

Genetic Variations of CYP2C9 in Thai Patients Taking Medical Cannabis

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Abstract : Medical cannabis can be used for treatment including pain, multiple sclerosis, Parkinson's disease, and cancer. However, medical cannabis leads to adverse effects (AEs), which is delta-9-tetrahydrocannabinol (THC). In previous studies, the major of THC metabolism enzymes are CYP2C9. Especially, the variation of CYP2C9 gene consist of CYP2C9*2 on exon 3 and CYP2C9*3 on exon 7 to decrease enzyme activity. Notwithstanding, there is no data describing whether the variant of CYP2C9 genes are a pharmacogenetics marker for the prediction of THC-induced AEs in Thai patients. We want to investigate the association between CYP2C9 gene and THC-induced AEs in Thai patients. We enrolled 39 Thai patients with medical cannabis treatment who were classified by clinical data. The CYP2C9*2 and *3 genotyping were conducted using the TaqMan real time PCR assay. All Thai patients who received the medical cannabis consist of twenty-four (61.54%) patients were female, and fifteen (38.46%) were male, with age range 27- 87 years. Moreover, the most AEs in Thai patients who were treated with medical cannabis between cases and controls were tachycardia, arrhythmia, dry mouth, and nausea. Particularly, thirteen (72.22%) medical cannabis-induced AEs were female and age range 33 - 69 years. In this study, none of the medical cannabis groups carried CYP2C9*2 variants in Thai patients. The CYP2C9*3 variants (*1/*3, intermediate metabolizer, IM) and (*3/*3, poor metabolizer, PM) were found, three of thirty-nine (7.69%) and one of thirty-nine (2.56%), respectively. Although, our results indicate that there is no found the CYP2C9*2. However, the variation of CYP2C9 allele might serve as a pharmacogenetics marker for screening before initiating the therapy with medical cannabis for the prevention of medical cannabis-induced AEs.

Keywords : CYP2C9, medical cannabis, adverse effects, THC, P450

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