Gender, Body Mass Index, and PPARγ Polymorphism Are Good Indicators in Hyperuricemia Prediction for Han Chinese.

Lee MF, Liou TH, Wang W, Pan WH, Lee WJ, Hsu CT, Wu SF, Chen HH.

Department of Nutrition and Health Sciences, Chang Jung Christian University, Tainan City, Taiwan, Republic of China.

Abstract

Hyperuricemia is closely associated with obesity and metabolic abnormalities, which is also an independent risk factor for cardiovascular diseases. The PPARγ gene, which is linked to obesity and metabolic abnormalities in Han Chinese, might be considered a top candidate gene that is involved in hyperuricemia. This study recruited 457 participants, aged 20-40 years old, to investigate the associations of the PPARγ gene and metabolic parameters with hyperuricemia. Three tag-single nucleotide polymorphisms, rs2292101, rs4684846, and rs1822825, of the PPARγ gene were selected to explore their association with hyperuricemia. Risk genotypes on rs1822825 of the PPARγ gene exhibited statistical significance with hyperuricemia (odds ratio: 1.9; 95% confidence interval: 1.05-3.57). Although gender, body mass index (BMI), serum total cholesterol concentration, or protein intake per day were statistically associated with hyperuricemia, the combination of BMI, gender, and rs1822825, rather than that of age, serum lipid profile, blood pressure, and protein intake per day, satisfied the predictability for hyperuricemia (sensitivity: 69.3%; specificity: 83.7%) in Taiwan-born obese Han Chinese. BMI, gender, and the rs1822825 polymorphism in the PPARγ gene appeared good biomarkers in hyperuricemia; therefore, these powerful indicators may be included in the prediction of hyperuricemia to increase the accuracy of the analysis.