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The circulating exosomal microRNA profile in patients with diabetic nephropathy

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Objectives: Diabetic nephropathy (DN) is associated with a high mortality rate. Exosomal microRNAs (miRNAs) regulate gene expression in a variety of tissues and play important roles in the pathology of various diseases. We hypothesized that the exosomal miRNA profile would differ between DN patients and patients without nephropathy.

Methods: We prospectively enrolled 74 participants, including healthy volunteers (HVs), diabetic patients without nephropathy, and those with DN. The serum exosomal miRNA profiles of participants were examined using RNA sequencing.

Results: The expression levels of 107 miRNAs differed between HVs and patients without DN, whereas the expression levels of 95 miRNAs differed between HVs and patients with DN. Among these miRNAs, we found 7 miRNAs that were uniquely up-regulated in DN patients compared to HVs, and 1 miRNA that was highly expressed in DN patients compared to patients without DN. A pathway analysis revealed that these eight miRNAs are likely involved in MAPK signaling, integrin function in angiogenesis, and regulation of the AP-1 transcription factor. Moreover, they were all significantly correlated with the degree of albuminuria.

Conclusions: In conclusion, patients with DN have a different serum exosomal miRNA profile compared to HVs and these miRNAs may be promising candidates for the diagnosis and treatment of DN.