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Association of PARK2 promoter polymorphisms and methylation with colorectal cancer in North Indian population

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Abstract

Different diseases have been associated with PARK2/PACRG overlapping promoter polymorphisms (rs2276201 and rs9347683) in the recent past. However association of these polymorphisms with cancer remain elusive till date. Thus in this study we evaluated association between these polymorphisms and colorectal cancer (CRC) incidences among North Indians. Genomic DNA was isolated using venous blood of 400 unrelated subjects (200 CRC cases and 200 healthy controls) of North Indian origin. Both SNPs were genotyped using PCR-RFLP method. Promoter methylation status in tumor DNA was checked using MS-PCR. Statistical analysis was performed using SPSS-17 software. *In-silico* predictions for transcription factor binding were performed using "PROMO" a freely available online tool. SNP rs2276201 showed statistically significant difference (P=0.047) among cases and controls while rs9347683 did not (P=0.113). The TC genotype (OR: 1.855, 95% CI: 1.021-3.369, P= 0.043), CC genotype (OR: 1.617, 95% CI: 1.042-2.510, P= 0.032), TT vs CT+CC genetic model (OR: 1.60, P= 0.0158) and allelic model (OR: 1.3931, 95% CI: 1.0498-1.8485, P= 0.0214) of rs2276201 showed significant risk for CRC. For rs9347683 AC genotype (OR: 1.604, 95% CI: 1.019-2.523, P= 0.041) and AA vs AC+CC genetic model (OR: 1.57, P= 0.039) showed significant risk. Haplotype CC provided significant risk (OR: 1.618, 95% CI: