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PHARMACOGENOMICS OF OPIOID CONSUMPTION AFTER ANTERIOR CRUCIATE LIGAMENT RECONSTRUCTION

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Introduction

According to the Centers for Disease Control and Prevention (CDC), the United States is in the midst of an opioid epidemic. Still, there remains a paucity of research regarding how one’s individual genetic composition may affect opioid consumption patterns. This study analyzed patients who underwent anterior cruciate ligament reconstruction (ACLR) to identify if a relationship between patient’s pharmacogenetics and their postoperative opioid consumption existed. This study seeks to illustrate the benefits of pharmacogenomic testing via non-invasive, low-cost buccal swabs to identify one's specific pharmacokinetic and pharmacogenomic responses to opioid medications. This knowledge will have the potential to shape the future of pain management by guiding physicians to create individualized pain management plans with unique drug regimens and educational content specific to each patient's needs.

Materials and Methods

The study is approved through the Institutional Review Board (IRB) of Emory University (IRB00002086). All participants provided informed consent prior to participation. Eligible subjects were contacted by phone via study personnel. If they elected to participate, subjects had the option to sign the consents electronically on their personal electronic device utilizing Research Electronic Data Capture (REDCap, Vanderbilt University, Nashville, TN, USA) or physically when they presented for buccal swab collection. Identifiers were stripped prior to providing specimens and data to our external collaborators and statisticians.

One hundred patients aged 18-50 years old were divided into cohorts based on their opioid tablet consumption patterns. Cohorts were defined as non, low, middle, high, and maximum opioid users. Participants' DNA was analyzed for genes relating to pharmacodynamics and pharmacokinetics including CYP3A4, CYP2D6, CYP3A5, OPRM1, and COMT.

Results/Case Report

The average age of study participants was 31 with 44% male and 56% female. When analyzing CYP2D6, there were differences identified in the number of opioid tablets consumed between the poor metabolizers and the normal metabolizers ($p<0.05$). For COMT, there were differences noted in the number of opioid tablets consumed between the high metabolizers and the low metabolizers ($p<0.05$). CYP3A4, CYP3A5, and OPRM1 were not found to have a significant effect on the number of tablets consumed.

Discussion

Both COMT and CYP2D6 were associated with higher metabolism rates and increased opioid usage within the study cohorts. This finding has the potential to shape the future of orthopedic care by guiding surgeons to create individualized postoperative pain management plans with unique drug regimens and educational content specific to each patient's needs. However, further research is required to better understand the effect of a patient's individual genetic composition on opioid consumption patterns.

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Disclosures

No

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