UTJMS 2025 June 30, 13(S3):e1-e2

Investigating the common genes involved in development of Sjogren's syndrome and Cardiomyopathy

Anwer Aldhaheri¹, Nezam Altorok², Sadik A. Khuder^{3*}

¹College of Medicine and Life Sciences, 3000 Arlington Avenue, The University of Toledo, Toledo OH 43615

²Professor, Program Director Rheumatology Fellowship, Director Internal Medicine Residency, Division of Internal Medicine, Department of Medicine, 3000 Arlington Avenue, The University of Toledo, Toledo OH 43615

³Professor, Division of Internal Medicine, Department of Medicine, 3000 Arlington Avenue, The University of Toledo, Toledo OH 43615

Email: sadik.khuder@utoledo.edu

Received: 2024-10-04

Accepted: 2024-10-09

Published: 2025-06-30

Background: Recent research has identified an association between SS and cardiomyopathy (CMP). However, the underlying mechanisms and shared genetic factors contributing to the coexistence of SS and CMP remain unclear.

Objectives: To identify common genes involved in the development of both SS and CMP.

Methods: Gene expression data for SS and CMP, including RNA sequencing (include the GSE number of each RNA-seq) and microarray (include the GSE number of each microarray dataset) datasets, were obtained from the Gene Expression Omnibus (GEO) database. GEO2R was used to identify the top 1,000 differentially expressed genes for each disease. The WGCNA package was used to identify co-expression modules significantly associated with each disease state. The DAVID database was used for Gene Ontology (GO) and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis. Hub genes were identified, and their associated pathways were examined.

Results: WGCNA revealed ten significant modules related to SS and CMP. Thirteen genes were selected based on the DAVID analysis results, with criteria including their known roles in disease development, shared pathways, and evidence from the literature. These genes—IFNLR1, IRF5, MDK, IL1RN, SOD2, PIAS4, SSPN, ELAVL1, TRAF3, TRAF6, CTNNB1, HIF1A, and JAK1—were differentially expressed and linked to both SS and CMP. IL1RN, for example, is protective against inflammation, but its polymorphisms are associated with various inflammatory, cancerous, and autoimmune conditions. INF genes overexpression

Dr. Lance D. Dworkin Department of Medicine Research Symposium

UTJMS 2025 June 30, **13**(S3):e1-e2

is known to recruit T cell for its inflammatory response. T cell activity in both SS and CMP drives tissue damage and inflammation, worsening disease progression.

Conclusion: This study identified 13 genes implicated in the shared development pathways of both SS and CMP. These findings provide new insights into the concurrent development of these diseases and offer potential targets for therapeutic intervention.

Keywords: Sjogren's Syndrome