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Simple Sequence Repeat DNA And Its Variability in the Alga *Chlamydomonas*

강 태진*

Department of Botany/Biology, North Dakota State University, USA.

Simple sequence repeats (SSR) have been found to be abundant and highly polymorphic in a number of eukaryotic genomes. The objective of this study was to determine the presence and variability of $(CA/GT)_n$ SSRs in the genome of the alga *Chlamydomonas*. A genomic DNA library of *C. reinhardtii* was screened with a radiolabeled $(AC)_{11}$ probe for the presence of $(CA/GT)_n$ repeats. The positive clones were sequenced. Three PCR primer sets flanking the $(CA/GT)_n$ sequences were constructed, and the Polymerase Chain Reaction (PCR) was used to specifically amplify these regions from several *Chlamydomonas* species and multiple isolates of *C. reinhardtii*. All three loci were highly polymorphic in the *C. reinhardtii* isolates. A simple Mendelian inheritance pattern was found for all three loci, which showed 2:2 segregation in the tetrads resulting from a cross between *C. reinhardtii* and *C. smithii*.

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Mutagenesis and Analysis of Fusogenic Activity of *Autographa californica* Nuclear Polyhedrosis Virus (AcNPV) gp64 Envelope Fusion Protein

김 희 진*, 양 재 명

Department of Biology, Sogang University, Seoul 121-742

The baculovirus gp64 glycoprotein is a major component of the envelope of budded virus (BV) and has been shown that it plays an essential role in the infection process, especially virus-cell membrane fusion. We have cloned AcNPV gp64 gene and expressed transiently in transfected insect cells. The cells expressing gp64 protein were examined for membrane fusion activity by using a syncytium formation assay under various conditions. The followings are optimal conditions required for inducing membrane fusion: 1) a pH 4.6 or lower 2) 15 min exposure time under acidic pH; 3) at least 1 μg of gp64 cloned plasmid DNA; 4) expose the cells to acidic pH at 72 hr post-transfection. In order to investigate the role of hydrophobicity for the membrane fusion, the two leucine residues (amino acid position at 229, 230) within hydrophobic region I were mutated to alanine by PCR and the membrane fusion activity of the mutant was analysed.