

## Genetic Analysis of colorectal carcinoma using high throughput SNP genotyping technique within the population of Jammu and Kashmir

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### Abstract

#### Background:

SNP genotyping has become increasingly more common place to understand the genetic basis of complex diseases like cancer. SNP-genotyping through massARRAY is a cost-effective method to quantitatively analyse the variation of gene expression in multiple samples, making it a potential tool to identify the underlying causes of colorectal carcinogenesis.

#### Methods:

In the present study, SNP genotyping was carried out using Agena massARRAY, which is a cost-effective, robust, and sensitive method to analyse multiple SNPs simultaneously. We analysed 7 genes in 492 samples (100 cases and 392 controls) associated with CRC within the population of Jammu and Kashmir. These SNPs were selected based on their association with multiple cancers in literature.

#### Results:

This is the first study to explore these SNPs with colorectal cancer within the J&K population. 7 SNPs with a call rate of 90% were selected for the study. Out of these, one SNP i.e. rs2229080 of DCC was found to be significantly associated with the current study and 6 were non-significantly associated with CRC within the studied population. The allelic OR observed for the variant rs2229080 of DCC was 1.5 (1.1-2.3 at 95% CI), p value = 0.02.

### Conclusion:

This is the first study to find the relation of Genetic variants with the colorectal cancer within the studied population using high throughput massARRAY technology. It is further anticipated that the variants should be evaluated in other population groups that may aid in understanding the genetic complexity and bridge the missing heritability.

### Keywords:

Colorectal Cancer; Single Nucleotide Polymorphism (SNPs), MassARRAY; Jammu and Kashmir