

## SUMMARY

Osteoarthritis (OA) is one of the most common musculoskeletal disorders, significantly reducing patients' quality of life. The causes of OA are complex and include both genetic and environmental factors. This study focuses on the role of microRNA (miRNA) in the pathogenesis of OA, with particular emphasis on their potential as diagnostic biomarkers.

MiRNAs are short, non-coding RNAs that regulate gene expression at the post-transcriptional level. Dysregulation in miRNA expression or processing has been linked to numerous diseases, including OA. Studies have shown changes in the levels of certain miRNAs in OA and their potential as diagnostic biomarkers for this disease.

The aim of this study was to investigate the role of miRNA in the pathogenesis of osteoarthritis (OA) and their potential as diagnostic biomarkers. The specific objectives were to determine the miRNA expression profile in cartilage and serum samples from patients with OA, to compare the miRNA expression profile between OA patients and a control group, to identify the relationship between the miRNA profile and demographic and environmental factors, and to assess the clinical significance of miRNA, providing a better understanding of the epigenetic mechanisms underlying the development of this disease.

Patients who provided written informed consent were included in the study. Samples were collected from 2014 to 2015, and the study group was recruited from patients at the Orthopedics and Traumatology Clinic of University Hospital No. 2 in Rzeszow. A total of 36 serum samples and 29 cartilage samples were obtained from patients diagnosed with OA. The control group consisted of patients with femoral neck fractures who did not experience joint pain before the injury and showed no signs of OA on radiological examination.

Data collected from patients included gender, age, BMI, age of disease onset, disease stage, presence of chronic comorbidities, pain in other joints, and lifestyle. Cartilage samples were collected during hip arthroplasty surgeries. All surgeries were performed in the same hospital by the same team of orthopedic surgeons.

Analysis showed significant differences in miRNA expression between OA patients and the control group. Of the 19 miRNAs analyzed, four (hsa-miR-138-5p, hsa-miR-146a-5p, hsa-miR-335-5p, and hsa-miR-9-5p) showed more than a twofold increase in expression in OA patients compared to the control group. Changes in the expression of these miRNAs were not significantly associated with clinical data.

The study of miRNA expression in the serum of OA patients also showed significant differences compared to the control group. Of the 20 miRNAs analyzed, there was a notable increase in miR-146a-5p and miR-98-5p, along with a reduction in miR-222-3p and miR-27a-3p. Despite these significant expression changes, the lack of correlation with clinical characteristics suggests that miRNAs may not be directly linked to disease progression. These findings highlight the need for further research into the role of miRNAs in different stages of OA and their potential clinical applications.

The conclusions of the study indicate that miRNAs can be valuable diagnostic tools in OA. MiR-146a-5p has potential as a biomarker for monitoring degenerative processes in the joint. Further studies on a larger cohort of patients are necessary to fully understand the role of miRNAs in OA and to develop effective therapeutic methods based on miRNA modulation.