



Investigation of genes in chronic and acute morphine-treated mice using microarray datasets

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ABSTRACT. Morphine is a psychoactive medication that is used as a standard analgesic treatment to relieve pain in clinics. Many patients rely on chronic or acute treatment of morphine to treat pain. However, morphine is a narcotic and has a reverse effect when inappropriately used. Therefore, it is necessary to study chronic and acute morphine treatment to improve pain relief. In this study, differentially expressed genes of acute and chronic morphine-treated mice were identified using Array Express datasets. The genes that were associated with these two types of morphine treatment are discussed. A co-expression network was constructed, and the hub genes were identified. Gene ontology enrichment analysis and pathway analysis were performed using the Gene Ontology website and Kyoto Encyclopedia of Genes and Genomes, respectively. Our study revealed genes that are associated with acute and chronic morphine treatment. Therefore, this study is

potentially useful for improving pain relief of patients by acute and chronic morphine treatment.

Key words: Chronic morphine treatment; Acute morphine treatment; Gene