Evidence of Economic Heterosis and Genetic Control of Fruit Yield and Yellow Vein Mosaic Virus Disease Severity Traits of Okra

Tania Seth1, Arup Chattopadhyay2*, Subrata Dutta3, Pranab Hazra4 and Bijendra Singh5

Abstract

Ten diverse genotypes of cultivated and wild species were crossed in half diallel fashion to produce 45 F1 hybrids to determine mode of gene action, extent of economic heterosis and dominance effect, and to estimate combining ability for eight quantitative traits. Predictability ratio revealed overwhelming response of non-additive gene action for controlling fruit length, number of fruits per plant, and fruit yield per plant; additive gene effects for days to 50% flowering, while both additive and non-additive genetic control for node number at first flowering, fruit weight, fruit girth, and PDI of YVMV disease. Appropriate breeding strategies for improvement of studied traits are highlighted here. Significant standard heterosis over two commercial hybrids, Shakti and Abantika was comparatively lower in magnitude for fruit yield per plant (4.62 % and 17.59 %, respectively) and higher in magnitude for PDI of YVMV disease (-71.28 % and -72.28 %, respectively). Partial- to over-dominance effects were involved in the inheritance of the studied traits. BCO-1 and 11/RES-6 were identified as potential donors for combining ability. Genetic analysis provides a guide line for the assessment of relative breeding potential of the parents or identifies best combiners in crops [15], which could be utilized either to exploit heterosis in F1 or to accumulate fixable genes to evolve variety. The information about the relative contribution of components of variation viz., additive and non-additive, is essential for effective crop improvement programme [16]. The analysis of diallel cross by the method proposed by Griffing [17] which partition the total genetic variation into general combining ability (GCA) of the parents and specific combining ability (SCA) of the crosses have been widely used. Such studies also simultaneously demonstrate the nature and magnitude of gene action involved in the expression of desirable traits and to predict the performance of the progenies.

Thus, the main aim of the present study was to determine the magnitude of economic heterosis and to estimate the dominance effect for fruit yield and its components, and YVMV disease severity, and to assess the nature of gene action for these traits in order to identify good combiners, as well as to formulate the breeding strategy for the genetic improvement of such traits.

Materials and Methods

Breeding material and procedure

Eight optimally diverse genotypes viz. BCO-1, VNR Green, VRO-6, 11/RES-6, 10/RES-6, 10/RES-4, Pusa Sawani, Arka Anamika belonging to Abelmoschus esculentus and two wild genotypes of Abelmoschus manihot (IC-140950) and Abelmoschus caillei (IC-433483) were selected on the basis of fruit characters, yield potentiality and YVMV disease severity as per our previous study [18]. Two standard private bred commercial okra hybrids (Shakti and Abantika) showing high tolerance against YVMV disease for the last couple of years under the Gangetic plains of eastern India were also taken to study the standard heterosis.

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Homozygous seeds of ten parents were sown in well-prepared plot having sandy loam soil (pH 6.5) during the third week of February, 2013 to raise 45 cross combinations in 10 × 10 half diallel mating design as per our previous study [12]. Seeds of 10 parents, 45 hybrids and 2 standard checks (Shakti and Abantika) were sown at a spacing of 60 cm (row to row) x 30 cm (plant to plant) in 3.6 m × 2.7 m plot during third week of July, 2014 following randomized complete block design with 3 replications in the research plots of All India Coordinated Research Project on Vegetable Crops, Bidhan Chandra Krishi Viswavidyalaya, West Bengal, India, situated at 23.5°N latitude and 89°E longitude at a mean sea level of 9.75 m. The period from July to September has been selected for screening of parents/hybrids against YVMV disease because of high population of viruliferous whiteflies which spread the maximum virus disease. Standard cultural practices were followed as per Chattopadhyay et al. [19,20]. No plant protection measures against sucking insect pests of okra were done in and around the experimental area to build up a reasonable amount of whitefly population. At the same time, one row of infected plants of local susceptible variety was sown after every plot of parents and hybrids to ensure sufficient virus inoculums.

Data recording

Data on days to 50% flowering, node number at first flowering, fruit length (cm), fruit diameter (cm), fruit weight (g), number of fruits per plant, and fruit yield per plant (g) were recorded from 20 randomly selected plants of each plot in each replication. Fifteen randomly selected fruits of marketable maturity (7 days after anthesis) were sampled from the selected plants per replication to record the observations on the following fruit characters. All harvested fruits of each plant were counted and weighed to determine average number of fruits per plant and total weight of fruits per plant which was recorded as fresh fruit yield per plant (g).

Monitoring of whitefly population

The incidence of YVMV disease depends on the population build up of the vector (Bemisia tabaci) and the presence of virus source. Whitefly populations were monitored from July to September and were recorded on five leaves, two each from lower, middle and one from upper canopy of the plants between 5.30 a.m. and 6 a.m. from 5 randomly selected tagged plants of each plot at 10-days interval starting from 20 days after sowing.

Estimation of yellow vein mosaic virus disease severity

Ten parents, forty hybrids and two standard checks were grown without any protective cover of insecticides to take data on percent disease index (PDI). PDI was recorded replication wise at five stages at an interval of 15 days starting from 30 days after sowing (DAS) to 90 DAS. Vein clearing symptom of any form in the plant was treated as disease incidence. The PDI was expressed as percentage taken from the cages and the feeding of vector on the plants was ensured since they were protecting inside the cages.

Data of all the eight characters were analyzed statistically using the standard methods of the randomized complete blocks design [21]. The magnitude of heterosis was estimated in relation to standard hybrids and was calculated as percentage increase or decrease of F 1's over standard hybrids (SH) values as per the formula suggested by Wynne et al. [22]. The dominance estimate (D.E.) usually referred to as “potence ratio” was computed using the following formula as suggested by Smith [23].

\[
\text{D.E.} = \frac{F_1 - MP}{0.5 \times P_2 - P_1}
\]

Where, \( F_1 \) mean of the hybrid; MP=mid-parent; \( P_2 \) mean of the highest parent; \( P_1 \) mean of the lowest parent. Over dominance is considered when D.E. exceeds ± 1; Complete dominance is realized when D.E.≥+1; while partial dominance is indicated when D.E. is between −1 and +1; D.E.=0 suggests absence of dominance. The ‘+’ and ‘−’ signs indicate the direction of dominance of either parent.

Combining ability variances and effects were worked out according to Griffing’s [17] Model 1 and Method 2 as parents and one set of non-reciprocal F 1’s were included. Statistical analyses were done using software SPSS Professional Statistics version 7.5 (SPSS Inc., Chicago, IL).

Results and Discussion

Genetic effects for different characters

The analysis of variance for combining ability based on Griffing’s Model 1 and Method 2 illustrated that components of gca and sca mean squares were highly significant for fruit yield per plant along with all other quantitative traits in F 1 generation (Table 1), indicated equal importance of both additive and non-additive gene actions in the inheritance of studied traits. The relative importance of genetic effects for quantitative traits is generally ascertained by the predictability ratio [24]. Preponderance of additive gene effects for days to 50% flowering was reflected as their predictability ratios were approaching unity (more than 0.80). In contrast, node number at first flowering, fruit diameter, fruit weight and PDI of YVMV disease
were controlled by both additive and non-additive gene action as their predictability ratios were between >0.50 and <0.80. On the other hand, the ratios <0.50 for fruit length, number of fruits per plant, and fruit yield per plant were indicative of non-additive genetic control of these traits (Table 2). In the present study, the GCA effects could not be considered to predict the performance of the parents, because most of the values of predictability ratio were much lower than the unity. Low predictability ratio highlighted the importance of SCA variance, and hence late selection would be practised based on better heterotic combinations rather than the performance of the parents involved in crossing programmes. Overwhelming response of non-additive gene action for the control of fruit length, number of fruits per plant and fruit yield per plant has been observed, hence selection will bring no or slow genetic improvement. In such case, heterosis breeding could be used to harness it by producing and marketing hybrids affordable to the resource-poor farmers of tropics for increasing okra productivity. The effects of non-additive gene actions for such traits are in a harmony with the findings of Das et al. [12]. On the other hand, selection for traits, such as node at first flowering, fruit weight, fruit diameter, and PDI of YVMV disease, that were governed by both additive and non-additive type of gene actions, might be deferred to later generations to allow a decrease in dominance, additive × dominance, and dominance × dominance effects [25]. The use of reciprocal recurrent selection could improve these traits [26]. Preponderance of both additive and non-additive gene action for the control of node number at first flowering was earlier reported by Jindal et al. [11]. The greater importance of additive gene effects ($\alpha_a$) in case of days to 50% flowering suggested the use of breeding systems that emphasize mainly $\alpha_a$. The amount of $\alpha_a$ contribution to the non-additive variance estimated for such traits is not known. However, if additive × additive epistatic variance was of importance, breeding system would change very little because additive × additive epistatic variance can be exploited by pedigree method. This type of epistatic variance increases during the selting process so that selection of traits governing earliness of the crop in early generations should be handled accordingly as suggested by Singh et al. [25]. Previous studies also suggested additive genetic control for days to 50% flowering [27].

**Standard heterosis and dominance effect of F₁ hybrids**

The number of F₁ hybrids displaying either significantly positive or negative heterosis over two standard commercial hybrids (Shakti and Abantika) is presented in Table 3. The cross BCO-1 × Arka Anamika expressed the maximum standard heterosis for fruit yield per plant and PDI of YVMV disease over Shakti (4.62%, -71.28%, respectively) and Abantika (17.59%, -72.28%, respectively). However, the hybrid VRO-6 × 11/RES-6 also exhibited desired significant standard heterosis for fruit yield per plant and PDI of YVMV disease over Abantika (12.00%, -55.82%, respectively) and also showed heterosis for PDI of YVMV disease over Shakti (-54.24%). In general, high yielding crosses exhibited low severity of YVMV disease and less population density of whiteflies as revealed from the Figures 1-2. The correlation study also depicted that fruit yield expressed strong inverse relations with PDI of YVMV disease and average whitefly population per leaf (Table 4). The highest mean (per se) performance for fruit yield per plant along with low severity of YVMV disease was recorded in BCO-1 followed by 11/RES-6 (Table 2). Thus, two promising crosses involved at least one parent having high yield potential with low disease severity. The hybrids with negative estimates of heterosis for days to 50% flowering, node number at first flowering and PDI of YVMV disease are desirable and could always be exploited. Our results are in well comparable with Jagan et al. [28] for node number at first flowering. Significant negative standard heterosis for PDI of YVMV disease has also been reported [29]. Fruit yield of crosses were highly influenced by YVMV disease severity and whitefly population density. The inverse relationships between yield and disease causing factors have also been reported from the Gangetic plains of eastern India [30]. On the other hand, positively significant standard heterosis for fruit length, fruit diameter, fruit weight, number of fruits per plant and fruit yield per plant found in our study, have also been reported [12,13,29,31,32] and could be useful for selection of high yielding hybrids. No problem of cross compatibility has been observed between cultivated (A. esculenta) and two wild species (A. manihot and A. cailei) as well as between two wild species. However, the expression of two wild species in a series of hybrid combinations with parents of cultivated species (A. esculenta) did not show any promise with regard to fruit yield and YVMV disease tolerance. These wild species might have acted as symptomless carrier of YVMV disease as reported earlier by Nariani and Seth [18]. Therefore, utilization of wild parent belonging to these species may be discouraged in hybrid development programme of okra.

The values of dominance estimates illustrated in 45 F₁ hybrids are presented in Table 5. Preponderance of partial dominance was reflected in most of hybrids in days to 50% flowering and fruit diameter. Overwhelming response of over dominance in majority of the hybrids was evident in conditioning of characters like node at first flowering, fruit length, number of fruits per plant, fruit yield per plant and PDI of YVMV disease. Thus the present study reflected various degrees of dominance; i.e., complete, partial to over-dominance or absence of dominance which involved in the inheritance of characters studied. To the best of our knowledge no previous works have been documented so far in okra to support our findings.

**Table 1: Analysis of variance (mean square) for combining ability of eight characters in okra.**

<table>
<thead>
<tr>
<th>Source of variation (d.f.)</th>
<th>D5OF</th>
<th>NFF</th>
<th>FL</th>
<th>FD</th>
<th>FW</th>
<th>FYPP</th>
<th>PDI</th>
</tr>
</thead>
<tbody>
<tr>
<td>GCA (9)</td>
<td>433.64**</td>
<td>24.67**</td>
<td>5.80**</td>
<td>0.53**</td>
<td>45.40**</td>
<td>65.08**</td>
<td>1501.19**</td>
</tr>
<tr>
<td>SCA (45)</td>
<td>4.30**</td>
<td>1.75**</td>
<td>0.64**</td>
<td>0.02**</td>
<td>3.16**</td>
<td>15.88**</td>
<td>1133.74**</td>
</tr>
<tr>
<td>Error (108)</td>
<td>1.98</td>
<td>0.02</td>
<td>0.0014</td>
<td>0.0007</td>
<td>0.11</td>
<td>0.09</td>
<td>6.24</td>
</tr>
<tr>
<td>$\alpha_a$</td>
<td>35.97</td>
<td>2.05</td>
<td>0.48</td>
<td>0.04</td>
<td>3.77</td>
<td>5.42</td>
<td>637.76</td>
</tr>
<tr>
<td>$\alpha_n$</td>
<td>2.32</td>
<td>1.73</td>
<td>0.64</td>
<td>0.02</td>
<td>3.05</td>
<td>15.80</td>
<td>1127.50</td>
</tr>
<tr>
<td>Predictability ratio</td>
<td>0.94</td>
<td>0.54</td>
<td>0.43</td>
<td>0.73</td>
<td>0.55</td>
<td>0.26</td>
<td>0.36</td>
</tr>
</tbody>
</table>

D5OF= Days to 50% flowering, NFF= Node at 1st flowering; FL= Fruit length (cm), FD= Fruit diameter (cm), FW= Fruit weight (g), NFPF= Number of fruits per plant, FYPPP= Fruit yield per plant (g), PDI= Percent Disease Index (%) of YVMV disease.

* Significant at 1% level
Choosing of good general and specific combiners

Two parents, BCO-1 and 11/RES-6 exhibited significant gca effects in desired direction in most of the heterotic hybrids for fruit yield per plant followed by number of fruits per plant, fruit per se performance of 10 parents for eight characters of okra. These best specific combiners could be identified as potential specific combiner for certain important traits. The negative SCA effects observed in some of the crosses for different characters might be due to the presence of unfavourable gene combinations in the parents for the respective traits. These best specific combiners having the highest magnitude of significant SCA effects in desired direction are recommended for heterosis breeding. The inter-crossing of these materials could, therefore, generate a population with a large gene pool, where genetic linkages and genetic blocks could be broken [33]. Significant sca effects in desired direction

Two crosses, BCO-1 × Arka Anamika and VRO-6 × 11/RES-6 expressed the maximum significant sca effects for fruit yield per plant along with number of fruits per plant, days to 50% flowering, and PDI of YVMV disease in desired directions (Table 3). Among the forty five hybrids, the per se performance of the hybrid BCO-1 × Arka Anamika was found to be the highest for fruit yield per plant and could be identified as potential specific combiner for certain important traits. The negative SCA effects observed in some of the crosses for different characters might be due to the presence of unfavourable gene combinations in the parents for the respective traits. These best specific combiners having the highest magnitude of significant SCA effects in desired direction are recommended for heterosis breeding. The inter-crossing of these materials could, therefore, generate a population with a large gene pool, where genetic linkages and genetic blocks could be broken [33].

### Table 2: Mean (per se) performance of 10 parents for eight characters of okra.

<table>
<thead>
<tr>
<th>Parents</th>
<th>D50F</th>
<th>NFF</th>
<th>FL</th>
<th>FD</th>
<th>FW</th>
<th>NFPP</th>
<th>FYPP</th>
<th>PDI</th>
</tr>
</thead>
<tbody>
<tr>
<td>BCO-1</td>
<td>47.33</td>
<td>6.50</td>
<td>8.35</td>
<td>1.45</td>
<td>9.01</td>
<td>25.07</td>
<td>177.53</td>
<td>9.56</td>
</tr>
<tr>
<td>VNR Green</td>
<td>49.00</td>
<td>5.03</td>
<td>6.93</td>
<td>1.46</td>
<td>9.90</td>
<td>12.17</td>
<td>113.88</td>
<td>17.25</td>
</tr>
<tr>
<td>VRO-6</td>
<td>46.67</td>
<td>4.07</td>
<td>7.86</td>
<td>1.52</td>
<td>9.02</td>
<td>13.33</td>
<td>111.09</td>
<td>60.23</td>
</tr>
<tr>
<td>11/RES-6</td>
<td>49.00</td>
<td>5.07</td>
<td>5.87</td>
<td>1.28</td>
<td>5.58</td>
<td>16.80</td>
<td>170.00</td>
<td>14.40</td>
</tr>
<tr>
<td>10/RES-6</td>
<td>46.00</td>
<td>4.50</td>
<td>7.72</td>
<td>1.60</td>
<td>9.59</td>
<td>16.40</td>
<td>111.80</td>
<td>45.86</td>
</tr>
<tr>
<td>10/RES-4</td>
<td>47.00</td>
<td>6.50</td>
<td>7.90</td>
<td>1.46</td>
<td>8.21</td>
<td>18.33</td>
<td>108.79</td>
<td>55.40</td>
</tr>
<tr>
<td>Pusa Sawani</td>
<td>48.00</td>
<td>6.03</td>
<td>9.00</td>
<td>2.20</td>
<td>8.75</td>
<td>5.63</td>
<td>48.46</td>
<td>74.29</td>
</tr>
<tr>
<td>Arka Anamika</td>
<td>49.67</td>
<td>6.00</td>
<td>8.20</td>
<td>1.42</td>
<td>7.40</td>
<td>6.47</td>
<td>55.18</td>
<td>64.02</td>
</tr>
<tr>
<td>A. mahhot</td>
<td>75.00</td>
<td>9.00</td>
<td>6.16</td>
<td>1.46</td>
<td>5.61</td>
<td>27.57</td>
<td>32.64</td>
<td>27.72</td>
</tr>
<tr>
<td>A. caillei</td>
<td>79.67</td>
<td>11.03</td>
<td>12.00</td>
<td>2.73</td>
<td>21.02</td>
<td>7.67</td>
<td>95.43</td>
<td>25.46</td>
</tr>
</tbody>
</table>

### Table 3: Selected crosses with high standard heterosis (%), their corresponding gca and sca effects, and type of cross combinations.

<table>
<thead>
<tr>
<th>Characters</th>
<th>Cross (es) with high standard heterosis (%) over Shakti</th>
<th>Cross (es) with high standard heterosis (%) over Abantika</th>
<th>Sca effects of crosses with per se performance</th>
<th>Type of combinations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Days to 50% flowering</td>
<td>BCO-1 × VNR Green (-10.39%**)</td>
<td>BCO-1 × VNR Green (-9.80%**)</td>
<td>-1.88 (46.00)</td>
<td>H x H</td>
</tr>
<tr>
<td>Node number at first flowering</td>
<td>VRO-6 × Pusa Sawani (-53.33%**)</td>
<td>VRO-6 × Pusa Sawani (-36.36%**)</td>
<td>-0.62 (4.50)</td>
<td>H x H</td>
</tr>
<tr>
<td>Fruit length (cm) None</td>
<td>A. caillei × Arka Anamika (25.24%**)</td>
<td>A. caillei × Arka Anamika (20.93%**)</td>
<td>0.52 (10.07)</td>
<td>H x H</td>
</tr>
<tr>
<td>Fruit diameter (cm) 10/RES-4 × A. caillei (44.70 %**)</td>
<td>Pusa Sawani × A. caillei (43.66 %**)</td>
<td>0.19 (2.32)</td>
<td>L x H</td>
<td></td>
</tr>
<tr>
<td>Fruit weight (g) BCO-1 × A. caillei (4.94 %)</td>
<td>BCO-1 × A. caillei (125.69 %**)</td>
<td>2.09 (18.37)</td>
<td>H x H</td>
<td></td>
</tr>
<tr>
<td>Number of fruits per plant</td>
<td>BCO-1 × Arka Anamika (48.41 %**)</td>
<td>BCO-1 × Arka Anamika (23.03 %**)</td>
<td>8.61 (23.40)</td>
<td>H x H</td>
</tr>
<tr>
<td>Fruit yield per plant (g/plant)</td>
<td>VRO-6 × 11/RES-6 (43.55%**)</td>
<td>VRO-6 × 11/RES-6 (25.55%**)</td>
<td>8.21 (22.63)</td>
<td>H x H</td>
</tr>
<tr>
<td>PDI (%) of YVMV disease</td>
<td>BCO-1 × Arka Anamika (-72.28 %**)</td>
<td>BCO-1 × Arka Anamika (-19.20 %**)</td>
<td>-22.39 (7.23)</td>
<td>H x L</td>
</tr>
</tbody>
</table>

Data in parentheses indicate per se values.

* Significant at 5% level, ** Significant at 1% level.
for node at 1st flowering [34] number of fruits per plant [35-37];
fruit length, fruit diameter, fruit weight and fruit yield per plant
[10]; PDI of YVMV disease [12] involving various combinations
of gca effects of the parents have also been reported. These two
promising hybrids along with one most susceptible hybrid (BCO-
1 × VRO-6) were grown under artificial inoculation condition
to confirm the tolerance against this virus. Out of twenty plants
inoculated with whiteflies none of the plants of the hybrid (BCO-1
× Arka Anamika) were developed any symptom of YVMV even after
30 and 45 days of inoculation and grow normally even after feeding
by the vectors. Only one plant after 60 days of inoculation showed
5.00 % disease incidence in BCO-1 × Arka Anamika as compared to
another promising hybrid VRO-6 × 2011/RES-6 which showed 15.00%
disease incidence. However, the susceptible hybrid BCO-1 × VRO-
6 exhibited 80.00 % disease incidence after 60 days of inoculation
(Table 6).

The perusal of different cross combinations revealed that the
crosses involved three types of combinations namely, H × H type;
H × L type and L × H type, where H stands for significant gca effect
and L for non-significant gca effect in desired direction of the parents
(Table 3). The result depicting the type of cross combinations for the
genetic control of the characters under study, both additive as well as
additive × additive type of epistatic interactions were involved in H ×
H type cross combinations and thus, can be exploited effectively for
the improvement of the traits through pedigree method of selection
[38]. On the other hand, crosses of H × L type or L × H type
involved one parent having either positive or negative significant
gca effect indicated that predominantly additive effect was present
in good combiner and possibly complementary epistatic effect in
poor combiner and these two gene actions acted in complementary
fashion to maximize the expression as suggested by Salimath and
Bahl [26].

Figure 1: Relationship between fruit yield (g/plant) and PDI (%) of YVMV disease in tolerant and susceptible hybrids of okra.

Figure 2: Relationship between fruit yield (g/plant) and average whitefly population per leaf in tolerant and susceptible hybrids of okra.
Table 4: Dominance estimate (DE) of F₁ hybrids for eight traits of okra.

<table>
<thead>
<tr>
<th>Crosses</th>
<th>D50F</th>
<th>NFF</th>
<th>FL</th>
<th>FD</th>
<th>FW</th>
<th>NFPP</th>
<th>FYPP</th>
<th>PDI</th>
</tr>
</thead>
<tbody>
<tr>
<td>BCO-1 × VNR Green</td>
<td>2.60</td>
<td>0.32</td>
<td>0.43</td>
<td>7.67</td>
<td>1.42</td>
<td>-1.12</td>
<td>-1.01</td>
<td>1.29</td>
</tr>
<tr>
<td>BCO-1 × VRO-6</td>
<td>-5.00</td>
<td>-0.64</td>
<td>2.11</td>
<td>-0.30</td>
<td>367.67</td>
<td>-0.90</td>
<td>0.20</td>
<td>-0.02</td>
</tr>
<tr>
<td>BCO-1 × 11/RES-6</td>
<td>1.40</td>
<td>-0.49</td>
<td>0.23</td>
<td>2.47</td>
<td>1.30</td>
<td>-2.27</td>
<td>-16.98</td>
<td>1.36</td>
</tr>
<tr>
<td>BCO-1 × 10/RES-6</td>
<td>-1.00</td>
<td>0.47</td>
<td>4.73</td>
<td>-0.06</td>
<td>8.69</td>
<td>-1.77</td>
<td>0.27</td>
<td>-0.18</td>
</tr>
<tr>
<td>BCO-1 × 10/RES-4</td>
<td>-1.00</td>
<td>0.00</td>
<td>6.66</td>
<td>3.00</td>
<td>8.52</td>
<td>-2.02</td>
<td>1.04</td>
<td>-0.17</td>
</tr>
<tr>
<td>BCO-1 × Pusa Sawani</td>
<td>1.00</td>
<td>7.29</td>
<td>0.51</td>
<td>-0.87</td>
<td>13.36</td>
<td>0.18</td>
<td>1.06</td>
<td>0.32</td>
</tr>
<tr>
<td>BCO-1 × A. caillei</td>
<td>-0.09</td>
<td>-1.44</td>
<td>-0.25</td>
<td>0.31</td>
<td>0.23</td>
<td>-1.26</td>
<td>-1.18</td>
<td>-1.22</td>
</tr>
<tr>
<td>BCO-1 × A. manihot</td>
<td>-0.20</td>
<td>0.20</td>
<td>-0.97</td>
<td>13.50</td>
<td>-1.35</td>
<td>-11.72</td>
<td>-0.64</td>
<td>-1.22</td>
</tr>
</tbody>
</table>

Table 5: Correlation comparison matrix between disease causing variables and fruit yield among tolerant and susceptible crosses of okra.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Fruit yield per plant (g)</th>
<th>PDI (%) of YVMV disease</th>
<th>Average whitefly population per leaf</th>
</tr>
</thead>
<tbody>
<tr>
<td>Fruit yield per plant</td>
<td>1.000</td>
<td>-0.976**</td>
<td>-0.972**</td>
</tr>
<tr>
<td>PDI (%) of YVMV disease</td>
<td>1.000</td>
<td>0.940*</td>
<td>1.000</td>
</tr>
</tbody>
</table>

** LSD at 1%.
Conclusion

The present study demonstrated the prevalence of non-additive gene effects in governing traits like fruit length, number of fruits per plant, and fruit yield per plant which could be improved through heterosis breeding. Pedigree method of selection is suggested for the improvement of days to 50% flowering controlled by additive gene effects. Reciprocal recurrent selection is ascertained to improve number at first flowering, fruit weight, fruit diameter, and PDI of YVMV disease influenced by both additive and non-additive gene effects. Two parents, BCO-1 and 11/RES-6 could be utilized as promising donors in future okra breeding programme for improvement in fruit yield and YVMV disease tolerance. Exploitation of parents belonging to wild species (A. manihot and A. caillei) for the development of desirable hybrids should not be encouraged. The cross BCO-1 × Arka Anamika emerged as outstanding hybrid in respect of fruit yield and level of tolerance against YVMV disease, and could be exploited at commercial level in the tropics after its critical evaluation. The dominance effects clearly demonstrated partial-to over-dominance reactions for the inheritance of fruit yield and other economically important traits in okra.

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References