Abstract

Massive differences in the response towards drugs exist among patients, it is generally affected by their genetic and phenotypic traits. To examine the effect of genetic variation of patients, a comprehensive association study was conducted using the whole genome sequence of the statin-treated patient. The human UGT1A gene is likely to significantly contribute in the improvement of drug efficacy as their genetic variability shows responsibility in ethnic diversity.

We hypothesized that the presence of the variants in UGT1A gene family would be associated with the variability of patient drug response undergoing statin therapy in Singaporean population. As the results, the study found 13 SNPs inside UGT1A gene cluster that were significantly associated with statin side effects –the risks of having myalgia– before the multiple test correction using PLINK was applied. More polymorphisms were to be found to affect the metabolites rate of the patients as multiple SNPs were associated with atorvastatin metabolism ratio and remain significant after multiple test correction. In conclusion, this study suspected that UGT1A variants may play minor role with the statin side effects but could be substantial with the drug metabolism; which will still need to be confirmed in more extensive studies.

Keywords: Pharmacogenomics, UGT1A, Statin, Single nucleotide polymorphisms (SNPs), Association Study, Genome-Wide Association Studies, Genetic Association Study.