

Potential For Adverse Effect Reduction With Pharmacogenomic Guided Dosing of Delta-9-Tetrahydrocannabinol

Intro:

Marijuana use has increased both medically and recreationally, and presents as a potential new therapy for a wide range of indications. Limited resources exist for prescribers to aid in prescribing and monitoring of new patients. This meta-analysis and clinical decision support looks to create a treatment dosing guideline for the use of dronabinol based upon genomic testing results.

Methods:

Pubmed, SCOPUS, and EBSCOhost platforms were utilized to complete primary literature searches using Boolean operators AND/OR combined with search terms and Medical Subject Headings (MeSH) to retrieve relevant information. Information on gene-drug interactions, allele functionality, and delta-9-tetrahydrocannabinol metabolism was utilized through Pharmacogenomic Knowledgeable and youscript.org.

Results:

Available research looking at metabolism and adverse effect profiles of THC have been able to show the associated hepatic enzymes and transporters involved in metabolite formation and elimination and dopamine regulation. CYP2C9 is the major enzyme involved in THC metabolism with data supporting pharmacokinetic changes with gene polymorphisms resulting in reduced function. COMT polymorphism and associated dopamine regulation effects has also been shown to have a potential role in adverse effect presentation and therapeutic efficacy. Dronabinol dosing recommendations were made utilizing youscript's clinical decision support database to assess CYP2C9 intermediate and poor metabolizer effects on drug exposure. Dosing decreases are recommended for intermediate or poor metabolizers, supported by data showing increases in THC AUC, C_{max}, and active metabolite formation and sedation data showing increased scores on reported sedation rating scales.

Conclusion:

Use of marijuana both medically and recreationally has increased nation-wide but clinical resources and treatment guidelines for the use of THC remain inadequate. Use of pharmacogenomic testing for potential patients can be an effective means of predicting patient response and proactively improving patient care through mitigation of adverse reactions.