Comparative analysis of Mitochondrial DNA (D-loop) variations associated with cervical cancer

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ABSTRACT

Cervical Cancer is the second most common gynecologic malignancy and constitute for significant public health problem globally. Several factors such as infections with Human Papilloma Virus (HPV), Human Immuno Deficiency Virus (HIV), poor personal hygiene, usage of oral contraceptives and genetic risk factors lead to disease pathogenesis. The human mitochondrial DNA (mtDNA) is a double stranded circular genome of 16569 Bp and containing 37 genes. Further, the mutation rates in mtDNA are 10 times higher than that of nuclear DNA. Genetic variations were observed in liver, breast, gastric, colorectal and cervical cancers in the highly variable non-coding displacement (D) loop region in the forms of insertions, point mutations, deletions and microsatellite variabilities. MtDNA is the target for high level alterations in various types of cancers and high incidences of somatic mutations have been reported in cervical malignancy. In this current study, we have analyzed the mitochondrial genomic sequences with reference to cervical cancer from NCBI-Nucleotide databank submitted from different geographical regions (Argentina, Mexico, U.S.A, and India) which were submitted from 1/1/2001 till 31/12/2017 along with the sequences from our study in South India. We have identified significant variations in the analyzed mtDNA genome sequences. The mtDNA mutations are hot spots and have the potential of being used as early biomarker in addition with available methods for improved cervical cancer diagnosis.

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