MTERF2, RPS6KA5, and SYNE2 define the link between systemic lupus erythematosus and breast cancer

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Background: Systemic lupus erythematosus (SLE) is a complex heterogenous systemic autoimmune disease. Previous studies have shown that SLE may be related to breast cancer (BC), but the mechanism underlying their relationship is still unclear.

Objectives: To explore the genetic molecular mechanisms common to and core genes shared by BC and SLE.

Methods: SLE (GSE175839) and BC (GSE183635) RNA-seq data were downloaded from the National Center for Biotechnology Information (NCBI) 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. Three core shared genes were screened out and validated using GEO2R differential expression analysis results.

Results: Using GEO2R, 44 genes were identified as shared by BC and SLE. Using WGCNA, two modules were identified as significantly correlated to SLE and BC, from which three core shared genes–MTERF2, RPS6KA5, and SYNE2–were screened out and validated by the GEO2R results. All three genes were significantly downregulated in both diseases.

Conclusion: The present study identified three core genes shared by SLE and BC that may be involved in the relationship between the two diseases.

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