Identification of Synovial Tissue Biomarkers in Late-Onset Rheumatoid Arthritis Patients

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Rheumatoid arthritis (RA) and osteoarthritis (OA) are distinct joint diseases presenting unique pathophysiologies. Because of the similar symptoms that RA and OA present, such as arthralgia, edema, and stiffness, late-onset RA is oftentimes misdiagnosed as OA. This confusion can be detrimental to patients' health as modes of treatment vary drastically and late diagnoses can inhibit quality of life. This study aimed to identify more reliable biomarkers of RA based upon an examination of genes that were significantly upregulated in RA synovial tissue samples compared to OA samples. Such biomarkers could prevent misdiagnosis in older age groups, thereby improving patient outcomes. Three distinct Gene Expression Omnibus datasets were obtained and a total of 112 differentially expressed genes (DEGs) were cross-identified in multiple sets; 67 genes were present in all three datasets. STRING and PANTHER databases were utilized to identify complex biological processes involved with the DEGs. Notably, the positive regulation of cell-to-cell adhesion had a 83.72 fold enrichment in RA patients and 9 key hub genes (CCL5, CXCL9, CXCL10, CXCL11, CXCL13, CCL13, CXCL8, CXCL5, and CXCL3) were involved in chemokine domains. Further exploration of the 67 common DEGs, particularly CXCL13, can potentially distinguish genetic biomarkers that may indicate the presence of RA and reduce the likelihood that it is falsely characterized as OA. Furthermore, gene expression results indicated that the interleukin-21 (IL-21) mediated signaling pathway experienced a fold enrichment of over 100 in RA patients. Results denote that focusing on IL-21 cytokine profiles in patients' blood test results can potentially be a more reliable standard of diagnosis than the current rheumatoid factor metric.

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