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Association of common genetic variants with colorectal cancer risk in a Romanian sample

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Abstract
Recently, several genome-wide association studies identified and validated loci at which common genetic variants influence the risk of colorectal cancer. We aimed to test the association between eight SNPs and colorectal cancer in a Romanian case-control sample. We genotyped rs10795668, rs16892766, rs3802842, rs4444235, rs4779584, rs4939827, rs6983267, and rs9929218 and we statistically tested the association with the disease. Five SNPs (rs6983267, rs4939827, rs3802842, rs4444235, rs10795668) showed an association with colon and rectal cancer. Three of them proved to be statistically significant: rs6983267 and rs4939827 risk alleles were significantly associated with rectal cancers (p=0.031 and p=0.004 for homozygous, p=0.002 and p=0.005 for heterozygous). For rs3802842 we found a greater risk for colon than rectal cancer with an OR of 2.26(CI=1.04-5.88, p=0.040) for the dominant model. The rs4444235 confirmed the risk for both homozygous and heterozygous carriers, with the greatest ORs of 1.49(CI=0.61-3.61) for heterozygote. For rs10795668 we found an increased risk for rectum cancer vs. controls with an OR of 1.46(CI=0.66-3.21), and for rectum cancer vs. colon cancer (OR=2.19; CI=0.87-5.55). This is the first Romanian study that confirms previously-identified associations with colorectal cancer risk for five out of eight SNPs investigated and underlines the necessity of extensive replication using larger samples.
Key words: colorectal cancer, SNPs, association study

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