

# Evaluating the Evidence for Genetics/Genomics in Chronic Pain: An Integrative Literature Review

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**Introduction.** Differences in DNA sequence and/or genomics account for an estimated 70% of the individual differences in pain sensitivity. While it is accepted that genetics/genomics play a role in determining pain burden, the present study was designed to identify the presence of clinical evidence for genetic factors as a determinant of chronic pain severity. This study seeks to fill that gap in knowledge and provide a systematic review of various genes for which evidence is available.

**Methods.** The Scale for the Assessment of Narrative Review Articles (SANRA) criteria guided this review. We employed PubMed/Medline to identify relevant articles using the primary database and search terms encompassing combinations of chronic pain, genetics/genomics, pharmacogenomics, opioid side effects in human subjects. After review by two independent reviewers for inclusion, 27 articles ultimately met the inclusion criteria.

**Results.** While only a small number of articles provided level II (randomized clinical trial) evidence for specific genes involved in chronic pain susceptibility and severity, we were able to identify level III evidence for genetics of chronic pain. Studies identified genes in several broad categories: opioid related genes, genes implicated in the development of pain, proteins, genes modulating inflammatory markers, genes affecting disease processes.

**Conclusions.** Evidence implicating genetic/genomic variation in the individual differences in chronic pain risk and severity, but that information is not being used to guide evidence-based medicine decision making. We found that this may be due to a lack of published evidence with the highest levels of science supporting their integration into practice.