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Virus tolerance in okra (Abelmoschus esculentus): Field screening strategies and sustainable management

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ABSTRACT

Viral diseases, particularly Yellow Vein Mosaic Virus (YVMV) and Okra Leaf Curl Virus (OLCV), pose significant threats to okra (Abelmoschus esculentus L. Moench) production, leading to severe yield losses. This study focuses on the field screening of virus-tolerant okra genotypes to identify those with natural resistance under high virus pressure. A diverse set of genotypes was tested using aRandomized Complete Block Design (RCBD) in virus-prone areas.Disease incidence, severity index, and yield performance were evaluated. Genotypes exhibiting lower infection rates, reduced disease severity, and minimal yield loss were identified as virus-tolerant. The results indicate that these virus-tolerant genotypes can be recommended for cultivation in regions vulnerable to viral outbreaks, reducing dependency on chemical control methods and improving sustainable okra production. This approach offers a viable solution to enhance food security and ensure better economic outcomes for farmers.

KEY WORDS

Sustainable management; Genotypes; Abelmoschus esculentus L. Moench; Virus; Food security

ARTICLE HISTORY

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Introduction

Okra (A. esculentus L. Moench), a member of the Malvaceae family, is a prominent vegetable crop grown in tropical and subtropical regions worldwide. Valued for its edible green pods rich in dietaryfiber, vitamins A and C, calcium, and antioxidants, okra holds considerable economic and nutritional significance, particularly in South Asia and sub-Saharan Africa. However, its productivity is threatened by several biotic stresses, with viral diseases emerging as the most damaging factors responsible for significant yield losses and quality degradation [1]. Among these, YVMV, OLCV, and Enation Leaf Curl Virus (ELCV) are the most common and destructive pathogens, severely impacting plant morphology, photosynthetic capacity, and reproductive development, often resulting in yield reductions of up to 80–100% undersevere infestations [2].

The epidemiology of okra viral diseases is closely associated with insect vectors, particularly the whiteflyBemisia tabaci which transmits begomoviruses in a persistent, circulative manner [3]. The rapid and widespread movement of vectors, high rate of virus recombination, and emergence of new viral strains have made chemical control increasingly ineffective and unsustainable. This has intensified the need for resistant or tolerant genotypes as the most viable and eco-friendly solution for managing viral diseases in okra. Host plant resistance remains a cornerstone in integrated pest management due to its cost-effectiveness, environmental safety, and compatibility with other agronomic practices [4]. In this context, the field screening of diverse okra genotypes under natural or artificial viral pressure becomes a critical first step in the identification, evaluation, and utilization of resistant genetic materials.

Field screening, especially under endemic conditions, offers a practical means of evaluating genotypic responses to virus infection across multiple growth stages and environmental fluctuations. It enables the assessment of real-time disease incidence, symptom expression, and agronomic performance in the presence of native vector populations and prevailing climatic influences. Previous studies have highlighted the utility of such screeningapproaches. For instance,Ghosh et al., conducted field evaluations of 50 okra genotypes and reported significant variability in their resistance levels to YVMV, identifying a few highly tolerant lines suitable for further breeding [5]. These evaluations typically involve visual scoring of disease symptoms,estimation of percent disease incidence (PDI), and severity grading based on standardized scales, thereby facilitating the categorization of genotypes into resistant, moderately resistant, susceptible, and highly susceptible classes.

Notably, resistance to okra viral diseases is often governed by polygenic traits, complicating selection efforts. Field-based screening allows the detection of genotypes exhibiting not only resistance but also tolerance plants that are infected yet sustain growth and yield, thus contributing to production stabilityunder viral stress.Such traits are especially valuable in small-holder farming systems where virus pressure is high, and access to chemical protection is limited. Research by Akinyele and Osekita demonstrated that tolerant genotypes displayed reduced symptom progression and sustained pod yield despite infection, underscoring the role of physiological and morphological adaptations such as thicker cuticles, leaf hairiness, and altered phloem chemistry in minimizing virus multiplication or vector feeding efficiency [6].

Despite its importance, field screening is not without limitations. Environmental variability, inconsistent vector populations, and mixed infections can complicate the interpretation of genotype performance. Therefore, multiple-season and multi-location trials are recommended to validate resistance stability and adaptability. Moreover, screening should ideally be supplemented with molecular diagnostictools like PCR or ELISA to confirm viral infections and rule out escapes or asymptomatic cases [7]. Marker-assisted selection (MAS) has emerged as a complementary

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tool, allowing breeders to trace resistance genes in segregating populations. Nonetheless, the identification of QTLs and resistance-linked markers in okra remains limited due to its complex genome and underdeveloped molecular resources.

To widen the resistance gene pool, wild relatives of okra such as Abelmoschus manihot and A. caillei have been explored as potential donors. Although these species often carry undesirable traits like poor fruit quality or late maturity, pre-breeding efforts have shown promise in transferring virusresistance into elite cultivars [8]. However, introgression of resistance genes must be followed by rigorous field screening to eliminate linkage drag and ensure agronomic suitability. National breeding programs in countries like India, Nigeria, and Bangladesh have incorporated field screening protocols into their variety development pipelines, leading to the release of cultivars like 'Arka Anamika', 'BARI Dherosh-1', and 'NH47-4', known for their improved tolerance to viral diseases [9].

Furthermore, the phenological behavior of genotypes, such as early flowering and pod maturity, can influence virus exposure and disease severity. Early maturing genotypes often escape peak vector activity and thus show lower disease incidence, which may be mistaken for resistance. Hence, field screening must also consider growth duration and vector dynamics to ensure accurate classification of genotypic tolerance [10].

Given the increasing pressure from climate change, which favors vector proliferation and virus spread, the urgency to identify and disseminate virus-tolerant okra genotypes through robust field screening programs has never been greater. This effort requires collaboration among plant breeders, plant pathologists, entomologists, and molecular biologists. The integration of high-throughput phenotyping, disease modeling, and genomic tools will enhance the efficiency of screening and accelerate the development of resilient okra varieties suited for virus-endemic regions.

In summary,field screening of virus-tolerant okra genotypes serves as a foundational stepin breeding programs aimed at mitigating yield losses and ensuring crop sustainability. It offers a practical approach to identifying stable, high-performing genotypes capable of withstanding the complex interplay of viral pathogens and their vectors. By combining conventional field trials with emerging molecular and diagnostic technologies, researchers can fast-track the development of virus-tolerant okra cultivars, ultimately contributing to enhanced food security and livelihood resilience in vulnerable agricultural systems.

Objective

- To select high yielding virus tolerant okra genotype.
- To develop potential virus tolerant hybrids.

Review of Literature

Okra (A. esculentus L. Moench) is an economically and nutritionally valuable vegetable crop cultivated extensively in tropical and subtropical regions. Rich in vitamins, minerals, and dietary fiber, okra plays a significant role in human nutrition and food security. However, its productivity is severely constrained by biotic stresses, particularly viral diseases, which can cause up to 80–100% yield loss under severe infestations depending on the susceptibility of the genotypeand environmental conditions. Among the major viral pathogens affecting okra are the YVMV, Okra Enation Leaf Curl Virus (OELCV), Bhendi Yellow Vein Mosaic Virus (BYVMV), and OLCV. These viruses, predominantly transmitted by vectors such as B. tabaci (whitefly), are responsible for substantial reductions in photosynthetic efficiency, flower and pod abortion, and overall plant vigor [11].

Several efforts have been made globally and regionally to identify and develop virus- tolerant okra genotypes through both conventional and molecular breeding approaches. Field screening under natural or artificial inoculation is a fundamental step in evaluating the tolerance of various genotypes against viral diseases. According to Mandal et al., field screening allows researchers to observe actual disease expression under diverse agro-climatic conditions, enabling the selection of truly resistant or tolerant genotypes suited for regional cultivation [12].

YVMV is considered the most prevalent and economically damaging virus among okra- infecting viruses in South Asia and parts of Africa. It is a monopartite begomovirus of the Geminiviridae family, causing distinctive yellow vein symptoms that extend across the leaf lamina. Several researchers have screened okra germplasm for YVMV resistance under field conditions. For instance, Ghosh et al., screened 42 okra accessions and reported that only two genotypes showed high levels of tolerance, characterized by reduced symptomseverity and delayedinfection onset [5]. The genetic variability among these accessions was crucial in identifying promising sources of resistance that could be utilized in breeding programs.

A similar field-based study by Akinyele and Osekita in Nigeria evaluated 20 okra genotypes for resistance to OLCV and reported that genotypes 'NH47-4' and 'LD88' exhibited low disease incidence and severity across two seasons [6]. The authors attributed this tolerance to possible genetic factors, including inherent resistance gene expression or morphological traits such as reduced vector attraction. Studies like these highlight the importance of multi-location and multi-season trials in confirming stable resistance across diverse environments.

Breeding for virus tolerance in okra has traditionally relied on phenotypic selection, but integrating molecular tools has improved the precision and speed of developing resistant cultivars. Recent work by Venkataravanappa et al., employed DNA markers to associate resistance loci with YVMV tolerance in a segregating F2 population [7]. Although such molecular approaches are promising, field screening remains indispensable, especially in early-generation breeding or germplasm evaluation phases, to validate resistance under real-world conditions.

Another dimension of virus tolerance in okra is the role of plant morphology and physiology. Virus-tolerant genotypes often exhibit traits such as thicker leaf lamina, dense trichomes, and altered stomatal density, which may reduce vector feeding and virus transmission [4]. Some studies also report that genotypes with early maturity escape the critical periods of vector activity, indirectly reducing disease incidence[10]. Thus, screening strategies must consider not only disease severity and incidence but also plant phenology and vector dynamics to accurately assess tolerance levels.

The deployment of virus-tolerant varieties is also a sustainable and environmentally friendly strategy to reduce the reliance on chemical control of vectors. Continuous use of insecticides to manage whiteflies not only poses risks to human and environmental health but also leads to resistance development in

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vector populations. Hence, incorporating virus tolerancethrough host plant resistance is both economically and ecologically desirable [13].

In many developing countries, limited access to certified virus-tolerant okra seeds remains a constraint. Public sector research institutions such as the Indian Council of Agricultural Research (ICAR) and the Bangladesh Agricultural Research Institute (BARI) have initiated breeding programs to develop and distribute tolerant cultivars. For example, the variety 'BARI Dherosh-1' has shown moderate tolerance to YVMV in multi-location trials in Bangladesh and is widely adopted by smallholder farmers [9].

Despite progress, the dynamic nature of virus-vector interactions and the emergence of new virus strains pose ongoing challenges. Field screening efforts must be updated regularly to evaluate existing and new genotypes against evolving pathogen pressures. Integration of resistant germplasm from wild relatives, such as Abelmoschus manihot and A. tuberculatus, has shown promisein expanding the genetic base for resistance [8]. However, these wild species often harbor undesirable agronomic traits, necessitating backcrossing and careful selection in breeding pipelines.

In conclusion, field screening for virus tolerance in okra genotypes is a critical component of breeding programs aimed at sustainable disease management. While molecular tools are advancing, the relevance of field-based evaluations remains high for identifying stable, location-specific sources of resistance. Combining traditional breeding with advanced genomics,vector ecology, and farmer participatory approaches will strengthen efforts to develop virus-tolerant okra cultivars adapted to diverse agro-ecologies.

Materials and Methods

The field experiment was conducted in the field of Bangladesh Agricultural Research Institute, Joydebpur, Gazipur. The materials and methods conducted for the experiment are presented under the following being:

Description of the experiment

Location of the experiment

The experiment was carried out at the field and laboratory of the Horticulture Division, Bangladesh Agricultural ResearchInstitute, BARI, Joydebpur, Gazipur. The experimental field is at 24° 05` N latitude and 90° 25` E latitudes having an elevation of 8.2m from the sea level.

Climatic condition

The climate of the experimental site from June to September was tropical which is characterized by typical monsoon season, high temperature, heavy rainfall, and elevated humidity.

Table 1. Temperature and weather condition.

Months	Minimum Temperature ©	Maximum Temperature	Average Temperature	Humidity (%)	Winds (km/h)	Average Rainfall (mm)	Sunshine hrs/day
June	30	33	28	80	25	300	4.6
July	31	33	26	90	30	400	6.5
August	30	32	27	80	15	300	6.2
September	30	32.7	28.8	75	20	250	4.2

Source: Bangladesh Meteorological Department weatheratlas 2023-24.

Soil and climatic characteristics

The soil

The Soil of the experimental area is Dark Grey Terrace Soil which belongs to the Madhapur Tract under AEZ 28. This is characterized by poorly fertile. The range of pH status in soil is recorded very strongly acidic to slightly acidic (4.00 to 6.00), the range of organic matter status was very low to high 1.01 to 3.37%. (Agro Ecological Zone–Banglapedia).

Climate

Average temperatures vary from 28°C to 32°C in summer, falling to 20°C in winter, with extreme lows of 10°C. Rainfall ranges between 1000 mm and 1500 mm annually.

Soil and climatic requirements

All the members of Brassica family of crops have similar soil and climate requirements.

Soil requirements

Loamy soils with a balance of sand, silt, and clay are ideal. However, okra can tolerate sandy soils with proper management, as long as they have good water retention capabilities.

Okra grows best in slightly acidic to neutral soil with a pH range of 6.0 to 7.0. Soils that are too acidic or too alkaline can lead to nutrient deficiencies or toxicities

Good drainage is essential. Raised beds or mounded rows can help improve drainage in heavy clay soils. Ensuring that the soil surface does not stay wet for prolonged periods helps prevent diseases and root issues.

Prior to planting, till the soil to a depth of about 12 inches (30 cm) to ensure good root development and improve soil structure. Removing weeds and debris helps reduce competition for nutrients (Figure 1).

Experiment materials

Polythene, Net, Electric Balance, Bucket, Data tag, Hand gloves, Hand Sickle

Layout in the field

Plot size 54m * 32m

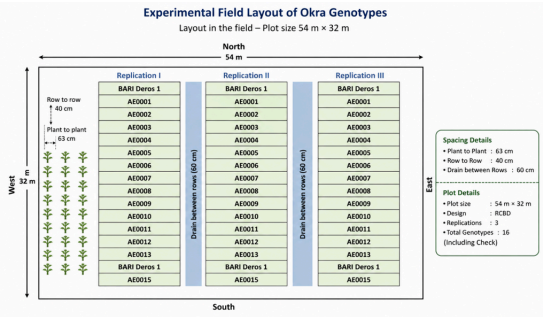


Figure 1. Experimental field layout showing the arrangement of okra genotypes under a Randomized Complete Block Design (RCBD) with three replications.

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Plot size and spacing



Figure 2. Okra field seed sowing after 20 days.

The size of plot was 1,728-meter square (54 m x 32 m). The plot had divided into 36 double rows. The size of experimental row was 40cm width and total 64 plants per plot, plant spacing of 63cm plant to plant, 40cm row to row was maintained. And also 60 cm drain was used between two rows (Figure 2).

Counting the insect data from every leaf

From Every plot counting the white fly. Every 6 plant are observedthe white fly. When plantage 20 days (Figure 3).



Figure 3 White fly counting, b. Virus affected leaf and plant. c. Counting the branch number of plant

Stem and Petiole

Observation the color of stem and petiole color (light green, green, and deep green) (Figure 4).



Figure 4. a. Observation of the color of petiole and stem, b. Tagging

Nameplate placement

Placing nameplates at the base of the plants.

Pubescence

Observation by hand how much pubescence are present there. (slight, Glaborous, conspiois)

Dry fruit collect

From every plant collected the dry fruit and put into the net bag and dry in the sun properly (Figure 5).



Figure 5. Collection of dry fruit weight.

Results and Discussion

Parameters of identified data

Number of fruits per plant

The number of fruits per plant varied significantly among the evaluated okra genotypes under field screening for virus tolerance (Figure 6). Genotype A007 produced the highest fruit number (32.0), followed by A009 (29.0) and A008 (23.0), indicating superior yield potential under virus pressure. In contrast, A001 and A012 exhibited the lowest fruit numbers (6.5 and 6.7, respectively), suggesting greater susceptibility. The observed differences may be attributed to genetic variation in virus tolerance, influencing reproductive performance. Thesefindings align with earlier reportsthat virus-tolerant genotypes maintain higher fruit set and yield under disease stress through reduced pathogen impact on flowering and pod development.

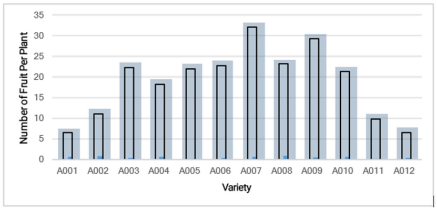


Figure 6. Number of fruits per plant of differentokra varieties.

Number of branches per plant

The number of branches per plant differed among the tested okra genotypes under virus stress conditions (Figure 7). Genotype A012 recorded the highest branching (4.45), followed by A007 and A009 (4.0 each), suggesting better structural growth and potential for higheryield. In contrast, A002 exhibited the lowest numberof branches (2.75), indicating reduced vegetative development, possibly due to higher susceptibility. Increased branching in tolerant genotypescan enhance photosynthetic capacity and reproductive sites, contributing to better performance under disease pressure [14]. These results are consistent with previous findingsthat virus-tolerant okra genotypes maintain vigorousbranching, which supportshigher yield stabilityunder stress.

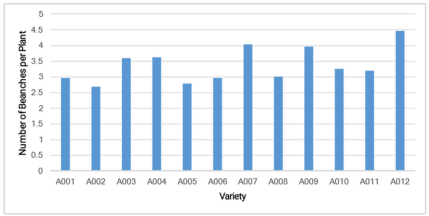


Figure 7. Number of branches per plant of different okra varieties.

Number of virus affected plants

The number of virus-affected plants varied notably among the evaluated okra genotypes (Figure 8). Genotypes A001 (0.72) and A002 (0.69) recorded the highest incidence, indicating high susceptibility to viral infection. Moderate infection was observed in A011 (0.18) and A012 (0.12), while A003, A004, and the remaining genotypesshowed negligible or zero infection, reflecting strong virus tolerance. The absence or minimal occurrence of infected plants in tolerant genotypessuggests the presence of inherent genetic resistance mechanisms [15]. These results agree with earlier studies reporting that virus-tolerant okra lines can suppress disease development, thereby

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maintaining better growth and yield stability under field conditions.

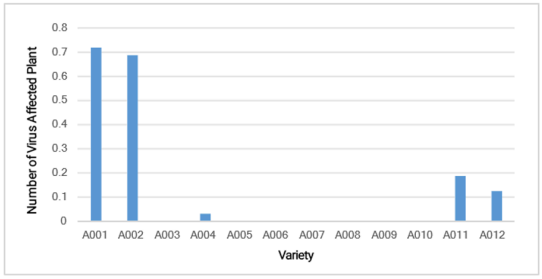


Figure 8. Number of viruses affected plant of differentokra varieties.

Number of insect-affected plants

Field screening of virus-tolerant okra genotypes revealed significant variation in insect- affected plants among the tested varieties (Figure 9). Varieties A011 and A012 exhibited the highest susceptibility, with over 0.55 affected plants, indicating poor insect tolerance. In contrast, varieties A002 and A005 showed the lowest incidence (<0.1), suggesting stronger resistance. Moderate susceptibility was observed in varieties A001, A003, A004, A007, A008, and A009. These differences highlight genetic variability in insect resistance, essential for selecting virus-tolerant lines with reduced insect attraction. Therefore, A002 and A005 may serve as promising candidates for breeding insect- and virus-resistant okra cultivars [16].

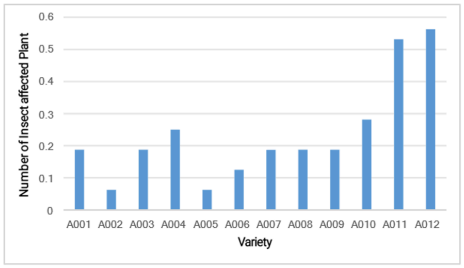


Figure 9. Number of Insect affected plant of differentokra varieties

Single fruit wt. (g)

Single fruit weight among the virus-tolerant okra genotypes varied considerably under field conditions (Figure 10). The highest fruit weight was recorded in variety A004 (18g), followed by A003 and A007 (17g), indicating superior yield potential. In contrast, A001 and A011 produced the lowest fruit weights (10–11g), suggesting reduced productivity. Most other genotypes, including A005, A006, A008, A009, and A010, showed moderate fruit weights (14–15g), reflecting stable performance [17]. These findings suggest that A004, A003, and A007 are promising candidates for high-yielding, virus-tolerant okra lines, suitable for further breeding and cultivation programs.

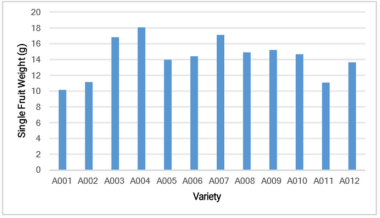


Figure 10. Single fruit wt. (g) per plant of different okra varieties.

Fruit wt. (g) per plant

The total fruit weight per plant among virus-tolerant okra genotypes exhibited significant variability under field conditions (Figure 11). Genotype A007 showed the highest fruit yield (540g), followed by A009 (450g) and A003 (370g), indicating superior performance. In contrast, A011 and A001 recorded the lowest yields (10g and 70g, respectively), suggesting poor productivity. Moderate yields were observed in A004, A005, A006, A008, and A010 (310–350g). These results highlight A007, A009, and A003 as high-yielding, virus-tolerant genotypes with strong potential for commercial cultivation and breeding programs aimed at improving okra productivity [18].

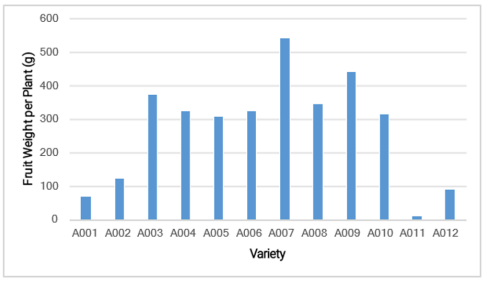


Figure 11. Fruit wt. (g) per plant of different okra varieties.

Yield\plot (gm)

The yield per plot among virus-tolerant okra genotypes varied widely, indicating significant genetic diversity(Figure 12). GenotypeA007 recorded the highest yield (35,000 g), followed by A009 (28,000 g) and A003 (24,000 g), demonstrating excellent productivity potential. Conversely, A002 and A001 showed the lowest yields (1,000 g and 4,000 g, respectively), indicating limited suitability for high-yield cultivation. Moderate yields were observed in A004, A005, A006, A008, and A010 (20,000–23,000 g). These results suggest that A007, A009, and A003 are promising virus-tolerant okra genotypes for commercial farming and future breeding programs aimed at maximizing yield.

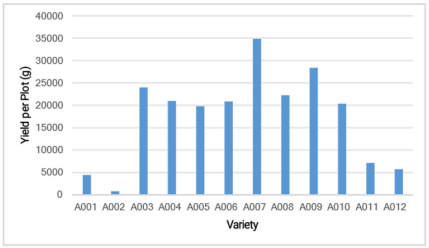


Figure 12. Yield per plot (g) of differentokra varieties.

Yield/plot (kg)

Yield per plot (kg) among virus-tolerant okra genotypes exhibited notable differences under field conditions (Figure 13). Genotype A007 recorded the highest yield (35 kg), followed by A009 (28 kg) and A003 (24 kg), indicating strong agronomic performance. In contrast, the lowest yields were observed in A001, A011, and A012 (4–7 kg), suggesting limited productivity. Genotypes A004, A005, A006, A008, and A010 demonstrated moderate yields (20–23 kg), reflecting stable performance under virus pressure. These findings suggest that A007, A009, and A003 are the most promising virus-tolerant okra genotypes for high-yield cultivation and varietal improvement.

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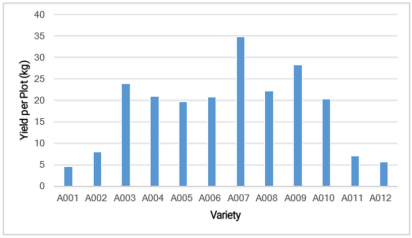


Figure 13. Yield per plot (kg) of different okra varieties.

Stem Color

Stem color variation among virus-tolerant okra genotypes showed moderate diversity, ranging between 1.3 and 1.8 (Figure 14), where 1 = green, 2 = light green, and 3 = deep green. Most genotypes exhibited stem color values close to 1.6–1.7, indicating a predominance of light green stems. Genotype A009 recorded the highest stem color rating (1.8), suggesting a deeper green hue, while A010 had the lowest (1.3), and indicating a greener stem. This variation in pigmentation may be linked to genetic differences and potential resistance traits. Genotypes A006, A008, and A009 may be preferred for their deeper green stems under field conditions [19].

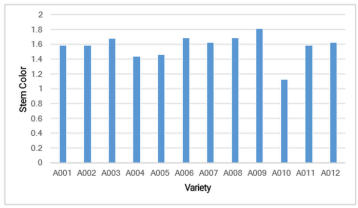


Figure 14. Stem Color of different okra varieties.

Petiole color

Petioles of virus-tolerant okra genotypes exhibited noticeable variation in color intensity, ranging from green (1) to light green (2) (Figure 15). Genotypes A006 and A009 recorded the highest petiole color values (1.7), indicating a stronger light green pigmentation, while A003 and A010 had the lowest values (1.1), signifying greener petioles. Most other genotypes, including A002, A004, A005, A007, and A011, showed intermediate values (1.5–1.6), suggesting a mix of green and light green shades [19]. These differences may reflect genotypic variation in chlorophyll content, potentially influencing light absorption and photosynthetic efficiency under virus stress.

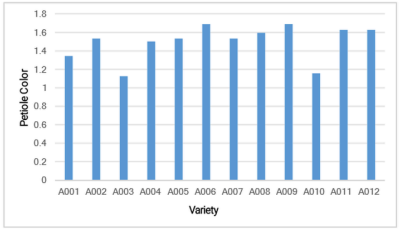


Figure 15. petiole color of different okra varieties.

Mature fruit color

Mature fruit color of virus-tolerant okra genotypes ranged from green (1) to light green (2), indicating moderate variation in pigmentation (Figure 16) [20]. Genotype A002 displayed the highest mature fruit color value (1.7), suggesting a distinctly light green pod, while A003 and A010 showed the lowest values (1.0–1.1), indicating greener fruits. Most genotypes, including A005, A006, A009, and A012, ranged between 1.5 and 1.6, reflecting intermediate coloration. These differences may influence market preference and consumer acceptance, as pod coloris a key quality trait.Genotypes with greener fruits, such as A003 and A010, may be preferred in local markets.

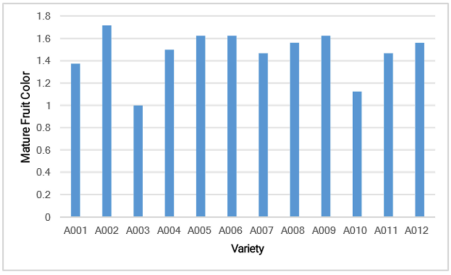


Figure 16. Mature fruit color of different okra varieties.

Immature fruit color

The immature fruit color of virus-tolerant okra genotypes ranged from green (1) to light green (2), reflecting distinct pigmentation differences (Figure 17). Genotypes A006, A009, and A012 showed the highest values(1.6+), indicating more pronounced lightgreen coloration. At the same time, A003 and A010 had the lowest scores (1.0–1.2), indicating greener immature fruits. Most other genotypes, such as A004, A005, A008, and A011, showed intermediate values (1.4–1.5). These differences may influence consumer preference and harvest timing, as fruit color is an important visual quality trait. Greener fruits (A003, A010) may be favored in markets preferring traditional okra appearance.

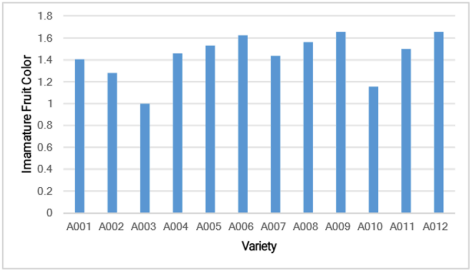


Figure 17. Immature fruit color of different okra varieties

Summary

Okra is an important vegetable crop, but it is highly susceptible to viral diseases like YVMV and OLCV. Developing and identifying virus-tolerant okra genotypes is essential to ensure stable yields and reduce losses caused by viral infections. Field screening involves selecting diverse genotypes, conducting trials under natural virus pressure, and measuring disease incidence, severity, and yield performance. Genotypes with lower infection rates, disease severity, and minimal yield loss are identified as virus-tolerant. This approach helps reduce reliance on chemical control, promotes sustainable agriculture, and contributes to food security.

Okra is vulnerable to viral diseasessuch as YVMV and OLCV, which significantly impact its yield. Field screening of virus-

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tolerant okra genotypes is crucial for identifying varieties with natural resistance. The screening process involves selecting diverse genotypes, conducting trials in virus- prone areas, and assessing disease incidence, severity, and yield performance. The goal is to identify genotypes that show lower infection rates and reduced yield losses under viral pressure.

Conclusion

Field screening is a critical step in the identification and development of virus-tolerant okra genotypes, providing a practical and sustainable solution for managing major viral diseases that severely affect crop productivity. Viral infections in okra often result in significant yield losses, poor fruit quality, and reduced economic returns for farmers. Therefore, the selection of tolerant genotypes through field evaluation under natural disease pressure is essential for improving crop resilience and long-term productivity. The use of virus-tolerant varieties can greatly enhance okra production by maintaining plant vigor, reducing disease incidence, and ensuring more stable yields under adverse conditions. In addition, these genotypes help reduce the dependence on chemical pesticides used for controlling insect vectors, thereby lowering production costs and minimizing environmental and health risks associated with excessive pesticide use. This approach also supports environmentally friendly and sustainable agricultural systems. By promoting the cultivation and adoption of resistant or tolerant okra varieties, farmers can achieve higher yields, better income, and improved livelihood opportunities. Furthermore, the widespread use of such genotypes can contribute significantly to food security, especially in regions where viral diseases are common and continue to threaten vegetable production. Thus, field screening remains an essential strategy in modern okra improvement programs.

Disclosure Statement

No potential conflict of interest was reported by the author.

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