Cell cycle checkpoint gene Tumor protein 53 (*Tp53*) has shown a drastic impact on the development of Oral cancer (OC) because it plays a crucial regulatory role in a number of cell signaling pathways. This study intended to determine how individuals with oral squamous cell carcinoma (OSCC) and a control group differed in their methylation patterns of the *Tp53* gene's promoter region. One hundred and one unrelated OSCC patient’s, clinically diagnosed at the Shaukat Khanum Memorial Hospital and Research center (SKMCH&RC), Lahore, Pakistan, and one hundred and one unrelated healthy controls (HC) samples from different geographic regions of Pakistan, were included in this study. Methylation status of the promoter region of the *Tp53* gene was detected by methylationspecific-polymerase chain reaction (MS-PCR). The correlation between *Tp53* gene promoter methylation profiles and clinic pathalogical characteristics were examined using the chi- square test. Analysis of MSP revealed that there was 42.57% methylation, 54.45% partial methylation and 2.97% methylation of *Tp53* gene in oral cancer. Whereas 34.5% methylation, 11.8% partial methylation and 1.8 % unmethylation was observed in *Tp53* gene of HC. The p-value is .00094. The result is significant at $p < .05$. The results show that promoter region methylation of the *Tp53*gene was not associated with OSCC development in the studied patient group. In addition, the methylation status of the *Tp53* gene promoter was found to be related to age, gender or tumor stage.