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A bioinformatics analysis of Runx1 and its related miRNA Involved in Colorectal Cancer metastases

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Background

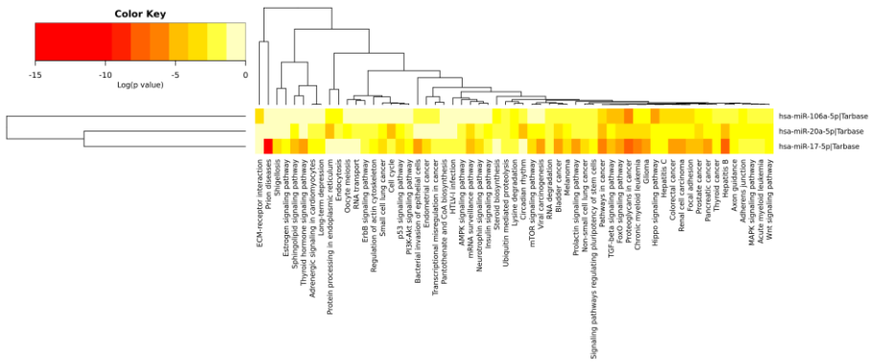
Colorectal cancer is one of the most frequent carcinoma worldwide; and it is also one of the most important causes of death in the world. MicroRNAs (miRNAs or miRs) are small single-stranded non-coding RNA molecules which play key roles as master regulators of many biological processes altered in cancers such as colorectal cancers. Additionally, they can be used to diagnose, treat and monitor cancer. Here, we aimed to examine the crosslink between some of these miRNAs and a specific gene in colorectal cancer. The association between the expression of genes and miRNAs is significant, and changes in their expression levels can onset cancer.

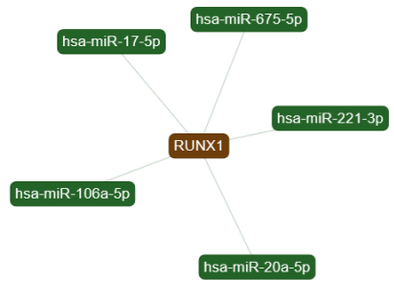
Materials and Methods

Runt-related transcription factor 1 (RUNX1) acts as an oncogene in tumors. Abnormal upregulation of RUNX1 has been suggested to contribute to the carcinogenesis of colorectal cancer. By using the miRTargetLink database, we found out that RUNX1 is strongly associated with certain miRNAs. Finally, using the Diana miRpath V.2 algorithm , we found out that it has a significant relationship with miR-106a-5p, miR-20a-5p and miR-17-5p.

Results

Data analysis showed that mir-106a-5p, mir-20a-5p and mir-17-5p were significantly associated with the Runx1 gene, which could be associated with the TGF-beta, p53, and foxO signaling pathways. Due to the effect of TGF-β signaling pathway on cell migration, this can affect cancer metastasis.





Conclusion

These results revealed RUNX1 could regulate colorectal cancer migration via TGF-β signaling pathway, and RUNX1 might serve as a potential target for preventing colorectal cancer metastasis.

References

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