Abstract

A negative regulator of the tumor protein p53 is encoded by the murine double minute 2 (*MDM2*) gene. It has been demonstrated that SNP309 T > G, a single nucleotide polymorphism (SNP) in the *MDM2* promoter, affects *MDM2* protein expression and speeds up the development of tumors. In this study, we aim to evaluate the association of *MDM2* SNP309 (rs2279744) and oxidative stress with the risk of hepatocellular carcinoma (HCC) development among Pakistani population. *MDM2* SNP309 polymorphism was investigated in 25 confirmed subjects with HCC and 25 cancer-free control subjects, using DNA extraction and PCR sequencing methods. SHEsis software was used to analyze the allelic and genotypic frequencies. The overall results of our study indicated that the allele frequencies of case subjects (T=0.300, G=0.700) were significantly different from those of control subjects (T=0.800, G=0.200) (p=0.0005). The genotypic frequency of GG of SNP309 in patients with HCC (GG=0.520) was significantly higher than that in control individuals (0.002) which showed G. We observed that compared with the TT genotype, the genotypes containing G allele [TG (OR, 2.19; 95% CI, 1.18–4.07; p = 0.013) or GG (OR, 3.63; 95% CI, 1.65–8.00; p = 0.001)] were associated with significant increased susceptibility to HCC. Together with the biochemical parameters being examined, oxidative stress is assessed. Patients with HCC showed reduced activity of the antioxidant enzymes glutathione peroxidase, superoxide dismutase, and catalase. It demonstrates the strong correlation between oxidative stress and HCC. Our findings suggest that *MDM2* promoter SNP309 G allele and oxidative stress is associated with presence of HCC in Pakistani population.