THE KOREAN SOCIETY OF NEPHROLOGY
APCN & KSN 2024
June 13(Thu) - 16(Sun), 2024 Coex, Seoul, Korea
Promoting Sustainable Kidney Health: The Asia-Pacific and Beyond

Abstract Submission No.: A-0833

Circulating microRNAs enriched in hemodialysis patients using medium cut-off dialyzers

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Objectives : Patients with end-stage kidney disease (ESKD) had a significantly higher risk of all-cause and cardiovascular mortality; however, the putative causes were not fully elucidated and remained the target of an active investigation. Circulating microRNAs (miRNAs) participated in biologic processes by regulation of target messenger RNAs (mRNAs) in a post-transcriptional manner. ESKD itself and the hemodialysis (HD) procedure, a therapeutic approach in patients with ESKD, could affect the generation or degeneration/removal of miRNAs. Thus, we investigated the effect of recently developed HD dialyzers, medium cut-off, on miRNAs.
Methods : We collected plasma from groups using medium cut-off dialyzers and those using conventional high-flux dialyzers. Each group had three patients, of which age and sex were matched. miRNAs were extracted from the plasma; then, next-generation sequencing (NGS) for miRNA was conducted. The expression of miRNA was compared between two groups and KEGG ontology analysis was performed.
Results : There were several miRNAs that enriched in group using medium cut-off dialyzers, including has-miR-1273c, has-miR-483-5p, has-miR-4271, has-miR-619-5p, has-miR-8485, and others. KEGG ontology analysis showed theses miRNAs were associated with cell-junction pathways, including focal adhesion, tight junction, and adherence junction, and with cell-signaling pathways, including Wnt, ErbB, p53, MAPK, and Jak-STAT signaling pathways.
Conclusions : There were several differentially expressed microRNAs between the two groups, using medium cut-off dialyzers and high flux. These differences in miRNA expression between the two groups might be contributed by the more effective removal of middle-molecule uremic toxin by the medium cut-off dialyzer.

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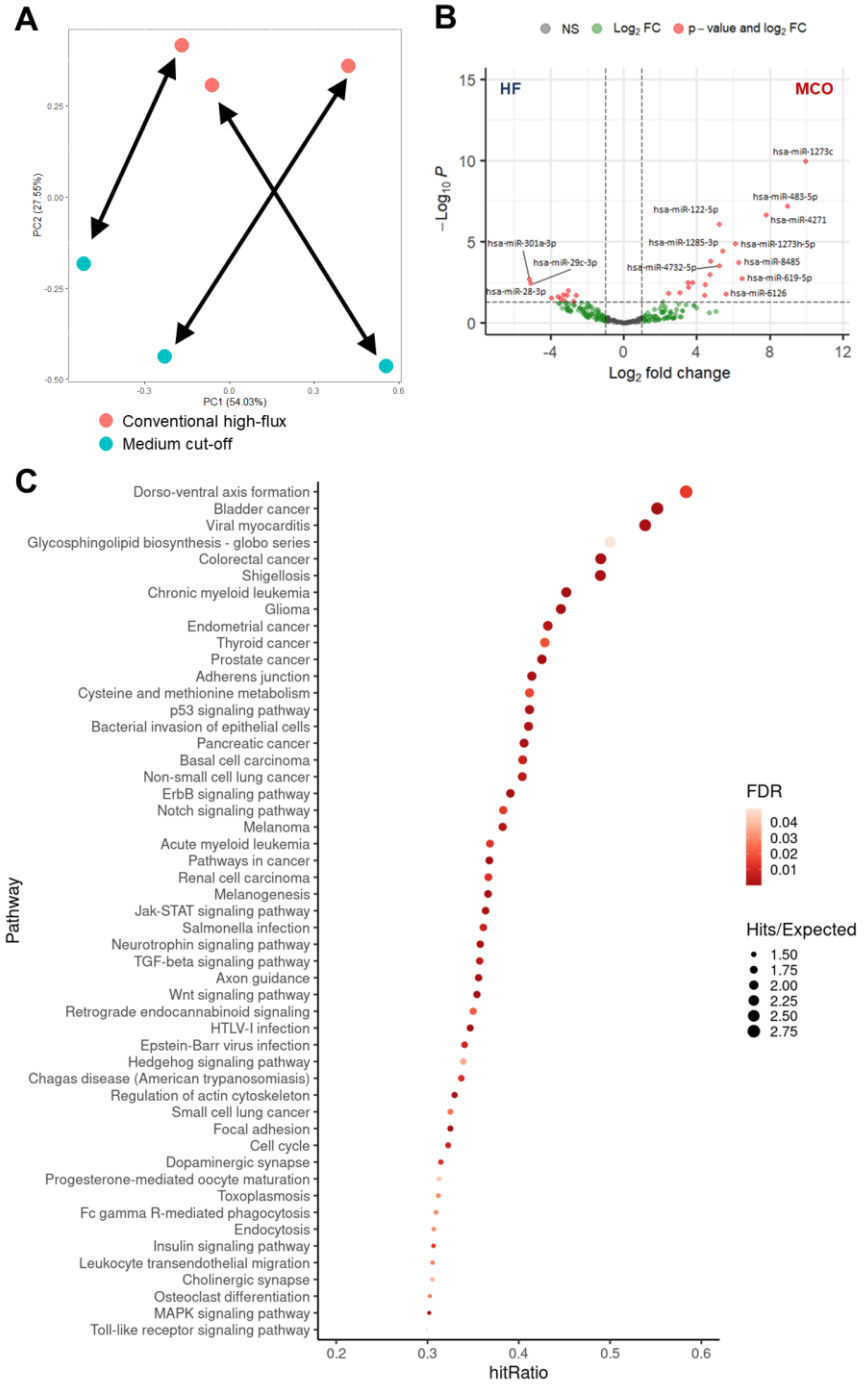

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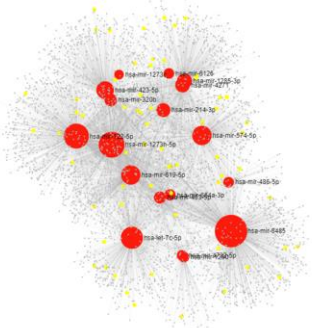
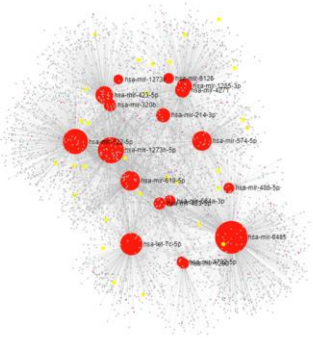
A. Focal adhesion



B. Tight junction



C. Adherence junction