

Nutrigenomic Effects of White Rice and Brown Rice on the Pathogenesis of Metabolic Disorders in a Fruit Fly Model

ABSTRACT

Consumption of white rice (WR) has been shown to predispose individuals to metabolic disorders. However, brown rice (BR), which is relatively richer in bioactive compounds, possesses anti-glycaemic and antioxidant effects. In this study, fifteen cultivars of paddy rice that are predominantly consumed in North West Nigeria were analysed for their nutritional composition, bioactive contents and effects on metabolic outcomes in a fruit fly model. Gene expression analyses were conducted on the whole fly, targeting dPEPCK, dIRS, and dACC. The protein, carbohydrate, and fibre contents and bioactives of all BR cultivars were significantly different ($p < 0.05$) from the WR cultivars. Moreover, it was demonstrated that the glucose and trehalose levels were significantly higher ($p < 0.05$), while glycogen was significantly lower ($p < 0.05$) in the WR groups compared to the BR groups. Similarly, the expression of dACC and dPEPCK was upregulated, while that of dIRS was downregulated in the WR groups compared to the BR groups. Sex differences ($p < 0.05$) were observed in the WR groups in relation to the nutrigenomic effects. Our findings confirm metabolic perturbations in fruit flies following consumption of WR via distortion of insulin signalling and activation of glycogenolysis and gluconeogenesis. BR prevented these metabolic changes possibly due to its richer nutritional composition