



REG4, CEACAM5 and OLFM4 are among the most recurrently fused genes in patients with colorectal cancer

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Abstract

Backgrounds: Colorectal cancer (CRC) is one of the leading causes of cancer-related deaths in both men and women, all around the world. Since current treatments are not really effective, molecular targeted therapy would be advantageous for CRC therapy. Next generation sequencing technologies provide new insight into the dynamics of cancer development. In this work, we focused on molecular dynamics of mRNAs at transcription level to identify some of the recurrent fusion genes in colorectal cancer.

Materials and Methods: This study was carried out using RNA-seq data from NCBI data bank (PRJEB27536 bio project). For this purpose, a total of 60 matched samples were analyzed with FusionCatcher V.1.20. A list of fusions was then constructed for all the cancer samples, and finally the frequency of recurrent fusions was evaluated.

Results: REG4, CEACAM5 and OLFM4 were the most recurrently fused genes present in cancer samples in comparison with their normal counterparts. REG4 is a very hyperactive mRNA in terms of transcriptional dynamics and is involved in the most frequent fusions in cancer such as PIGR-REG4, MUC2-REG4 and KRT8-REG4. Other recurrent fusions were CEACAM5-MUC2, CEACAM5-KRT8 and OLFM4-PIGR.

Conclusion: Our study revealed that REG4, CEACAM5 and OLFM4 are among the most frequent fusions found in our cancer data. The oncogenic role of these fusions can be investigated with further functional analysis. Some of these fusions can be druggable and might be good candidates for molecularly targeted therapy.

Keywords: Colorectal cancer, Transcriptome analysis, Fusion transcripts, Recurrent fusion