Molecule identification to explore effects of blood cell storage time on uterine corpus endometrial carcinoma

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ABSTRACT

OBJECTIVE: MiRNA participates in the post-transcriptional regulation of gene expression primarily via gene silencing. We hypothesized that miRNAs in red blood cells (RBCs) used in clinical treatment play crucial roles at the molecular level in the pathogenesis and disease progression of some cancers. We explored the potential molecules and pathways active in the pathogenesis and prognosis of cancers in patients transfused with RBCs with different storage times.

METHODS: Differentially expressed miRNAs (DEmiRNAs) and mRNAs were screened using Gene Expression Omnibus and The Cancer Genome Atlas databases. Candidate mRNAs were selected and validated using the Gene Expression Profiling Interactive Analysis tool after pathway enrichment and survival analyses.

RESULTS: A total of 27 and 22 DEmiRNAs from storage days 7 and 28, respectively, were identified in the GSE114990 dataset. After prediction and integrated analysis, MiR-381 and candidate 18 intersected mRNAs were selected to construct the survival analysis model. Finally, a model which revealed substantial differences in survival rates between different risk groups were conducted.

CONCLUSIONS: Collectively, the progression and prognosis of cancer in patients transfused with RBCs with different storage times are affected by miR-381-mediated regulation of mRNAs and cancer-related pathways.

Key Words: miRNA, mRNA, blood transfusion, survival analysis

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