REPLICATION OF HEIGHT GWAS IN KOREAN POPULATION AND EVALUATION OF HEIGHT PREDICTION MODEL IMPLEMENTED WITH THE GENETIC MARKERS

Ji Eun Lim[1], Jong Sik Kim[2], Kwang Man Woo[2], Seung Hwan Lee[2] and Bermseok Oh[1]

[1]Department of Biomedical Engineering, School of Medicine, Kyung Hee University
[2]DNA analysis lab., Forensic Science Division, Supreme Prosecution Service

Height is one of the classic complex traits and has been studied in various ways to explain the genetic architecture with common variants. Nineteen height genome-wide association studies (GWASs) have been carried out from European, African and Asian population. In this study, we examined previously reported height-related SNPs in unrelated male Koreans (n=2,841). The association of height was analysed by linear regression adjusted for age and recruitment area using PLINK. Twenty-four of the 99 height SNPs were replicated in Korean ($P < 0.05$). We also analysed the genomic prediction of human height in training (n=2,741) and validation (n=100) sample. The height GWAS was carried out in training set to identify more SNP markers for improving prediction accuracy. Among 24 SNPs which replicated in Korean and 428 GWAS significant SNPs ($P < 1*10^{-3}$), 244 SNPs were selected for prediction model. These SNPs explained 55% of the height variation in training samples and 56 individuals of 100 validation samples were predicted within errors ranged ± 4cm. In this study suggests that many more height SNP markers need to be identified to explain large amount of missing heritability and to implement height prediction model to use practically in forensic science area.