Screening and utilization of soybean germplasm for breeding resistance against Mungbean Yellow Mosaic Virus

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Soybean are susceptible to about fifty different viruses. Under Indian conditions Mungbean yellow mosaic virus (MYMV), Soybean mosaic virus (SMV) and Groundnut bud necrosis virus (GBNV) are of prime importance.

The incidence of YMV was limited to north plain zone but since last few years it has been reported to spread to central zone as well. Central zone accounts for the 90% of the soybean production in the country. Singh et al. (1998) in order to determine the incidence of stem fly (Melanagromyza sojae), whitefly (Bemisia tabaci) and yellow mosaic virus, fields of 20 villages were observed during kharif in 1996. they found that virus incidence occurred in patches in most of the area.

Yellow seeded soybean was introduced during nineteen sixties in India. At that time only three exotic varieties namely Bragg, Clark and Lee, found to be suitable under Indian conditions, were available to farmers. These varieties being highly susceptible to MYMV created general impression of a agricultural non-feasibility of yellow seeded soybean in India. Although this problem has been over come to some extent with the release of new varieties under All India Coordinated Research Project (AICRP) on soybean. However, the resistance is not durable. Varieties showing field resistance at the time of release become susceptible to MYMV over a period of time.

The problem may be because of prevalence of different isolates of the causal virus. Biswas and Varma (2000) reported five naturally occurring variants of mungbean yellow mosaic virus (MYMV), one from Vigna mungo (Bg3D from Delhi), two from Vigna radiata (MbD from Delhi and MbS from Sriganganagar), one from Phaseolus aconitifolia (MoL from Ludhiana) and one from Cajanus cajan (Pp1D from Delhi). Based on the host reactions a set of differentials was selected, which could be used for differentiating the five variants of MYMV. The variants of MYMV could be further distinguished by nucleic acid spot hybridization (NASH) using full length and fragment probes to MYMV-Bg3D DNA-A and DNA-B. The variants Pp1D and MbD reacted weakly with all the probes but these isolates could also be differentiated by using a smaller concentration of viral DNA. Based on the degree of hybridization the five variants appeared to fall into two distinct groups i.e. Pp1D in one group and Bg3D, MbS and MoL in the other.

Usharani et al., (2004) studied various isolates from India on the basis of host range. Genomic components of the begomovirus causing yellow mosaic disease (YMD) in soybean in Delhi, India, were cloned, sequenced and evaluated for infectivity. Nucleotide sequence analysis of the virus isolate revealed more than 89% identity with mungbean yellow mosaic India virus (MYMIV); therefore, it is designated as a soybean isolate of MYMIV (MYMIV-Sb). Total nucleotide and predicted amino acid sequence analysis of MYMIV-Sb with other yellow mosaic virus isolates infecting legumes established dichotomy of the isolates into two species, namely, MYMIV and mungbean yellow mosaic virus (MYMV). The involvement of at least two distinct viruses in the etiology of soybean YMD in India is reported.

There are conflicting reports about genetics of resistance to MYMV. However, in most cases susceptibility has been shown to be dominant and governed by two genes. The strains can be distinguished from each other.

At present essentially two sources of resistance is being used in AICRP on soybean, namely G. Max cv. UPSM-534 and the wild species G. sojae (Ram et al., 1984) . There is an urgent need to identify newer sources of resistance and to understand the nature of resistance.