Genetic variation in \textit{WDR1} is associated with gout risk and gout-related metabolic indices in the Han Chinese population

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\textbf{ABSTRACT.} Gout is the most common form of inflammatory arthritis affecting men, and current evidence suggests that genetic factors contribute to its progression. As a previous study identified that WD40 repeat protein 1 (\textit{WDR1}) is associated with gout in populations of European descent, we sought to investigate its relationship with this disease in the Han Chinese population. We genotyped six \textit{WDR1} single nucleotide polymorphisms in 143 gout cases and 310 controls using
Sequenom MassARRAY technology. The SPSS 16.0 software was used to perform statistical analyses. Odds ratios (ORs) and 95% confidence intervals (CIs) were calculated by unconditional logistic regression, with adjustments for age and gender. In an analysis using an allelic model, we identified that the minor alleles of rs3756230 (OR = 0.64, 95%CI = 0.450-0.911, P = 0.013) and rs12498927 (OR = 1.377, 95%CI = 1.037-1.831, P = 0.027) were associated with gout risk. In addition, we found that the “A/A” genotype of rs12498927 was associated with increased risk of gout under codominant (OR = 2.22, 95%CI = 1.12-4.40, P = 0.042) and recessive models (OR = 2.24, 95%CI = 1.20-4.17, P = 0.012). We also determined the “A/G” genotype of rs12498927 to be significantly associated with higher urea levels in gout patients (P = 0.017). Our data shed new light on the association between genetic variations in the WDR1 gene and gout susceptibility in the Han Chinese population.

**Key words:** WDR1; Single nucleotide polymorphism; Gout; Case-control study