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## Commentary

### DRUG ANALYSIS USING CAPILLARY ELECTROPHORESIS

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## INTRODUCTION

Wines are complex matrices known for their exceptional flavor and pleasant aroma. Traditional Chinese liquor known as baijiu (white wine) has a pleasant mouthfeel, a sweet flavor, and a persistent aftertaste. Solid fermentation is used to distill sorghum and wheat into baijiu. The microbial ecosystem of Baijiu, like that of wines, has a significant impact on aroma and consumer preferences. Baijiu's microbial diversity has been the subject of extensive research. It is essential to keep in mind that probiotics are primarily intended to improve health. They are a mixture of bacteria and yeast. Our research aimed to identify probiotic-specific microbes in the microbial ecosystem of Zaopei Baijiu Daqu (ZBD) starter cultures. A metagenomic 16S rRNA approach was used to characterize the bacterial and fungal diversity in ZBD starter DNA samples. In the bacterial community, *Weissella cibaria* dominated, while *Saccharomycopsis fibuligera* dominated the fungal community. Additionally, unique pathways related to microbial diversity that are relevant to functional innovation were discovered through functional prediction analysis. Fermentation, the metabolism of amino acids, the metabolism of carbohydrates, the metabolism of energy, and membrane transport are among the associated pathways [1].

## DISCUSSION

This study found beneficial microbes in the starter culture, paving the way for more in-depth analysis by isolating and evaluating those microbes for their potential to play a useful role in *in vitro* and *in vivo* research. One of the best white wines or traditional liquors from China is called baijiu. It is made by distilling wheat and sorghum through solid-state fermentation. Baijiu has a unique history that dates back to the Western Han Dynasty. It has a special place in traditional Chinese culture. It is made with simple ingredients like grain (Zaopei) and water to make a complex flavor. It comes in several different varieties and is made after being brewed for four years in urns. The authentic liquor that is produced in the China town of Moutai, which is located on the Chishui River's shore in the Guizhou Province, is well-known. One of China's most popular flavored liquors is Baijiu with a Zaopei flavor. It contains thousands of volatile compounds and has a distinctive aroma and flavor that lasts [2].

The mass production of branded Baijiu involves two main steps: Daqu preparation is the first step,

followed by fermentation and the final production of liquor. Due to its substantial size, the solid-state fermentation starter culture known as Daqu is shaped like a brick. While less is known about Daqu's specific function and composition, its higher microbial diversity and richer flavor are the result of its complicated production process compared to other straightforward starters. Daqu is home to a wide variety of bacterial and fungal species. The production of organic acids that are responsible for the development of liquor aroma is greatly influenced by the bacterial effect. When applied to the body or consumed, probiotics are viable bacterial or fungal species that benefit the human body's health. They can be found naturally in yogurt, fermented foods, and beverages, or they can be added artificially to various food items, such as brand-name capsules. A composite microbial community makes up every fermented product, including food. There are indigenous microorganisms in this microbiota that are connected to the raw materials naturally, on the apparatus or equipment, in the environment where the process is carried out, and on the surfaces of processing sites [3].

On the other hand, starter cultures can be made with specific microorganisms. Therefore, the starters' microbes are the players in fermentation and flavor development. The microbial communities and the crucial role they play in liquor fermentation were previously studied using a variety of traditional methods. Specific microbes in alcohol fermentation have been identified using conventional microbiological methods like isolation, culturing, identification, and PCR-DGGE (analysis). The beneficial role of microbes in starter cultures has received less attention and research in recent years. Metagenomics data on all culturable and non-culturable microbes in any environment is now possible thanks to recent advancements in sequence-based methods. They support quick massive sequence data that cover and reveal a wide variety of microbes and their functional roles, which may provide a more comprehensive picture of the microbes in the starter culture. After being isolated, characterized, and validated, these microbes may be suitable for use as probiotic strains, and this study may serve as a guide for determining their beneficial function [4].

Using 16S/18S rDNA and ITS sequencing to identify bacterial and fungal communities is the most reliable sequencing method. While other related bioinformatics tools provide insight for associated functional analysis of those microbes, these two methods are appropriate for identifying the present microbes. These methods look at the diversity of the microbiome in a variety of environments, including Chinese liquors. They show that these liquors have complex microbes and that their traditional fermentation methods are secret. Commercial starter cultures contain microorganisms like fungal and bacterial species that are utilized in the wine industry. In most cases, those starter cultures contain a lot of bacteria that make lactic acid. The exceptional flavors and aromas of Baijiu are thought to be a result of these intricate microbial compositions. Based on literature mining, the purpose of this study was to investigate the functional role of the microbes in Baijiu Zaopei starter culture by examining the entire microbial diversity of the branded starters to identify the highly abundant microbial taxa, including fungi and bacteria. Improved comprehension of the beneficial role of the microbes and potential future applications of traditional wine preparation methods will result from the discovery of these essential microbes and their roles in fermentation [5,6].

## **CONCLUSION**

We discovered the functional gene composition of the starter microbiome and the microbial composition of branded starter samples in this study. The starter culture contained beneficial

microbes, according to this study. By isolating these microbes and evaluating their beneficial role in paved the way for more in-depth research on them. In particular, the study determined that *Saccharomycopsis fibuligera* and the bacterial strain *Weissella cibaria* were the predominant species found in all of the samples. *Weissella cibaria*'s strong beneficial role has been demonstrated in previous studies, which serves as a foundation for further characterization of our strain, which will be processed for its probiotic activity through isolation, whole genome sequencing, and follow-up *in vitro* and *in vivo* studies.

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