Investigating the Association of rs6982267 Polymorphism in (CCAT2) long non-coding RNA with Gastric Cancer Risk

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Introduction: Gastric cancer (GC) is classified into cardia and non-cardia types depending on tumor site. Various epigenetic and genetic variations are implicated in gastric carcinogenesis. CCAT2, a long non coding RNA (lncRNA) in the 8q24 has been attributed to the progression of multiple human cancers. Its up regulation has been reported in gastric cancer, making it a potential biomarker for GC diagnosis and prognosis. Accumulating evidence suggests the functionality of lncRNAs in cancer development and introduces their variations as genomic biomarkers for determining cancer predisposition and treatment outcomes. rs6983267 is a single nucleotide polymorphism within CCAT2 lncRNA that its association with GC has been reported in some ethnic populations, although, its mechanism of action remain unclear. Therefore, present study has been done to investigate the association of rs6983267 with different types and histological grades of GC.

Materials & Methods: TaqMan genotyping assay was used to determine the genotypes of 68 patient and 82 control DNA samples. GC samples composed of 38 non-cardia and 30 cardia types. Chi2 test was used to find association of this SNP with gastric cancer susceptibility. Stratified analysis was also done for association in cardia and non-cardia and different grades of GC.

Results: TaqMan genotyping assay was used to determine the genotypes of 68 patient and 82 control DNA samples. GC samples composed of 38 non-cardia and 30 cardia types. Chi2 test was used to find association of this SNP with gastric cancer susceptibility. Stratified analysis was also done for association in cardia and non-cardia and different grades of GC.

Conclusion: Our results suggest that G allele is more frequent in more aggressive tumors, pointing to its involvement in tumor invasion and metastasis, but it needs a greater sample size to be able to draw a conclusive conclusion