Original Paper

Bioinformatics analysis to predict potential Micro-RNAs inhibiting processes of angiogenesis in cancer

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Abstract

Background and Objective: Tumor size results in hypoxic and acidic environment leading to the production of several types of growth factors required for the formation of blood vessels. Afterwards, metastasis of cancerous cells occurs via blood vessels. Therefore angiogenesis inhibition can be a new way of cancer treatment. This study was done to determine the bioinformatics analysis to predict potential Micro-RNAs inhibiting processes of angiogenesis in cancer.

Methods: In this descriptive study, micro-RNAs that are able to connect to MMP genes involved in tumor angiogenesis (MMP1-2-3-8-9-10-11-13) were detected using miRwalk database. Effective Micro-RNAs selection was based on the number of binding sites in 3'UTR genes. MicroRNA data base was used to find sample base pairing sequences.

Results: mir-1302, mir-516a, mir-512, mir-511, mir-516b and mir-548 were determined with the most number of binding sites in genes involved in angiogenesis.

Conclusion: MicroRNAs are worthy options for cell culture and laboratory examination in order to find new ways to prevent the development of cancer by angiogenesis inhibition.

Keywords: Bioinformatics, Angiogenesis, MMPs, MicroRNA

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