KSN 2021
FULLY VIRTUAL MEETING
September 02 (Thu) - 05 (Sun)

Oral Communication Abstract
Presentation No. OC4-03 (Abstract Submission No. 2442)

Oral Communications 4 Sep. 2 (Thu), 16:40-17:40

The effect of DNA methylation in the development of CKD in middle aged general population: an Epigenome-Wide Association Study using Korean Genome and Epidemiology Study database.

Ji Eun Kim[1], Jung An Kim[2], Min Jee Jo[1], Shin Young Ahn[1], Young Joo Kwon[1], Gang Jee Ko[1]
[1]Department of Internal Medicine-Nephrology, Korea University Guro Hospital, Korea, Republic of
[2]Department of Medical Science Research Center, Korea University College of Medicine, Korea, Republic of

Objectives: Although there is increasing evidence for genetic factors influencing kidney disease, epigenetic profiles which related to chronic kidney disease is not fully elucidated. We aimed to identify DNA methylation sites (CpG-sites) associated with decreased renal function and test whether identified CpG-sites are associated with CKD development.

Methods: We analyzed DNA methylation data of 440 general population who have eGFR >= 60 at baseline from Korean Genome and Epidemiology Study. CKD development was defined as decrease of eGFR < 60 at any time in 10 years of follow up.

Results: Of total 403,129 CpG sites which analyzed, we found increasing methylation of 114,154 CpG site correlated with baseline eGFR decrease (FDR<0.05) by simple linear regression analysis. Among the CpG sites which showed negative correlation with eGFR, the increasing percentage of methylation in 49 CpG sites showed significantly elevated the risk of CKD in univariable logistic regression. Furthermore, the methylation on seven CpG-sites from six genes including *PRMT7*, *ZSCAN2*, *RSPO3*, *LRRC24*, *F12* and *C13orf38* showed significant association with the risk of CKD development for 10 years, even after adjusting for age, sex, body mass index, diabetes, hypertension and baseline eGFR.

Conclusions: Our study suggests that DNA methylation on specific genes in Korean general population with normal kidney function might be related to the deterioration of kidney function.