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

S. Baruah\(^1,2\), M.K. Sarma\(^1\*) and D. Baishya\(^2\)

\(^1\)Biotech Hub, BN College of Agriculture, Assam Agricultural University, Biswanath Chariali, Assam-784176, India
\(^2\)Department of Bioengineering and Technology, Gauhati University, Guwahati, Assam-781014, India

*Corresponding author

**A B S T R A C T**

Yellow Mosaic Virus disease (YMD) is a serious viral disease of soybean. Considering a very less attempt in studying the disease this investigation was carried out in order to arrive at the genetic basis of Yellow Mosaic Virus disease resistance of soybean. Crosses were made between highly resistant soybean varieties (DS 9712 and DS 9814) and two highly susceptible varieties (JS 335 and MAUS 609). The four cross combinations were MAUS 609 × DS 9712, MAUS 609 × DS 9814, JS 335 × DS 9712 and JS 335 × DS 9814. All true hybrids of F\(_1\) population were observed to be resistant with the score zero (0) presenting a clear visible evidence of resistance to be dominant over susceptibility. The F\(_2\) plants resulted from all four crosses were observed to segregate for YMD resistance at 3 (Resistance): 1 (Susceptible) ratio indicating the genes for resistance in the concerned parents under study to be monogenic in nature. Chi square (\(\chi^2\)) test for all the four crosses showed a good fitness to 3 (Resistance): 1 (Susceptible) ratio in the F\(_2\) population at 5 \% probability level indicating the monogenic dominance nature of the resistance gene. The present investigation clearly suggests that the YMD resistance trait is governed by a single dominant gene.

**Keywords**
Soybean, Yellow Mosaic Virus Disease, Resistance, Inheritance, Monogenic Dominance

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**Introduction**

Soybean *Glycine max* (L.) Merr. (2n = 40) is the unique grain legume known for its dual use as pulse and oilseed providing both quality edible protein (38-44 \%) and oil (18-22 \%). Although soybean is not commercially grown in North East India, it is quite popular as a source of traditional food among the ethnic communities of this region besides being consumed as soya chunks and oils. Soybean production has been challenged by a number of biotic and abiotic stresses. Among different biotic stresses Yellow Mosaic Virus disease (YMD) is one of the predominant viral diseases, especially in North, North East and Central India causing yield loss as high as 80 \%. Yellow Mosaic Virus disease (YMD) is a viral disease transmitted by white fly *Bassimia tabacci*. The begomovirus causing YMD has two species, *viz.*, Mungbean Yellow Mosaic India Virus (MYMIV) and Mungbean Yellow
Mosaic Virus (MYMV) (Fauquet and Stanley, 2003). Both MYMIV and MYMV are prevalent in India causing YMD epidemics on various legume crops including mungbean, blackgram, soybean, cowpea, pigeonpea and horsegram (Usharani et al., 2004). The affected plants turn yellow and lose its vigor. In severe cases, the growing tip stops growing and becomes a clump of un-opened leaves. Pod setting gets drastically reduced with eventual loss of yield. The situation demands devising effective control mechanism to sustain rather increase soybean production in the country. The incidence of YMD in soybean is most pronounced in North Eastern India as well as Northern India (Annual Report, AICRP-soybean, 2000 - 2002, 2004 - 05 and 2005 - 06, 2008 - 09, 2009 - 10). So, further spread of this disease may bring disaster towards soybean industry in our country. Although chemical or cultural strategy for controlling YMV disease is in practice, neither of these approaches are known to be fully effective or environment friendly. Hence, the most advisable way to control Yellow Mosaic Virus infection is the deployment of genetic resistance of the host against the viral pathogen. Having a clear understanding about the inheritance pattern of YMD resistance is prerequisite to design breeding programme leading to the development of YMD resistant lines. The present investigation was undertaken with a view to study the inheritance pattern of resistance against YMD in native location and environmental condition of North Eastern part of India so as to aid in formulating effective resistance breeding programme on soybean for the region.

**Materials and Methods**

**Material**

Materials for the present investigation comprised of four soybean genotypes with complete resistance and susceptibility for Yellow Mosaic Virus disease viz., DS 9712, DS 9814, JS 335 and MAUS 609. DS 9712 and DS 9814 were two highly resistant varieties against YMD whereas JS 335 and MAUS 609 were highly susceptible ones.

**Hybridization to obtain F₁ plants**

In order to study the inheritance of YMV resistance of soybean selected resistant and susceptible genotypes were used as parents for hybridization programme (Fig. 1). Crosses were performed in different combinations viz., MAUS 609 × DS 9712, MAUS 609 × DS 9814, JS 335 × DS 9712 and JS 335 × DS 9814 (Table 1) by performing pollination without emasculation as described by Talukdar and Shivakumar, (2012). Selection of flower for hybridization is of prime importance in an artificial crossing programme. The flowers, which are going to open in the next morning, were selected for hybridization. Moreover, the season of crossing also affects the success of hybridization. Warm weather favors successful hybridization while crossing performed in winter leads to wrong selection of flower buds for crossing. Mature pollen was extracted from selected fully opened fresh flower to pollinate the flower bud. The pollination was performed early morning. The selected flower bud was made ready for pollination by carefully removing the sepals and exposing the ring of stamens. The yellow colored dusty pollen was then distributed on stigma carefully. The buds were covered with moist cotton to prevent drying of stigma. The plants were tagged properly after pollination. A large number of F₁ seeds were obtained from the crosses.

**Test of hybridity**

In order to test whether the plants developed from a F₁ seed is hybrid or self-fertilized,
hybridity of the F₁ plants was tested. For this purpose, a set of two markers viz., Satt177 and Satt656 was selected which showed polymorphism between parents.

The genomic DNA extracted from the parents was amplified with these two markers. Plants producing two bands each corresponding to maternal and paternal genotype were identified as true hybrid and rests were rejected as self-fertilized plants.

Testing for goodness of Fit

The recorded resistant and susceptible plants ratios were subjected to $\chi^2$ (Chi-square) tests for goodness of fit at 5 % probability level and significance of the test was studied following Panse and Sukhatme, (1967). The formula used as follows:

$$\chi^2 = \frac{(O_i - E_i)^2}{E_i}$$

Where $O_i$ = Observed value against ith class, $E_i$ = Expected value in the ith class.

Results and Discussion

Test of Hybridity

Soybean, being a highly self-pollinated crop shows very low level of 0.2 % of out crossing (Talukdar and Shivakumar, 2012). Improper crossing leads to self-pollinated crops. Hence, testing the hybridity of F₁ plants is a must to ensure successful crossing programme. Both morphological and molecular markers can be used to test the hybridity of test plants.

In the present experiment, all the four cross combinations between susceptible and resistant genotypes generated satisfactory number of F₁ plants. Further, while testing for true hybrids with polymorphic SSR marker viz., Satt177 and Satt656, ample number of plants exhibited bands corresponding to both paternal and maternal parents indicating successful flower bud selection and crossing. The number of F₁ plants respective to all four cross combination along with the number of true hybrids are listed in Table 3.

The cross between YMD susceptible genotype MAUS 609 and resistant genotype DS 9712 generated a total of seventy two F₁ plants among which sixty five were found to be true hybrid. 80 % of total F₁ obtained from the cross MAUS 609 × DS 9814 showed true
hybridity while 83 % of F₁ were true hybrid for the cross JS 335 × DS 9712. The cross JS 335 × DS 9814 generated a total of seventy F₁ plants among which sixty two plants showed true hybridity. Test of hybridity results revealed high rate of accuracy during the crossing experiment. Results also indicated that the climatic condition of hybridization experiment was appropriate. Talukdar and Shivakumar, (2012) reported that successful crossing depends on the stage of flower bud taken and also on the season of hybridization.

**Inheritance study of YMV**

All true hybrids of F₁ population were observed to be resistant showing the score zero (Table 3). The number of F₂ plants screened for YMD resistance and number of F₂ plants exhibiting resistance and susceptibility against YMD are listed in Table 4. The F₂ plants resulted from all four crosses were observed to segregate for YMD resistance at clear cut 3 (Resistance): 1 (Susceptible) ratio. Number of resistant plants for the four cross combination are 153, 115, 90 and 123, respectively. On the other hand, in the present investigation, 47, 35, 22 and 47 plants showed susceptibility for YMV among all the F₂ plants screened. The disease reaction in the sergeants appeared to be qualitative in nature which was expected based on the contrasting parents taken for the crossing. Appearance of no intermediate sergeants indicated the genes for resistance in the concerned parents under study were monogenic in nature.

Chi square ($\chi^2$) test for all the four crosses showed a good fitness to 3 (Resistance): 1(Susceptible) ratio in the F₂ population fit at 5 % probability level (Table 5). Under the present investigation, all the F₁ plants generated through crosses showed resistance against YMV. This presents a clear visible evidence of resistance to be dominant trait over susceptibility. The F₂ plants resulted from all four crosses were observed to segregate for YMV resistance at clear cut 3 (Resistance): 1(Susceptible). The entire cross combinations were found to be non-significant when tested against actual 3:1 ratio.

Further, the insignificant $\chi^2$ and high P-value showed complete goodness of fit to the ratio. Hence, results of F₂ segregation and Chi square ($\chi^2$) test confirmed that the resistance is governed by single dominant gene. Similar observations that YMD resistance was controlled by single dominant gene was also reported by Bhattacharyya et al., (1999) and Talukdar et al., (2013). However, contrary to this Singh and Mallick, (1978) reported two recessive genes controlling the YMD resistance.

This monogenic dominance pattern of inheritance of resistance against YMD has been reported in other crops like mungbean too (Sandhu et al., 1985; Verma and Singh, 1988, Ammavasai et al., 2004). On the contrary, some reports revealed the dominance of susceptibility over resistance against YMD in Mungbean (Sudha et al., 2013).

They observed dominance of susceptibility over resistance indicating a monogenic recessive inheritance of the resistance. Similar results of single recessive genes inheritance of the MYMV resistance in mungbean have been reported by other workers too (Basak et al., 2004; Saleem et al., 1998). Further, Khattak et al., (2000) mentioned role of some modifying genes monogenic recessive control of YMD resistance in mungbean.

These contradictory results regarding the genetics of YMD may possibly arise from variation of genotypes of host. Difference in viral strain specific to that area may also influence the inheritance pattern. Climatic condition also affects the phenotypic
appearance of traits among genotypes. Moreover, a susceptible genotype may also be rated as resistant in presence of insufficient disease pressure or uneven spread of the vectors in the field. Although contradictory reports on inheritance of YMD resistance has been reported by various worker, all the experiments were carried out in different region taking different genotypes for studying the inheritance pattern.

Table.1 Cross combination of highly resistant and highly susceptible soybean genotypes for Yellow Mosaic Virus to generate F_1 generation

<table>
<thead>
<tr>
<th>Sl. No.</th>
<th>Parents</th>
<th>Disease response</th>
<th>Disease response</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>DS 9712</td>
<td>Resistant</td>
<td>MAUS 609</td>
</tr>
<tr>
<td>2</td>
<td>DS 9814</td>
<td>Resistant</td>
<td>MAUS 609</td>
</tr>
<tr>
<td>3</td>
<td>DS 9712</td>
<td>Resistant</td>
<td>JS 335</td>
</tr>
<tr>
<td>4</td>
<td>DS 9814</td>
<td>Resistant</td>
<td>JS 335</td>
</tr>
</tbody>
</table>

Table.2 Scoring criteria for YMD incidence (Lal et al., 2005)

<table>
<thead>
<tr>
<th>Score</th>
<th>Symptom</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>No symptoms on any plant</td>
</tr>
<tr>
<td>3</td>
<td>Yellow mottle on 10% or fewer plant</td>
</tr>
<tr>
<td>5</td>
<td>Necrotic mottle on most plants, no reduction in plant growth, no yield loss.</td>
</tr>
<tr>
<td>7</td>
<td>Yellow mottle not covering whole leaf on most plants, reduction in leaf and plant growth</td>
</tr>
<tr>
<td>9</td>
<td>Yellow mottle on most plant, severe reduction in yield, leaf and plant growth</td>
</tr>
</tbody>
</table>

Table.3 Number of true hybrids in F_1 population obtained from all four crosses combinations

<table>
<thead>
<tr>
<th>Cross Combination</th>
<th>F_1 Obtained</th>
<th>True Hybrid F_1</th>
<th>% hybridity</th>
<th>Score</th>
<th>YMD response</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAUS 609 × DS9712</td>
<td>72</td>
<td>65</td>
<td>90%</td>
<td>0</td>
<td>Highly Resistant</td>
</tr>
<tr>
<td>MAUS 609 × DS 9814</td>
<td>60</td>
<td>48</td>
<td>80%</td>
<td>0</td>
<td>Highly Resistant</td>
</tr>
<tr>
<td>JS 335 × DS 9712</td>
<td>60</td>
<td>50</td>
<td>83%</td>
<td>0</td>
<td>Highly Resistant</td>
</tr>
<tr>
<td>JS 335 × DS 9814</td>
<td>70</td>
<td>62</td>
<td>88%</td>
<td>0</td>
<td>Highly Resistant</td>
</tr>
</tbody>
</table>

Table.4 Disease response of F_2 plants against YMV caused disease

<table>
<thead>
<tr>
<th>Cross Combination</th>
<th>F_2 plants Screened (Number)</th>
<th>Resistant plant against YMD (Number)</th>
<th>Susceptible plants for YMD (Number)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAUS 609 × DS 9712</td>
<td>200</td>
<td>153</td>
<td>47</td>
</tr>
<tr>
<td>MAUS 609 × DS 9814</td>
<td>150</td>
<td>115</td>
<td>35</td>
</tr>
<tr>
<td>JS335 × DS9712</td>
<td>112</td>
<td>90</td>
<td>22</td>
</tr>
<tr>
<td>JS335 × DS 9814</td>
<td>170</td>
<td>123</td>
<td>47</td>
</tr>
</tbody>
</table>
### Table 5: Chi Square test to check goodness of fit of F<sub>2</sub> plant to Mendelian ratio

<table>
<thead>
<tr>
<th>Cross Combination</th>
<th>Number of F&lt;sub&gt;2&lt;/sub&gt; plants screened</th>
<th>Phenotypic class</th>
<th>Expected number of plants as per Mendelian ratio 3:1 (E&lt;sub&gt;i&lt;/sub&gt;)</th>
<th>Observed Number of Plants (O&lt;sub&gt;i&lt;/sub&gt;)</th>
<th>O&lt;sub&gt;i&lt;/sub&gt; - E&lt;sub&gt;i&lt;/sub&gt;</th>
<th>(O&lt;sub&gt;i&lt;/sub&gt; - E&lt;sub&gt;i&lt;/sub&gt;)&lt;sup&gt;2&lt;/sup&gt;</th>
<th>(O&lt;sub&gt;i&lt;/sub&gt; - E&lt;sub&gt;i&lt;/sub&gt;)&lt;sup&gt;2&lt;/sup&gt; / E&lt;sub&gt;i&lt;/sub&gt;</th>
<th>χ&lt;sup&gt;2&lt;/sup&gt; = ∑(O&lt;sub&gt;i&lt;/sub&gt; - E&lt;sub&gt;i&lt;/sub&gt;)&lt;sup&gt;2&lt;/sup&gt; / E&lt;sub&gt;i&lt;/sub&gt;</th>
</tr>
</thead>
<tbody>
<tr>
<td>MAUS 609 × DS 9712</td>
<td>200</td>
<td>R</td>
<td>150</td>
<td>153</td>
<td>3.00</td>
<td>9.00</td>
<td>0.06</td>
<td>0.24</td>
</tr>
<tr>
<td></td>
<td></td>
<td>S</td>
<td>50</td>
<td>47</td>
<td>-3.00</td>
<td>9.00</td>
<td>0.18</td>
<td></td>
</tr>
<tr>
<td>MAUS 609 × DS 9814</td>
<td>150</td>
<td>R</td>
<td>112.5</td>
<td>115</td>
<td>-2.50</td>
<td>6.25</td>
<td>0.06</td>
<td>0.23</td>
</tr>
<tr>
<td></td>
<td></td>
<td>S</td>
<td>37.5</td>
<td>35</td>
<td>2.50</td>
<td>6.25</td>
<td>0.17</td>
<td></td>
</tr>
<tr>
<td>JS335 × DS 9712</td>
<td>112</td>
<td>R</td>
<td>84</td>
<td>90</td>
<td>6.00</td>
<td>36.00</td>
<td>0.43</td>
<td>1.71</td>
</tr>
<tr>
<td></td>
<td></td>
<td>S</td>
<td>28</td>
<td>22</td>
<td>-6.00</td>
<td>36.00</td>
<td>1.3</td>
<td></td>
</tr>
<tr>
<td>JS335 × DS 9814</td>
<td>170</td>
<td>R</td>
<td>127.5</td>
<td>123</td>
<td>4.50</td>
<td>20.25</td>
<td>0.16</td>
<td>0.64</td>
</tr>
<tr>
<td></td>
<td></td>
<td>S</td>
<td>42.5</td>
<td>47</td>
<td>-4.50</td>
<td>20.25</td>
<td>0.48</td>
<td></td>
</tr>
</tbody>
</table>

P<sub>0.05</sub> = 3.841 at degree of freedom (d.f) = 1.

**Fig.1** Parents for hybridization

Right: Female parent: YMV resistant soybean genotype DS 9712, Left: Male parent: YMV susceptible soybean genotype JS 335
It is also possible that different soybean genotype has different resistance mechanism (Fu et al., 2006). However, no evidence of contradictory inheritance pattern of MYMV resistance has been reported from same soybean genotypes or area.

This investigation recorded YMD resistance to be governed by single dominant gene. Hence, simple hybridization method can be used to transfer the gene to recipient genotypes followed by its selection. Elucidation of the inheritance pattern of YMD resistance will enable workers to design and identify molecular marker linked with YMD resistance gene for effective Marker Assisted Selection (MAS). This will lead to identification of the concerned gene conferring resistance to YMD.

Moreover, development of high yielding varieties devoid of YMV infection can also be attained with the help of the clear inheritance pattern. Breeding for cultivars with resistance is suggested to be very effective in controlling and preventing viral diseases of plants (Sudha et al., 2013). A better understanding about the genetic background of resistance against YMD will enable breeders to incorporate resistance into agronomically poor but desirable genetic resources. This will lead to the development of improved varieties with better yield, withstanding the viral infection. The result of the present study suggested that the resistant sources viz., DS 9712 and DS 9814 may be used in back cross breeding programme to transfer the resistance gene into the high yielding but disease susceptible varieties. Recently, two Simple Sequence Repeat markers have been found to be linked with the gene for YMD resistance in Soybean (Glycine max L. Merr) by the approach of association breeding (Kumar, 2013). Molecular markers linked to resistance against YMV and SMV (Soybean Mosaic Virus) was reported in blackgram too (Souframanien and Gopalakrishna, 2006; Ma et al., 2010). Thus, the above genotypes (both susceptible and resistant) may also be used for identification of the particular resistance gene and its mapping on the chromosome.

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References


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