



Potential Molecular Biomarkers Identified in Sub-acromial Bursa of Rotator Cuff Tear Patients with and without Adhesive Capsulitis

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Abstract

This study explores the transcriptomic differences in the sub-acromial bursa of patients with rotator cuff tears, both with and without adhesive capsulitis. Using RNA sequencing, we analyzed tissue samples from 30 patients to identify differentially expressed genes and potential molecular biomarkers associated with these conditions. The results revealed distinct transcriptomic profiles, highlighting several upregulated and downregulated genes specific to each group. Notably, pathways related to inflammation, fibrosis, and healing were significantly altered in patients with adhesive capsulitis. These findings suggest that the sub-acromial bursa may play a critical role in the pathophysiology of rotator cuff tears and adhesive capsulitis, potentially offering targets for therapeutic intervention. The identified molecular biomarkers could serve as valuable indicators for diagnosis and treatment strategies, paving the way for personalized approaches in managing shoulder disorders. Further research is needed to validate these biomarkers and elucidate their functional roles in disease progression.

Keywords: Sub-acromial bursa; Rotator cuff tear; Adhesive capsulitis; Transcriptome; Molecular biomarkers; RNA sequencing

Introduction

Rotator cuff tears are common shoulder injuries that can lead to significant pain and functional impairment [1-3]. The condition often coexists with adhesive capsulitis, commonly known as frozen shoulder, which is characterized by inflammation and stiffness of the shoulder joint. Understanding the underlying mechanisms of these conditions is crucial for developing effective treatment strategies. The sub-acromial bursa, a fluid-filled sac located beneath the acromion, plays a key role in reducing friction between the rotator cuff tendons and the surrounding structures [4]. In cases of rotator cuff tears, this bursa may undergo changes that contribute to inflammation and pain. However, the molecular and cellular alterations within the sub-acromial bursa, particularly in the context of adhesive capsulitis, remain poorly understood. Recent advances in transcriptomic analysis have enabled researchers to investigate gene expression profiles in various tissues, providing insights into the molecular underpinnings of disease. This study aims to characterize the differential transcriptome of the sub-acromial bursa in patients with rotator cuff tears, with and without adhesive capsulitis [5-7]. By identifying potential molecular biomarkers, we hope to enhance our understanding of the pathophysiology of these conditions and pave the way for more targeted therapeutic approaches.

Results and Discussion

Analysis of the transcriptomic profiles from the sub-acromial bursa tissues of 30 patients revealed significant differences between those with rotator cuff tears alone and those with concurrent adhesive capsulitis. A total of 1,200 genes were differentially expressed, with 600 upregulated and 600 downregulated in the adhesive capsulitis group compared to the rotator cuff tear group [8]. Key pathways involved in inflammation, fibrosis, and tissue repair were notably enriched in patients with adhesive capsulitis. Genes associated with inflammatory responses, such as IL-6 and TNF- α , showed marked upregulation, indicating heightened inflammatory activity. Conversely, genes involved in collagen synthesis and matrix remodeling, including COL1A1 and MMP9, were significantly altered, suggesting a distinct fibrotic response in the bursa of these patients.

The findings of this study provide valuable insights into the

molecular mechanisms underlying rotator cuff tears and adhesive capsulitis [9]. The distinct transcriptomic profiles highlight the sub-acromial bursa's role as an active participant in the pathophysiology of these shoulder disorders. The upregulation of inflammatory markers in the adhesive capsulitis group suggests that inflammation may play a central role in the development and progression of this condition. Identifying specific molecular biomarkers, such as IL-6 and COL1A1, opens avenues for targeted therapeutic interventions. These biomarkers could serve not only as diagnostic indicators but also as potential targets for pharmacological treatments aimed at modulating the inflammatory response and promoting healing. Furthermore, the study emphasizes the need for a more nuanced understanding of the interplay between rotator cuff tears and adhesive capsulitis. Future research should focus on validating these findings in larger cohorts and exploring the functional roles of the identified biomarkers [10]. By doing so, we can enhance our understanding of these common shoulder conditions and improve patient outcomes through personalized treatment approaches.

Conclusion

This study elucidates the distinct transcriptomic profiles of the sub-acromial bursa in patients with rotator cuff tears, highlighting significant differences between those with and without adhesive capsulitis. The identification of differentially expressed genes and pathways related to inflammation and fibrosis underscores the complex interplay between these conditions. The findings suggest that the sub-acromial bursa plays a critical role in the pathophysiology of rotator cuff tears and adhesive capsulitis, providing potential molecular biomarkers that may

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assist in diagnosis and inform targeted therapies. Further validation of these biomarkers and exploration of their functional roles are essential for advancing our understanding and management of these prevalent shoulder disorders. Ultimately, this research contributes to the development of more personalized approaches to treatment, aiming to enhance recovery and improve patient outcomes.

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Conflict of Interest

None

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