(Notification) 528/2023 **Date 25/01/2023**

Name: Mohammad Taleb Abdelrazeq Mohsen

Under the supervision of: *Prof. Seemi Farhat Basir* (Supervisor) *& Dr. Mausumi Bharadwaj* (Co-Supervisor)

Thesis title: Study on Single Nucleotide Polymorphisms in microRNAs and their correlation with susceptibility to Colorectal cancer in Indian population

Department of Biosciences
Faculty of Natural Sciences
Jamia Millia Islamia
New Delhi-110025

Findings

Key words: Colorectal cancer, microRNAs, *miR-146a*/rs2910164, *miR-196a2*/rs11614913, *miR-499a*/rs3746444

Based on CRC patient's tissues, a total of 153 CRC patients were recruited. However, 10 of them were excluded and considered as dropouts. Surgically resected tissues comprising of 143 tumor tissues and equal number of adjacent control regions of primary sporadic CRC were collected. Genomic DNA isolation followed by genotyping via PCR-RFLP, and the results were confirmed by sequencing. For genotyping and clinicopathological statistical analyses, SPSS Statistics, excel 365 version and GraphPad_Prism_8.0.2.263 were used. Chi-square, ANOVA, 95% CI, P value, and OR tests were performed.

Analysis of polymorphic T→C (rs3746444) has revealed that TT genotype, T allele and T dominant model were associated with increased risk of CRC. While CC genotype and recessive model were associated with reduced risk of CRC. Further analysis of synergistic relation has revealed significant decreased CRC risk in the presence of genetic combinations of *miR-146a/miR-499*: GG/CC & GC/CC and *miR-196a2/miR-499*: CC/CC & TC/CC.

rs11614913 (C→T) analysis has revealed that TC genotype was associated with lower CRC risk. However, all other genotypes and allelic models were not associated to the risk of CRC. In addition, the genetic combinations with *miR-146a* [GG/TC] and *miR-499* [CC/CC & TC/CC] have shown decreased CRC risk significantly.

rs2910164 (G→C) analysis has revealed that GC genotype was associated with decreased risk of CRC, while G allele and recessive model (GC+CC) were associated with increased CRC risk. Moreover, combined analysis of *miR-146a/ miR-196a2* [GG/TC] and *miR-146a/miR-499* interactions [GG/CC and GC/CC] were associated significantly with decreased CRC risk.

Clinicopathological features in association with rs2910164, rs11614913 and rs3746444 did not show significant correlation, except for rs2910164/CC genotype, which was linked with increased CRC risk in non-smokers and G dominant allele has shown association with increased risk in non-vegetarian patients.

In conclusion, this study is the first of its type in Indian population, incorporating tumor tissue and their adjacent normal controls to study rs2910164, rs11614913 and rs3746444. Results provide the evidence that the studied SNPs, individually and synergistically are correlated with CRC risk and may have the prospect emerge as CRC biomarkers.