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## Genetic Instability and Allelic Loss on Chromosome 2, 3 in Gastric Carcinomas

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We studied genetic instability with gastric carcinomas in 56 Korean patients. We screened RER(+/-) and LOH on the chromosome 2p, 3p, p53, APC, DCC, CDKN2 with 14 microsatellite markers by polymerase chain reaction analysis. The MSI phenotypes were observed in 20 of 53(38%) gastric carcinomas. Frequencies of RER(+) phenotypes and LOH were 13%(7 of 53) and 30%(16 of 53), respectively. Frequencies of MSI was detected in poorly differentiated adenocarcinomas(43%). Several cases(high frequency of MSI, MSI-H) showed RERs at many microsatellite loci simultaneously. Allelic losses (LOH) on chromosome 2p, 3p were shown in only MSI-H and non-RER cases. LOH frequency(7%) of D2S123 and D3S1038 loci was close to that of TP53 locus. Mismatch repair genes(hMSH2, hMLH1) on the chromosome 2p, 3p may not be responsible for microsatellite instability in gastric carcinomas. It is postulated that putative tumor suppressor genes in gastric carcinoma may be lie in 2p15-16 and 3p23-3pter.

**F814**The mitochondrial genome of Silkworm (*Bombyx mori*) : Complete DNA Sequence, Genome Organization, and Comparisons with Mitochondrial Genome of Other Insects.

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The entire 15,640 bp mitochondrial genome was cloned and sequenced from the silkworm *Bombyx mori*. With respect to the protein-coding genes(Cyt b, CO I-III, ATPase 6 and 8, ND 1-6, ND4L), rRNA(12S and 16S) genes and the A+T rich control region, the gene order was identical to that reported for other insects. There were significant differences, however, in the position and orientation of several tRNA loci. The overall nucleotide composition was heavily based toward adenine and thymine which accounted for 81.2% of all nucleotides. Comparisons were made with the mitochondrial genomes of other insects on the basis genome size and gene organization, DNA and putative amino acid sequence data, codon usage and bias, patterns of AT enrichment, and secondary structure of two ribosomal RNA gene.