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Analysis of the regulatory sequence of the *vir*E promoter in *Agrobacterium tumefaciens*.

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In order to investigate the regulatory mechanisms of the *vir*E operon, we constructed various deletion mutants in the 5'-nontranscribed region of the *vir*E promoter. The mutant deleted from 5'end to position -12 showed 4.7% promoter activity. The mutant deleted to position -48 3.7% promoter activity. On the other hand, the mutant that CCGAGT on putative -35 sequence were substituted for TTGACA and the region from 5'end to -50 was deleted showed 63.4% promoter activity. The same mutant as the about-mentioned substitutional mutant with the exception of the deletion from -68 to -50 instead of the deletion from 5'end to -50 indicated 74% of the native promoter activity. Therefore, we concluded that *vir*E promoter in functional without *vir* box if the putative -35 sequence of *vir*E promoter was substituted for *E. coli* -35 sequence.

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Cloning of the Kinesin-Related Gene in *Schizosaccharomyces pombe*

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It has been known that kinesin gene has an important role in transport of cell organelles. Kinesin is composed of the heavy chain and light chain. Kinesin heavy chain-related genes were cloned in *Saccharomyces cerevisiae, Aspergillus nidulans*, and *Drosophila melanogaster* and they had major roles in movement of chromosomes and separation of spindle poles. In this study, we have tried to clone the kinesin-related gene in *Schizosaccharomyces pombe* using PCR technique. The primer was constructed with the highly conserved area in kinesin-related genes in other organisms. *S. pombe* genomic DNA was amplified with primer and the part of the gene was cloned. By use the part of the gene as a probe, we cloned the two whole genes from *S. pombe* cDNA library. The cloned genes are in the middle of sequencing.