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## Significance of mitochondrial and detoxifying nuclear gene polymorphisms related to gastric cancer susceptibility in Mizo-Mongloid population, Northeast India

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To investigate the possible role of mtDNA mutations in stomach cancer, the mitochondrial control (900 bp) and COI (700 bp) regions were sequenced from stomach cancer patients in Mizoram. In the case of COI gene, 96 point mutations were found out of 103, including, one single-nucleotide deletion. Eighteen of these mutations resulted in amino acid substitution. Most of the mutations were C>T or T>C base substitutions. In case of control region, a novel 292A>AA... microsatellite instability was found. This particular microsatellite instability position is the TFI binding Y site for human mitochondrial DNA. This could be a potential pathogenic site for stomach carcinogenesis. We also found a novel 316C>CC... microsatellite instability in the conserved position of control region. Our study showed the simultaneous presence of both the GSTM1 and the GSTT1 null genotypes associated with gastric cancer. Concerning the GST P11le105Val (rs1695) gene polymorphism showed a significant relation to gastric cancer susceptibility or phenotype. The allele frequencies of the GSTT11 and M1 null genotypes were found for individuals with gastric cancer risk in the presence of H. pylori. Consumption of smoked-meat/ vegetables was also significantly associated with the increase in the incidence of gastric cancer. Mitochondrial and detoxifying nuclear gene alterations may attribute for stomach cancer risk in Mizoram, Northeast Indian population. The analysis of D-loop and COXI alterations might help to identify patients at high risk for stomach cancer diagnosis.

## **Biography**

Nachimuthu Senthil Kumar has completed his PhD during 1997 from Bharathiar University and Postdoctoral studies from Sun-Yat-sen University, China. He is the Professor of Biotechnology at Mizoram University, Aizawl. He has published more than 35 papers in reputed journals and serving as an editorial board member of repute. His area of specialization is molecular markers, mutation studies and bioinformatics.

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