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Contribution of microRNA-149, microRNA-146a, and microRNA-196a2 SNPs in colorectal cancer risk and clinicopathological features in Tunisia

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ABSTRACT

Background and aim: Colorectal cancer (CRC) is a worldwide leading cause of mortality. Genetic studies have associated single nucleotide polymorphisms in genes encoding microRNAs with CRC risk but results are mostly inconclusive across variable ethnicities. In this study, we investigated the association of *hsa-mir-149* rs2292832 C/T, *hsa-mir-146a* rs2910164 G/C and *hsa-mir-196a2* rs11614913 C/T and explored their roles in clinicopathological features of CRC progression in an Eastern Tunisian cohort.

Subjects and methods: Three hundred thirteen subjects were enrolled in our retrospective study including 152 CRC cases and 161 controls. Genotyping was assayed by RFLP-PCR (Restriction Fragment Length Polymorphism-Polymerase Chain Reaction) method. SPSS v.18.0, R and SNP Stats online software performed statistical analysis.

Results: Significantly higher *hsa-mir-149* C/T rs2292832 minor allele frequency was associated with increased risk of CRC [p=0.03; OR= 1.54 (1.08-2.19)]. In addition, significant crude associations of *hsa-mir-149* C/T rs2292832 polymorphism were detected under codominant, dominant and additive models of inheritance. After adjusting for covariates and performing FDR correction, these associations did not remain. No associations were detected for *hsa-mir-146a* G/C rs2910164 and *hsa-mir-196a2* C/T rs11614913. When performing stratified analysis of clinicopathological features according to genotypes, a significant association (p=0.004) was found between *hsa-mir-146a* G/C rs2910164 and tumour differentiation grade. Regression analysis according to CRC progression features had demonstrated a trend toward significance in overdominant model of inheritance for *hsa-mir-149* C/T rs2292832 with a protective effect [p=0.05 ; OR=0.51 (0.26-1.02)].

Conclusion: Hsa-mir-149 C/T rs2292832 and *hsa-mir-146a* G/C rs2910164 may influence CRC risk in an ethnicity-dependent manner by interfering with CRC progression parameters in Tunisian cohort.

List of abbreviations