

**Abstract Submission No.: A-0956****Prediction of risk of chronic kidney disease using multi-ethnicity and multiple polygenic risk score in Korean population**

**Yunmi Ji**<sup>1</sup>, Boram Weon<sup>2</sup>, Ara Ko<sup>3</sup>, Seughyun Han<sup>3</sup>, Jung Pyo Lee<sup>2</sup>, Sungho Won<sup>4</sup>, Jeonghwan Lee<sup>2</sup>

<sup>1</sup>Department of Bioinformatics, College of Natural Sciences, Seoul National University, Seoul, Republic of Korea, Korea, Republic of

<sup>2</sup>Department of Internal Medicine-Nephrology, Seoul National University Boramae Medical Center, Korea, Republic of

<sup>3</sup>Department of Internal Medicine-Nephrology, Seoul National University Hospital, Korea, Republic of

<sup>4</sup>Department of Public Health Sciences, Institute of Health & Environment, Seoul National University, Seoul, Republic of Korea, Korea, Republic of

**Objectives :** Chronic kidney disease(CKD) is a complex disease influenced by genetic factors, in addition to environmental factors like lifestyle and nutrition. Although the genetic mechanisms underlying complex diseases have been revealed, most of these studies were conducted on Caucasians, and studies on East Asians are relatively unknown. The aim of the study is to assess the genetic impact on CKD in the Korean population and analyze its interaction with various factors.

**Methods :** To evaluate the genetic effects on CKD, we calculated polygenic risk score(PRS) of eGFR using 71,514 Korean subjects. We considered diverse PRS methods. Specifically, we employed the newly developed trans-ethnic PRS approach that constructs PRS by combining genome-wide association study results from multiple ethnic groups. We also developed a multiple-PRS model by including PRS for comorbidities and related traits as covariates. Finally, a logistic regression was used to verify the association between genetic factor and covariates on baseline CKD.

**Results :** In the CKD model considered only genetic factors, we observed that trans-ethnic PRS<sub>eGFR</sub>(AUC = 0.604) outperforms PRS<sub>eGFR</sub>(AUC = 0.598) from a single ethnicity. Furthermore, the multiple PRS model(AUC = 0.611), which included PRS for BMI, SBP and T2DM, showed a marked improvement. The results of logistic regression analysis showed that the significant associations between the baseline CKD and trans-ethnic PRS<sub>eGFR</sub>(OR = 0.674 with P < 0.001), alcohol consumption(OR = 0.631 with P < 0.001, urate(OR = 2.034 with P < 0.001), hypertension(OR = 1.721 with P < 0.001), diabetes mellitus(OR = 1.948 with P < 0.001), depression(OR = 1.484 with P < 0.001), HDL(OR = 0.987 with P < 0.001) and sodium intake (OR = 0.938 with P = 0.004)

**Conclusions :** This study demonstrates that trans-ethnic PRS functioned as a risk factor for CKD and provides valuable insights into the genetic factors contributing to CKD.