phosphate, acetic acid, citric acid, Folin reagent, sodium hypochlorite, sodium carbonate, trichloroacetic acid, sodium acetate, potassium permanganate,

etc. All reagents were of analytical grade and purchased from Chengdu Kelong Chemicals Co., Ltd.



Fig 1. Cross-Sections of Normal Daqu and Black-Colored Daqu

2.2. Instruments and Equipment

UV-2400 UV-Vis spectrophotometer, Shanghai Unico Instrument Co., Ltd. 5430R high-speed refrigerated centrifuge, Eppendorf, Germany. C1000 PCR machine and Gel Doc RX gel imager, Bio-Rad, USA. NanoDrop2000 DNA content analyzer, Thermo Fisher Scientific, USA.

2.3. Experimental Methods

2.3.1. Detection of Daqu Quality Indicators

Physicochemical indices and main enzymatic activities of Daqu were detected with reference to QB/T 4257-2011 General Analytical Methods for Liquor-making Daqu.

2.3.2. Total DNA Extraction and Sequencing of Daqu

Daqu DNA was extracted using the elution plus SDS-based extraction method [6]. The bacterial 16S rRNA gene was PCR-amplified with primers 27F (5'-AGRGTTYGATYMTGGCTCAG-3') and 1492R (5'-RGYTACCTTGTACGAC TT-3'), and the fungal ITS gene was amplified with primers ITS1 (5'-CTTGATCATT TAGAGGAAGTAA-3') and ITS4 (5'-TCCTCCGCTTATTGATATGC-3'). The constructed amplicon libraries were sequenced on the Illumina Miseq Pcbio sequencing platform by Shanghai Meiji Biomedical Technology Co., Ltd.

2.4. Data Processing

Raw sequences were processed using the Majorbio Bioinformatics Cloud Platform (<http://www.majorbio.com/>), and online tools were used for species composition analysis and microbial-physicochemical correlation analysis.

3. Results and Analysis

3.1. Microbial Community Diversity and Composition

To compare the microbial community differences between black qu blocks (B) and normal Daqu (W), high-throughput sequencing was used to analyze the microorganisms in both types of samples. A total of 112,974 valid bacterial sequences and 149,832 valid fungal sequences were obtained from black and normal Daqu samples across different time periods.

The results of microbial α -diversity analysis are shown in Table 1. In the α -diversity analysis, the Chao 1 indices of fungi and bacteria in normal Daqu were significantly higher than those in black qu blocks, indicating that normal Daqu had higher species richness than black qu blocks. Additionally,

both types of Daqu showed higher bacterial diversity than fungal diversity.

Table 1. Microbial α -Diversity Indices

| α Diversity Index | Microbial Type | Normal Daqu | Black Qu Blocks |
|--------------------------|----------------|---------------|-----------------|
| Chao 1 Index | Fungi | 164.28±14.31a | 24.79±8.45b |
| Chao 1 Index | Bacteria | 209.88±8.72a | 86.85±14.39b |

Note: Different letters in the same row indicate significant differences ($P < 0.05$).

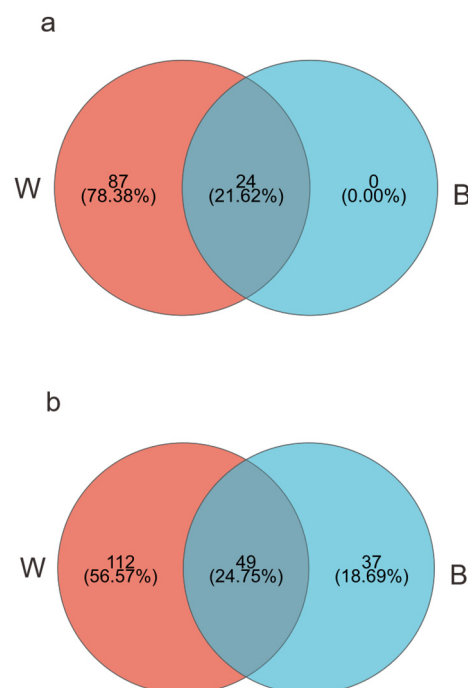


Fig 2. Venn Diagram Comparing Community Structures of Different Daqu Samples

The Venn diagram shows the overlap in microbial species composition between normal Daqu and black qu blocks of Daqu. The normal Daqu had 111 fungal OTUs, of which 87 (78.38%) were unique species, while 24 species (21.62%) were shared by normal Daqu and black qu blocks. The black qu blocks had only 24 fungal OTUs, and no unique species were observed in the black qu blocks, with all species shared with normal Daqu (see Figure 2-a). The normal Daqu

contained 198 bacterial species, of which 112 (56.57%) were unique to normal Daqu and 49 (24.75%) were shared with black qu blocks. The black qu blocks had a total of 86 bacterial species, of which 37 (18.69%) were unique to the black qu blocks (see Figure 2-b).

The fungal microbial community structure of black qu blocks was relatively simple, with the highest relative abundance being the thermophilic fungus *Thermomyces lanuginosus* (59.58% average relative abundance), followed by *Walleimia mellicola* (25.32%) and *Aspergillus chevalieri* (12.60%). These species are adapted to high-temperature environments and possess strong carbohydrate-degrading abilities, capable of producing highly active cellulase and xylanase, which may aid in the initial degradation of complex starches [7][8][9]. Normal Daqu contains various molds and yeasts: *Candida tropicalis* and *Cyberlindnera fabianii* can produce large amounts of ethanol and other volatile flavor compounds during fermentation, which combine with organic acids to form esters [10]. Additionally, *Wickerhamomyces anomalus* exhibits antibacterial activity, inhibiting the growth

of undesirable microbes and enhancing fermentation stability [11]. *Thermoascus aurantiacus* demonstrates excellent enzymatic activity under high temperatures, particularly in producing cellulase and xylanase [12].

The bacterial community of black qu blocks was dominated by a single species, *Staphylococcus gallinarum* (95.02%). In contrast, normal Daqu showed higher bacterial diversity, including various lactic acid bacteria (LAB) and bacilli. *Bacillus licheniformis* and *Bacillus amyloliquefaciens* secrete multiple enzymes (e.g., protease, amylase) to promote the degradation of complex organic matter, generating amino acids and other substances that not only supply energy for microbial fermentation and growth metabolism but also provide precursor materials for the formation of aromatic substances like esters [13][14]. Furthermore, lactic acid bacteria such as *Enterococcus faecalis* and *Weissella confusa* help produce lactic acid and other organic acids, regulating the pH of the fermentation environment [15][16]. The diverse bacterial community in normal Daqu thus contributes to a broader spectrum of metabolic products.

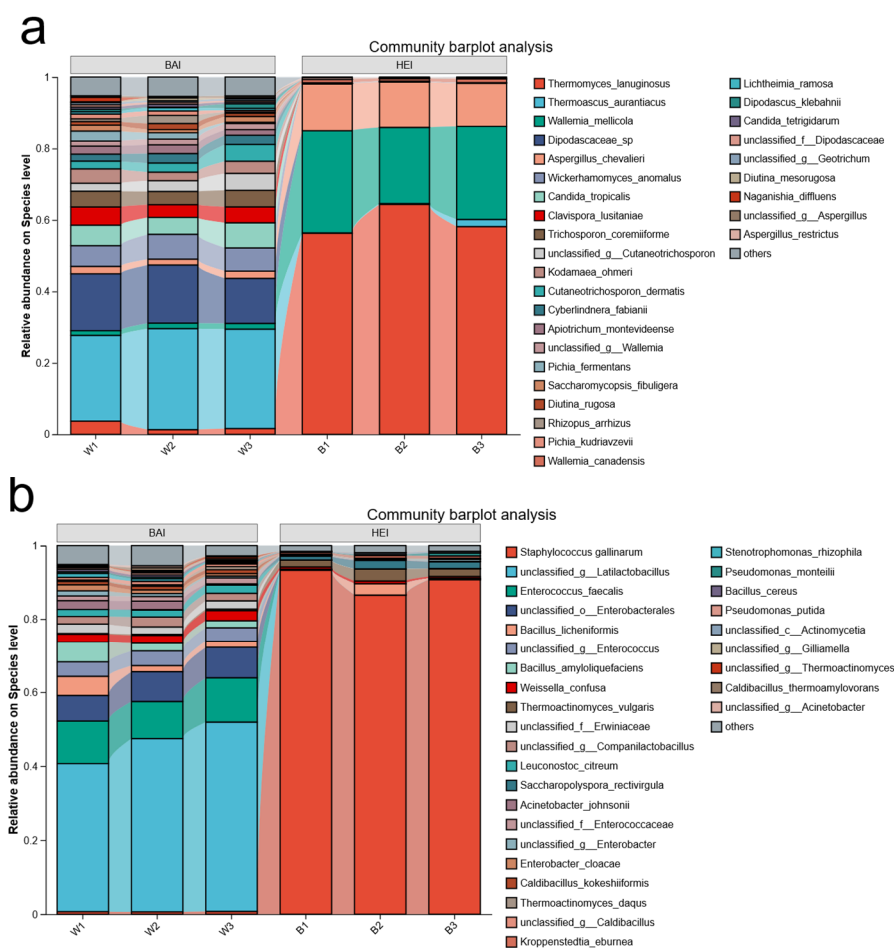


Fig 3. Microbial Community Structures of the Two Types of Daqu

To further identify the differential microbial species between the two types of Daqu, LEfSe analysis at the species level was performed. The differentially abundant fungal microbes in black qu blocks were *Aspergillus chevalieri*, *Thermomyces lanuginosus*, and *Walleimia mellicola*. In normal Daqu, the differential fungal microbes included *Apiotrichum montevidense*, *Candida tropicalis*, *Clavispora lusitaniae*, *Cutaneotrichosporon dermatis*, *Cyberlindnera fabianii*, *Diascus*, *Kodamaea ohmeri*, *Thermoascus aurantiacus*, *Trichomonascus ciferrii*, *Trichosporon coremiiforme*, and *Wickerhamomyces anomalus*. For bacteria,

the differential microbes in black qu blocks were *Thermoactinomyces vulgaris* and *Staphylococcus gallinarum*, while those in normal Daqu included *Bacillus licheniformis*, *Enterococcus faecalis*, *unclassified Erwiniaceae*, *unclassified Bartonella*, *unclassified Companilactobacillus*, *unclassified Enterococcus*, *unclassified Latilactobacillus*, and *unclassified Enterobacteriales*.

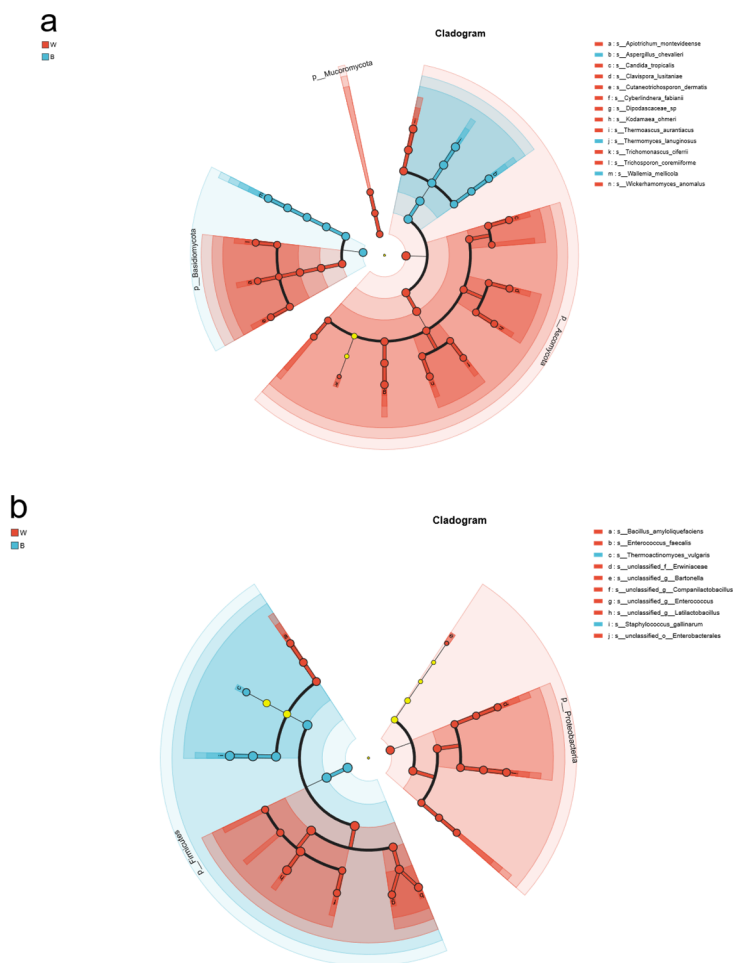


Fig 4. LfSe Analysis of Species Differences Between Two Types of Daqu

3.2. Analysis of Physicochemical Property Differences

Physicochemical indices and enzymatic activity indices are

important criteria for evaluating Daqu quality. The differences in physicochemical indices and enzymatic activity indices between the two types of Daqu were analyzed by one-way ANOVA, and the results are shown in Table 2 below.

Table 2. Physicochemical Properties and Enzyme Activity Indices of the Two Types of Daqu

| Physicochemical Index | Normal Daqu | Black Qu Blocks |
|---|-----------------------------|----------------------------|
| Moisture content/% | 9.90 ± 0.03 ^a | 20.00 ± 0.02 ^b |
| Acidity/% | 0.81 ± 0.06 ^a | 0.47 ± 0.04 ^b |
| Saccharification capacity/[mg·(g·h) ⁻¹] | 279.52 ± 12.66 ^a | 401.10 ± 5.42 ^b |
| Fermentation capacity/[g·(0.5g·72h) ⁻¹] | 0.51 ± 0.07 ^a | 0.23 ± 0.02 ^b |
| Liquefaction capacity/[g·(g·h) ⁻¹] | 0.90 ± 0.05 ^a | 1.70 ± 0.09 ^b |

Note: Different letters in the same row indicate significant differences (P < 0.05).

From the table, it can be seen that the moisture content of black qu blocks was significantly higher than that of normal Daqu. High moisture content increases microbial growth activity but may also lead to fermentation perishability and instability [17]. Conversely, the low moisture content of normal Daqu enhances its storage stability, prolongs service life, and avoids excessive fermentation or spoilage during storage [18]. The acidity and fermentation capacity of black qu blocks were significantly lower than those of normal Daqu, while their saccharification and liquefaction capacities were significantly higher. Fermentation capacity reflects the ability to produce alcohol and other volatile aroma substances; higher fermentation capacity indicates that normal Daqu has advantages in generating alcohol and aroma compounds, which are crucial for flavor richness [19]. Saccharification

and liquefaction capacities are key indicators for evaluating starch decomposition during fermentation, collectively reflecting the efficiency of converting starch into fermentable sugars. Black qu blocks showed higher saccharification capacity (401.10 mg·(g·h)⁻¹) and liquefaction capacity (1.70 g·(g·h)⁻¹) than normal Daqu (279.52 mg·(g·h)⁻¹ and 0.90 g·(g·h)⁻¹, respectively), indicating stronger starch decomposition and sugar production capabilities. This suggests that black qu blocks can rapidly convert starch into sugars, providing abundant substrates for fermenting microbes and potentially improving early-stage fermentation efficiency [20][21].

3.3. Correlation Analysis Between Microbial Communities and Physicochemical Properties

Canonical Correlation Analysis (CCA) was used to interpret the correlations between differential microbes and Daqu physicochemical indices, as shown in Figure 5.

Fungal Analysis: In normal Daqu, *Thermoascus aurantiacus* and *Dipodascaceae sp.* were significantly

correlated with acidity and fermentation capacity. Studies show that *Thermoascus* maintains high activity under high temperatures and low pH, secreting various hydrolases critical for degrading complex polysaccharides and advancing fermentation [22]. Additionally, *Dipodascaceae* metabolizes aroma-producing secondary metabolites, significantly influencing fermentation product flavors [23]. Thus, low acidity and strong fermentation performance may be important factors in normal Daqu formation.

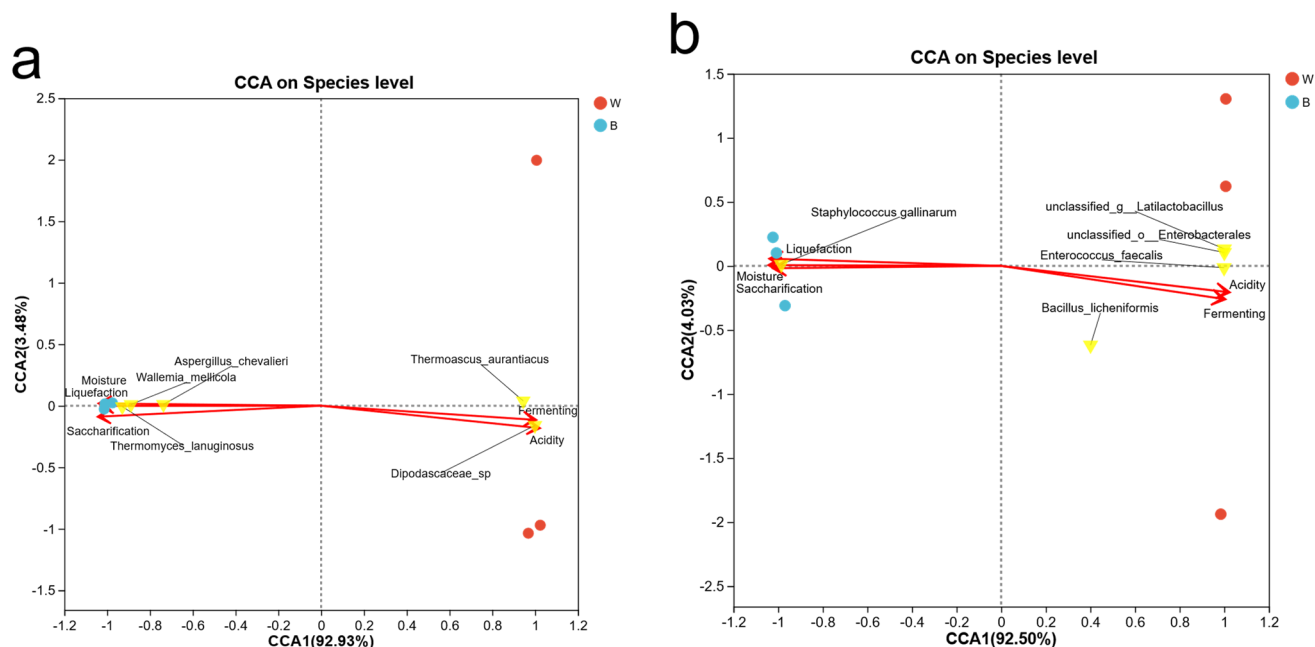


Fig 5. Correlation Analysis Between Differential Microorganisms, Physicochemical Properties, and Key Enzyme Activities

In contrast, black qu block samples had higher moisture, saccharification, and liquefaction capacities, under which fungal communities exhibited specific ecological adaptability. *Walleimia mellicola*, *Aspergillus chevalieri*, and *Thermomyces lanuginosus* were significantly correlated with moisture content, saccharification, and liquefaction capacities. Research indicates that *Walleimia mellicola* is sugar-loving and survives in high-sugar environments, offering obvious advantages during saccharification and liquefaction [24]. Moreover, *Thermomyces lanuginosus* is recognized as an effective decomposer of cellulose and hemicellulose, providing key cellulase and xylanase during saccharification to facilitate sugar release in fermentation [25]. *Aspergillus chevalieri* efficiently decomposes plant cell wall components in humid environments, supplying carbon sources for subsequent microbial communities, which has been widely applied in various fermented products [26].

Bacterial Analysis: In normal Daqu, unclassified lactobacilli, *Enterococcus faecalis*, and *Bacillus licheniformis* showed high activity and were significantly correlated with acidity and fermentation conditions. Existing studies demonstrate that *Enterococcus* generates diverse acidic metabolites during fermentation, effectively inhibiting pathogenic bacteria and improving fermented product safety and flavor characteristics [27]. Additionally, *Bacillus licheniformis* produces degradation enzymes (e.g., protease, amylase) that decompose complex matrix components to form unique flavor substances [28].

By contrast, black qu blocks exhibited specific microbial activities in high-moisture, high-saccharification, and high-liquefaction environments. *Thermoactinomyces vulgaris* and

unclassified staphylococci were positively correlated with moisture, saccharification, and liquefaction capacities, indicating their adaptability to high-moisture conditions. *Thermoactinomyces* efficiently decomposes cellulose and starch during fermentation, enhancing saccharification efficiency [29].

4. Conclusion

This study systematically compared the physicochemical properties and microbial community structures between black qu blocks and normal Daqu in Luzhou-flavor Daqu, revealing significant differences in their ecological adaptability and fermentation quality. The results showed that normal Daqu had higher microbial community diversity and richness, in which lactic acid bacteria, bacilli, and various yeasts significantly improved fermentation stability and flavor compound production through metabolic activities. In contrast, the microbial community of black qu blocks was dominated by thermophiles, adapted to high-temperature and high-humidity environments, and exhibited strong cellulose and starch decomposition capabilities. Physicochemical analysis indicated that normal Daqu had higher acidity and fermentation capacity, which could inhibit the growth of undesirable microbes and optimize the fermentation environment. Black qu blocks, however, showed superior saccharification and liquefaction capacities, suitable for rapid production of fermentable sugars, but their high moisture content increased the risks of fermentation instability and spoilage. The microbial community of normal Daqu was significantly correlated with acidity and fermentation

performance, while the thermophilic fungal community of black qu blocks was closely linked to high moisture and saccharification capacity.

Overall, black qu blocks exhibit high sugar production efficiency in the early fermentation stage, making them suitable for rapid fermentation requirements, but their simple microbial community structure may lead to insufficient flavor complexity. Normal Daqu, by contrast, demonstrates higher aroma layers and fermentation quality due to its rich microbial community and diverse metabolic products. This study provides a scientific basis for further understanding the formation mechanism of black qu blocks and their impact on Daqu fermentation quality, while offering important references for optimizing the fermentation process of Luzhou-flavor Daqu.

References

- [1] Hu Y, Dun Y, Li S, et al. Changes in microbial community during fermentation of high-temperature Daqu used in the production of Chinese 'Baiyunbian' liquor[J]. *Journal of the Institute of Brewing*, 2017, 123(4): 594-599.
- [2] Chen Y, Li K, Liu T, et al. Analysis of difference in microbial community and physicochemical indices between surface and central parts of Chinese special-flavor Baijiu Daqu[J]. *Frontiers in microbiology*, 2021, 11: 592421.
- [3] Wen Z, Han P J, Han D Y, et al. Microbial community assembly patterns at the species level in different parts of the medium temperature Daqu during fermentation[J]. *Current Research in Food Science*, 2024, 9: 100883.
- [4] Deng, Ling, et al. "Comparative analysis of physicochemical properties and microbial composition in high-temperature Daqu with different colors." *Frontiers in microbiology* 11 (2020): 588117.
- [5] Pang Z, Li W, Hao J, et al. Correlational analysis of the physicochemical indexes, volatile flavor components, and microbial communities of high-temperature daqu in the northern region of China[J]. *Foods*, 2023, 12(2): 326.
- [6] Ye, Xin, Yang, et al. Effects of different DNA extraction methods on the DNA extraction effect and amplicon library of Daqu genome [J]. *Food and Fermentation Industries*, 2024, 50(12): 118-126.
- [7] Li, X., Ma, H., & Sun, Z. (2018). *Thermomyces lanuginosus*: Properties of an efficient cellulolytic and xylanolytic enzyme producer. *Applied Microbiology and Biotechnology*, 102(15), 6305-6316. doi:10.1007/s00253-018-9141-8.
- [8] Zalar, P., de Hoog, G. S., Schroers, H. J., Frank, J. M., & Gunde-Cimerman, N. (2005). Taxonomy and phylogeny of the halophilic and halotolerant fungi in the *Wallemia sebi* species complex. *Anton van Leeuwenhoek*, 87(4), 311-328. doi:10.1007/s10482-004-6854-1.
- [9] Jiang, Z., Xu, B., & Zhang, J. (2015). *Aspergillus*: a traditional fermentation fungi for Chinese liquor production. *Applied Biochemistry and Biotechnology*, 176(5), 1509-1517. doi:10.1007/s12010-015-1689-y.
- [10] Yan, D., Hu, B., Liu, Y., & Han, X. (2022). Impact of yeast strains on aroma compounds in Chinese light-flavor liquor production. *Food Chemistry*, 385, 132680. doi:10.1016/j.foodchem.2022.132680.
- [11] Gonçalves, C., Moreira, J. M., & Pina, C. (2017). Biological and technological significance of *Wickerhamomyces anomalus* in food and beverage fermentations. *Food Research International*, 91, 89-98. doi: 10.1016/j.foodres.2016.11.003.
- [12] Bai, Y., Zhi, R., & Chen, H. (2020). Role of *Thermoascus aurantiacus* in traditional Chinese liquor fermentation: High temperature adaptability and its influence on flavor. *Journal of Applied Microbiology*, 129(2), 493-502. doi:10.1111/jam.14646.
- [13] Yan, D., & Hu, B. (2022). *Bacillus* species in high-temperature fermentation. *Food Chemistry*, 385, 132680. doi:10.1016/j.foodchem.2022.132680.
- [14] Bai, Y., & Zhi, R. (2020). *Bacillus licheniformis* and *amyloliquefaciens* in traditional liquor production. *Journal of Applied Microbiology*, 129(2), 493-502. doi:10.1111/jam.14646.
- [15] Gonçalves, C., & Moreira, J. M. (2017). Lactobacilli in fermentation and flavor development. *Food Research International*, 91, 89-98. doi: 10.1016/j.foodres.2016.11.003.
- [16] Zhao, X., Wu, S., & Liu, Y. (2020). Dynamics of bacterial communities in Baijiu fermentation. *Food Research International*, 138, 109767. doi:10.1016/j.foodres.2020.109767.
- [17] Liu, Y., Cheng, Y., & He, Z. (2019). Role of microbial community in Chinese liquor fermentation. *Frontiers in Microbiology*, 10, 1640. doi:10.3389/fmicb.2019.01640.
- [18] Zhao, X., Wu, S., He, L., & Liu, Y. (2020). Microbial diversity and dynamics in fermentation of Chinese traditional strong-flavor liquor (Baijiu). *Food Research International*, 138, 109767. doi: 10.1016/j.foodres.2020.109767.
- [19] Jiang, Z., Xu, B., & Zhang, J. (2015). Metabolic activities of microbial communities in liquor fermentation. *Applied Biochemistry and Biotechnology*, 176(5), 1509-1517. doi: 10.1007/s12010-015-1689-y.
- [20] Chen, X., Feng, Y., Wang, Q., & Li, L. (2019). Enzyme activity in high-temperature liquor fermentation. *Journal of Food Science*, 84(6), 1378-1386. doi:10.1111/1750-3841.14682.
- [21] Ma, C., Zhang, Y., & Liu, L. (2020). Effect of high starch degradation on flavor development in Chinese liquor. *LWT - Food Science and Technology*, 134, 110212. doi: 10.1016/j.lwt.2020.110212.
- [22] Liu, X., Dong, H., Zhang, Y., and Zhao, S. (2020). Thermophilic fungi and their enzymatic potential in the fermentation industry: A review. *Journal of Industrial Microbiology & Biotechnology*, 47(6-7), 527-538. doi:10.1007/s10295-020-02277-y.
- [23] Wang, X., Liu, Y., and Li, Y. (2019). Fungal biodiversity and its impact on aroma production during traditional fermentation. *Food Research International*, 115, 67-76. doi:10.1016/j.foodres.2018.08.030.
- [24] Rosas-Saavedra, C., and Stojanovic, O. (2016). Adaptation and survival mechanisms of *Wallemia* spp. in osmotic stress conditions. *Frontiers in Microbiology*, 7, 1096. doi:10.3389/fmicb.2016.01096.
- [25] Cai, W., Zhang, S., and Zhang, X. (2021). Role of thermophilic fungi in biomass degradation: Potential applications in bioenergy production. *Renewable and Sustainable Energy Reviews*, 135, 110361. doi:10.1016/j.rser.2020.110361.
- [26] Samson, R. A., Houbraken, J., Thrane, U., Frisvad, J. C., and Andersen, B. (2014). Food and indoor fungi. *CBS-KNAW Fungal Biodiversity Centre, Utrecht, The Netherlands*.
- [27] Wu, Q., Chen, L., and Xu, Y. (2013). Impact of a selected lactic acid bacterial starter on the volatile compounds in Chinese rice wine. *Journal of Agricultural and Food Chemistry*, 61(40), 9703-9712. doi:10.1021/jf4034484.
- [28] Xu, Y., Xie, G., Zhang, S., and Li, P. (2020). Fermentation performance and metabolic profiles of *Bacillus licheniformis* in traditional fermentation process. *Food Chemistry*, 319, 126548. doi:10.1016/j.foodchem.2020.126548.
- [29] Liu, D., Zhang, R., Yang, X., Zheng, H., and Zhang, X. (2019). High-temperature-resistant microorganisms in the fermentation process of Chinese strong-flavor liquor: A review. *Journal of Food Science*, 84(9), 2438-2448. doi:10.1111/1750-3841.14720.