LV OP 3-1

Novel SNPs for screening of nonalcoholic fatty liver disease: a Korean population-based study

Min-Su PARK

Surgery, Kyunghee University, Korea

Introduction : Genetic susceptibility plays a key role in the development of nonalcoholic fatty liver disease (NAFLD). The fatty liver index (FLI) is a simple and accurate noninvasive method for predicting NAFLD. The aim of this study was to identify novel susceptibility genes associated with NAFLD as assessed by the FLI by performing a genome-wide association study (GWAS).

Methods : A prospective cohort study of 6284 adults (2333 men and 3951 women) aged 40–70 years was examined. Patients were classified into three groups by FLI (FLI <30, no NAFLD; FLI ≥60, NAFLD; and 30≤ FLI <60, intermediate FLI). We investigated single-nucleotide polymorphisms (SNPs) related to NAFLD.

Results : After adjusting for age, sex, and body mass index, 20 SNPs in 12 genes (rs10790162, rs9326246, rs2075290, rs2266788, rs964184, rs7350481, rs780093, rs780094, rs1260326, rs10401969, rs671, rs11066280, rs11066015, rs150401869, rs1109501, rs3782886, rs76178990, rs61737409, rs201338826, and rs1448349) showed significant associations with the susceptibility to NAFLD (P < 0.0001). Five genes (BUD13, GCKR, KCNQ2, MUC7, and C12orf51) of 12 genes were duplicated and meaningful. Seven SNPs in 3 genes (rs780093, rs1260326, rs1109501, rs1448349, rs780092, rs780094, and rs11249502) showed significant associations with the severity of liver fibrosis based on the NAFLD fibrosis scores.

Conclusions : We demonstrated that 20 SNPs in 12 genes are significantly associated with the presence of NAFLD in a Korean population. These findings suggest the value of genetic factors in the pathogenesis of NAFLD.

Corresponding Author. : **Min-Su PARK** (ikireida@hanmail.net)