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# Research Progress on Microbial Fermentation Assisted Extraction Method Of $\beta$ - Glucan from Barley

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## Abstract

This study explores advancements in the microbial fermentation-assisted extraction of  $\beta$ -glucan from highland barley, a highly nutritious grain primarily cultivated on the Qinghai-Tibetan Plateau. Highland barley, known for its high protein and dietary fiber content, is particularly rich in  $\beta$ -glucan—a polysaccharide linked through  $\beta$ -1,3- and  $\beta$ -1,4-glycosidic bonds, which provides numerous health benefits, including glycemic control, lipid regulation, and anti-tumor effects. The research focuses on different microbial strains' efficacy of various microbial strains in extracting  $\beta$ -glucan, including homolactic fermentation bacteria such as *Lactobacillus acidophilus* and *L. reuteri*, as well as other strains such as *Lactiplantibacillus plantarum* and *Saccharomyces cerevisiae*. Notably, *Lactobacillus* species enhanced the soluble dietary fiber content significantly more than *S. cerevisiae*, which in some cases reduced  $\beta$ -glucan content. The traditional Tibetan fermentation starter, Tibetan Qu, was also studied, revealing its complex microbial composition's ability to improve both the quantity and quality of  $\beta$ -glucan extracted during fermentation. Our findings indicate that the choice of microbial strain plays a crucial role in the fermentation process, impacting the molecular weight, viscosity, solubility, and antioxidant activity of  $\beta$ -glucan. This has implications for both the health benefits and industrial applications of the final product.

**Keywords:** Highland Barley;  $\beta$ -Glucan; Microbial Fermentation; *Lactobacillus acidophilus*; *Lactobacillus reuteri* *Saccharomyces cerevisiae*; Tibetan Qu

**Abbreviations:** LAC: *Lactobacillus acidophilus*; L reuteri: *Lactobacillus reuteri*; SDF: Soluble dietary fiber; IDF: Insoluble dietary fiber; L plantarum: *Lactobacillus plantarum* S. *cerevisiae*: *Saccharomyces cerevisiae*.

## Introduction

Highland barley, too alluded to as dehulled or exposed grain, could be an exceedingly nutritious grain developed on the Qinghai-Tibet Plateau in China. It is known for its tall protein and dietary fiber content [1]. Highland barley is rich in  $\beta$ -glucan, a polysaccharide compound that has appeared to control blood sugar and cholesterol

levels too showing anti-tumor properties [2].  $\beta$ -glucan comprises of glucose molecules linked through  $\beta$ -1,3- and  $\beta$ -1,4-glycosidic bonds [3]. The most basic units of  $\beta$ -glucan are trisaccharides (DP3) and tetra saccharides (DP4), and the proportion of these units (DP3:DP4) decides the source, dissolvability, and physiological



action of the compound [4]. The thickness, dissolvability, and atomic weight of  $\beta$ -glucans determined from highland barley change based on extraction strategies, with atomic measure impacting their antioxidant action and fat assimilation capacity. Beta-glucans have pulled in critical investigations due to their wide-ranging well-being benefits. Ponders have illustrated that beta-glucans can enact resistant cells, such as macrophages and characteristic executioner cells, improving the body's antiviral resistances. Also, beta-glucans can hinder tumor development by balancing the tumor microenvironment or applying coordinate cytotoxic impacts on tumor cells

### The Effect of Different Strains on Beta-Glucan Content

#### Lactobacillus acidophilus (LAC) and Lactobacillus reuteri (L. reuteri)

LAC and *L. reuteri* are Gram-positive, rod-shaped bacteria commonly utilized in the food industry. LAC, a homolactic fermenter, is transcendently found within the human and other creatures' gastrointestinal tracts. In this anaerobic environment, LAC matures

carbohydrates, creating lactic corrosive and carbon dioxide, in this manner illustrating critical fermentative capacity [5]. *L. reuteri* produces a non-protein antimicrobial substance called 'reuterin,' which shows Broad spectrum antibacterial activity against Gram-positive and Gram-negative microscopic organisms, yeasts, organisms, and different pathogens [6]. Within the think-about conducted by Shunzhang Ma and others [7] the tests were carried out in a sterile environment. The strategy included vaccinating 6% LAC into highland barley and refining it at 37°C for 60 hours, whereas 6% *L. reuteri* was immunized into highland barley and refined for 30 hours. A while later, the fermented grains was dried, ground, and sieved to evaluate its nutritional content. Compared to unfermented grain, the soluble dietary fiber substance expanded by 46.8% (coming to 9.84 g) and 11.6% (coming to 7.48 g) for LAC and *L. reuteri*, respectively. Insoluble dietary fiber content rose by 6.0% (reaching 12.95 g) and 9.7% (reaching 13.33 g) for LAC and *L. reuteri*. Additionally, beta-glucan content increased by 16.8% (reaching 4.86 g) and 13.4% (reaching 4.72 g) for LAC and *L. reuteri*. This study indicates that LAC is more effective at increasing soluble dietary fiber, whereas *L. reuteri* enhances insoluble dietary fiber to a greater extent.

**Table 1:** Comparison of Nutrients Fermented by Different Bacterial Strains

	SDF(g/100g)	IDF(g/100g)	$\beta$ -glucan(g/100g)
BR	6.70 $\pm$ 0.11c	12.15 $\pm$ 0.24b	4.16 $\pm$ 0.03b
LAC	9.84 $\pm$ 0.14a	12.95 $\pm$ 0.16ab	4.86 $\pm$ 0.03a
<i>L. reuteri</i>	7.48 $\pm$ 0.37b	13.33 $\pm$ 0.51a	4.72 $\pm$ 0.01a

Table Abbreviations: Soluble dietary fiber (SDF), Insoluble dietary fiber (IDF)

#### Lactobacillus plantarum (L. plantarum), Saccharomyces cerevisiae(S. cerevisiae)

*Lactobacillus plantarum* is a widely distributed bacterium found in plant materials, fermented foods, and the human gastrointestinal tract. It is an anaerobic or facultatively anaerobic Gram-positive bacterium, known for its role in food fermentation and health benefits. *L. plantarum* produces various enzymes that aid in the degradation of complex carbohydrates, such as starch and cellulose, in plant matter. It can also produce antibacterial substances that inhibit the growth of pathogens [8]. *S. cerevisiae* is a single-celled fungus widely used in winemaking, bread making, and biotechnological fields. It possesses a thick cell wall and is rich in organelles, containing most of the enzyme systems required for fermentation. In a ponder by Bai et al. [9] highland barley flour was to begin drying at 40°C and after that sieved through an 80-mesh screen to get a homogeneous test. *L. plantarum* and *S. cerevisiae*

were included, either independently or together, in a 1:7 blend of highland barley flour and deionized water, taken after fermentation at 30°C for 24 hours. After fermentation, the supernatant was collected through high-speed centrifugation and dried utilizing vacuum freeze-drying for consequent examination. The comes about appeared that fermentation with *L. plantarum* alone altogether expanded the beta-glucan substance by 157.1%, coming to 6.97 grams. In differentiation, fermentation with *S. cerevisiae* driven to a 93.3% diminish in beta-glucan substance, decreasing it to 0.18 grams.

Co-fermentation with both microorganisms comes about in a beta-glucan substance of 0.32 grams. These discoveries recommend that *L. plantarum* fermentation significantly enhances beta-glucan levels and mostly mitigates the utilization of beta-glucan by *S. cerevisiae*.

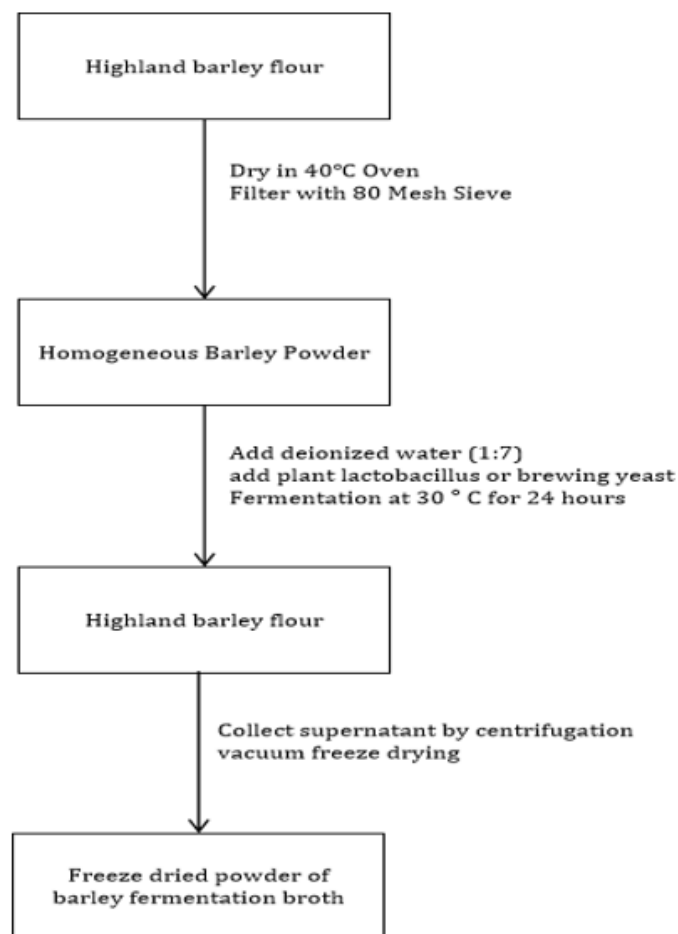


Figure 1:

## Tibetan Qu

Tibetan Qu is a basic common yeast starter utilized within the traditional brewing of Tibetan highland barley wine. It is essentially composed of an assorted microbial community counting Proteobacteria, Firmicutes, Cyanobacteria, Actinobacteria, and Bacteroidetes. These organisms are involved in the saccharification and fermentation of the grain, changing it into an alcoholic beverage with an interesting flavor. The generation of Tibetan Qu includes blending fixings such as grain and peas in certain proportions, taken after by natural fermentation to create the yeast cake, which is at that point air-dried beneath appropriate conditions to guarantee its essentialness and effectiveness during brewing. This normal yeast not as it were gives a particular smell and taste to the grain wine but also improves its dietary esteem. In a think about conducted by Lihua Chen et al. [10] highland barley was at first doused in water at 55°C for 12 hours, at that point depleted until its water assimilation came to 30% of the barley's weight. Sterilized highland barley was at that point immunized with 1.5% Tibetan Qu and subjected to solid-state fermentation at 30°C for 36 hours. Taking after this, twofold the volume of sterile water

was included for an extra 36-hour liquid fermentation, with tests collected every 12 hours. The ponder uncovered that after 24 hours of fermentation, the  $\beta$ -glucan substance within the highland barley wine treated with Tibetan Qu was 2.983 mg/mL, which was 9.7% higher than that of commercially accessible grain wine. By 72 hours, the  $\beta$ -glucan substance expanded to 10.683 mg/mL, speaking to a 293.1% increment compared to the commercial item.

## Conclusion

### Result

After a comparative investigation of methods and the impacts of utilizing diverse microbial strains to extricate  $\beta$ -glucans from highland barley through fermentation, it has been decided that the choice of strains plays a pivotal part in the extraction handle. For instance, *Lactobacillus acidophilus* and *Lactobacillus royi* significantly enhance the  $\beta$ -glucan content, whereas *Lactobacillus plantarum* and brewer's yeast exhibit varying effects when used alone or in combination for fermentation. The Tibetan Yeast with its diverse microbial community, effectively increases the quantity and quality of  $\beta$ -glucan extracted.

## Future work

However, several limitations remain in this field. Firstly, current research predominantly employs single strains or simple combinations of strains, lacking studies that investigate complex microbial community systems. Furthermore, there is insufficient metagenomic and metabolomic research to support mixed-strain fermentation methods, which hinders a comprehensive understanding of complex microbial interactions and their impact on the fermentation process. Therefore, future research should incorporate metagenomic and metabolomic techniques to explore the potential and optimization strategies of multispecies symbiotic fermentation systems for extracting  $\beta$ -glucans from highland barley. This approach could not only enhance the yield and quality of  $\beta$ -glucans but also offer new insights into the development of other functional components in highland barley.

## Acknowledgements

None.

## Conflict of Interest

None.

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