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Characterization of Okra Genotypes for Yellow Vein Mosaic Virus Resistance and Yield-Related Traits

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ABSTRACT

Yellow vein mosaic disease (YVMD) is a major constraint to okra production, necessitating the identification of genotypes combining disease resistance with desirable yield attributes. The present study evaluated seven genetically diverse okra genotypes (G1–G7) for YVMD response and yield-related performance under artificial whitefly-mediated inoculation during 2026. The experiment was conducted in a randomized complete block design with three replications. Six yield-related traits, including days to first flowering, plant height, primary branches plant⁻¹, fruits plant⁻¹, average fruit weight, and fruit yield, were evaluated along with disease incidence and severity. Significant differences ($P < 0.001$) were observed among genotypes for all traits. Days to first flowering ranged from 46.0 days (G1) to 57.0 days (G6), while plant height varied from 119.33 to 152.33 cm. G6 recorded the highest number of primary branches (6.90 plant⁻¹), fruits (36.33 plant⁻¹), average fruit weight (19.93 g), and fruit yield (11.85 kg plot⁻¹). In contrast, G1 had the lowest disease incidence (18.33%) and severity (1.20), whereas G6 exhibited the highest disease incidence (84.00%) and severity (4.60). G2 and G3 showed comparatively lower disease incidence (25.33 and 32.33%, respectively) while maintaining relatively good fruit yield (9.29 and 9.98 kg plot⁻¹). Correlation analysis showed a significant positive association between fruits plant⁻¹ and fruit yield ($r = 0.64^*$), while disease incidence and severity were strongly correlated ($r = 0.76$). Overall, G1 was identified as the most promising genotype for YVMD tolerance, whereas G2 and G3 showed potential for combining relatively lower disease response with improved productivity. The findings provide useful phenotypic selection criteria and contrasting genetic material for breeding okra cultivars with improved YVMD resistance.

Introduction

Okra (*Abelmoschus esculentus* L. Moench) is an important vegetable crop cultivated widely in tropical and subtropical regions and valued for its tender fruits, nutritional properties, and diverse food and nutraceutical uses. However, productivity remains constrained by genetic and environmental limitations, particularly biotic stresses that adversely affect plant growth, fruit production, and quality (Gemede et al., 2015; Kumar et al., 2021). Among these constraints, yellow vein mosaic disease (YVMD), associated with begomoviruses and transmitted predominantly by the whitefly *Bemisia tabaci*, is one of the most destructive diseases of okra. Infection causes characteristic vein yellowing, mosaic symptoms, reduction in photosynthetic capacity and, under severe infection, substantial reductions in fruit yield and quality (Kumar et al., 2017; Singh et al., 2023; Davis & Thompson, 2024). Recent reviews emphasize that the complex begomoviruses–whitefly–okra interaction and efficient vector-mediated transmission make YVMD difficult to manage through conventional approaches alone (Davis & Thompson, 2024).

Host-plant resistance is therefore considered one of the most economical, environmentally sustainable, and effective approaches for managing YVMD. Considerable variation in resistance has been identified among cultivated and wild *Abelmoschus* germplasm, providing useful sources for varietal improvement (Venkataravanappa et al., 2022; Noopur et al., 2022). Genetic studies have demonstrated that YVMV resistance can involve different genetic mechanisms, including complementary dominant and recessive gene effects, highlighting the complexity of resistance inheritance (Khade et al., 2020; Singh et al., 2023). Furthermore, recent molecular studies have identified SSR markers linked with YVMD resistance, demonstrating increasing opportunities for integrating phenotypic screening with marker-assisted breeding (Singh et al., 2023). Mutagenesis-based approaches have also generated promising YVMV-resistant okra mutants, reinforcing the importance of identifying and characterizing diverse resistance sources (Hazra et al., 2024).

Alongside disease resistance, genetic variability for yield and its component traits is essential for developing productive okra cultivars. Recent studies have reported substantial variability for plant height, flowering time, number of branches, number of fruits, fruit weight, and fruit yield, with fruit number and fruit weight frequently showing strong associations with yield (Pathania et al., 2024; Behera et al., 2025; Yadav et al., 2024). However, most previous investigations have considered YVMV resistance and yield performance separately, whereas simultaneous evaluation of disease incidence, disease severity, and major yield-related traits under controlled disease pressure remains comparatively limited. This is particularly important because selection exclusively for high yield may inadvertently favor disease-susceptible genotypes, while selection solely for resistance may compromise productivity.

Climate change is expected to further complicate okra production by altering temperature regimes, rainfall patterns, and pest and pathogen dynamics. Increasing temperatures can influence the population growth, feeding activity, and geographic distribution of insect vectors such as *Bemisia tabaci*, potentially increasing the transmission and spread of begomoviruses responsible for yellow vein mosaic disease. Changes in temperature and other environmental conditions may also modify host–vector–virus interactions and disease development, increasing the vulnerability of susceptible cultivars (Gautam et al., 2022; Singh et al., 2023). Therefore, developing climate-resilient okra cultivars that combine YVMV resistance with stable yield potential is becoming increasingly important for sustainable vegetable production. Screening genetically diverse germplasm under controlled disease pressure can help identify genotypes capable of maintaining desirable agronomic performance under changing disease environments.

The novelty of the present study lies in the integrated evaluation of seven genetically diverse okra genotypes under artificial *B. tabaci*-mediated YVMV inoculation, combining disease incidence and severity with six yield-related traits and their correlations. This approach provides a basis for identifying genotypes with simultaneous YVMV tolerance and acceptable productivity, which is particularly relevant for developing climate-resilient okra cultivars under increasing pest and disease pressure.

Materials and Methods

Experimental Site and Plant Material

The experiment will be conducted at the research farm of Plant Protection Research Institute, Ayub Agricultural Research Institute, Faisalabad, during 2026 under open-field conditions. The study comprised seven genetically diverse approved varieties of okra (*Abelmoschus esculentus* L. Moench) Healthy, genetically pure, and uniform seeds of each genotype were obtained from the Vegetable Research Institute, Ayub Agricultural Research Institute, Faisalabad (Fig. 1).

Table 1: Detail of germplasm Used for studying the disease and yield related parameters in seven Okra Varieties

SR No	Designation	Variety name
1	G1	Sabaz Pari
2	G2	Hari Bhari (VRI-OK-1900)

3	G3	Pusa Sawani
4	G4	Okra-3
5	G5	Punjab Selection
6	G6	Green Wounder
7	G7	Super star

Experimental Design and Field Establishment

The experiment will be established using a Randomized Complete Block Design (RCBD) with seven genotypes and three replications, resulting in 21 experimental plots. Each genotype will be randomly assigned to one plot within each replication. A plot of approximately 3.0 m × 2.4 m will be used, depending on the available field area, with rows maintained at approximately 60 cm apart and plants at approximately 30 cm within rows (Venkataravanappa et al., 2022). The field will be prepared according to standard production technology published by AgriPunjab (Anonymous, 2025).

Artificial Inoculation of Virus through Whitefly

Adult *Bemisia tabaci* will be collected from virus-free colonies maintained on healthy host plants and allowed to acquire the virus from symptomatic source plants. For acquisition access, approximately 20–30 adult whiteflies per source plant will be confined on symptomatic leaves using clip cages or suitable insect-proof cages for approximately 24 hours. After the acquisition period, viruliferous whiteflies will be transferred individually or in groups to healthy test plants at the 2–3 true-leaf stage. Approximately 5–10 viruliferous whiteflies per test plant will be used for inoculation. The insects will be confined on young leaves using clip cages for approximately 24 hours to provide sufficient inoculation access. Following inoculation, the whiteflies will be removed manually or using an appropriate insecticide under controlled conditions, and the plants will subsequently be maintained under insect-proof conditions to prevent uncontrolled secondary transmission. This whitefly-mediated artificial inoculation approach is consistent with established protocols for screening okra genotypes against yellow vein mosaic disease (Venkataravanappa et al., 2013; Singh et al., 2023; Davis & Thompson, 2024).

Yield-Related Traits

Six yield-related traits will be recorded for each genotype, including days to first flowering, plant height (cm), number of primary branches plant⁻¹, number of fruits plant⁻¹, average fruit weight (g), and fruit yield (kg plot⁻¹). Days to first flowering will be recorded as the number of days from sowing to the opening of the first flower, while plant height will be measured from the soil surface to the apical growing point at the final growth stage. Primary branches will be counted from the main stem, whereas the total number of marketable fruits harvested from tagged plants throughout the harvesting period will be recorded to determine fruits plant⁻¹. Fruits will be harvested at the tender edible stage at regular intervals, and average fruit weight will be calculated from the total weight and number of representative fruits. Cumulative fruit yield will be determined by weighing all marketable fruits harvested from each plot across successive pickings and expressed as kg plot⁻¹. All observations will be taken from competitive plants in the central rows while avoiding border plants, and uniform harvesting and measurement procedures will be followed for all genotypes.

Assessment of Yellow Vein Mosaic Disease

Disease Incidence (%)

Viruliferous *Bemisia tabaci* will be introduced for artificial inoculation when the okra plants reach the 2–3 true-leaf stage. Disease incidence will be recorded at the vegetative stage (15 days after inoculation), flowering stage (30 days after inoculation), and fruiting stage (45 days after inoculation) by calculating the percentage of symptomatic plants in each plot. The final disease incidence recorded at the fruiting stage will be used for comparison among the seven genotypes. This assessment approach is consistent with established phenotypic screening procedures used for evaluating okra genotypes against yellow vein mosaic disease (Kumar et al., 2015; Venkataravanappa et al., 2022).

Percent disease incidence will be calculated at each assessment using the number of symptomatic plants relative to the total number of plants assessed within each plot:

$$\text{Disease incidence (\%)} = (\text{Number of symptomatic plants} / \text{Total number of plants assessed}) \times 100$$

Disease Severity Score

Disease severity will be assessed on the same plants at the vegetative stage (15 days after inoculation), flowering stage (30 days after inoculation), and fruiting stage (45 days after inoculation) using a standardized 0–5 disease severity scale, where 0 represents absence of symptoms and 5 represents severe yellow vein mosaic symptoms with pronounced plant damage. The

mean severity score of the assessed plants will be calculated for each plot, and the final score at the fruiting stage will be used to characterize the relative response of the genotypes to YVMV (Kumar et al., 2015; Venkataravanappa et al., 2022).

Sampling Procedure

For yield and disease observations, plants located in the central portion of each experimental plot will be selected to minimize border effects. A predetermined number of plants, for example 10 plants per plot, will be tagged immediately after establishment and used consistently for plant-level observations. The same tagged plants will be used for plant height, primary branches, fruits plant⁻¹, and disease severity observations whenever possible. Disease incidence, however, will be calculated using the total established plant population of the plot rather than only the tagged plants, because disease incidence is intended to represent the proportion of the entire experimental unit affected by disease.

Fruit harvesting will be performed from the whole experimental plot rather than only the tagged plants when calculating plot yield. This distinction is essential because plant-based observations should not be substituted for plot yield, as doing so can introduce sampling error and may bias the estimate of total productivity. The same harvesting schedule and maturity criteria will be followed for all seven genotypes.

Statistical Analysis

Data for six yield-related and two disease-related traits will be subjected to analysis of variance (ANOVA) under RCBD at $P \leq 0.05$. Pearson correlation analysis will be performed to determine the association between YVMV incidence/severity and yield-related traits. All statistical analyses will be performed using Statistix 8.1.

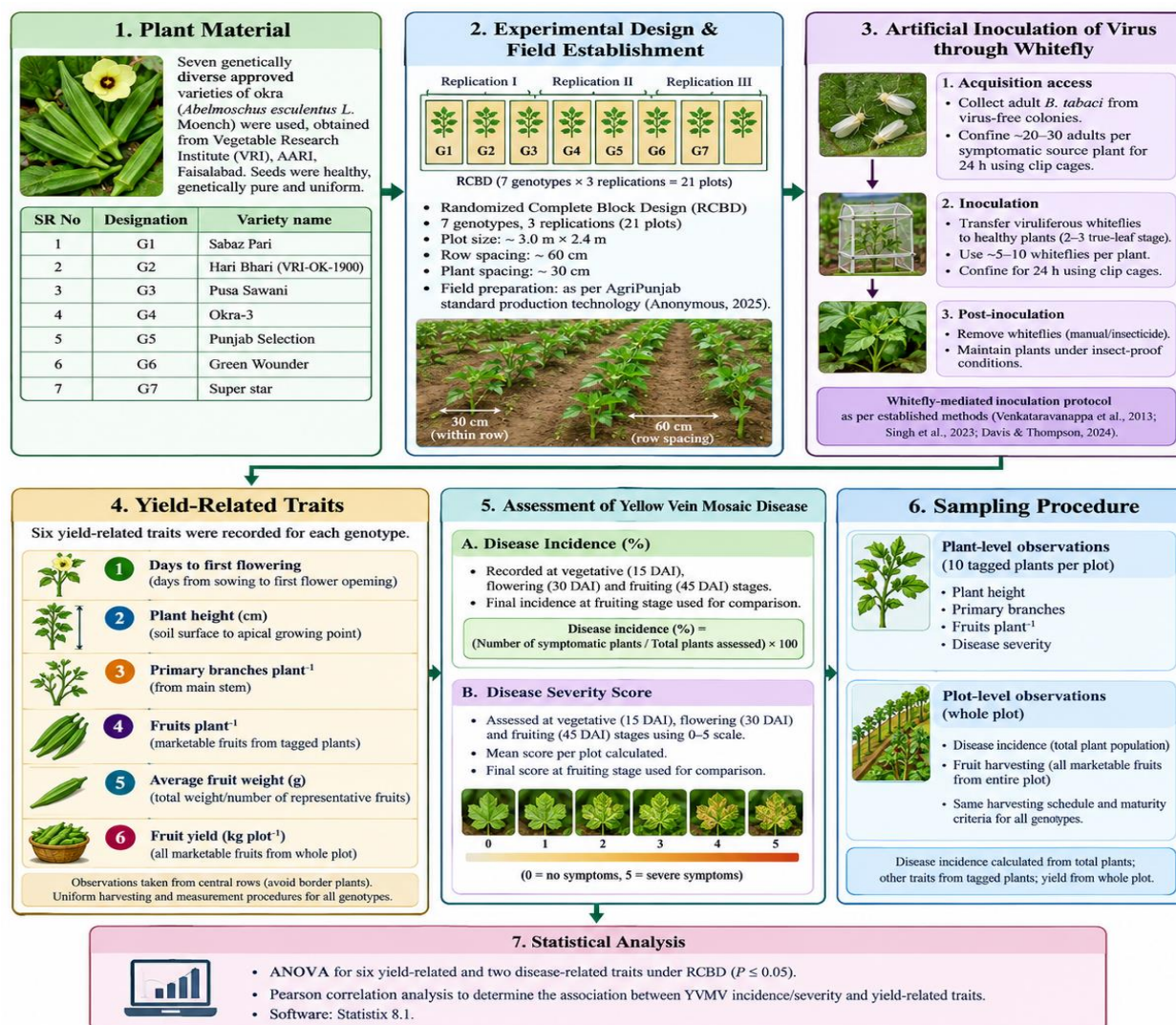


Figure 1: Flow chart of study conduction for evaluation of Okra genotypes of yield and disease related characters

Results and Discussion

The results showed clear and significant variation among the seven okra genotypes for both yield-related attributes and YVMV response (Fig. 2). Days to first flowering ranged from 46.0 days in G1 to 57.0 days in G6, while plant height varied from 119.3 to 152.3 cm. G6 exhibited the highest number of primary branches (6.90 plant^{-1}), fruits (36.33 plant^{-1}), average fruit weight (19.93 g), and fruit yield ($11.85 \text{ kg plot}^{-1}$), whereas G1 showed the lowest values for most of these traits. G7 also performed relatively well, particularly for fruit yield ($10.36 \text{ kg plot}^{-1}$). The progressive increase in vegetative growth and yield attributes among genotypes indicates substantial genetic variability for productivity. Such differences among okra genotypes are consistent with previous reports demonstrating considerable genetic variation for agronomic performance and disease response, which can be exploited in varietal selection and breeding programs (Kumar et al., 2015; Venkataravanappa et al., 2013).

A contrasting pattern was observed for YVMV response. Disease incidence increased markedly from 18.33% in G1 to 84.00% in G6, while disease severity increased from 1.20 to 4.60, respectively. Thus, although G6 produced the highest yield under the present conditions, it was also the most susceptible genotype, indicating that superior yield potential did not necessarily correspond to YVMV resistance. In contrast, G1 showed the lowest disease incidence and severity, suggesting comparatively better tolerance/resistance, while G2 and G3 also maintained relatively low disease levels. G4 and G7 displayed intermediate reactions, whereas G5 and G6 were highly susceptible. Similar genotype-dependent variation in YVMV incidence and severity has been documented, with disease expression influenced by host genotype, infection timing and virus-vector interactions (Venkataravanappa et al., 2013; Venkataravanappa et al., 2022). Recent studies further confirm substantial differences in virus multiplication and defence responses between contrasting resistant and susceptible okra genotypes, supporting the use of phenotypic screening for identifying useful resistance sources (Muthaiah et al., 2024). Therefore, G1 appears particularly promising as a YVMV-tolerant genotype, whereas G6 may be useful as a high-yielding but susceptible genotype. Importantly, resistance should ideally be confirmed over seasons and, where possible, through virus detection because symptom expression alone can vary with environmental conditions and inoculum pressure. Large-scale screening has similarly demonstrated substantial variation from highly resistant to highly susceptible responses among okra germplasm.

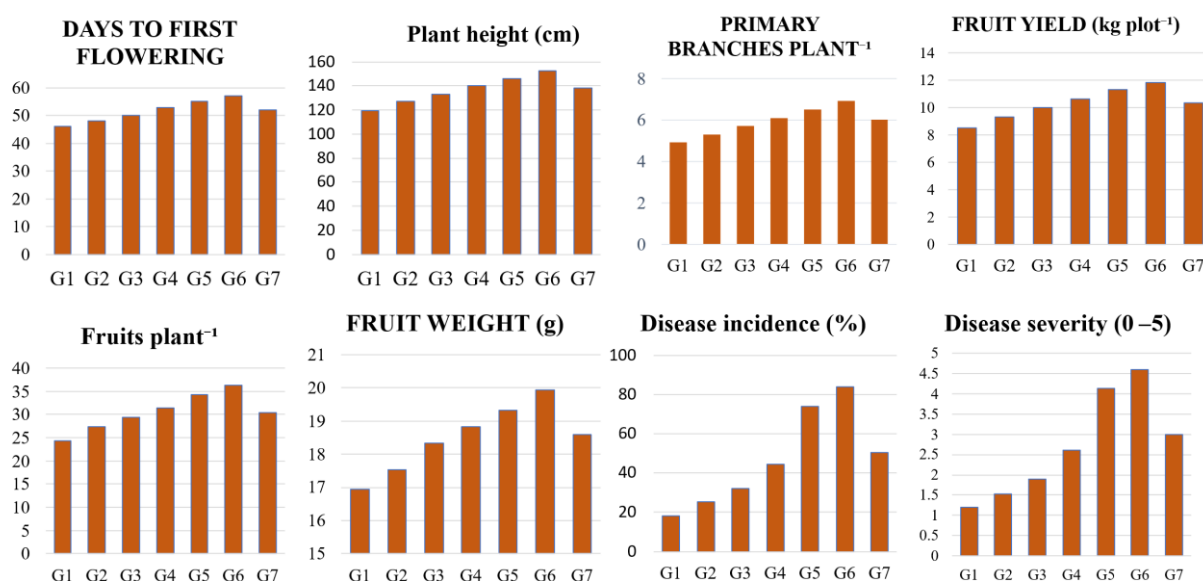


Figure 2: Average data of seven Okra genotypes evaluated for yield and disease related parameters

The analysis of variance revealed highly significant differences ($P < 0.001$) among genotypes for all eight traits, demonstrating substantial genetic variability in the evaluated okra material. The genotype mean square was highest for disease incidence (1811.27), followed by plant height (376.381), fruits plant^{-1} (49.4286), days to first flowering (44.8571), fruit yield (3.89209), average fruit weight (3.14333), disease severity (5.00746), and primary branches plant^{-1} (1.40429). The very low coefficients of variation for most traits further indicate good experimental precision. Particularly strong genotype effects for fruit yield and disease parameters suggest that genetic differences were important determinants of both productivity and YVMV response.

The genotype means showed a clear contrast between productivity and disease resistance. G6 recorded the highest fruit yield ($11.85 \text{ kg plot}^{-1}$), fruits plant^{-1} (36.33), fruit weight (19.93 g), plant height (152.33 cm), and branches plant^{-1} (6.90), but was also the most susceptible genotype, with 84.0% disease incidence and a severity score of 4.60. In contrast, G1 showed the lowest disease incidence (18.33%) and severity (1.20), although its yield was comparatively low ($8.53 \text{ kg plot}^{-1}$). G2 and G3 exhibited relatively low disease levels while maintaining better yield attributes than G1, suggesting greater potential for combining productivity with disease tolerance. G4 and G7 displayed intermediate responses, whereas G5 and G6 were highly susceptible. This variation agrees with previous studies demonstrating substantial genetic differences in okra response to yellow vein mosaic disease and emphasizing genotype-dependent disease development (Venkataravanappa et al., 2022). Recent transcriptomic work has also demonstrated markedly different molecular responses and viral multiplication between contrasting YVMV-tolerant and susceptible okra genotypes, supporting the strong genetic component of resistance observed in the present study (Muthaiah et al., 2024).

The simultaneous occurrence of high yield and high disease susceptibility in G6 indicates that selection solely for yield may increase vulnerability to YVMV. Therefore, G2 and G3 appear particularly promising for further evaluation, because they combined comparatively lower disease incidence/severity with improved yield performance, while G1 may serve as a useful source of disease tolerance. Similar genotype-dependent differences have been reported under artificial whitefly-mediated inoculation, confirming that artificial screening can effectively discriminate resistant and susceptible okra genotypes (Venkataravanappa et al., 2013). The identification and utilization of genotypes combining acceptable yield with YVMV resistance is considered an important breeding strategy for sustainable management of this disease (Venkataravanappa et al., 2022; Muthaiah et al., 2024).

Table 2: Mean Sum of Square (MSS) values obtained from analysis of variance of seven okra genotypes evaluated for yield and disease related parameters

Trait	Genotype MSS	P Value
Days to first flowering	44.85*	0.03
Plant height (cm)	376.38*	0.04
Primary branches plant^{-1}	1.40*	0.02
Fruits plant^{-1}	49.42*	0.01
Average fruit weight (g)	3.14*	0.03
Fruit yield (kg plot^{-1})	3.89*	0.02
Disease incidence (%)	1811.27*	0.01
Disease severity (0-5)	5.01*	0.03

Correlation Analysis

The correlation analysis revealed predominantly positive associations among the measured traits, indicating that improvement in several agronomic attributes may occur simultaneously in the evaluated okra genotypes. *Number of fruits per plant (NFP) showed a significant positive correlation with fruit yield ($r = 0.64$ **), demonstrating that fruit number was an important yield-contributing trait. Similarly, positive associations of fruit yield with days to first flowering ($r = 0.43$), disease incidence ($r = 0.54$), disease severity ($r = 0.16$), fruit weight ($r = 0.34$), and plant height ($r = 0.36$) indicate that yield was influenced by several component traits rather than a single character. Recent studies in okra have likewise reported strong positive associations of yield with number of fruits per plant and fruit weight, with these traits frequently identified as useful selection criteria for yield improvement (Behera et al., 2025; Yadav et al., 2024).

A strong positive relationship was observed between days to first flowering and NFP ($r = 0.73$ **), while plant height was also positively associated with NFP ($r = 0.76$), suggesting that relatively vigorous and later-flowering plants tended to produce more fruits. The relationship between fruit weight and disease incidence was also significant ($r = 0.54$), whereas fruit weight showed a positive association with fruit yield ($r = 0.34$). Such positive relationships among fruit number, fruit weight, plant stature and yield have been reported in recent okra germplasm studies, supporting their usefulness as indirect selection criteria (Pathania et al., 2024; Behera et al., 2025).

The disease-related traits showed particularly strong interrelationships. Disease severity was strongly correlated with disease incidence ($r = 0.76$), indicating that genotypes with a greater proportion of diseased plants generally also exhibited greater symptom severity. Disease incidence also showed positive associations with days to first flowering ($r = 0.46$), fruit yield ($r = 0.54$), and fruit weight ($r = 0.54$), while disease severity was positively associated with days to first flowering ($r = 0.61$) and fruit weight ($r = 0.65$). However, these positive correlations should not be interpreted as evidence that YVMV increases yield; in this dataset, they likely reflect the contrasting genetic pattern in which some vigorous/high-yielding genotypes, particularly G5 and G6, simultaneously expressed greater disease susceptibility. This is important because previous okra studies have

reported negative associations between YVMV incidence and fruit yield, indicating that disease can reduce productivity when disease pressure directly limits plant growth and fruit production (ND et al., 2021; Sharma et al., 2022).

The exceptionally high correlations involving primary branches per plant (NPB) with several traits ($r = 0.90-0.99$) indicate that branching was closely associated with the overall growth and productivity pattern of the genotypes. In particular, its strong association with fruit weight, plant height and fruit number suggests that more highly branched plants possessed greater structural capacity for fruit production. Recent studies have similarly identified number of branches, fruit number and fruit weight as important traits associated with yield in okra, and path analyses have frequently demonstrated substantial contributions of fruit number and fruit weight to yield formation (Yadav et al., 2024; Usha et al., 2026).

Table 3: Correlation analysis of seven okra genotypes evaluated for yield and disease related parameters

	NFP	DFF	DI	DS	FY	FW	NFP	NPB
DFF	0.73*							
DI	0.47*	0.46						
DS	0.46*	0.61	0.76					
FY	0.35*	0.43	0.54	0.16				
FW	0.36	0.45	0.54*	0.65	0.34			
PH	0.76	0.65*	0.25	0.63	0.36	0.54		
NPB	0.26	0.9752	0.9652	0.96*	0.9*	0.99*	0.99*	
NFP	0.54	0.65	0.45	0.63	0.64*	0.65	0.14	0.18**

DFF= Days to first flower, DI= Disease Incidence, DS= Disease Severity, FY= Fruit yield, FW= Fruit Weight, PH=Plant Height, NBP= Number of Primary Branches, NFP=Number of fruits per plant

Conclusion

The study revealed significant genetic variability among seven okra genotypes for yield and YVMD response. G6 recorded the highest fruit yield (11.85 kg plot⁻¹) but was highly susceptible (84.0% incidence; 4.60 severity), whereas G1 showed the lowest disease incidence (18.33%) and severity (1.20). G2 and G3 showed a better balance between disease tolerance and yield, making them promising for further evaluation. Overall, the identified variation provides useful material for breeding okra cultivars with improved YVMD resistance and productivity.

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