Current Understanding of DNA Methylation in the Pathogenesis of Neuropathic Pain

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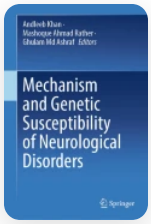

Mechanism and Genetic Susceptibility of Neurological Disorders

Hayate Javed, Aishwarya Mary Johnson & Andleeb Khan

Abstract

Lesion or disease in the somatosensory nervous system is the root cause of neuropathic pain, which has a major negative influence on the quality of life. Injury to peripheral sensory nerves is well documented to change the expression of genes in the neurons and sensory nerves, which has a significant impact on the spinal cord's synaptic plasticity and the onset and progression of chronic pain. N-methyl-D-aspartate (NMDA) receptors and α2δ1 are examples of pro-nociceptive genes, while potassium channels, opioid, and cannabinoid receptors are examples of anti-nociceptive genes. However, there is still more to learn about

epigenetic mechanisms controlling the transcription of these genes. In this chapter, we explored the current research on the role of histone changes and DNA methylation in the development of neuropathic pain. We discussed the importance of neurotransmitter receptors and ion channels expressed transcriptionally under the regulation of these proteins in the dorsal root ganglia following nerve injury, which is frequently utilized in neuropathic pain models. A deeper understanding of the epigenetic reprogramming involved in the transition from acute to chronic pain may lead to the development of innovative neuropathic pain treatments.

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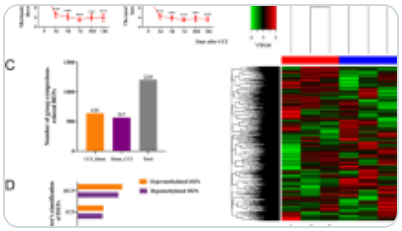

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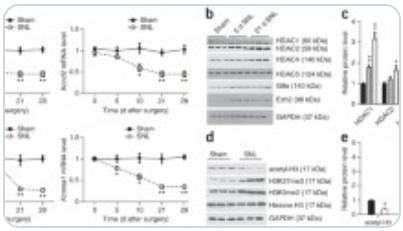

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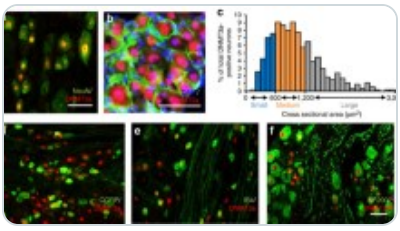

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Ethics declarations

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