

Z601 **The Complete DNA Sequences of the *Crassostrea gigas* mtDNA**

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We analyzed the genetic structure and the complete DNA sequences of the *C. gigas* mtDNA (Bivalvia: Mollusca) for evolutionary and population studies. The total length of the molecule was 18,224 base pairs. It contained 12 protein encoding genes (cytochrome C oxidase subunit I-III, NADH dehydrogenase 1-6, 4L, Cytochrome b, ATPase subunit 6) and two ribosomal RNA genes. The *C. gigas* does not contain a gene for ATPase subunit 8. The mitochondrial genetic code of *C. gigas* is proposed to be the same as that of invertebrate. Predicted initiation codons are ATG and ATA, and termination codons are TAA, TAG, and incomplete termination codon T. Only 18 putative tRNA genes were identified, although there was sufficient unassigned sequence to encode the remainder of the expected total of 22 tRNA genes. And one additional sequences in *C. gigas* mtDNA could be folded into structures resembling tRNA-Lys. The small subunit ribosomal RNA(12S rRNA) gene was duplicated, and two non-coding regions existed. The arrangement of genes in *C. gigas* mtDNA is remarkably unlike that found in any other known metazoan mtDNA.

Z602 **Tumor Necrosis Factor Receptor 2 (TNFR2) Exon 6 Single Nucleotide Polymorphism In Koreans**

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Tumor Necrosis Factor Receptor 2 (TNFR2) is a 75 kDa type I transmembrane protein expressed primarily on cells of hematopoietic lineage. *TNFR2* on chromosome 1p36 contains 10 exons encoding cysteine-rich extracellular domains, thought to be important for ligand binding, and serine-rich cytoplasmic domains. *TNFR2* participates in signaling for cytotoxicity, and regulates proliferation and cytokine secretion in T cells. There is an amino acid substitution, M196R, in fourth extracellular domain resulted from the ATG->AGG single nucleotide polymorphism (SNP) for the exon 6 of *TNFR2*. We analyzed the exon 6 of *TNFR2* by PCR-SSCP from 245 unrelated healthy Koreans. The genotype frequencies of 196*R/196*R, 196*R/196*M, and 196*M/196*M in Koreans were 3.3%, 24.5%, and 72.2%, respectively. The 196*R allele frequency of *TNFR2* in Koreans (0.16) is lower than that in Spanish and UK Caucasoids (0.23 and 0.28), and similar to that in Japanese (0.10).