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Low glycemic index rice: a healthier diet for countering diabetes epidemic in Asia

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Abstract

The global prevalence of type 2 diabetes is rising, particularly in Asia, where rice is a staple food. Most commercially available rice varieties have a high glycemic index (GI), increasing the risk of diabetes. Therefore, promoting the consumption of low-GI rice is crucial. Through a multi-omics analysis, we identified key genes, including OsSBEIIb (starch branching enzyme IIb) and OsEnS-34 (prolamin box binding factor), associated with low GI (GI < 55) and high protein content (14–16 %) in a high-yielding background. To develop rice with these enhanced nutritional traits, we employed two complementary strategies: conventional breeding using recombinant inbred lines and gene editing of target genes. The resulting varieties exhibited significantly improved nutritional profiles compared to the parent variety, Samba Mahsuri, and other popular rice varieties ($p < 0.05$). Multi-omics analysis further revealed a metabolic shift from starch biosynthesis toward amino acid, lipid, and phenylpropanoid pathways. To evaluate the potential impact of low-GI rice adoption on diabetes prevalence in rice-consuming countries, we developed a predictive model incorporating factors such as weighted GI and glycemic load based on caloric intake. The model demonstrated a strong correlation (adjusted $R^2 = 0.51$), underscoring its predictive power in assessing the benefits of low-GI rice adoption. For instance, in India, adopting low-GI rice could lead to an estimated 33 % reduction in type 2 diabetes cases. Additionally, our study provides country-specific estimates of diabetes risk reduction based on low-GI rice adoption. These findings offer valuable insights for breeding nutritionally enhanced rice varieties and support dietary interventions to mitigate diabetes risk in rice-dependent populations.

Keywords: Diabetes, glycemic index, low GI, multi-omics

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