



Comparative Quantitation of KDR Gene Signature in Parallel Tumor Tissues and Adjacent Non-tumor Counterparts in Colorectal Cancer

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Abstract

Introduction & Aim: Colorectal cancer (CRC) is one of the most common types of cancers in the world. Vascular endothelial growth factor (VEGF) has an essential role in tumor angiogenesis and involved in the growth and progression of CRC. KDR (VEGFR2) is the main pro-angiogenic receptor for VEGF and seems to play an important crucial role in tumor angiogenesis. The aims of this study were to measure relative expression of KDR gene in tumor and marginal tissues in CRC patients and to assay the correlation of KDR mRNA expression level with clinico-pathological factors.

Methods: 47 Human colorectal cancer tissues and 47 non-tumor (marginal) tissues were obtained. After RNA extracting and then cDNA synthesizing by RT-PCR, the mRNA expression levels of KDR gene were assessed using real-time PCR. For data analysis, The Relative Expression Statistical Tool (REST) and SPSS software were used.

Results: Analysis showed that KDR mRNA expression level was similar between tumor tissues and adjacent non-tumor counterparts ($p=0.059$). Also, there was no association between mRNA expression level of KDR gene and Clinicopathological features.

Conclusions: Although our results demonstrated that KDR gene is expressed in colorectal cancer patients, but the mRNA expression level of KDR has no prognostic value in CRC. Hence, whether this gene might be useful as a clinically reliable predictive marker remains to be solved.

Keywords: Colorectal Cancer, Expression, KDR, Real-Time PCR