Progress in Microbes and Molecular Biology • Volume 6, Issue 1 • 4 January 2023 • Article number a0000343

Document type
Article

Source type
Journal

ISSN
26371049

DOI
10.36877/pmmb.a0000343

Publisher
HH Publisher

Original language
English

View less

A Panel of Three MicroRNA Signatures as a Potential Biomarker for CRC Screening Based on Stages and Functional Prediction Using Bioinformatic Analysis

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Abstract

(1) Background: MicroRNA (miRNA) has been linked to colorectal cancer (CRC) tumorigenesis due to its post-transcriptional mechanism in targeting cancer-associated genes. Although miRNAs appear to be promising screening biomarkers, functional prediction analysis is required to shed light on their role in CRC tumorigenesis. Therefore, this study aims to identify the significantly deregulated miRNAs in CRC tumorigenesis. (2) Methods: Three upregulated miRNAs (hsa-miR-20a-5p, hsa-miR-21-5p, and hsa-miR210-3p) from 14 significant differentially expressed miRNAs (DEMs) were chosen from microarray profiling to be validated in plasma. Bioinformatics analyses showed that these miRNAs generally contributed to tumorigenesis, but only hsa-miR-20a-5p and hsa-miR-21-5p were specifically linked to CRC. Only two miRNAs showed a positive correlation when compared to their expression in plasma. However, further analysis showed that all three miRNAs in plasma were significantly difference between

the early and advanced stages of CRC. ROC curve analysis was used to evaluate miRNAs' diagnostic performance in the early and advanced stages. (3) Results: Collectively, hsa-miR-20a-5p showed the highest discriminative value (AUC= 0.82, sensitivity = 86%, and specificity= 88%) in discriminating early CRC, while both hsa-miR-21-5p and hsa-miR-210-3p give a perfect performance for advance CRC. In addition, the performance of all miRNAs' combinations also gives a perfect performance for diagnosis in both early and advanced CRC, except the combination of hsa-miR-20a-5p and hsa-miR-210-3p. (4) Conclusions: A few potential miRNA panels as CRC biomarker is needed for better prediction of disease. The reflective circulating miRNAs can be contributed to by minimal invasive screening tools.

Author keywords

Biomarker; Colorectal cancer (CRC); MicroRNA (MiRNA); Receiver Operating Curve (ROC); Target prediction

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