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The Association of ABCB1 Gene Polymorphism and Postoperative Chronic Opioid Use Following Lower Extremity Total Joint Arthroplasty

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Introduction

Total joint arthroplasty, including total knee arthroplasty (TKA) and total hip arthroplasty (THA), is one of the most common elective procedures performed in the United States. It is associated with moderate-to-severe postoperative pain and the resultant incidence of chronic opioid use has been reported to range from 10-40%.1 Interindividual differences in opioid analgesia associated with genetic variability have been well-documented in the surgical population.2 Expanding genomic medicine to total joint arthroplasty pain management has the potential to reduce opioid dependence and chronic pain development. In this study, we tested the association of various genes with pain and opioid metabolism and the development of chronic opioid use following TKA and THA.

Materials and Methods

Our institutional review board approved this study and waived the consent requirement. We performed a retrospective case-controlled study in which we identified patients that underwent unilateral primary TKA or THA that either did not or did require ongoing opioid use ≥3 months following surgery. These patients underwent pharmacogenomic (PGx) screening for various single nucleotide polymorphisms, including the following genes: ABCB1, CYP3A4, CYP3A5, CYP2C9, and CYP2D6. Via manual chart review, we extracted data from postoperative orthopedic clinic visits and recorded whether opioid use was persistent at their ≥3 month follow-up visit. We performed logistic regression to measure the association of each genotype to our outcome of interest. We report odds ratio (OR) and 95% confidence interval (CI). A p value < 0.01 was considered statistically significant based on Bonferroni correction (five genotypes).

Results/Case Report

There were 283 patients included in this study, in which 29 (10.2%) were found to continue opioid use after ≥ 3 months based on chart review. While no association was found with the cytochrome P genes, we found that those with the homozygous wild-type genotype for ABCB1 compared to heterozygous genotypes were associated with chronic opioid use (OR 3.23, 95% CI 1.36 – 7.68, $p = 0.008$). When controlling for age, sex, and body mass index, the association of ABCB1 remained significant (OR 3.53, 95% CI 1.44 – 8.66, $p = 0.006$).

Discussion

We found an association of ABCB1 and chronic opioid use after surgery. ABCB1 is a P-glycoprotein transporter and an important efflux transporter at the blood-brain-barrier and has been reported to be associated with opioid metabolism and pain relief variability.2,3 This is an important finding and needs to be validated in future prospective trials. Pharmacogenomics may play a key role in establishing personalized pain management for those patients considered high risk for developing opioid dependence.

References

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Disclosures

Yes

Tables / Images