



A system approach to the pharmacogenetics of migraine

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Background and Aims: Migraine is recurrent headaches and known as the most common neurological disorder. Despite recent advances, the pathophysiology of migraine remains incompletely understood. In this study a systems pharmacology approach used for better understanding the genetic factors might determine a role in apparition of the migraine symptoms.

Methods: The genomic data directly and indirectly associated with the name 'migraine' was extracted from GENE in NCBI. All proteins, about 800 proteins, related to these genes were characterized from uniprot and protein-protein interaction database and clustered as a network by Cytoscape.

Results: Among the proteins there were about 70 ones which were highly connected to other proteins in the network. IL6, TNF- α , HTR1B, NFKB1, DRD4 and IL1B had the higher interaction to the others which shows the importance of involving them to the process of initiation of the migraine.

Conclusions: We used highthroughput computational analysis of regulatory networks to reveal some genomic factors related to migraine. Inappropriate activation of the genes of IL6, TNF- α , HTR1B, NFKB1, DRD4 and IL1B may affect the central glutamate synapse, via NMDA receptors. All of these proteins are associated with neurological disorders may have a critical role in developing migraine attack and could be the target of new drug design in the prevention or treatment of migraine.

Keywords: Systems pharmacology; Migraine; Pharmacogenetics