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Distribution of *CYP2C9* variant genes in the healthy Thai population associated with medical cannabis metabolic pathway

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Medical cannabis consists of tetrahydrocannabinol (THC) and cannabidiol (CBD). *CYP2C9* is a major metabolizer of THC and the frequency of *CYP2C9* genotypes vary between populations worldwide. THC-induced adverse effects (AE) can be explained in terms of *CYP2C9* gene variants in pharmacogenetics. This study aims to investigate the impact of the frequency of *CYP2C9* variants related to THC metabolic pathways in the healthy Thai population. We have recruited a set of unrelated healthy Thai subjects (n=160). Genotyping for *CYP2C9* (*2 and *3) were subsequently analyzed through real-time PCR. We found that *CYP2C9**1 alleles is the most common form of the *CYP2C9* gene among the Thai population, comprising a percentage frequency of approximately 95.94%. *CYP2C9**3 alleles were found to occur at only 4.06%. However, *CYP2C9**2 alleles were absent among the subjects. Furthermore, in the aspect of phenotypes and genotypes, we found that the phenotype of extensive metabolizers (EM) (*CYP2C9**1/*1, wild-type) genes have the highest frequency. Intermediate metabolizers (IM) (*1*3) and poor metabolizers (*3*3) were also found from the samples, respectively 6.88% and 0.62%. Our results for *CYP2C9**1/*3 and *3/*3 frequency is also similar to previous studies in Asian populations. The allelic variants *CYP2C9**2 and *CYP2C9**3 have been presented to experience decreased enzymatic activity in the THC metabolism pathway. In conclusion, the distribution of *CYP2C9**3 in Thai populations might be associated with THC-induced serious adverse effects through metabolic pathways.

Keywords: *CYP2C9* gene, Thai population, Cannabis

Biography

I am Bunnalin Liamputhong and I am currently studying in Regent's International School of Bangkok as a senior high school student in the Twelfth grade. I have a strong interest in medicine and aspire to continue my studies in a medical university. An area which I find quite fascinating is pharmacogenetics, hence the reason why I carried out this research.