GENETICS OF YELLOW MOSAIC VIRUS (YMV) RESISTANCE IN CULTIVATED SOYBEAN [GLYCINE MAX (L.) MERR.]


Division of Genetics,
Indian Agricultural Research Institute, New Delhi-110 012

Received: 03-08-2012
Accepted: 15-12-2012

ABSTRACT

In the present study, 100 soybean germplasm were screened for three years (2009-2011) in New Delhi, a hot-spot for YMV disease in order to identify resistant sources. A set of 29 genotypes, mostly improved varieties of Northern India were identified with higher level of resistance consistently over the years. The inheritance of YMV resistance studied in F1 and F2 populations of three crosses involving two highly resistant varieties DS9712 and DS9814 and two highly susceptible genotypes JS335 and PI542044 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 three F2 populations viz., PI542044 x DS9712, PI542044 x DS9814 and JS335 x DS9712. 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.

Key words: Bemisia tabacci, Inheritance, Resistance, Soybean, YMV.

INTRODUCTION

Soybean is the numero uno oilseed crop in India. Currently, it is grown in nearly 10.0 mha area with average production of about 10.0 mt. However, its average productivity (~ 1.0 t/ha) is far below the world average (2.5 t/ha). Among other factors, pest and diseases are the most important ones for such low productivity. The yellow mosaic virus (YMV) disease caused by Gemini virus and transmitted by white fly (Bemisia tabacci) is the most important disease of soybean. Besides India, it is prevalent in Sri Lanka, Bangladesh, Pakistan and Thailand. The economic loss caused by YMV disease is 30-50%; however, it may go up to as high as 80% in extreme cases (Nene 1972). Since it is a viral disease, its control through chemical or cultural practices is not effective, nor is it environment friendly. Deployment of genetic resistance is the best approach for management of YMV. 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 (G soja) to possess resistance against YMV. Bhattacharyya et al. (1999) reported the resistance in G soja 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 a large number of soybean germplasm in Delhi, a hot-spot for YMV, in order to identify useful sources of resistance to YMV diseases. Segregating generations developed through intra-specific (Glycine max) crosses involving resistance and susceptible genotypes were evaluated in the field to study the genetics of YMV resistance in cultivated soybean (G max L. Merr.).

*Corresponding author’s e-mail: akshay.talukdar1@gmail.com.
MATERIALS AND METHODS

Germplasm evaluation: A set of 100 soybean germplasm lines was obtained from the germplasm collection maintained at the Division of Genetics, Indian Agricultural Research Institute (IARI), New Delhi-12. The germplasm lines were comprised of exotic and indigenous collections, varieties and advanced breeding lines. The genotypes were genetically diverse and had varied morphological features including days to maturity, flower color, seed color, seed size, growth habit and seed yield. For testing reaction against YMV, the genotypes were grown in 3-meter-rows at a spacing of 45cm from row to row and 15cm from plant to plant in the experimental field of IARI, New Delhi, a hot-spot for YMV disease. In order to maintain uniform disease pressure across the field and to ensure proper spread of the disease, spreader rows of highly susceptible genotypes viz., JS335 and PI542044 were grown after every 5 rows and around the experimental plot as border rows. The screening was performed consecutively for 3 years (2009, 2010 and 2011) during kharif season.

Genetics of YMV resistance: Two highly resistant varieties viz., DS9814 and DS9712 were crossed with two highly susceptible genotypes PI542044 and JS335 in different combinations to produce three $F_1$ populations viz., PI542044 x DS9712, PI542044 x DS9814 and JS335 x DS9712. The three $F_1$ and their corresponding $F_2$ populations were grown during 2010 and 2011, respectively in the experimental field of IARI with spreader rows in between and around the field.

Scoring: 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. In a similar fashion, the $F_2$ populations were scored for the disease responses and the ratios of resistant and susceptible plants were subjected to $\chi^2$ (Chi-square) test for goodness of fit.

RESULTS AND DISCUSSIONS

Evaluation of germplasm for YMV resistance:
Evaluation of the 100 germplasm of soybean for YMV disease resistance was started during kharif season of 2009. Out of 100 genotypes, 34 showed complete resistance to YMV disease; rest of the genotypes showed expression of the disease and were rated as susceptible through highly susceptible. The highly resistant genotypes included both indigenous and exotic collections, as well as varieties particularly of North-India. In fact, YMV is more a serious problem in North-Indian states. It is however, spreading at alarming rate towards central and South-Indian states which is a matter of serious concern for the soybean industry because, central-Indian states, Madhya Pradesh in particular are the hub of soybean in the country. Nearly all the popular varieties grown in central and southern states are susceptible to YMV. Talukdar et al. (2010) emphasized the importance of improving such varieties through incorporation of genetic resistance for sustainable production and survival of soybean.

**TABLE 1:** List of genotypes showing resistance reaction in field evaluation during 2009-2011.

<table>
<thead>
<tr>
<th>Particular</th>
<th>N. o. of genotype</th>
<th>Name of the genotypes</th>
</tr>
</thead>
<tbody>
<tr>
<td>for 3 years of testing</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genotypes showing resistance</td>
<td>6</td>
<td>KG831, IC416879, J576257, J581607, J59329, J(SH)9616</td>
</tr>
<tr>
<td>for 2 years of testing</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genotypes showing resistance</td>
<td>5</td>
<td>IC144409, PK1225, EC456554, L291, EC456533</td>
</tr>
<tr>
<td>for one year of testing</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
industry in the country. The resistant genotypes indentified in this study may serve as starting material for incorporation of resistance in the central and south-Indian soybean varieties.

In evaluation of germplasm in the field, it often happens that ‘Disease escape’ gets recognized as ‘Disease resistant’. It would therefore be prudent to repeat such experiment over years or across locations. In this study, the 100 genotypes screened during 2009 were subjected to screening further during 2010 and 2011 under similar set of conditions for confirmation of the result. The number of genotypes identified as completely resistant were 38 and 36 during 2010 and 2011, respectively. It thus happened that a few genotypes identified as resistant (disease-escape?) in a particular year appeared as susceptible in the subsequent year(s). This may be attributed to the variation in disease pressure or non-uniform distribution of the disease in the field leading to disease-escape. The weather condition during crop growing period plays a definite role in multiplication and/or distribution of the white fly, the vector of the disease in the field. Repetition of the experiment over years as has been done in the present study can help avoid such ambiguity.

**Inheritance of YMV disease resistance:** 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. The information is not available for its resistance in the cultivated soybean (*G max* L. Merr.). In this study, it was found that all the three *F*₁ populations exhibited higher level of resistance indicating that the resistance to YMV in the cultivated soybean (*G max* L. Merr.) is dominant. The *F*₂ plants of all the three 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 2). The insignificant $\chi^2$ and high p-value showed complete goodness of fit to the ratio. Thus, it revealed that like in *G soja*, the resistance in *G max* 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. Repetition of the experiment over the years as has been done in the present study can help avoid such ambiguity.

<table>
<thead>
<tr>
<th>Cross combination</th>
<th>No. of <em>F</em>₁ plants screened</th>
<th>No. of <em>F</em>₂ plants screened</th>
<th>No. of resistant <em>F</em>₂ plants</th>
<th>No. of susceptible <em>F</em>₂ plants</th>
<th>$\chi^2$ (3:1)</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>PI542044 x DS9712</td>
<td>62</td>
<td>259</td>
<td>191 (194.5)</td>
<td>68 (64.75)</td>
<td>0.217</td>
<td>0.5-0.7</td>
</tr>
<tr>
<td>PI542044 x DS9814</td>
<td>48</td>
<td>115</td>
<td>89 (86.25)</td>
<td>26 (28.75)</td>
<td>0.343</td>
<td>0.5-0.7</td>
</tr>
<tr>
<td>JS335 x DS9712</td>
<td>52</td>
<td>138</td>
<td>101 (103.5)</td>
<td>37 (34.5)</td>
<td>0.241</td>
<td>0.5-0.7</td>
</tr>
</tbody>
</table>

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

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. Recently, Kumar et al. (2012, under publication) has identified two simple sequence repeat (SSR) markers linked to the gene for YMV resistance in G max L. Merr. Similarly, 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 PI542044 is devoid of trypsin inhibitor, an anti-nutritional factor present in the soybean seeds. It could be used as donor of null allele for trypsin inhibitors in breeding programs for development of trypsin inhibitor free soybean varieties. However, high susceptibility of the genotype to YMV disease has reduced its applicability as donor. Transferring the YMV resistance gene into it would increase its value in breeding program. JS335 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). The resistant genotypes identified in this study are primarily released varieties. Use of such improved varieties as donor of resistance gene will exclude the problem of linkage drag; rather it might contribute some more useful genes to the recipient genotypes. 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.

**CONCLUSION**

Through three years of field evaluation of 100 soybean germplasm for YMV resistance in Delhi (a hot-spot for YMV), 26 genotypes have been identified as promising source of resistance that showed consistent resistance against YMV. Field evaluation of three $F_1$ and their corresponding $F_2$ populations developed through hybridization between YMV resistant and susceptible genotypes indicated that YMV resistance in cultivated soybean (G 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.

**REFERENCE**


