

Impact of Genetic Polymorphisms on Opioid Misuse: A Scoping Review

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Opioids misuse has led to almost 52,000 Americans deaths in year 2015. Genetic polymorphism has been hypothesized to augment the effects of opioids either by reduced metabolism (pharmacokinetics) or by increasing neuropsychological effects (pharmacodynamics). There have been few efforts in the past to synthesize knowledge about the associations of pharmacokinetic- and pharmacodynamic- genetic variations with the opioid misuse. The main goal of this study is to synthesize knowledge about associations of genetic polymorphisms with opioid misuse. We conducted a scoping review using key terms. For this study, we defined opioid misuse is a clinically diagnosed dependence or a serious medical event as a result of opioid misuse (e.g., intoxications). We selected relevant publications from following databases: Medline®, EMBASE®, CINAHL®, Psychinfo®, and SNPedia®. The SNPedia® is a specific database that catalogues studies evaluating Single Nucleotide Polymorphism (SNP) associated with various health conditions including opioids misuse. The findings were summarized as qualitative description. Our scoping review indicated that there are almost 57 genes with 106 single nucleotide polymorphism (SNPs) that were associated with opioid misuse. The effects of these genetic variations could be classified as pharmacokinetics or pharmacodynamics responses. For example, several studies indicated that genetic variations in opioid receptors OPRM1, ORPD1, ORKD1, and TPH1 caused more opioid consumption for pain relief leading to dependence and depression. SNPs at the following genes were also associated with pharmacokinetic effects of opioids: COMT, SLC6A4, ABCB1, ANKK1, CACNA2D2, KCNC1, KCNG2, and KCNJ6. Alternately, we noted that genetic variations for dopamine receptors, i.e., DRD2 and MTHFR augmented the effects of opioid use. We conclude that genetic-polymorphisms might explain some of the population-level variations in opioid misuse. We propose to build on our efforts to further develop comprehensive review and improved data collection of these variations.