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Bring back the nutrition to rice: Unraveling the genetic diversity and nutritional component of coloured rice

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Abstract

Over half of the world's population relies on rice for caloric and dietary requirements. Screening a large diversity panel of rice for its metabolite content and nutritional properties is crucial to secure the dietary targets among rice-consuming countries. Metabolomic analysis revealed that pigmented rice exhibited a significant variation of bioactive compounds. Pathway analysis demonstrated that flavonols and anthocyanins accumulate in purple rice, while catechin and procyanidins were detected at elevated levels in red rice samples. Genome-wide association studies (GWAS) have determined Rc, IPT5, and OsENS genes are associated with high proanthocyanidin levels in red rice. Correlation network analyses revealed that proanthocyanidins are the primary metabolite responsible for anti-colon cancer activities. The elite cultivars with high catechin content also exhibited a lowering of the glycemic index. The allelic variation between the inferior and superior lines is significant. Molecular docking simulations revealed the potential interaction of the metabolites with cancer receptors, and it exhibited comparable binding energy results with the reference drug. Germination has shown that it can alter the nutritional properties of rice by enhancing the antioxidants and micronutrients. It can increase the free phenolics and micronutrients in rice. Furthermore, it altered the flavonoid pathway by favouring the accumulation of certain phenolic compounds. Classification models were used to cluster coloured rice for their multi-nutritional properties with anticancer activities. This work provided new insights into the genes regulating the phenolic metabolites. Furthermore, the model developed in this study can be useful in screening a large diversity panel of rice for their dietary attributes.

Keywords: Anticancer, GWAS, proanthocyanidin, rice

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