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Germination enhances the multi-nutritional properties of pigmented rice revealed through metabolomic and machine-learning techniques

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Abstract

Enhancing the dietary properties of rice is crucial to contribute to alleviating hidden hunger and non-communicable diseases in rice-consuming countries. Germination is a bioprocessing approach to increase the nutritional properties of seeds. However, there is scarce information on how germination impacts the overall nutritional profile of pigmented rice sprouts. Herein, we demonstrated that germination could increase certain dietary compounds, such as phenolics, GABA, and micronutrients, and induce new flavonoid glycosides. Minerals such as Ca, Na, Fe, Zn, and vitamins such as riboflavin and biotin increased upon germination. In addition, this process decreased toxic elements like aluminum. This process allowed for a decrease in bound phenolics leading to an increase in free phenolics, corroborating the increased minerals. Metabolomic analysis revealed the preferential accumulation of flavonoid compounds in the germination process. Genome-wide association studies of the altered metabolites revealed the activation of specific genes responsible for increasing certain flavonoid compounds. Notably, the activation of the CHS1 gene boosted the naringenin and the compounds along this pathway. Likewise, the UGT gene is responsible for the formation of flavonoid glycosides derived from kaempferol, caffeic, ferulic, and quercetin. Haplotype analyses showed a significant difference ($p < 0.05$) between alleles associated with this genetic region. Genetic markers associated with these flavonoids were incorporated into the random forest model, improving the accuracy from 89.7% to 97.7%. Consistent with this feature, the improved model has a faster prediction speed in a shorter training time. The elite cultivars can breed rice with multi-nutritional properties, and the model could screen rice with several dietary benefits.

Keywords: Germination, machine-learning, metabolomics, rice