Analysis of miRNAs in Rheumatoid arthritis: Correlation with Disease Activity

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April 05, 2024

Abstract

Rheumatoid arthritis (RA) is a chronic, severe inflammatory disease, characterized by progressive bone, cartilage, and joint destruction.miRNAs are epigenetic regulatory mechanisms that participated in broad and long-term changes in gene expression and involved in various pathophysiological pathways related to several autoimmune diseases such as RA. The regulated expression of miRNAs in synovia, T cells, or Peripheral blood mononuclear cells (PBMCs) from RA patients is associated with inflammation, angiogenesis, osteoclastogenesis, innate immunity, and cartilage synthesis. This work is designed to analyze the expression of certain miRNAs in PBMCs of 30 RA patients compared to 20 healthy controls using quantitative real-time polymerase chain reaction (qRT-PCR). Selected miRNAs were categorized into 3 main groups: miRNA participating in the inflammatory response (miR-16, miR-146a, and miR-155), miRNA participating in the angiogenesis process (miR-17 - miR-221 and miR-222) and muscle-specific myomiR (miR-133b and miR-206). The data showed significant elevation in the fold change expression levels of all studied miRNAs in PBMCs of RA patients as compared with those in healthy controls. The receiver operator characteristic curve (ROC) curve analysis of miR-206 showed the best sensitivity and specificity value among studied miRNAs (70% sensitivity and 85% specificity). Our results suggest that the elevated expression of tested miRNAs might be involved in RA pathology including inflammation, angiogenesis, and bone affection leading to joint destruction and bone deformity. A better understanding of the role of these miRNAs will enable a new advanced strategy to ameliorate disease progression in RA.

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