Identification of differentially expressed circulating exosomal lncRNAs in IgA nephropathy patients

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Abstract

Background: Immunoglobulin A nephropathy (IgAN) is one of the most prevalent primary glomerular disease. Non-invasive biomarkers are urgently needed for IgAN diagnosis. We investigate the difference in expression profiles of exosomal long non-coding-RNAs (lncRNAs) in plasma from IgAN patients compared with their healthy first-degree relatives, which may reveal novel non-invasive IgAN biomarkers.

Methods: Exosomes were isolated from the plasma of IgAN patients and their healthy first-degree relatives. High-throughput RNA sequencing and real-time quantitative polymerase chain reaction (qRT-PCR) was used to validate lncRNA expression profiles. Pathway enrichment analysis was used to predict their nearest protein-coding genes.

Results: lncRNA-G21551 was significantly down-regulated in IgAN patients. The nearest protein-coding gene was found to be encoding the low affinity receptor of the Fc segment of immunoglobulin G (FCGR3B).

Conclusion: Exosomal lncRNA-G21551, with FCGR3B as the nearest protein-coding gene, was down-regulated in IgAN patients, indicating its potential to serve as a non-invasive biomarker for IgAN.

Full-text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed.

However, the manuscript can be downloaded and accessed as a PDF.

Tables

Due to technical limitations, tables are only available as a download in the supplemental files section

Figures

Figure 1

Characterization of exosomes isolated from plasma. (A) The distribution of exosome size by DLS analysis. (B) Flow cytometry analysis of the exosomal surface markers CD63 and CD81. (C) Transmission Electron Microscope (TEM) images of isolated exosomes. Scale bar, 100 nm.

Figure 2

Differential expression profile of lncRNA in IgAN patients of RNA-seq (n=6) and relatives (n=6) of RNA-seq. (A) Heatmap of 70 lncRNAs that are differentially expressed between the two groups. The row z-score depict the lncRNAs expression values (B) Volcano plot of the differentially expressed lncRNAs between the two groups, the green, red and black dots represent down-regulated, up-regulated, and non-significance lncRNAs respectively. Cutoff:

FDR < 0.05, fold change > 2.

Figure 3

Validation of differentially expressed lncRNAs by qRT-PCR between IgAN patients and their healthy first-degree relatives. (A) lncRNA-G21551. (B) lnc-SPATA31E1-10. (C) lncRNA-G111779. Gene expression was calculated by the $2^{-\Delta\Delta Ct}$ method and normalized to external reference λ polyA+ RNA compared with the maximum ΔCt .

Supplementary Files

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