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MiR-485-3p И miR-4728-5p КАК СУПРЕССОРЫ ОПУХОЛЕВОГО РОСТА В ПАТОГЕНЕЗЕ КОЛОРЕКТАЛЬНОГО РАКА^{1, 2}

© 2022 г. Т. Gurer^{a, *}, А. Aytakin^{b, **}, Е. Caki^a, S. Gezici^c^aDepartment of Biology, Faculty of Science and Literature, Gaziantep University, Gaziantep, 27310 Turkey^bDepartment of General Surgery, Faculty of Medicine, Gaziantep University, Gaziantep, 27310 Turkey^cDepartment of Medical Biology and Genetics, Faculty Medicine, Gaziantep University, Gaziantep, 27310 Turkey

*e-mail: turkanayte@hotmail.com

**e-mail: taytekin@gantep.edu.tr

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МикроРНК – класс малых некодирующих РНК, главные функции которых связаны с развитием и прогрессией колоректального рака (CRC), где они действуют как супрессоры опухолевого роста или онкогены. Изучена роль микроРНК miR-485-3p и miR-4728-5p в патогенезе CRC. Образцы опухолей и прилегающих морфологически нормальных тканей получены от 59 больных CRC (37 образцов рака толстой кишки и 22 образца рака прямой кишки). Профили экспрессии miR-485-3p и miR-4728-5p определяли, используя количественную обратную транскрипцию с последующей полимеразной цепной реакцией. Регуляторные сети факторов транскрипции (TF), связанных с микроРНК, конструировали с использованием TransmiR v2.0. Регулируемые TF гены-мишени определяли, используя Human.mirFFL.DB и TRRUST v2.0, функциональную аннотацию и анализ обогащения с помощью DIANA-mirPath v3.0 и -Tarbase v7.0. Показано значительное снижение уровней экспрессии miR-485-3p, и miR-4728-5p в тканях CRC (кратность изменений составила 0.42 ± 0.70 и 0.59 ± 1.06 соответственно; $p = 0.000$). С другой стороны, более низкие уровни экспрессии miR-485-3p выявлены и в прямой, и в толстой кишке. Более того, снижение уровней экспрессии miR-4728-5p коррелировало с увеличением возраста. Эти различия были статистически незначимыми (FDR-значения p составили 0.126 и 0.168 соответственно). С помощью биоинформатического анализа идентифицированы TF, связанные с miR-485-3p и miR-4728-5p. Некоторые из этих TF, а именно, AR, CREB1, SEBPB, FOXA1, GTF2I, MAZ, NCOR2, NFIC, NRF1, SIN3A, SREBF1, SREBF2, TP53 и YY1, по-видимому, ассоциированные с CRC, выбраны для конструирования потенциальных мишеней сетей микроРНК-TF-ген для ранней диагностики и терапии CRC. Анализ обогащения путей показывает, что сигнальный путь Hippo строго регулируется miR-485-3p. Предполагается, что снижение экспрессии miR-485-3p и miR-4728-5p может быть ассоциировано с развитием CRC.

Ключевые слова: колоректальный рак, микроРНК ОТ-ПЦР, опухолевые супрессоры, факторы транскрипции, биоинформатика

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miR-485-3p AND miR-4728-5p AS TUMOR SUPPRESSORS IN PATHOGENESIS OF COLORECTAL CANCER

T. Gurer¹*, A. Aytakin²*, E. Caki¹, and S. Gezici³

¹ Department of Biology, Faculty of Science and Literature, Gaziantep University, Gaziantep, 27310 Turkey

² Department of General Surgery, Faculty of Medicine, Gaziantep University, Gaziantep, 27310 Turkey

³ Department of Medical Biology and Genetics, Faculty of Medicine, Gaziantep University, Gaziantep, 27310 Turkey

*e-mail: turkanayte@hotmail.com

**e-mail: taytekin@gantep.edu.tr

MicroRNAs (miRNAs) are a class of small noncoding RNAs that have major functions in the development and progression of colorectal cancer (CRC) as tumor suppressors or oncogenes. The aim of the current research was to assess the role of miR-485-3p and miR-4728-5p in the pathogenesis of CRC. In this study, fresh tumor and adjacent non-tumor tissue samples were obtained from a total of 59 CRC patients, 37 from colon and 22 from rectum. The expression profiles of miR-485-3p and miR-4728-5p were determined using qRT-PCR. miRNA-related transcription factor (TF) regulatory networks were constructed using the TransmiR v2.0, TF-regulated target genes were determined using the Human.mirFFL.DB and TRRUST v2.0, functional annotation and pathway enrichment analyses were performed using DIANA-mirPath v3.0 and -Tarbase v7.0. The results demonstrated that the expression levels of both miR-485-3p and miR-4728-5p were

very significantly downregulated in CRC tissues (fold changes = 0.42 ± 0.70 and 0.59 ± 1.06 , respectively; both $p = 0.000$). On the other hand, lower expression levels of miR-485-3p were detected in the both rectum and colon. Moreover, the decrease in the expression levels of miR-4728-5p was correlated with increasing age. However, these differences were not statistically significant according to the FDR-related p -values (0.126 and 0.168, respectively). By bioinformatics analyses, miR-485-3p and miR-4728-5p-related TFs were identified. Some of these TFs, namely, AR, CREB1, CEBPB, FOXA1, GTF2I, MAZ, NCOR2, NFIC, NRF1, SIN3A, SREBF1, SREBF2, p53 and YY1, appeared to be associated with CRC and were, therefore, selected to construct miRNA–TF-gene networks of potential targets for the early diagnosis and treatment of CRC. Pathway enrichment analysis indicated Hippo signaling pathway as heavily regulated by miR-485-3p. It seems that the decrease in expression levels of miR-485-3p and miR-4728-5p might be associated with development of colorectal cancer.

Keywords: colorectal cancer, qRT-PCR, microRNA, tumor suppressor, transcription factor, bioinformatics