SL204 The sensing of plant signal molecules by *Agrobacterium* and characterization of an unusual sensor gene (*virA*) of *Agrobacterium*

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The virulence(*vir*) genes of *Agrobacterium tumefaciens* are induced by low molecular weight phenolic compounds and monosaccharides through a two component regulatory system consisting of the VirA and VirG proteins. However, it is not clear how the phenolic compounds are sensed by the VirA/VirG system. We tested the *vir*-inducing abilities of different phenolic compounds using wild type *A. tumefaciens* strains. We analyzed the relationship between the structures of the phenolic compounds and the levels of *vir* gene expression in these strains. In strain KU12, the *vir* genes were not induced by phenolic compounds containing 4-hydroxy, 3- and 5-methoxy groups such as acetosyringone which strongly induced the *vir* genes of the other *Agrobacterium* strains. On the other hand, the *vir* genes of KU12 were induced by phenolic compounds containing only a 4-hydroxy group such as 4-hydroxyacetophenone which did not induce the *vir* genes of the other *Agrobacterium* strains. By transferring different Ti plasmids into isogenic chromosomal backgrounds, we showed that the phenolic sensing determinant is associated with the Ti plasmid. Subcloning of the Ti plasmid indicates that it is the *virA* locus which determines which phenolic compounds can function as *vir* gene inducers. These results suggest that the VirA protein directly senses the phenolic compounds for *vir* gene activation. To gain some understanding of the basis for these differences in sensing ability, we sequenced the entire *virA* locus of pTiKU12, including its promoter region and compared this sequence with five different published *virA* sequences which respond in different ways to inducing compounds. The *virA* gene of KU12 is composed of an open single reading frame coding for 851 aa. At the aa level, the VirA protein of pTiKU12 is 45, 45, 49, 49 and 64% identical to the VirA proteins from pTiA6, pTi15955, pRiA4, pTiC58 and pTiAg162, respectively. The transcription start sites of pTiKU12 and pTiA6 *virA* genes differed significantly when mapped by primer extension. Unlike all other *vir* genes except *virA* gene of pTiAg162, pTiKU12 *virA* is constitutively expressed and its synthesis is not induced by phenolic compounds. The lack of induction is accounted for by the fact that the promoter region does not has the conserved VirG-binding dodecadeoxynucleotide sequence (*vir*-box) which was previously identified in all promoter regions of inducible *vir* genes.