OPiOD analgesics are the most widely used drugs to treat moderate to severe pain. High individual variability has been reported in both pain intensity and in response to pharmacological analgesia. Furthermore, patients’ responses vary for both analgesic efficacy and side effects to different opioids, despite the fact that most clinically used opioids are selective for μ-opioid receptors (OPRM1). Thus, there is a considerable need to identify predictive biological markers of opioid therapy outcomes, and genetic markers are among those that have generated both interest and hope. In this issue, Hwang et al.1 present a meta-analysis in which the influence of the OPRM1 A118G polymorphism on postoperative opioid requirement and analgesic response is evaluated, thereby contributing to a body of literature suggesting that understanding the heritable factors related to analgesic control may provide objective guidance to clinicians.

The single nucleotide polymorphism A118G codes for an amino acid substitution Asp to Asn at the codon 40 and it is the most widely studied genetic variant of OPRM1. Minor allele G, with 24% frequency in Hispanics, 25 to 47.4% in Asians, and 14% in Caucasians was proposed to mediate a significant proportion of the observed variability in clinical effects. However, the molecular and cellular mechanisms by which the A118G polymorphism contributes to OPRM1 receptor activation and function are not fully understood. For example, the minor G allele has been shown to increase the affinity of the receptor for β-endorphin by three-fold.2 But others have reported no difference in binding affinity, functional coupling, or internalization of receptor.3,4 Alternatively, a substantial reduction in the expression of the G variant allele at both the RNA and protein levels has been reported.4,5 In line with the latter findings, it has been reported that the G variant introduces a new CpG-methylation site into the OPRM1 gene locus, resulting in greater epigenetic control over receptor expression down-regulation.6 It is plausible that opposite molecular regulatory events are affected by the minor G allele and the net result of the substitution depends on cell type, state of the cell activation, and nature of ligand.

In parallel with molecular genetic studies, a multitude of association analyses have been conducted for A118G variation and its relationship to various phenotypes including risk of opioid or alcohol dependence, prediction for naltrexone treatment response, and opioid analgesic efficacy. Although meta-analysis of the association between OPRM1 A118G and naltrexone efficacy for treatment of alcoholism has shown convincing consistency, clinical studies of A118G contribution to opioid analgesic sensitivity have displayed widely varying levels of association. Moreover, the directionality of the minor allele effect(s) is not uniform, with some evidence for G allele carries being less sensitive to opioids.7

The current study makes a step toward clarifying the seemingly inconsistent prior findings with a very well-controlled meta-analysis that reveals the essential elements of the relationship between OPRM1 genotype and opioid analgesia. Using PubMed, EMBASE, and the Cochrane Library, the essential studies were identified in which OPRM1 polymorphism and pain phenotypes were measured in the same-ethnicity population after only surgical procedures in patients who were not suffering from chronic pain before surgery. By analyzing the findings from 18 published studies including 4,607 participants, the authors found that the effect of OPRM1 A118G on postoperative pain is greatly driven by ethnicity and is most obvious in Asian but not Caucasian patient populations. In agreement with prior studies showing significant differences in pain between ethnic groups,8 Hwang et al.1 report that ethnicity strongly predicts postoperative need for opioid analgesia and shapes the effect of the OPRM1 genotype on analgesic response in the way

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Accepted for publication June 11, 2014. From the Department of Anesthesiology, University of Pittsburgh, Pittsburgh, Pennsylvania (I.B., E.E.Y.); and Alan Edwards Centre for Research on Pain, McGill University, Montreal, Quebec, Canada (L.D.).

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that minor G allele carriers require more opioid analgesics. Although the underlying mechanism(s) for the effects of ethnicity and its interplay with genetic factors are unknown, the authors offer a number of plausible hypotheses that include the relatively low frequency of G allele in Caucasians, the potential for differences in genotypic structure between Asian and Caucasian populations, variations in single nucleotide polymorphism \times\text{ single nucleotide polymorphism} interaction within and outside of \text{OPRM1} locus, and divergence of environmental pressures.

Furthermore, the authors report that the predictive power of \text{OPRM1} genotype for postoperative analgesic need is prominent only when patients have undergone visceral as opposed to somatic surgeries. Prior research has shown that \text{μ}-opioid agonists can effectively manage postoperative somatic pain but are not particularly well suited to treatment of visceral pain due in part to constipating and dysmotility effects which add significantly to symptom burden.\textsuperscript{6} As a result, visceral pain is more medically difficult to treat; and higher doses of \text{OPRM1} agonists that could potentially offer pain relief are contraindicated due to their effects on gastrointestinal function. Perhaps, the strong effect of \text{OPRM1} genotype on visceral pain is driven by an interaction of these two latter factors: visceral surgery patients require more opioids but they also have stronger side effects which contributes to exacerbation of symptom burden.

Finally, only the \text{OPRM1} effect on morphine but not fentanyl analgesia has been found to be significant. Although this result may be a consequence of difference in the size of the analyzed opioid treatment subgroups, with morphine being the biggest treatment group, this finding may also reflect differential receptor dynamics upon binding different opioid ligands. Along these same lines, both the report of \textit{in vitro} endorphin-specific effects of minor G variants binding\textsuperscript{2} and the recent report in a humanized mouse model,\textsuperscript{10} where sensory neurons expressing the 118GG gene displayed reduced morphine (but not fentanyl) potency and efficacy compared with 118AA, would suggest that pharmacogenetic response to opioid agonists may be ligand dependent.

This study has a number of strengths including the careful definition and adherence to selection criteria for the published reports that produced the most homogeneous patient groups for combining the meta-analysis and sufficient power to detect the genetic effect produced by this method compared with original reports that had limited representation of homozygote groups within studied populations. In fact, the study exemplifies how a meta-analysis method compared with original reports that had limited power to detect the genetic effect produced by this patient groups for combining the meta-analysis and sufficient power to detect the genetic effect produced by this patient groups for combining the meta-analysis and suf

Competing Interests

The authors are not supported by, nor maintain any financial interest in, any commercial activity that may be associated with the topic of this article.

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References


Anesthesiology 2014; 121:678-80