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mircoRNA-3162-3p is a potential biomarker to identify new infections in HIV-1-infected patients

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Abstract

Background Identification of new HIV infections (HIV incidence) is critical for monitoring AIDS epidemic and assessing the effectiveness of intervention measures. However, current methods for distinguishing new infections from newly diagnosed HIV-1 patients are still imperfect. We explored utilizing miRNAs as biomarker to identify HIV new infections.

Methods According to the HIV-1 status and the estimated duration of infection (EDI), we enrolled participants and divided them into three groups: healthy control, new infection (within 1 year), and old infection (longer than 1 year). Participants were assigned into screening set or validation set. miRNA microarray was performed in screening set and the differentially expressed miRNAs were screened out. The differentially expressed miRNAs were further confirmed in validation set and HIV-1 IIIB-MT2 cells infection system.

Results In screening set, 5 miRNAs including miR-1291, miR-3609, miR-3162-3p, miR-874-5p and miR-4258 were screened out for their differential expression in plasma among three groups. In validation set, down- trend of miR-3162-3p was validated from healthy control, new infection to old infection groups. In HIV-1 IIIB-MT2 system, the levels of miR-3162-3p also decreased along with infection duration *in vitro*. Sensitivity and specificity for miR-3162-3p to distinguish new infection from old infection were 100.0% and 71.43%, respectively, with the cut-off value of 0.916.

Conclusion miR-3162-3p in plasma could be a potential microRNA biomarker to identify HIV new infections in HIV-1 infected patients.