## RIPK1 gene polymorphism as a prognostic marker for survival in patients with colorectal cancer

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Background: Since apoptosis plays a key role in cancer progression, we hypothesized that single nucleotide polymorphisms (SNPs) of apoptosis-related gene can affect survival after curative resection in patients with colorectal cancer.

Patients and methods: Three hundred and ninety seven patients with colorectal cancer who underwent surgery with curative intent were enrolled in the present study. The genomic DNA was extracted from fresh colorectal mucosal tissue, and the 19 SNPs of 15 apoptosis-related genes (CASP3, CASP6-10, FAS, FAS ligand [FASLG], TNSFR1A, TNSFR10B, RIPK1, BCL2, BCL2 ligand [BCL2L], TP53, and PTGS2) were determined using a PCR-RFLP assay. Results: The median age of the patients was 63 years (range, 21-85), and 218 (54.9%) patients had colon cancer and 179 (45.1%) patients rectal cancer. Pathologic stages after surgery were as follows: stage 0/I (n=86, 21.7%), stage II (n=146, 36.8%), stage III (n=145, 36.5%), and stage IV (n=20, 5.0%). Multivariate survival analysis including pathologic stage, differentiation, age, and CEA level showed that relapse-free survival for the patients with the GA+AA genotype of RIPK1 (Receptor interacting serine/threonine kinase 1) +83G>A (rs2272990) was worse than for the patients with the GG genotype (hazard ratio [HR]=1.66, 95% confidence interval [CI]=1.03-2.68, p=0.038). However, no associations were observed between the polymorphisms and overall survival (OS) in a multivariate analysis.

Conclusion: RIPK1 gene polymorphism can be considered as a possible prognostic marker for survival after curative resection in patient with colorectal cancer.