

Genetics of Resistance to Peanut Mottle Virus in Soybean

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(ABSTRACT)

Soybean (*Glycine max* L. Merr.) is one of the most important crops of the world. Among the various viruses infecting soybean, peanut mottle virus is most commonly found on soybeans in areas where they are grown in close proximity to peanuts. This research was conducted with the primary objective of identifying new genes for resistance to peanut mottle virus. To assign a gene symbol to the resistance gene in cultivar CNS, it was crossed with 'Peking'. Both the F_2 and $F_{2:3}$ lines segregated in a ratio which is expected when one dominant and one recessive gene at two different loci are segregating. Previous studies indicate the presence of one dominant gene in CNS and one recessive gene in Peking for resistance against PMV. This clearly suggests that Peking and CNS possess different resistance genes, which are non-allelic to each other. Now that, all the allelism tests are complete, the resistance gene in CNS can be assigned a gene symbol of *Rpv3*. PI 486355, a resistant line, was crossed with susceptible cultivars Lee 68 and Essex to study the mode of inheritance of resistance. This PI was found to possess two independent dominant genes for resistance to peanut mottle virus. It was also crossed with 'York' and CNS which are known to have resistance genes at the *Rpv1* and *Rpv3* loci, respectively. Data from inoculations of F_2 and $F_{2:3}$ progenies indicated that one gene was allelic to *Rpv1* and the other is at a locus different from both *Rpv1* and *Rpv3*. PI 398593 was crossed

with Lee 68, York, Peking and CNS for studying the nature of resistance genes present in it. No certain conclusions can be drawn regarding the nature of the resistance gene(s) at this stage because of inconsistent behavior of the PI itself. The F_2 data of the crosses of PI 398593 with Lee 68, York and CNS supported a recessive nature of the resistance gene present in the PI. F_2 plants of the cross PI 398593 x Peking segregated but, not in the expected ratio. $F_{2:3}$ data of only one cross (PI 398593 x York) supported the recessive nature of the PI resistance gene whereas the other two crosses (PI 398593 x CNS and PI 398593 x Peking) did not support these findings. From the data available it appears that the resistance is at least partially influenced by the environment. The mode of inheritance of resistance in PI 96983, 'Kwanggyo', 'Toano', 'Jizuka', 'Raiden' and 'Suweon 97' was studied by crossing these cultivars with PMV susceptible cultivars and inoculating the F_2 populations of these crosses. In all these cultivars resistance is governed by a single dominant gene. PI 96983, Toano, Jizuka and Suweon 97 were also crossed with York to determine the allelic relationships. Resistance genes in all these cultivars were found to be allelic to *Rpv1*. Since each of the cultivars also has a single dominant gene at the same locus for resistance to soybean mosaic virus, it is possible that resistance to both viruses is controlled by the same gene.

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