ORIGINAL RESEARCH REPORT NIGER. J. PLT. PROT. 40(2):123-134(2026)

Field Evaluation of Tomato (*Solanum lycopersicum* L.) Genotypes for Yield and Viral Disease Response in Southwest Nigeria

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ABSTRACT

Tomato production in Nigeria is severely constrained by viral diseases, leading to significant yield losses and reduced farm income among resource poor farmers in the country. This study evaluated the yield performance and viral disease response of selected tomato varieties and advanced breeding lines under open-field rainfed conditions. Eight genotypes, including commercial hybrids and advanced breeding lines were assessed using a randomized complete block design with three replications across two growing seasons. Data were observed for fruit yield, disease incidence, and severity. Although no significant differences ($p > 0.05$) was observed in fruit yield among genotypes, notable numerical variation was recorded with breeding line NHTo128-1 exhibiting the highest yield. Disease severity differed significantly at eight weeks after transplanting ($p < 0.05$), with NHTo128-1 and NHTo29-2/1 showing the lowest (2.61) and the highest (4.38) severity scores respectively. Regression analysis revealed significant negative relationship between disease severity and yield ($R^2 = 0.398$, $p = 0.0016$) indicating that increased disease severity substantially reduced productivity. The results of the trial revealed NHTo128-1 as a high yielding genotype with potential for tolerance to tomato virus diseases under open field conditions.

Keywords: Tomato, viral disease severity, genotype evaluation, virus tolerance, yield loss, breeding lines.

INTRODUCTION

Tomato (*Solanum lycopersicum* L.) is one of the most economically important and widely cultivated vegetable crops worldwide. It is good source of bioactive compounds such as lycopene, which confers antioxidant, health-promoting benefits, vitamins (especially vitamin C), and including potassium, phosphorus, magnesium, calcium, and iron (1) Globally, tomato production exceeds 186–189 million tonnes annually from approximately 5 million hectares, with China as the top producers (2; 3). In Nigeria, tomato ranks top as a staple vegetable and a key driver of food security, income generation, and rural livelihoods, particularly for smallholder farmers who dominate production. Nigeria produces an estimated 3.6–4.1 million tonnes annually, positioning it as the second-largest producer in Africa (after Egypt) and among the top 11–13 globally (4). The crop supports over 3 million people across the value chain, from farming to marketing and processing, with growing urban demand

fueling a processing industry valued at over USD 1 billion as of recent estimates (5).

Despite its importance, tomato productivity in Nigeria remains substantially below global averages, often limited to 4–10 t/ha compared to higher yields in more intensive systems (6, 4). This yield gap arises from multiple factors ranging from abiotic constraints such as heat, drought, poor soil fertility, erratic rainfall and biotic such as blight, fruit borers, Tuta absoluta and viral diseases, which represent one of the most devastating biotic factors in solanaceous crop, especially tomato production (7; 5; 8). Viral disease can cause significant losses especially begomoviruses infestation transmitted by the whitefly vector *Bemisia tabaci*, causes severe symptoms such as leaf curling, mottling, chlorosis, stunting, reduced fruit set, and poor fruit quality, frequently leading to crop failure and substantial economic losses (9).

Among these, *Tomato yellow leaf curl virus* (TYLCV) disease and related begomovirus complexes of *Tomato leaf curl virus*, ToLCV) are predominant in Nigeria and sub-Saharan Africa, with prevalence documented across major production zones (10). TYLCV and similar viruses can induce yield losses of 20–100% in susceptible genotypes, particularly under high vector pressure during early growth stages, with severe infections often exceeding 50–90% reduction in marketable fruit (11). Other viruses such as *Tomato mosaic virus* (ToMV) contribute additional losses of 15–25% in affected fields (12). These pathogens are challenging to manage due to their efficient whitefly transmission, rapid spread in tropical climates with high vector populations, and limited efficacy of conventional controls like insecticide applications, which are costly, environmentally unsustainable, and prone to resistance development in vectors (13).

Chemical vector suppression and cultural practices of rouging, reflective mulches provide only partial and temporary relief, which often proves uneconomic for resource-limited smallholders farmers (14). Consequently, breeding and deployment of resistant or tolerant varieties offer the most effective, durable, and environmentally friendly strategy for sustainable management (15, 16). While progress has been made globally in identifying and introgressing resistance genes (e.g., *Ty-1*, *Ty-2*, *ty-5*), performance under controlled conditions does not always translate to field stability in virus-prone tropical environments with mixed infections and high natural inoculum pressure (17).

Unfortunately, there is limited report of field-based evaluations of advanced tomato breeding lines under ambient viral exposure and this constrains the selection of genotypes that combine high yield potential with stable virus resistance. This gap hinders the development of resilient virus tolerant tomato cultivars tailored to local agro-ecological conditions.

Thus, the present study evaluated selected commercial tomato varieties and advanced breeding lines from National Horticultural Research Institute (NIHORT) for yield and response to natural viral disease pressure under open-field trials in Ibadan, Nigeria.

MATERIALS AND METHODS

Study Area

The field experiment was conducted during the early (April–July 2025) and late cropping season (November 2025–February 2026) at the experimental field of the National Horticultural Research Institute (NIHORT), Ibadan, Oyo State, southwestern Nigeria (7°30′N, 3°54′E). The site lies within the humid tropical agro-ecological zone, characterized by a bimodal rainfall pattern, mean annual rainfall of

1200–1500 mm, and average temperature ranging from 25–32 °C. The soil at the experimental site is classified as sandy loam with moderate fertility.

Plant Materials

The plant materials comprised of eight tomato genotypes consisting of two commercial hybrid varieties (Platinum F1 and Cobra F1), one released NIHORT variety (HORTITOM 1) and five advanced breeding lines developed and maintained under the tomato breeding programme of National Horticultural Research Institute (NIHORT), Ibadan.

Nursery Activities

The tomato seedlings were raised **in the** nursery for five weeks before transplanting to the field. Basal fertilizer was applied using NPK (15–15–15**) at the rate of 300 kg/ha**, and top-dressing was carried out as required. Pest management was conducted using standard integrated pest management practices, excluding treatments that could interfere with natural viral infection. Adequate watering with **a** watering can and hand pulling of weeds at regular intervals **was** maintained throughout the nursery period.

Experimental Design and Field Layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with three replications. The tomato seedlings were transplanted to each experimental plot measured 3 m × 2 m, accommodating 20 plants per plot. The seedlings were transplanted at a spacing of 50 cm between rows and 50 cm within rows. Standard agronomic practices were uniformly applied across all plots.

Data Collection

Disease Assessment

These lines were evaluated alongside commercial varieties to determine their response to viral disease infestation and yield performance under open field rainfed conditions. As viral disease incidence and severity were assessed under natural field conditions due to their differential performance on the experimental field

Disease incidence (%) was calculated as:

$$\text{Incidence} = \left\{\frac{\text{Number of infected plants}}{\text{Total number of plants}}\right\} \times 100$$

Disease severity was scored as the area or proportion of plant that were symptomatic using a 1–5 scale, where:

1 = No visible symptoms

2 = Mild symptoms (slight leaf curling or mottling)

3 = Moderate symptoms (clear mosaic and leaf distortion)

4 = Severe symptoms (stunted growth and pronounced distortion)

5 = Very severe symptoms (plant death or complete yield loss) (9)

Disease assessments were conducted at 7-day intervals after transplanting. At each assessment, individual plants were scored using the 1–5 severity scale. The mean disease severity score for each treatment was calculated by summing the severity scores of all assessed plants within the treatment and dividing by the total number of plants assessed

The resulting mean scores were used for statistical analysis.

Data were collected on: Number of fruits per plant, Average fruit weight (g), Total fruit yield per plot (kg) and later converted to yield per hectare (t/ha). All data were subjected to analysis of variance (ANOVA) using Statistical Analysis System (SAS) version 9.4. Treatment means were separated using Least Significant Difference (LSD) at a 5% probability level ($p < 0.05$). Data expressed in percentages were arcsine-transformed prior to analysis to stabilize variance, although untransformed means are presented for clarity.

RESULTS

Yield Performance and Fruit Production

The analysis of variance indicated that fruit yield did not differ significantly among the evaluated tomato genotypes (Fig. 1). However, observable numerical variation was evident across the entries, with the advanced breeding line NHTo128-1 exhibiting the highest mean yield and number of fruits per plant, coupled with superior performance under natural viral disease pressure. Tomato lines NHTo29-2/1 and NHTo37L recorded consistent low yields (4.8 t/ha and 5.2 t/ha, respectively). From the results, significant variation (p = 0.029) was recorded for the number of fruits per plant among the genotypes (Fig. 2). The tomato genotypes generally expressed a low fruiting pattern across the plots, with the exception of the NHTo128-1 genotype that recorded a significantly higher fruit yield.

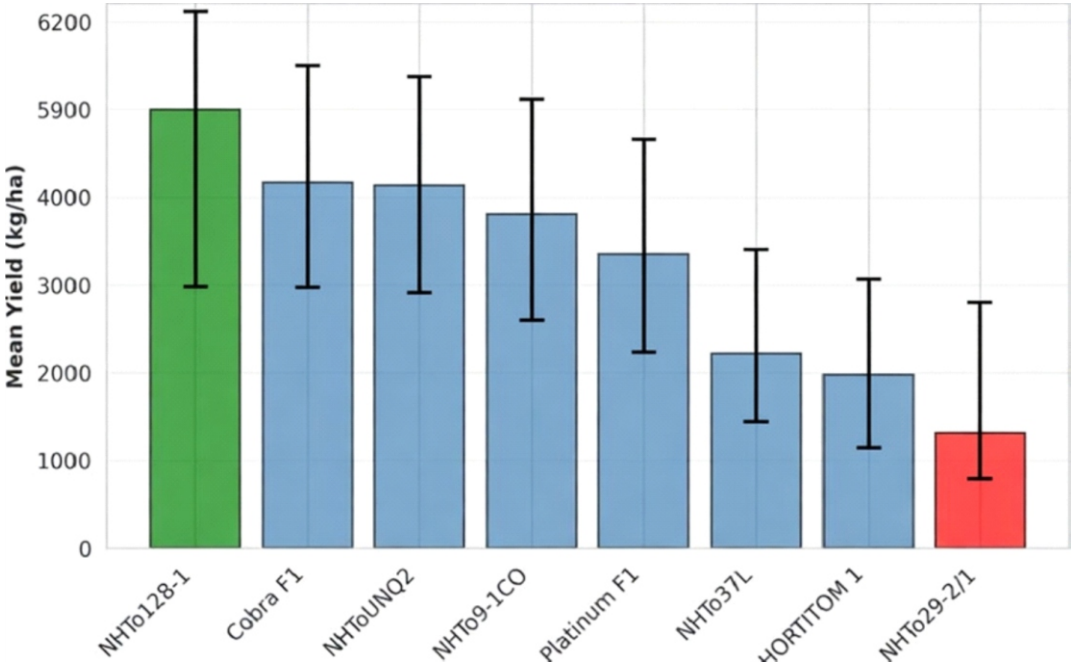


Figure 1: Mean Yield by Genotype

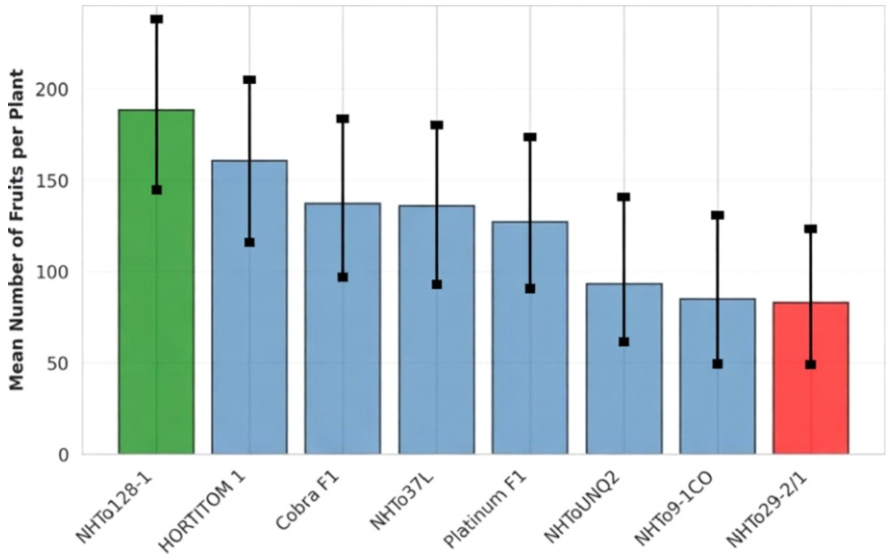


Figure 2: Mean Fruit Production by Genotype

Virus Disease Incidence

Disease incidence increased progressively with no statistical significance ($p > 0.05$, Table 1) from 6 to 8 weeks after transplanting (WAT) across all the eight tomato genotypes evaluated, with mean incidence ranging from 82.5% to 96.7% at 6 WAT and from 90.0% to 100% at 8 WAT. However, the advanced breeding line NHTo29-2/1 recorded the highest incidence (96.7% at 6 WAT and 100% at 8 WAT), while NHTo128-1 exhibited a lower disease incidence (85.0% at 6 WAT and 92.5% at 8 WAT). The commercial hybrids Platinum F1 (88.3% at 6 WAT and 95.0% at 8 WAT) and Cobra F1 (90.0% at 6 WAT and 96.7% at 8 WAT), and the NIHORT registered variety HORTITOM 1 (87.5% at 6 WAT and 94.0% at 8 WAT) fell within the intermediate range, with no pairwise differences.

Table 1: Mean Disease Incidence (%) at 6 and 8 Weeks After Transplanting (WAT)

Genotype	Incidence 6 WAT (%)	Incidence 8 WAT (%)
NHTo128-1	85.0 a	92.5 a
Platinum F1	88.3 a	95.0 a
Cobra F1	90.0 a	96.7 a
HORTITOM 1	87.5 a	94.0 a
NHToUNQ2	86.7 a	93.3 a
NHTo9-1CO	92.0 a	97.5 a
NHTo37L	91.3 a	98.0 a
NHTo29-2/1	96.7 a	100.0 a
p-value (ANOVA)	Ns	Ns

Mean followed by the same letter in each column do no differ significantly from each other at $p \leq 0.05$ according to new Duncan Multiple Range Test (DMRT)

Virus Disease Severity

Disease severity assessed at six weeks after transplanting (SEV6) did not differ significantly among genotypes ($p = 0.085$, Fig. 3). Breeding line NHTo29-2/1 had the highest disease severity score (4.38) while NHTo128-1 exhibited the lowest severity score of 2.61. Pairwise comparisons showed a significant difference ($p = 0.019$) between NHTo128-1 and NHTo29-2/1.

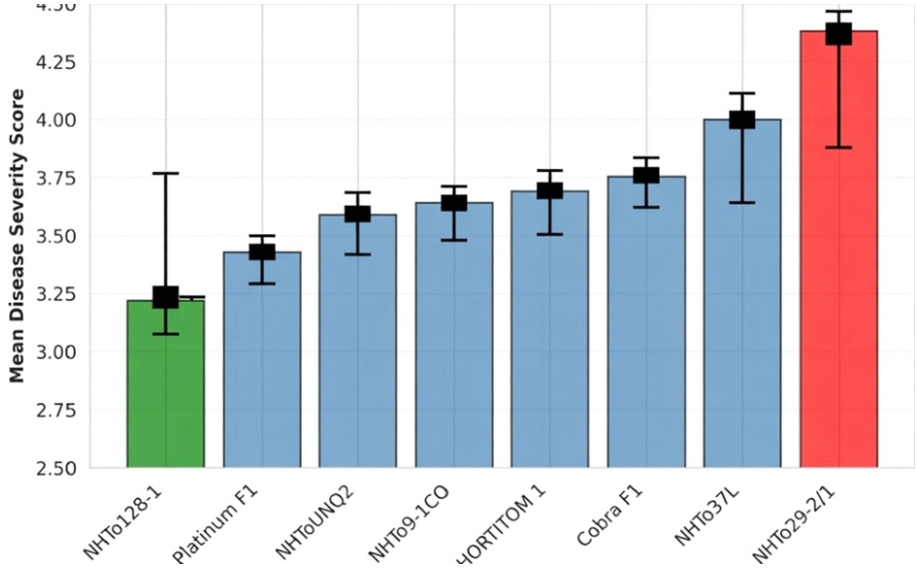


Figure 3: Disease Severity at 8 Weeks After Transplanting

Relationship Between Disease Severity and Yield

From the regression analysis, a significant negative relationship was observed between virus disease severity, yield and yield-contributing traits ($R^2 = 0.398$, $p = 0.0016$; Figure 4), such as number of fruits and fruit length.

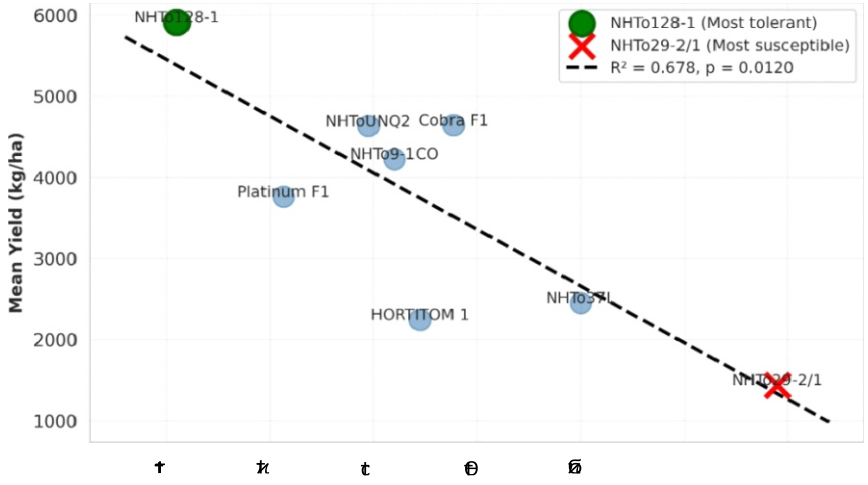


Figure 4: Relationship: Disease Severity vs Yield parameters (Kg).

DISCUSSION

The results obtained from the two-season field evaluation under natural viral disease pressure demonstrated that fruit yield did not differ significantly among the evaluated tomato genotypes, although clear numerical superiority was observed in the advanced breeding line NHTo128-1. This might be as a result of effective selection during development and advancement in favor of yield and yield contributing traits leading to breeding lines expressing similar yield potential. This is in agreement with earlier findings of Bhandari *et al*. (18), Meena *et al*. (19), Shastri (20) and Prapthi *et al*. (21), that reported superior yield potential among advanced tomato breeding lines in their study. Furthermore, absence of statistically significant difference in yield recorded in this trial might also be attributed to the presence of high virus pressure during the trial. This is consistent with earlier reports from virus-endemic production systems, where high inoculum pressure and continuous activity of the whitefly vector (*Bemisia tabaci*) tend to suppress the expression of yield potential across genotypes (22; 23). Under such conditions, even moderately tolerant genotypes may exhibit comparable yields due to overwhelming infection pressure, thereby masking inherent genetic differences.

The absence of significant variation in disease severity at the earlier growth stages of tomato suggested a relatively uniform early-stage infection across all genotypes. This could be attributed to the lag phase in virus replication and systemic movement within host tissues, which often delays phenotypic differentiation among resistant and susceptible genotypes (24). However, at 8 WAT the disease severity increased but with no significant different in the incidence rate observed which indicated that disease severity increased with crop age even at no significant different of the incidence which provided better discrimination of genotypic responses to viral disease under field conditions.

The significantly lower disease severity observed in NHTo128-1 confirms its superior tolerance to viral infection compared to other entries, particularly the highly susceptible NHTo29-2/1. Furthermore, the findings of this trial might be attributed to the polygenic nature of resistance usually associated with begomoviruses such as *Tomato yellow leaf curl virus* (TYLCV), where tolerance is often governed by quantitative trait loci (QTLs) including Ty-1, Ty-2, Ty-3, and ty-5 (25; 26). However, since the viral pathogens responsible for the symptoms observed in this study were not confirmed through molecular diagnosis, the observed tolerance cannot be attributed specifically to begomovirus resistance. These resistance mechanisms typically do not confer complete immunity but function by reducing viral replication, delaying symptom development, and maintaining physiological activity under infection pressure (27). The performance of NHTo128-1 suggests the presence of partial resistance or tolerance mechanisms, although molecular validation is required to confirm the specific viral pathogens and resistance mechanisms involved.

The consistently high disease incidence (above 85% across genotypes) further confirmed the intense natural viral disease pressure at the experimental site, likely driven by favorable environmental conditions for whitefly proliferation usually associated with high humid tropical environments. The symptoms observed during the trial, including leaf curling, mottling, mosaic, leaf distortion, stunted growth, and reduced fruit set, were

consistent with viral disease symptoms commonly reported in tomato; however, these symptoms cannot be used alone to confirm infection by a specific virus or virus group. Similar high incidence levels have been reported across sub-Saharan Africa by (5; 28), where mixed begomovirus infections are prevalent and difficult to manage using conventional control measures. The lack of significant differences in incidence among genotypes suggested that infection was widespread and relatively uniform, reinforcing the importance of focusing on disease severity and yield response as more reliable indicators of tolerance.

The significant negative relationship between disease severity and fruit yield ($R^2 = 0.398$; $p = 0.0016$) showed the substantial impact of viral diseases on tomato productivity. This finding corroborates earlier studies demonstrating that increased field severity is directly associated with reduced photosynthetic efficiency, impaired assimilate partitioning, and ultimately lower fruit yield (23; 11). The implication is that even moderate reductions in disease severity, as observed in NHTo128-1, can translate into meaningful yield advantages under field conditions.

The superior performance of NHTo128-1 might further be attributed to multiple physiological and ecological mechanisms, including restricted virus movement within phloem tissues, reduced vector feeding preference, or enhanced tolerance to oxidative stress induced by viral infection (24; 27). In contrast, the high susceptibility of NHTo29-2/1 suggests a lack of such defense mechanisms, resulting in severe symptom expression, stunted growth, and reduced fruit set. The intermediate performance of commercial hybrids (Platinum F1 and Cobra F1) and HORTITOM 1 might be an indication of partial tolerance and may not be sufficient under high natural infection pressure typical of most open-field conditions in Nigeria.

A key limitation of this study is the reliance on symptom-based disease assessment without molecular confirmation of specific viral species or strains. Given the complexity of tomato viromes and the frequent occurrence of mixed infections in field conditions, visual scoring alone may not fully capture the diversity and dynamics of viral pathogens present (28). Future studies should therefore integrate serological and PCR-based diagnostics, alongside marker-assisted selection for resistance genes, to enhance the accuracy of genotype evaluation and breeding efficiency (26; 25).

Thus, the findings in this study reinforced the critical role of host plant resistance as a sustainable and economically viable strategy for managing viral diseases in tomato production systems, particularly in sub-Saharan Africa where chemical control of vectors is often ineffective, costly, and environmentally unsustainable (15). The identification of NHTo128-1 as a promising tolerant genotype provides a valuable resource for breeding programs aimed at improving tomato resilience and productivity under virus-prone conditions.

CONCLUSION

In open-field conditions that mimicked smallholder tomato farming in Nigeria, the advanced breeding line NHTo128-1 demonstrated the lowest viral disease severity coupled with the highest numerical yield, although fruit yield did not differ significantly among the evaluated genotypes. NHTo128-1 showed potential for improved field tolerance to viral disease coupled with good adaptation to open-field

tomato growing conditions in southwestern Nigeria. Thus, NHTo128-1 can be considered a promising tolerant parent for use in breeding programs aimed at developing high-yielding tomato varieties with improved tolerance to viral diseases and adaptation to virus-endemic production regions in Nigeria.

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