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SIRT1 Gene Polymorphisms and Its Protein Level in Colorectal Cancer

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Abstract : Colorectal cancer (CRC) is a major cause of mortality and morbidity and accounts for over 9% of cancer incidence worldwide. Silent information regulator 2 homolog 1 (SIRT1) gene is located in the nucleus and exert its effects via modulation of histone and non-histone targets. They function in the cell via histone deacetylase (HDAC) and/or adenosine diphosphate ribosyl transferase (ADPRT) enzymatic activity. The aim of this work was to study the relationship between SIRT1 polymorphism and its protein level in colorectal cancer patients in comparison to control cases. This study includes 2 groups: thirty healthy subjects (control group) & one hundred CRC patients. All subjects were subjected to: SIRT-1 serum level was measured by ELISA and gene polymorphisms of rs12778366, rs375891 and rs3740051 were detected by real time PCR. For CRC patients clinical data were collected (size, site of tumor as well as its grading, obesity) CRC patients showed high significant increase in the mean level of serum SIRT-1 compared to control group ($P<0.001$). Mean serum level of SIRT-1 showed high significant increase in patients with tumor size ≥5 compared to the size < 5 cm ($P<0.05$). In CRC patients, percentage of T allele of rs12778366 was significantly lower than controls, CC genotype and C allele C of rs 375891 were significantly higher than control group. In CRC patients, the CC genotype of rs12778366, was 75% in rectosigmoid and 25% in cecum & ascending colon. According to tumor size, the percentage of CC genotype was 87.5% in tumor size ≥5 cm. Conclusion: serum level of SIRT-1 and T allele, C allele of rs12778366 and rs 375891 respectively can be used as diagnostic markers for CRC patients.

Keywords : CRC, SIRT1, polymorphisms, ELISA
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