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Original Research Article

Genetics of Yellow Mosaic Virus (YMV) Disease in Soybean [*Glycine max* (L.) Merr.]

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A B S T R A C T

The inheritance of YMV resistance studied in F_1 and F_2 populations of four crosses involving two highly resistant varieties UPSM-534 and PK-416 and two highly susceptible genotypes JS-335 and AMS-353 indicated that the resistance is dominant and is controlled by single major gene. The chi-square test showed complete fitness to 3 resistant: 1 susceptible ratio in all the four F_2 populations *viz.*, JS-335 X UPSM-534, JS-335 X PK-416, AMS-353 X UPSM-534 and AMS-353 X PK-416. The findings of the study will pave the way for mapping the gene for YMV resistance with linked molecular marker. The segregating populations generated will act as starting materials for developing improved lines with YMV resistance.

Keywords

Glycine max, *Bemisia tabacci*, Inheritance, Soybean, YMV resistance

Introduction

Soybean [*Glycine max* (L.) Merrill] (2n = 40), the major oilseed crop of the world including India, is susceptible to about fifty different diseases caused by virus. Yellow mosaic virus (YMV), Soybean mosaic virus (SMV) and Groundnut bud necrosis virus (GBNV) are the major viral diseases of soybean in India (Lal *et al.,* 2007). Yellow mosaic virus (YMV) is serious and widespread disease of soybean in the Northern India, parts of South India, Sri Lanka, Bangladesh, Pakistan and Thailand (Bhattacharyya *et al.,* 1999). At first, it was observed in North India in the early 1970s and since then it was being spread at alarming proportions. Its expansion towards central India or the hub of the country for soybean cultivation might be fatal to the soybean industry. Secondly, nearly all the major varieties grown in the central India are susceptible to YMV. The magnitude of yield loss due to YMV in soybean has been reported to be as high as 80 per cent (Nene, 1972). Therefore, there is an urgent need to tackle the disease before it causes serious damage to the soybean industry.

YMV is transmitted by white fly (*Bemisia tabaci*); therefore, control of this disease is indirectly related to the control of its vector. Its chemical or cultural control has not been found to be economical and environmental friendly. Only deployment of genetic resistance has been proved the way of its control or management. For such approach to be effective, it is important to understand the genetic control of the disease. Singh *et al.,* (1974 a, b) has identified the wild type

soybean (*Glycinesoja*) to possess resistance against YMV. Bhattacharyya *et al.,* (1999) reported the resistance in *Glycinesoja* to be dominant and controlled by single gene. However, Singh and Mallick (1978) reported the resistance to be controlled by two recessive genes. Thus, there is need to study and establish the genetic control of the disease beyond doubt for adopting effective approaches to YMV resistance breeding.

The resistance of genotypes may vary from region to region depending upon the strain of virus prevalent in the area. Usharani *et al.,* (2004) indicated that the species of YMV prevalent in Northern India are different from that prevalent in South India. The present study was therefore, designed to evaluate segregating generations developed through intra-specific (*Glycine max*) crosses involving resistance and susceptible genotypes in the field to study the genetics of YMV resistance in cultivated soybean (*Glycine max* L. Merr.).

Materials and Methods

Hybridization Programme

Two highly resistant genotypes *viz.,* UPSM-534 and PK-416 were crossed with two highly susceptible genotypes JS-335 and AMS-353 using an improved hybridization technique during *kharif* 2014. The genotypes JS-335 and AMS-353 has been used as female/susceptible parent whereas UPSM-534 and PK-416 was used as male/donor parent in hybridization programme.

Generation Advancement (F_1 toF_2)

About half quantity of F_0 seeds obtained was used for generation advancement during *kharif* 2015. F_1 plants were confirmed on the basis of characters carried from male parent and harvested separately.

Screening and Scoring of F_1 and F_2 Population

The four (*viz.*, JS-335 X UPSM-534, JS-335 X PK-416, AMS-353 X UPSM-534 and AMS-353 X PK-416) F_1 and F_2population / plants were tested for disease reaction at research field, Department of Agricultural Botany, Dr. PDKV, Akola during *kharif* 2016. Spreader rows were used to spread the disease uniformly across the plots. The seeds of Greengram (Var. Kopergaon) were also sown randomly to have early infestation of yellow mosaic virus disease.

No insecticide was spayed to facilitate the natural buildup of white flies. Responses of the genotypes to YMV disease was scored using 0–9 scale. The scoring was done only after the highly susceptible genotypes (spreader rows) were completely infected by YMV disease. Genotypes were categorized as resistant and susceptible based on disease score. Score '0' was given when there was no disease symptoms on any plants while score '9'was given upon observing yellow mottle symptoms on most of the plants; severe reduction in leaf and plant growth as well as pod formation. Plants with score 0 and 9 were rated as highly resistant and highly susceptible, respectively. The F_2 populations were scored for the disease responses and the ratios of resistant and susceptible plants were subjected to χ^2 (Chi-square) test for goodness of fit.

Results and Discussion

The genetics of YMV resistance in soybean is not clearly depicted in the available literature. It has been reported to be governed by single dominant gene (Bhattacharyya *et al.,* 1999) and two recessive genes (Singh and Mallick, 1978) from the studies conducted in inter-specific and inter-varietal crosses.

Table.1 Responses to YMV disease in F_1 and F_2 population and testing for goodness of fit

Cross combination	F_1 plants		F_2 plants			χ^2(3:1)	P value
	No. of plants screened	Disease reaction	No. of plants screened	No. of resistant plants	No. of susceptible plants		
JS-335 X UPSM-534	79	Resistant	281	214 (210.75)	67 (70.25)	0.201	0.5-0.7
JS-335 X PK-416	64	Resistant	156	114 (117.00)	42 (39.00)	0.307	0.5-0.7
AMS-353 X UPSM-534	68	Resistant	167	128 (125.25)	39 (41.75)	0.241	0.5-0.7
AMS-353 X PK-416	53	Resistant	146	107 (109.50)	39 (36.50)	0.228	0.5-0.7

(Figure in parenthesis indicate the expected number of plants in each category)

The information is not available for its resistance in the cultivated soybean (*Glycine max* L. Merr.). In this study, it was found that all the four F_1 populations exhibited higher level of resistance indicating that the resistance to YMV in the cultivated soybean (*Glycinemax* L. Merr.) is dominant. The F_2 plants of all the four crosses segregated for YMV resistance showing a clear-cut 3 resistant: 1 susceptible ratio indicating the resistance to be governed by a single dominant gene (Table 1). The insignificant χ^2 (Chi-square) test and high p-value showed complete goodness of fit to the ratio. Thus, it revealed that like in *Glycinesoja*, the resistance in *Glycinemax* L. Merr. is also governed by a single gene in a dominant fashion. The report of two recessive genes governing YMV resistance in soybean may be due to imprecise and faulty screening in the field. Owing to insufficient disease pressure or uneven spread of the vectors, a susceptible genotype may also be rated as resistant.

The clear genetics of YMV disease established in this study will help in designing breeding program for YMV resistance. Since resistance is governing by a single dominant gene, it would be easy to transfer the gene to recipient genotype(s) through simple hybridization followed by selection. It would further help in identification of linked molecular marker(s) for effective marker assisted selection (MAS). Since the symptom of resistance and susceptibility are clear and distinct, association mapping approach would fit appropriately for this purpose. Souframanien and Gopalakrishna (2006) reported identification of ISSR markers linked to MYMV (Mungbean Yellow Mosaic Virus) resistance in blackgram (*Vigna mungo* L. Hepper). Ma *et al.*, (2010) have mapped and identified markers linked to the gene for Soybean Mosaic Virus (SMV) resistance. Closely linked markers would facilitate selection of resistant plants even in the absence of the virus and the vectors. The F_2 populations developed in this study would serve as valuable material for transferring YMV resistance to the respective recipient parents. The genotype AMS-353 is pod shattering resistant and having high germ inability. It could be used as donor for pod shattering resistant and seed germ inability in breeding programs for improving seed quality in soybean varieties. However, high susceptibility of this genotype to YMV disease has reduced its applicability as

donor. Transferring the YMV resistance gene into it would increase its value inbreeding program. JS-335 is the most popular variety of soybean in India; however, it is highly susceptible to YMV disease limiting its cultivation to YMV-free areas only. Making it resistant through incorporation of YMV resistance would increase its acreage coupled with higher production. The significance of the findings of this study is that it would pave the way for YMV resistance breeding in soybean. Because, transferring genes from wild relatives comes with penalty of linkage drag (Singh *et al.*, 1974 a, b; Ram *et al.*, 1984). Use of linked SSR marker would open vistas for molecular breeding to improve the popular varieties with incorporation of the gene for YMV resistance. The improved genotypes with YMV resistance would act as barrier against spread of the disease to newer areas and thus boost production of soybean in the country.

Field evaluation of four F_1 and their corresponding F_2populations developed through hybridization between YMV resistant and susceptible genotypes indicated that YMV resistance in cultivated soybean (*Glycine max* L. Merr.) is dominant and controlled by a single major gene. The information would pave the way for YMV resistance breeding and mapping of the gene with linked molecular marker. The F_2 populations developed in this study would serve as valuable material for transferring YMV disease resistance to the respective recipient parents. The segregating populations generated will act as starting materials for developing improved lines with YMV disease resistance.

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