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Characterization of the Virulence Region and the *virG* Gene of pTiKU12 DNA

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Agrobacterium tumefaciens KU12, a Korean strain, exhibits some different characters in *vir* gene induction by phenolic compounds, tumor formation ability, and plant host range from those of other *Agrobacterium* strains that have been studied so far. Recently an octopine Ti plasmid pTiKU12 was isolated from the strain and partially characterized. In this study the virulence gene *virG* gene was characterized and compared with those of other Ti plasmids as a step for elucidation of the different characteristics at the molecular level. Complete nucleotide sequence of the *virG* gene locus was identified. It contains an open reading frame (ORF) of 726 nucleotides and has much lower homology (about 77%) to the *virG* sequences of other octopine Ti plasmids than those (above 98%) already known within octopine Ti plasmids. Also it uses GTG as a translation start codon instead of TTG in other Ti plasmids. Analysis of 5'-untranslated region reveals that the pTiKU12 *virG* has two *vir* boxes instead of three *vir* boxes of pTiA6 *virG*. In addition only one putative promoter region which has homolgy with P1 promoter of pTiA6 and pTiC58 in sequence and alignment is seen in this region. Meanwhile, the conserved direct repeat sequence 5'-ATTTTGTC-3' and ribosome binding site are homologous to those of pTiA6 and pTiC58. The pTiKU12 *virG* contained in pUCDG was able to complement a *virG* mutant strain *Agrobacterium tumefaciens* Mx19 in β -galactosidase activity assay and on plant tumor tests. The pTiKU12 VirG protein overproduced in *E. coli* as a fusion protein with maltose binding protein (MBP) is 27kDa and has cross reactivity with anti-VirG (of pTiA6) monoclonal antibody.