AUTOIMMUNE CONNECTIVE TISSUE DISEASES

GENOME-WIDE SCREENING AND FUNCTION ANALYSIS OF LONG NONCODING RNA EXPRESSION IN CD4+ T CELLS OF SYSTEMIC LUPUS ERYTHEMATOSUS

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Introduction: The mechanism of CD4+ T cells dysfunction in systemic lupus erythematosus (SLE) has not been fully understood. Increasing evidence showed that long noncoding RNAs (lncRNAs) can regulate immune response and take part in some autoimmune diseases such as SLE. However, little is known about the lncRNAs expression and function in CD4+ T of SLE.

Objective: We aimed to detect the profile of lncRNAs expression in lupus CD4+ T cells and explore the potential lncRNAs involved in the pathogenesis of SLE.

Methods: The expression levels of lncRNAs and mRNAs in CD4+ T cells from SLE and healthy controls were detected by microarray. Bioinformatics analysis was done to investigate the potential roles of lncRNAs. 6 differentially expressed lncRNAs were randomly chosen for validation by quantitative PCR (qPCR).

Results: A total of 1887 lncRNAs and 3375 mRNAs were aberrantly expressed in CD4+ T cells of SLE compared to healthy controls. The expression patterns of 6 chosen lncRNAs were consistent between microarray data and qPCR results. GO and KEGG pathway analysis indicated that 27 gene regulations and 53 signaling pathways related to differentially expressed mRNAs. A list of lncRNAs might play roles in the pathogenesis of SLE by comparing the difference between co-expression networks. Co-expression network recognized several lncRNAs as core genes.

Conclusion: Our results showed that the lncRNAs expression profile is altered in CD4+ T cells of SLE, which providing a potential target for further mechanistic studies of SLE pathogenesis.