Opinion Article

Genomic Characterizationof Rice Bran Fermented with Mono-and Di-Strain Probiotics

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DESCRIPTION

Rice bran is a valuable agricultural by product, abundant in nutrients and bioactive compounds. The purpose of this study was to evaluate the effects of fermentation on the bacterial populations and metabolic processes of rice bran using *Bacillus subtilis*, *Lactobacillus plantarum* and a combination of both. The results indicated that probiotic fermentation led to a reduction in Crude Fiber (CF), phytic acid and Trypsin Inhibitor Activity (TIA), while increasing levels of Trichloroacetic Acid-Soluble Protein (TCA-SP), Reducing Sugars (RS) and Total Phenols (TP) in rice bran. There were ten prominent taxa found with relative abundances greater than 1% and the relative abundances of *Enterobacter*, *Kasakonia* and *Pantoea* were dramatically reduced by fermentation. A comprehensive investigation revealed that probiotic fermentation increased the levels of organic acids, phenolic compounds and essential amino acids, resulting in the identification of 63 Differentially Expressed Metabolites (DEMs), with further analysis showing that probiotic fermentation improved the levels of essential amino acids, phenolic compounds and organic acids in rice bran. Notably, the co-fermentation of *Bacillus subtilis* and *Lactobacillus plantarum* promoted the growth of beneficial microbiota, including *Limosilactobacillus*, *Prevotella* and *Dialister*, along with the production of bioactive compounds such as lactic acid, catechol, and beta-tyrosine. In conclusion, co-fermenting these di-strain probiotics is an effective approach to producing functional compounds and improving the health-promoting properties of rice bran.

In this study, rice bran was fermented using single strains of *Bacillus subtilis*, *Lactobacillus plantarum* and their mixture. The alterations in bacterial populations and metabolic processes in the fermented rice bran were examined using genomics approaches, demonstrating the complementary effects of *Bacillus subtilis* and *Lactobacillus plantarum* during fermentation. This research provides theoretical support for co-fermenting rice bran with di-strain probiotics and the development of potential compounds for functional ingredients.

Nutritional improvements: Probiotic fermentation reduced crude fiber, phytic acid and trypsin inhibitor activity, while increasing levels of trichloroacetic acid-soluble protein, Reducing Sugars (RS) and Total Phenols (TP).

Microbial composition: Ten dominant genera with relative abundances exceeding 1% were identified, with significant decreases in the abundances of *Enterobacter*, *Kasakonia* and *Pantoea*.

Beneficial microbiota and bioactive compounds: Co-fermentation of *Bacillus subtilis* and *Lactobacillus plantarum* promoted the growth of beneficial microbiota, including *Limosilactobacillus*, *Prevotella* and *Dialister*, as well as the production of bioactive compounds like lactic acid, catechol and beta-tyrosine.

CONCLUSION

This study systematically analyzed the bacterial communities, metabolite profiles and their correlations in fermented rice bran. The findings indicated that probiotic fermentation optimized bacterial communities by reducing the abundance of *Enterobacter* and other potentially dangerous genera of *Proteobacteria*, while increasing the levels of amino acids and organic acids through the catabolism of proteins and carbohydrates. Furthermore, di-strain fermentation improved the presence of beneficial genera such as *Limosilactobacillus*, *Prevotella* and *Dialister* and promoted the production of bioactive compounds like lactic acid, catechol and beta-tyrosine, thereby boosting the nutritional value and potential health benefits of rice bran. Correlation analysis revealed that changes in metabolite profiles were linked to variations in the microbiota during fermentation. Overall, this analysis of bacterial communities and metabolite profiles in rice bran fermented with mono- and di-strain probiotics provides theoretical support for the synergistic effects of *Bacillus subtilis* and *Lactobacillus plantarum*, highlighting a novel approach for probiotic co-fermentation to improve the functional properties of rice bran.