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Perspective

Chronic Spinal Disorders and Genetic Modifications

Mark Boldin*

Department of Molecular and Cellular Biology, Beckman Research Institute, California, USA

DESCRIPTION

Degenerative spinal stenosis is a common and difficult degenerative spine illness that affects the older population and has a significant impact on their quality of life. Degenerative spinal stenosis can occur as a result of a variety of pathologic conditions compressing the spinal cord or nerve roots, which results in symptoms like pain, numbness, and weakness. Spinal degenerative spondylolisthesis, facet joint hypertrophy, intervertebral disc protrusion, and spinal ligament overlap or thickening can all result in a narrowing of the spinal canal. The Supraspinous Ligament (SSL), Posterior Longitudinal Ligament (PLL), Ligamentum Flavum (LF), Capsular Ligament (CL), Interspinous Ligament (ISL), and Anterior Longitudinal Ligament (ALL) make up the spinal ligaments anatomically. Due to their roles in the creation of the spinal canal's anterior and posterior walls, respectively, PLL and LF are the two main spinal ligaments that are considered to be of the utmost importance. A significant body of work has shown that the pathophysiology of degenerative spinal stenosis is directly related to the aging and degeneration of the ligamentum flavum and posterior longitudinal ligament. The most prevalent forms of spinal ligament aging at the beginning and progression of spinal stenosis are PLL ossification and LF ossification or hypertrophy. The deterioration of the spinal ligament has been linked to a number of genetic, epigenetic, and environmental variables, according to evidence. Additionally, it was shown that a number of important signal transduction pathways have a functional role in the ligamentum flavum's fibrosis, hypertrophy, ectopic ossification, and calcification. The current focus of study is still on the fundamental mechanisms of spinal ligament aging, which have not yet been distinctly identified.

Contrary to genetics, epigenetics describes the heritable and reversible changes in a gene's or genome's function that take place without any change to the primary DNA sequence. DNA methylation, histone modifications, and non-coding RNA (ncRNA) regulation are the most common epigenetic alterations, albeit they are not the only ones. These pathways are linked functionally. Epigenetic changes have a key role in the pathogenesis and advancement of numerous diseases, in addition to their involvement in physiological processes. Particularly, epigenetic changes have been linked to a number of age-related chronic musculoskeletal disorders. One of the most prevalent degenerative musculoskeletal disorders, Osteoarthritis (OA), is the main cause of pain and disability in adult and aged populations. The defective epigenetic regulation of DNA methylation, histone modifications, and non-coding RNAs in the articular cartilage has been shown to be a key factor in the pathogenesis of OA. The main cause of lower back discomfort, known as Intervertebral Disc Degeneration (IDD), which places a heavy strain on the global healthcare system, is widely acknowledged. Studies are increasingly concentrating on noncoding RNA regulatory apparatus in nucleus pulposus cells function and fate during IDD progression, reversible histone acetylation/deacetylation, and DNA methylation profiling. Another essential epigenetic method for controlling the expression of genes is chromatin remodeling. The involvement of chromatin remodeling in IDD and other degenerative musculoskeletal diseases has also been demonstrated by recent studies.

Epigenetic alterations, particularly those linked with age-related chronic musculoskeletal disorders, are functionally involved in both physiological processes and the aetiology of different diseases in humans. A widespread and intricate degenerative spine disorder called spinal ligament aging involves a number of hereditary, epigenetic, and environmental variables. Studies are increasingly focusing on reversible histone acetylation/deacetylation, DNA methylation profiling, and noncoding RNA regulatory apparatus in nucleus pulposus cells function and fate during IDD progression. Chromatin remodeling is a crucial epigenetic technique for regulating the expression of genes. Recent investigations have also shown that chromatin remodeling has a role in IDD and other degenerative musculoskeletal illnesses.

Epigenetic changes play a functional role in both physiological processes and the aetiology of several human diseases, especially those connected to age-related chronic musculoskeletal ailments. Spinal ligament ageing, a common and complex degenerative spine disorder, involves a number of inherited, epigenetic, and environmental factors.

Correspondence to: Mark Boldin, Department of Molecular and Cellular Biology, Beckman Research Institute, California, USA, E-mail: boldinmark.res@gmail.com

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