Single nucleotide variation analysis in microRNA target regions in colorectal cancer

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Colorectal cancer is the third most common cancer in the world. In 2012, The Cancer Genome Atlas Network Consortium reported that different colorectal tumor samples have distinct genetic alterations. MicroRNA (miRNA) is a key player in the control of eukaryotic gene expression. This family consists of small noncoding RNAs that prevent translation of target messenger RNAs (mRNAs), thus reducing the expression of the gene encoded in the mRNA. The region responsible for the miRNA target recognition is termed seed. Single nucleotide polymorphism (SNP) is commonly found in different types of cancer and this alteration is characterized by a change of a single nucleotide at a particular position in the genome. SNPs have been described in several regions associated with miRNAs in tumor samples, such as seed regions. This project intends to evaluate, qualitatively and quantitatively, the frequency of SNPs in miRNAs target regions and their adjacent genomic regions in colorectal cancer samples. Small RNA high throughput sequencing data of 5 rectal tumor samples and matched normal tissue were obtained in TCGA database (downloaded: 01/2016). SNP call was performed using the VARSCAN2 and information concerning the target regions of miRNAs were obtained in the TargetScan database. We investigated SNP effect in four different regions: seed region, miRNA pairing region outside seed region, 200 nucleotides upstream target region and 200 nucleotides downstream target region. SNPs in several genes were found common to all patients analyzed, as follows: 17 genes presented alterations in the target seed region, while 407 genes in the region 200 nucleotides upstream, 39 genes in the microRNA region outside seed and 384 genes in the region 200 nucleotides downstream. These preliminary results motivate us to expand this analysis to other 25 paired colon adenocarcinoma samples; we believe this project will help improve our understanding of the changes in microRNA regulation and its role in colorectal cancer. The effects of these modifications still need further study so that it can be possibly used in the future in therapy and cancer prevention.

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