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Inheritance and mapping of resistance against cowpea mild mottle virus (CPMMV) strain D1 in soybean

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A distinct strain of *Cowpea mild mottle virus* (CPMMV) infecting soybean was reported from India in 2013. Until now there are no resistant sources against CPMMV disease. In the present study 133 genotypes were first screened in the field and three sources of resistance against CPMMV in soybean were identified. The resistance in the three identified lines was confirmed by sap inoculation. The presence of the virus in sap inoculated plants was also confirmed through RT-PCR by designing primer specific to coat protein gene and NaBp region of CPMMV genome. The virus strain was also confirmed through particle size observed in the electron microscopy of the leaves of the sap inoculated plants and sequence alignment of the 1065 base pair PCR product with other strains of CPMMV. The lines which were found to be resistant were further used to develop mapping population. The inheritance of resistance to *Cowpea mild mottle virus* (CPMMV) strain D1 was studied. The resistant genotypes, DS 12-5 and SL958 were crossed with susceptible genotypes F4C7-32 and JS335 respectively. For testing the resistance individual F₂ plants and the parent as well as the F₂ derived F₃ families were sap inoculated in an insect proof net house. Resistance reactions of F₂ plants and individual F₂ plant derived F₃ families indicated that resistance was controlled by a single dominant gene. Mapping with Bulk Segregant method showed that SSR markers Satt635 and UO8405 were linked to resistance gene and it is located on linkage group H.