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# Genome-Wide Association Study Identifies Two Novel Loci with Sex-Specific Effects for Type 2 Diabetes Mellitus and Glycemic Traits in a Korean Population (*Diabetes Metab J* 2014;38:375-87)

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Type 2 diabetes is a multigenic disorder where genetic and environmental factors and their interactions play crucial roles in the pathogenesis. The recent technological advancement in genome analyses enabled us to identify at least 70 genetic loci for type 2 diabetes [1,2]. Collaborative efforts led by Korea National Institute of Health have laid the basis for the Asian Genetic Epidemiology Consortium and have identified eight novel genetic variants associated with type 2 diabetes in more than 54,000 East Asians subjects including Korean, Chinese, Japanese, Taiwanese, and Singaporeans [3].

The article entitled "Genome-wide association study identifies two novel Loci with sex-specific effects for type 2 diabetes mellitus and glycemic traits in a korean population" [4] is a two staged genome-wide association study on type 2 diabetes in a Korean population. In this study, the authors investigated more than 4.5 million genotyped and imputed single nucleotide polymorphisms to identify genetic risk factors for type 2 diabetes. The authors found that genetic variants in or near *CDKAL1* (rs7754840) and *CDKN2A/2B* (rs10811661) genes are associated with diabetes with odds ratio of 1.30 and 1.29, respectively, at genome-wide significance level of $P<5.0\times10^{-8}$. These two variants are also strong genetic risk factors in Europeans and other population, which suggests that genetic risk factors are shared across ethnicities [5]. The novel finding of this study is the association between variants in *CCDC63* (rs11065756) and *C12orf51* (rs2074356) with the risk of type 2 diabetes.

This study deserves much attention as it provides detailed information on genetic risk factors of type 2 diabetes in Koreans. However, it should be clarified whether the novel genetic association between variants in *CCDC63* and *C12orf51* and type 2 diabetes is confounded by alcohol consumption. In a previous study using the same discovery set, the very same variants (rs11065756 in *CCDC63* and rs2074356 in *C12orf51*) were significantly associated with alcohol consumption [6]. When the direction of association is considered, it is also true that alleles associated with increased risk of diabetes are associated with increased alcohol consumption. The fact that the association of these two variants with type 2 diabetes was only specific to men is also true for alcohol consumption. It could be possible that the variants have pleiotropic effect and are associated with both alcohol consumption and type 2 diabetes in an independent manner. This could be clarified by reanalyzing the data with an adjustment to the amount of alcohol consumption.

## CONFLICTS OF INTEREST

No potential conflict of interest relevant to this article was reported.

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