RNA-seq data analysis uncovers a link between systemic lupus erythematosus and glioblastoma

Nahshon A. Puente[1], Mahasin A. Osman[2], Sadik A. Khuder[3*]

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

[2]Associate Professor, Division of Hematology and Oncology, Department of Medicine, 3000 Arlington Avenue, The University of Toledo, Toledo OH 43615

[3]Professor, 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: Systemic lupus erythematosus (SLE) is a complex heterogenous systemic autoimmune disease. Our previous study using US Healthcare Cost and Utilization Project (HCUP) 2020 National Inpatient Sample (NIS) data showed that SLE may reduce the risk of glioblastoma (GB), but the mechanism underlying this reduction is still unclear.

Objectives: To explore the genetic molecular mechanisms and core genes underlying GB risk reduction in SLE.

Methods: SLE and GB RNA-seq data were downloaded from the National Center for Biotechnology Information (NCBI) Gene Expression Omnibus (GEO) database. GEO2R was used to identify the top 1000 differentially expressed genes for each disease. Weighted gene co-expression network analysis (WGCNA) was used to identify co-expression modules that were significantly correlated with each disease state. Six core shared genes were screened out and validated using GEO2R differential expression analysis results.

Results: Using WGCNA, three modules were identified as significantly correlated to SLE and GB. Six core shared genes–CEMIP, GIMAP6, NCAM1, RPS6KA5, SBSPON, and UHRF1–were screened out. Of these genes, CEMIP, GIMAP, RPS6KA5, and SBSPON were significantly downregulated in both diseases. Interestingly, NCAM1, and UHRF1 showed differences in their expression between SLE and GB and may contribute to the reduction in GB risk observed previously.

Conclusion: The present study identified six core genes shared by SLE and GB, of which two–NCAM1, and UHRF1–may be involved in GB risk reduction.

Keywords: Lupus, Glioblastoma

https://dx.doi.org/10.46570/utjms-2025-1458