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Plasma microRNA profiles in heart transplant recipients with acute rejection: a single-center cohort study

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The aim of this study was to estimate the circulating plasma non-coding RNAs (ncRNA) profile in heart transplant recipients (HTRs) with acute cardiac allograph rejection. The study enrolled 28 HTRs (aged 18-74 years), who underwent heart transplantation in the Almazov National Medical Research Center from 2012 to 2023. A total of 28 plasma samples were collected concurrently with endomyocardial biopsies (EMB), which were performed at time points defined by standard clinical protocols. Transplant rejection (TR) was diagnosed based on histopathological and immunological evaluation of EMB, following current ISHLT grading criteria within 10 years post-transplant. Consequently, four groups were formed: no rejection, cellular rejection, humoral rejection, and patients with TCAD. Small RNA libraries were generated using TruSeq Small RNA Library Prep Kit (Illumina, USA) according to manufacturer's recommendations. Non-coding RNA were detected in all comparison groups and miRNAs being the most represented. Venn diagram showed that there are 73% (317) of miRNAs shared between all groups studied. In the non-rejection and humoral rejection groups, 5% (22) unique miRNAs were identified. Patients with TCAD had 2% (8) unique miRNAs, while patients with cellular rejection had 1% (4). Differential analysis and heat maps did not reveal a clear miRNAs profile for the comparison groups. Significant differences in four miRNAs (hsa-miR-193b-3p, hsa-miR-5588-5p, hsa-miR-193b-5p, hsa-miR-483-5p) were found between patients without rejection and those with humoral rejection. The obtained results suggest that miRNAs may serve as potential biomarkers for the development of acute humoral rejection. Further verification is required, considering time since heart transplantation.

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