Association of an insertion/deletion polymorphism in IL1A 3'-UTR with risk for cervical carcinoma in Chinese Han Women.

Emerging evidence has demonstrated that polymorphisms of interleukin-1 (IL-1) may be involved in human tumorigenesis by regulating the production of this cytokine. Previous studies have investigated the association between two genetic variants (rs3783553 and rs17561) of IL1A and many diseases. The present study was conducted to evaluate whether these two variants are associated with cervical carcinoma (CC). These two polymorphisms were genotyped in 319 CC patients and 424 healthy controls by polymerase chain reaction polyacrylamide gel electrophoresis (PCR-PAGE) and polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). Significantly reduced CC risk was observed to be associated with the insertion allele of rs3783553 (P=0.014, OR=0.71, 95% CI=0.57-0.88). Stratification analysis based on different certain clinical features showed that patients with the heterozygous genotype were associated with a reduced predisposition advancing to clinical stage II-III or developing non-squamous cell carcinoma. Furthermore, patients with the insertion homozygous genotype were also associated with a reduced risk to have a poor tumor differentiation. No significant association was observed between rs17561 and CC. The present study provided evidence that the rs3783553 in IL1A 3'-UTR is inversely associated with CC risk, suggesting an important role IL-1α may play in cervical carcinogenesis.