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Genetic analysis and inheritance patterns of YVMV resistance in okra [*Abelmoschus esculentus* (L.) Moench]

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Abstract
A research was conducted at the vegetable research centre in GBPUA&T Pantnagar in 2022 showed that the YVMV Trait's complicated genetic inheritance pattern for disease tolerance. Generation means analysis involving six generations (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) was evaluated in randomized block design with two replications at performed to investigate okra traits. However, generation mean analysis demonstrated that the inheritance of disease tolerance includes both additive and non-additive effects. Thus, the current study provides more evidence that the disease resistance against YVMV characteristic is controlled by a complex genetic inheritance pattern. The key genes for tolerance may be inherited by other okra crossings, but the virus strains that break tolerance may prevent them from maintaining tolerance over time. A persistent tolerance phenotype in okra may thus need the accumulation of additional genes.

Keywords: Disease tolerance, gene, non-additive, sustainable, trait

Introduction
The most important vegetable crop in India is okra (*Abelmoschus esculentus* (L.) Moench), commonly referred to as lady's fingers, gumbo, or Bhindi. It originates in the old world, probably in one of the African countries. It belongs to the family Malvaceae and the genus *Abelmoschus*. (De Candolle, 1883; Vavilov, 1951) [4, 13] Ethiopia is where it initially originated. However, according to Zeven and Zhukovsky (1975) [16], it came from the Hindustani centre of origin, specifically the regions of India, Pakistan, and Burma. It is an often cross-pollination vegetable crop. It has a somatic chromosomal number of 2n = 130, and is amphidiploid of *Abelmoschus tuberculatus* with 2n = 58, and is an unidentified species with 2n = 72. The flower bud may be seen in the axil of each leaf node between the 6th to 8th leaf, depending on the species and takes about 22-26 days from initiation to full bloom. According on the cultivar, temperature, and humidity, anthesis occurs between 8 and 10 am (Purewal and Randhawa, 1947) [17].

For maximal growth and production, the crop has been adapted to tropical climates and vigorous, warm, humid weather. It is susceptible to drought and cold Nights temperature. The ideal soil moisture and temperature range for seed germination between 25–35 °C, with rapid germination observed at 35 °C and seeds fail to germinate below 17 °C. Most cultivars' flower buds have a tendency to desiccate and drop at temperatures over 42 °C, which reduces production. The ideal temperature range for growth is between 20 and 30 °C, and sunshine is just as crucial for okra yields. The first three weeks after sowing, a 50% reduction in sunshine had a negative impact on yield. (Adekiya *et al*., 2017) [1]. The crop is simple to grow, making it particularly appealing to women who work in agriculture as a source of income and employment. Furthermore, it is grown using conventional farming methods with little or no focus on production. (Ariyo, 1990) [2]

Vitamins, calcium, potassium, and other minerals are present in okra. Consumable unripe Bhindi fruits have 18mg of vitamin C, 10.4g of dry matter, 3,100 calories, 1.8g of protein, 90mg of calcium, 1.0mg of iron, 0.1mg of carotene, 0.07mg of thiamin, 0.08mg of riboflavin, and 0.08mg of niacin per 100g. (Thirumalaikumar *et al*., 2014) [12]. 20–24% protein and 13-22% edible oil are the two elements found in the dry seeds. Compared to green veggies, okra is more profitable.

In many other nations, including Brazil, West Africa, and India, fresh okra fruits are valued and consumed as vegetables.

India is the world's leading producer of okra. Okra was grown throughout the whole country over an area of 0.528 million hectares, producing 6.41 million tonnes of green fruits at a productivity of 11.60 tonnes per hectare. It produced 33.24 lakh metric tonnes from an area of 3.47 lakh hectares, placing it next to the tomato in the fifth spot among vegetables in the nation. Okra makes up 5.9 percent of the total area and 3.9 percent of the total production of vegetables. Okra production is dominated by Andhra Pradesh, whereas Jammu and Kashmir has the highest yield (NHB 2021-22).

The most serious and devastating virus that affects okra is Yellow Vein Mosaic Virus (YVMV). All phases of crop growth are affected by the disease, which substantially decreases growth and produce by 50 to 94 percent. It spreads by the vector, the white fly. The most economical and ecologically friendly way to increase okra output potential is to improve host tolerance to viruses, which is one of the primary defenses against the okra yellow vein mosaic disease. However, there has been a significant desire for YVMV-resistant, higher-yielding cultivars. Consequently, the development of YVMV-resistant cultivars or hybrids is necessary. (Shetty *et al.*, 2013) [11]. Because of the widespread incidence of a disease known as Yellow Vein Mosaic Virus (YVMV), which damage crops at all growth stages (Verma, 1952) [14] resulting in loss of yield ranging from 50 to 90%, okra production has been in danger for a while (Sastry and Singh, 1974) [9].

Material and Method

An aggregate of six generations was utilized in the experiment. *viz.*, P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2 of each of four different Okra crosses were sown during *kharif*, 2022 in Randomized Block Design replicated twice. Each plot consisted three row of P_1, P_2, F_1, BC_1P_1 and BC_1P_2 and eight rows of F_2. Each row was three meter long. Plant-to-plant and row-to-row spacing were both kept at 30 cm and 50 cm, respectively. The crop was successfully raised by using the other recommended procedures. Data on two YVMV disease-related traits days to first appearance of YVMV and Percent Disease Index of YVMV were evaluated. Days to first appearance of YVMV disease were recorded from the date of sowing to the date when first appearance of disease in each entry had flowered population. Diseases verity grade is to be recorded at 30DAS, 45DAS, 60DAS, 75DAS and 90DAS. Record the disease verity grade based on diseases verity range given bellow.

Table 1: Disease scale for YVMV

Severity range%	Disease scale/grade	Disease reaction
0	0	Immune (I)
1-10	1	Highly Resistant (HR)
11-25	2	Moderately Resistant (MR)
26-50	3	Tolerant (T)
51-60	4	Moderately Susceptible (MS)
>60	5	Susceptible (S)

$$PDI(\%)=\frac{Sum\ of\ all\ disease\ rating}{Maximum\ grade\times\ total\ number\ of\ leaves}\times 100$$

(Senjam *et al.*, 2018) [10].

Result and Discussion

Screening of genotypes against YVMV

On the basis of visual evaluations conducted at various phonological stages *i.e*. 30, 45, 60, 75, and 90 DAS, the prevalence of the YVMV disease under natural circumstances was reported. The outcome was that cross EC-169400 showed high percent disease index at 75 days and cross EC-169435 x 15/RES-4 showed least infection of YVMV among the parental lines. In F_1 cross IC-117123 x 15/RES-4 showed lowest infection and EC-169430 x 15/RES-4 recorded high percent disease index at 75 days. In F_2 cross EC-169435 x 15/RES-4 showed lowest infection and IC-117123 x 15/RES-4 recorded high percent disease index at 75 days. In F_1 cross IC-117123 x 15/RES-4 showed lowest infection and EC-169430 x 15/RES-4 recorded high percent disease index at 75 days. In BC_1P_1 cross IC-117123 x 15/RES-4 showed lowest infection and EC-169400 x 15/RES-4 recorded high percent disease index at 75 days. In BC_1P_2 cross IC-117123 x 15/RES-4 showed lowest infection and EC-169430 x 15RES-4 recorded high percent disease index at 75 days.

Days to first appearance of YVMV disease

It was found that the YVMV disease had a high infection rate once symptoms initially developed. The plants that had been infected with the YVMV disease before flowering exhibited the lowest yield.

Therefore days to firs appearance of YVMV disease was found key indicator governing susceptibility/ resistance of okra parents and crosses. It was found that early appearance of YVMV were recorded in cross EC-169430 and late appearance of YVMV disease found in cross 15/RES-4 among the parental line, while in F_1 late appearance of YVMV disease found in cross EC-169430 x 15/RES-4. F_2 late appearance of YVMV disease found in cross EC-169430 x 15/RES-4. In BC_1P_1 & BC_1P_2 generation cross IC-117123 x 15/RES-4 was observed late for appearance of YVMV disease.

Quantitative genetic analysis

Days to first appearance of YVMV disease

The significant of scaling test B, C and D in cross I under study indicated that inadequacy of additive-dominance model (table-2) thus, the presence of all three types of non-allelic gene interaction, *viz*. additive × additive (i), additive × dominance (j), dominance × dominance (l) were confirmed through the digenic-epistasis six parameter model (table-3). In addition to that, the significant values of all the gene effects revels the presence of additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The value of (h) and (l) were of the different sign which indicate the presence of duplicate type of epistasis.

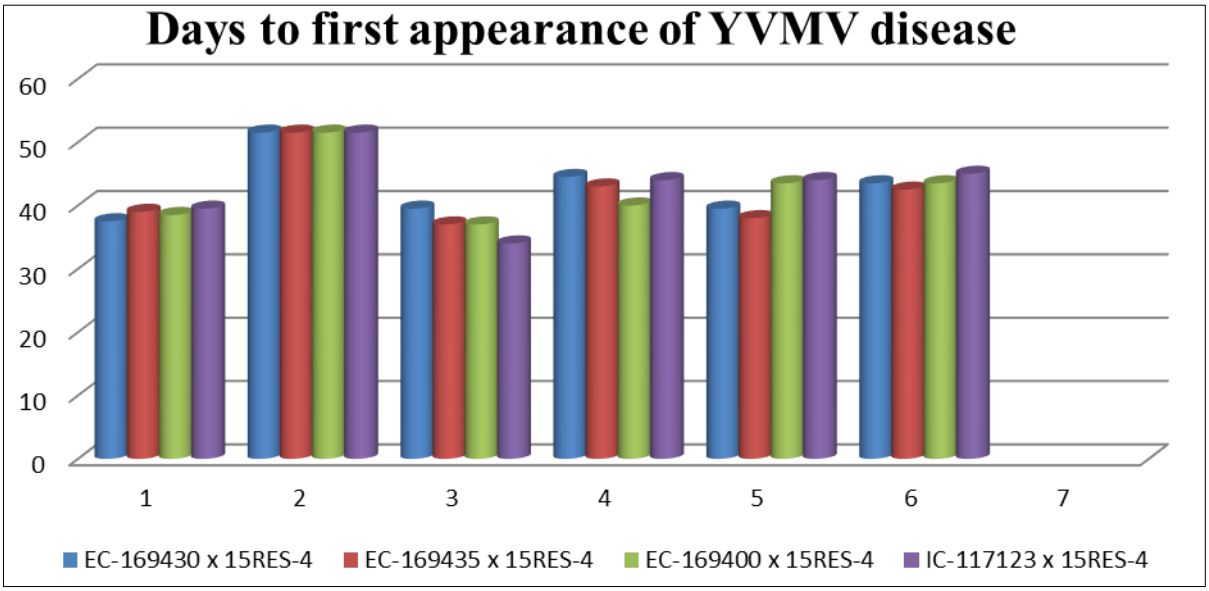
Gene interaction for cross II were found significant for scaling test B indicated the presence of all the three types of nonallelic gene interaction, namely (i), (j) and (l) and significant value of (d), (h), (l) and (j) gene effects revels the presence of additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The value of (h) and (l) were of the different sign which indicate the presence of duplicate type of epistasis.

Significant value of A and D scales in case of cross III indicated the presence of all the three types of nonallelic gene interaction, namely (i), (j) and (l) and significant value of (d), (h), (l) and (j) gene effects revels the presence of additive (d),

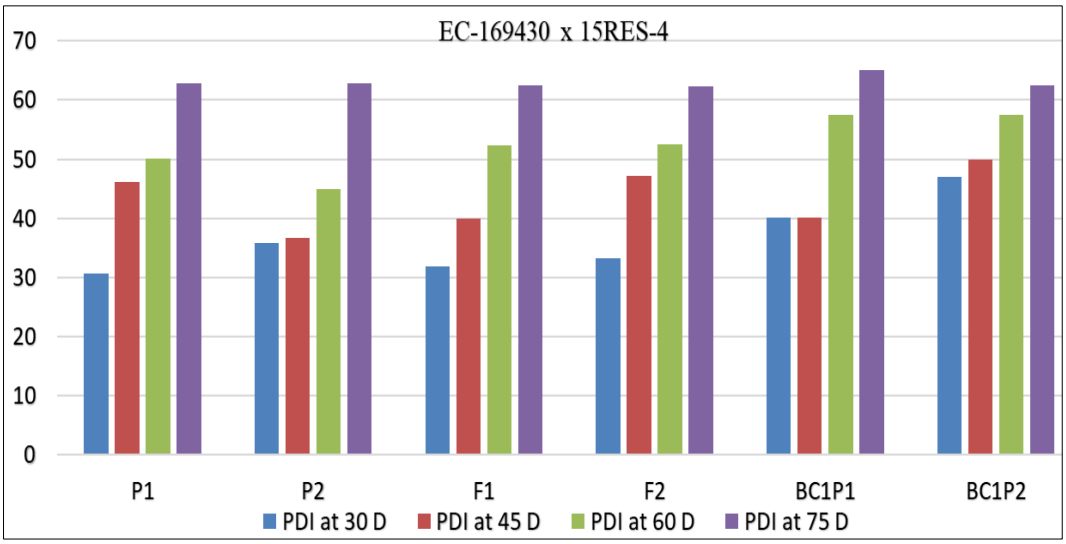
dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The value of (h) and (l) were of the different sign which indicate the presence of duplicate type of epitasis.
Significant value of A, B and C scales in case of cross IV indicated the presence of all the three types of nonallelic gene interaction, namely (i), (j) and (l) and significant value of (d), (h), (l) and (j) gene effects revels the presence of additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The value of (h) and (l) were of the different sign which indicate the presence of duplicate type of epitasis. However the magnitude of dominance × dominance (l) was higher compared to additive × additive (i) and additive × dominance (j) for all the four crosses, all with negative sign, suggested that pedigree breeding followed by intense selection of desirable sergeants through later generation would be most favourable for the improvement of this trait of okra.

Percent disease index of YVMV at 75 days

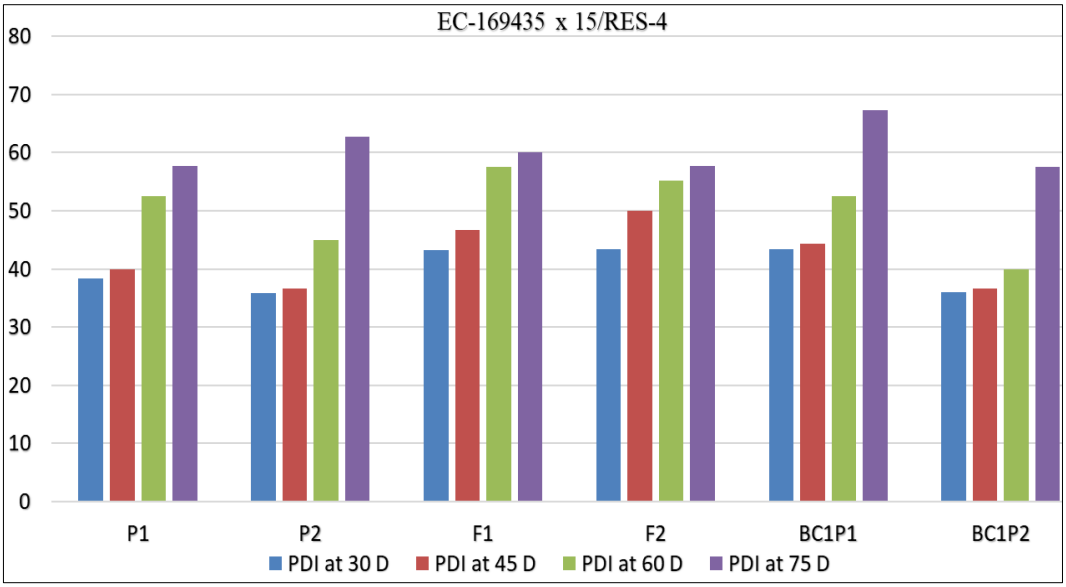
The significant of scaling test A, and D for cross I, the findings of the investigation revealed that the additive-dominance model was inadequate (table-2) thus, whenever all three non-allelic interaction types are present, *viz*. additive × additive (i), additive × dominance (j), dominance × dominance (l) were confirmed through the digenic-epistasis six parameter model (table-3). In addition to that, the significant values of all the gene effects revels the presence of additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The value of (h) and (l) were of several signs that point to the occurrence of duplicate epistasis. The significant value effect in cross I, I proposed that selection of suitable segments exhibiting late YVMV appearances as well as heterosis breeding would be similarly effective for this attribute.
Gene interaction for cross II were found significant for scaling test A, B, C and D indicated the presence of all the three types of nonallelic gene interaction, namely (i), (j) and (l) and significant value of (d), (h), (l) and (j) gene effects revels the presence of additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The value of (h) and (l) were of the different sign which indicate the presence of duplicate type of epistasis.
Significant value of A, B, C and D scales in case of cross III showed that all three forms of nonallelic gene interaction were present namely (i), (j) and (l) and significant value of (d), (h), (l) and (j) gene effects revels the presence of additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The value of (h) and (l) were amongst the several symptoms indicating epitasis of the duplication kind was present.
Significant value of A, B and C scales in case of cross IV indicated the presence of all the three types of nonallelic gene interaction, namely (i), (j) and (l) and significant value of (d), (h), (l) and (j) gene effects revels the presence of additive (d), dominance (h), additive × additive (i), additive × dominance (j) and dominance × dominance (l). The value of (h) and (l) were of the same sign which indicate the presence of complimentary type of epitasis. However the magnitude of dominance × dominance (l) was higher compared to additive × additive (i) and additive × dominance (j) for all the four crosses, They're all negative, suggested the best approach to improving this characteristic of okra would be pedigree breeding, followed by a stringent selection of desirable sergeants through subsequent generations.
Both the additive and non-additive type gene impacts were shown to be essential to the emergence of both the YVMV-related character in the current investigation. However, the magnitudes of dominance × dominance was higher compared to additive × additive and additive × dominance for all four crosses, have negative sign, and recommended that the best method for enhancing this feature for okra would be pedigree breeding followed by a intense selection of appropriate segregates over the following generations. While compared to the other two interactions, the PDI exhibited a greater degree of dominant influence than additive effect as well as a higher magnitude of dominance × dominance, usually with a negative sign. This study showed that the selection of disruptive sergeants was next in importance to heterosis breeding and recombination breeding in terms of improving this population for this trait.



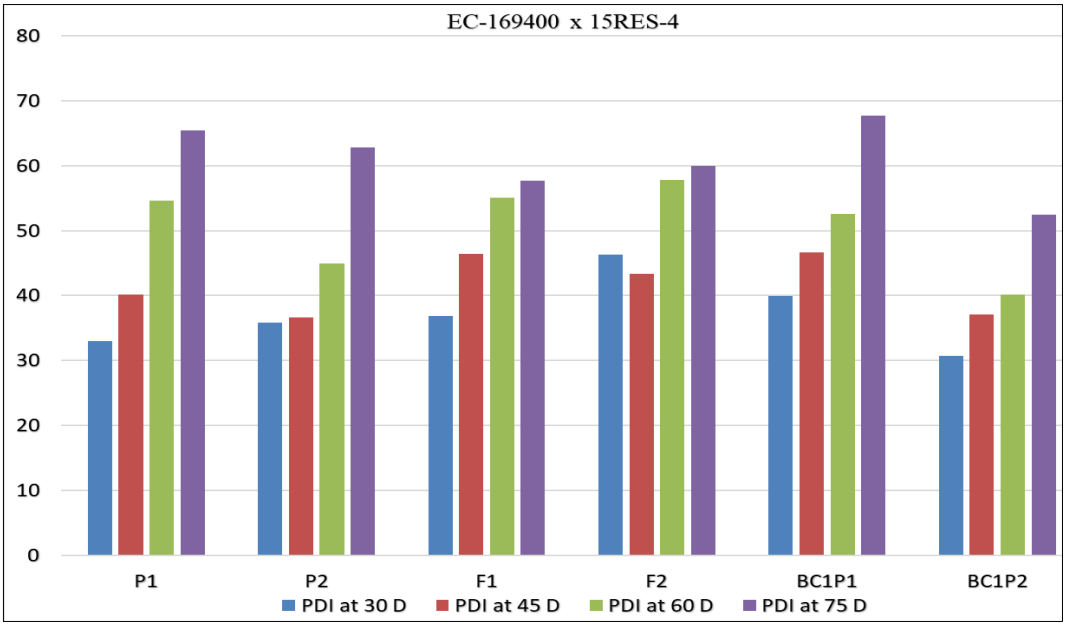
Graph 1: Mean performance of six generations for days to first appearance of YVMV disease in 4 crosses of Okra



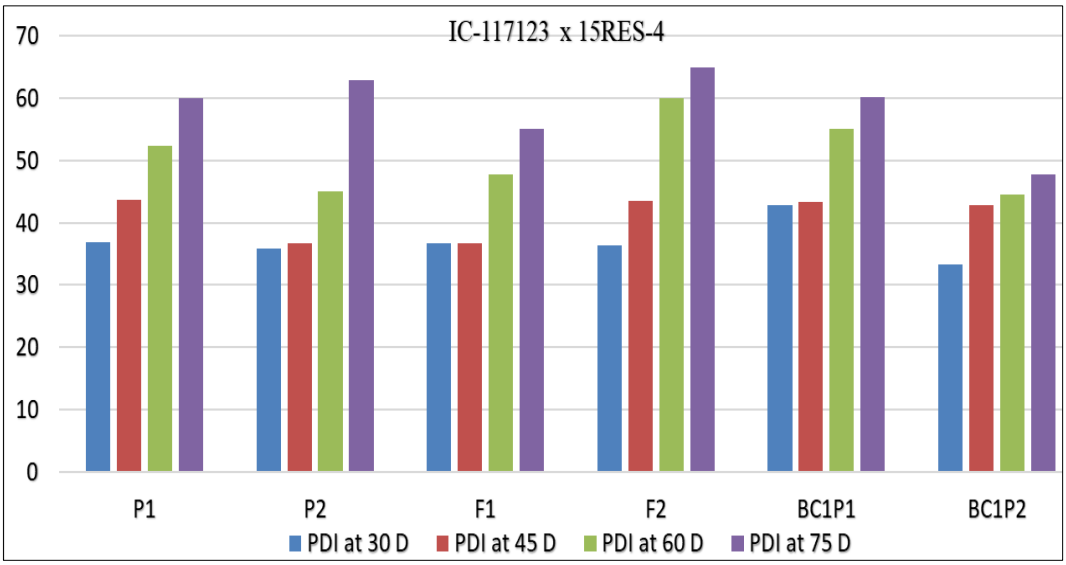
Graph 2: Mean performance of six generations for percent disease index for YVMV in Okra for cross EC-169430 x 15/RES-4



Graph 3: Mean performance of six generations for percent disease index for YVMV in Okra for cross EC-169435 x 15/RES-4



Graph 4: Mean performance of six generations for percent disease index for YVMV in Okra for cross EC-169400 x 15/RES-4



Graph 5: Mean performance of six generations for percent disease index for YVMV in Okra for cross IC-117123 x 15/RES-4

Table 1: Gene effect estimates based on a scaling test

Character and crosses	A	B	C	D
Days to first appearance of YVMV disease				
EC-169430 x 15RES-4	2.00±0.22	-4.00**±1.22	10.00**±2.35	6.00**±1.01
EC-169435 x 15RES-4	0.00±4.58	-3.50±0.29	7.50±1.15	5.50**±0.96
EC-169400 x 15RES-4	11.50**±5.02	-1.50±2.29	-4.00±9.62	-7.00**±1.13
IC-117123 x 15RES-4	14.50**±2.87	4.50**±2.06	17.00**±2.70	-1.00±2.24
Percent disease index of YVMV at 30 days				
EC-169430 x 15RES-4	17.80**±1.63	-26.29**±1.91	2.75±3.18	20.67**±0.51
EC-169435 x 15RES-4	0.24±0.16	-7.09**±1.51	7.86**±0.82	7.36**±0.66
EC-169400 x 15RES-4	10.16**±0.38	-11.39**±1.55	42.70**±1.67	21.97**±0.97
EC-117123 x 15RES-4	12.18**±1.22	-5.99**±0.78	-0.74±1.71	-3.47**±0.85
IC-169430 x 15RES-4	17.80**±1.63	-26.29**±1.91	2.75±3.18	20.67**±0.51
Percent disease index of YVMV at 45 days				
EC-169430 x 15RES-4	5.80**±0.67	23.43** ±0.38	26.06**±2.18	4.22±1.00
EC-169435 x 15RES-4	1.97**±0.04	-9.99**±0.02	30.28**±0.25	19.15**±0.12
EC-169400 x 15RES-4	6.75**±0.25	-8.88**±0.93	3.86**±0.49	3.00±0.46
IC-117123 x 15RES-4	6.38** ±0.35	-3.64**±0.97	20.23**±0.59	0.72±0.54
Percent disease index of YVMV at 60 days				
EC-169430 x 15RES-4	12.72**±0.18	17.51**±0.24	10.37**±0.36	-9.93**±0.09
EC-169435 x 15RES-4	-4.98**±0.08	-22.51**±0.02	8.10**±0.64	-17.79**±0.32
EC-169400 x 15RES-4	-4.73**±0.36	-19.79**±0.35	21.35**±1.31	22.93**±0.64
IC-117123 x 15RES-4	9.94**±0.32	-22.31**±0.92	47.18**±0.55	20.44**±0.44
Percent disease index of YVMV at 75 days				
EC-169430 x 15RES-4	4.75** ±0.25	-0.32 ±0.31	-1.57 ±1.08	-3.00 **±0.50
EC-169435 x 15RES-4	16.91** ±0.43	-7.80** ±0.31	-9.54** ±1.08	-9.33** ±0.53
EC-169400 x 15RES-4	12.26 **±0.76	-15.56** ±0.40	-3.81** ±0.55	-0.26 ±0.25
IC-117123 x 15RES-4	5.23** ±0.23	-22.31**±0.59	27.19** ±0.31	22.14** ±0.28

Table 2: Gene effect estimates based on the scaling test for each of the six parameters okra intervarietal cross model

Character and crosses	M	D	H	I	J	L	Type of epistasis
Days to first appearance of YVMV disease							
EC-169430 x 15RES-4	44.50**±0.50	-4.00**±0.71	-17.00**±2.52	-12.00**±2.45	3.00**±0.79	14.00**±1.67	Duplicate
EC-169435 x 15RES-4	43.00**±0.01	-4.50**±2.06	-19.25**±4.62	-11.00**±4.12	1.75±2.14	14.50**±9.23	Duplicate
EC-169400 x 15RES-4	40.00**±2.00	0.00±1.58	6.00**±2.01	14.00**±8.60	6.50±0.37	-24.00**±1.51	Duplicate
IC-117123 x 15RES-4	44.00**±1.00	-1.00±1.00	-9.50**±4.91	2.00±4.47	5.00**±1.06	-21.00**±2.96	Complementary
Percent disease index of YVMV at 30 days							
EC-169430 x 15RES-4	33.23**±0.11	-6.89**±0.46	39.92**±1.87	41.34**±1.01	-4.25**±0.67	-85.43**±3.68	Duplicate
EC-169435 x 15RES-4	43.38**±0.05	7.38**±0.65	-11.09**±1.37	-14.71**±1.31	3.66**±0.75	21.56**±2.72	Duplicate
EC-169400 x 15RES-4	46.31**±0.35	9.32**±0.67	-41.54**±1.98	-43.93**±1.93	10.78**±0.79	45.16**±3.14	Duplicate
IC-117123 x 15RES-4	36.32**±0.34	9.55±0.51	7.24±1.77	6.93**±1.70	9.09**±0.72	-13.12**±2.65	Duplicate
Percent disease index of YVMV at 45 days							
EC-169430 x 15RES-4	47.16**±0.50	-9.87**±0.12	-9.96**±2.05	-8.43**±1.99	-14.62**±0.28	-9.20**±2.23	Complementary
EC-169435 x 15RES-4	50.06**±0.06	7.65**±0.02	-29.97**±0.25	-38.30**±0.25	5.98**±0.02	46.33**±0.26	Duplicate

EC-169400 x 15RES-4	43.38**±0.05	9.54**±0.45	2.07±0.95	-5.99**±0.92	7.81**±0.45	8.12**±1.87	Complementary
IC-117123 x 15RES-4	43.45**±0.12	0.49±0.49	-4.98**±1.09	-1.43±1.07	-3.03**±0.51	-17.37**±2.03	Complementary
Percent disease index of YVMV at 60 days							
EC-169430 x 15RES-4	52.51**±0.02	0.11±0.09	24.68**±0.25	19.86**±0.18	-2.39**±0.09	-50.09**±0.50	Duplicate
EC-169435 x 15RES-4	55.16**±0.16	12.53**±0.03	-26.84**±0.64	-35.58**±0.64	8.76**±0.04	63.06**±0.66	Duplicate
EC-169400 x 15RES-4	57.81**±0.31	12.36**±0.17	-40.57**±1.30	-45.86**±1.29	7.53**±0.24	70.37**±1.47	Duplicate
IC-117123 x 15RES-4	60.00**±0.00	10.44**±0.44	-41.78**±0.92	-40.88**±0.88	6.79**±0.45	34.58**±1.84	Duplicate
Percent disease index of YVMV at 75 days							
EC-169430 x 15RES-4	62.25**±0.25	2.50±0.00	5.72**±1.02	6.00**±1.00	2.53±0.20	-10.43**±1.08	Duplicate
EC-169435 x 15RES-4	57.75**±0.25	9.82**±0.18	18.36**±1.08	18.65**±1.06	12.36**±0.27	-27.76**±1.29	Duplicate
EC-169400 x 15RES-4	60.00**±0.00	15.26**±0.25	-5.89**±0.64	0.51±0.51	13.91**±0.39	2.79±1.28	Duplicate
IC-117123 x 15RES-4	65.00**±0.00	12.37**±0.28	-50.68**±0.57	-44.27**±0.55	13.77**±0.32	61.35**±1.15	Duplicate

Conclusion

The existence of duplicate epistasis in both traits showed that the conventional selection process would be delayed because duplicate epistasis would lead to less diversity in F_2 and subsequent generations. Recurrent selection in biparental progenies would be beneficial for examining these kinds of non-allelic interaction since it causes a high frequency of good recombination and a concentration of alleles with functional consequences in the population. Although it was additionally discovered that a complementary form of epistasis existed in cross IV for days to first appearance of disease was exciting, because of the late emergence and minimal disease infection of the ne recombinants generated through this kind of epistasis, their yield is more extensive. Therefore, utilizing the hybrid breeding procedure, the above characteristics of this particular cross could have been improved. The most effective and easiest way to utilize every type of gene effect and aid in selecting superior lines with higher tolerance levels for YVMV disease in okra could be concluded to be a followed by a few phases of recurrent selection and the pedigree procedure.

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