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Influence of Field and Storage Diseases and Pests on Tuber Yield and Quality of Exotic and Local Yam (*Dioscorea* spp.) Genotypes

Musa Decius Saffa [1], Francess Sia Saquee [2,3], Prince Emmanuel Norman [4,*], Nyasha John Kavhiza [2], Diakite Simbo [2], Meisam Zargar [2,*], Marina Lyashko [2], Elena Pakina [2] and Valentin Vvedenskey [2]

[1] Crop Protection Department, School of Agriculture and Food Sciences, Njala University, Freetown 00232, Sierra Leone; m.saffa21@yahoo.com
[2] Department of Agrobiotechnology, Institute of Agriculture, RUDN University, 117198 Moscow, Russia; 1042215055@pfur.ru (F.S.S.); njkavhiza@rocketmail.com (N.J.K.); diakitesimbo88@gmail.com (D.S.); lyashko-mu@rudn.ru (M.L.); pakina-en@rudn.ru (E.P.); vvedenskiy-vv@rudn.ru (V.V.)
[3] Faculty of Development Agriculture & Natural Resources Management, Eastern Technical University of Sierra Leone, Combema Road, Kenema City 00232, Sierra Leone
[4] Germplasm Enhancement and Seeds System, Sierra Leone Agricultural Research Institute (SLARI), Tower Hill, Freetown 00232, Sierra Leone
* Correspondence: norman.prince64@gmail.com (P.E.N.); zargar-m@rudn.ru (M.Z.)

Abstract: Field and storage trials were conducted to assess the response of exotic and local yam genotypes to major diseases (anthracnose, yam mosaic virus (YMV) and dry rot) and pests (i.e., mealy bug and nematodes) for the identification of parents with desired complementary traits for crossing. The experiment was conducted at the Njala Agricultural Research Centre (NARC) experimental site in Sierra Leone during two cropping seasons, 2020 and 2021. A total of 113 genotypes of yam comprising 15 *D. rotundata*, 4 *D. prahensilis*, 7 *D. esculenta*, 74 *D. alata*, 7 *D. bulbifera*, and 4 *D. cayenensis* were assessed. Results showed a significant ($p < 0.001$) linear relationship between yield and disease severity among yam genotypes. In-field disease (anthracnose and yam mosaic virus) infection accounted for 38% of the total variation observed in the fresh tuber yield. Findings on fresh tuber yield revealed that for every ton increase in yield of yams, anthracnose and YMV severities at five months after planting (MAP) decreased by 0.5 and 3.1 units, respectively. About 30 genotypes had low infection of disease, of which two belonged to *D. rotundata* (TDr 205 and TDr 96/00587), two belonged to *D. prahensilis* (PSLY074-13 and BMSLY085-13), three belonged to *D. bulbifera* (MOSLY022-12, MOSLY024-12 and KESLY09-12), and one belonged to *D. esculenta* (WRSLY083-13), while the remaining were *D. alata*. About 27 genotypes had intermediate infection, and 14 had high disease susceptibility, all of which belonged to *D. alata*. Storage disease infection had a highly significant ($p < 0.002$) linear relationship among yam genotypes. Dry rot, mealy bug, and nematode infection accounted for 15.1% of the total variation in fresh tuber weight loss. The findings were relevant for selecting parents with complementary traits of interest targeted at yam population improvement.

Keywords: field and storage trials; key diseases; pests; *Dioscorea* spp.

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1. Introduction

Yam (*Dioscorea* spp.) is a large genus that has species that are important as food and as sources of bioactive substances used in different ranges of applications due to its high nutritional benefits [1,2]. Yam is a primary staple food in many parts of the world, especially in Sub-Saharan Africa, where it serves as a valuable source of livelihood for many farmers, including Sierra Leone [3,4]. It is considered the third most important root and tuber crop after cassava (*Manihot esculenta*) and sweet potato (*Ipomoea batatas*) [5]. Yam is a valuable source of carbohydrates for the people of tropical and subtropical Africa, central and southern America, parts of Asia, the Caribbean, and the Pacific Islands [6,7].

Nevertheless, the traditional yam production belt is across West Africa [8]. With an average yield of 8.5 t ha^{-1}, over 74.9 million tons of yam tubers are produced annually, with Ghana, Benin, Côte d'Ivoire, Nigeria, and Togo accounting for 93.9% of global yam production. Yam production in West Africa increased from 8.3 million tons in 1961 to 74.2 million tons in 2019 [9,10]. Nigeria also produces 66.9% of the world's yam crops [10]. In a recent study from 2019 to 2022, yam is a precious food crop in tropical countries of west Africa. It is mainly integrated into their social, economic, cultural, and religious beliefs, serving as an essential food product in such communities [10].

Despite its socioeconomic significance, a number of issues, including the high cost and scarcity of clean "seeds," pests and diseases [11–13], severely limit yam yield. Diseases (bacteria, fungi and viruses) and pests including insects and nematodes directly affect production and quality. The viruses are the prime issues since they are the most difficult to control, they spread quickly through planting materials, and they have been observed in every place where yams are grown worldwide [11,13–15]. In addition, the International Committee (ICTV) has recognized twenty-five virus species infecting Yam on Taxonomy of Viruses (https://ictv.global/). Yam mosaic virus (YMV) is a potyvirus originating from Africa, which generally exhibits a narrow host range and is transmitted by over 200 species of aphids in a non-persistent and non-circulative manner [16,17]. The increasing infestation of yam diseases both in the field and during storage, as well as the high cost of production, are among the significant factors that limit its increased productivity [4,18]. The large size and relative fragility of tubers make them vulnerable to physical damage during harvesting and transportation for storage, and the crop also suffers from a range of foliar and tuber pests and diseases [19,20].

Declining yam quality at the market outlets due to the various pest and disease attacks, poor harvesting practices, and poor storage conditions is a challenge bedeviling the agricultural enterprise of yam [20,21]. One of the most economically significant foliar diseases of yam in Sierra Leone is yam anthracnose disease (YAD) caused by *Colletotrichum gloeosporioides* [3]. Anthracnose can depress yield by 67 to 80% especially in intensive and extensive yam production areas. Severe infection during early establishment may result in a total loss of planting material. Seed yam production is very low in most parts of the world due to low-yielding cultivars, poor agronomic packaging, and a lack of high-quality seeds, making growers become more involved in the seed scheme for crops that are vegetatively propagated than for crops that are propagated through seed [22–24]. Yam anthracnose disease, YMV and other diseases and pests are bottlenecks affecting commercial yam production [25]. Yam diseases and pests spread through the exchange of infected/or infested yam germplasm [26] and naturally through animal vectors (aphids, pollination) [27]. The infectious or infested genotypes provide an opportunity to investigate the infectivity of the disease or pest infestation, host range, symptom expression and localization with plant host. Disease such as YMV travels through the vegetative propagation of infected tubers or vines as well as transmission by the aphids [28].

Virus elimination through in vitro culture techniques has been successfully applied for the production of virus-free plants. Some of these established techniques are shoot–tip or meristem culture, micrografting, chemotherapy, thermotherapy, and shoot–tip cryotherapy [29–31]. Ita et al. [11] noted the elimination of YMV from *D. rotundata* genotypes by the cryotherapy of axillary buds of infected stocks. According to Shin et al. [32], YMV-free *D. opposita* plantlets were produced using the cryotherapy of shoot tips. Umber et al. [33] reported the elimination of yam viruses using a combination of thermotherapy and meristem culture. The water-dissolved ozone technique was reportedly utilized for the sanitation of potyvirus during the in vitro propagation of *D. cayenensis-rotundata* [34].

Several biological, serological and nucleic acid-based diagnostic methods have been described for the detection of diseases including YMV. Some of these techniques include triple antibody sandwich enzyme-linked immunosorbent assay (TAS-ELISA) and immunocapture reverse transcription-polymerase chain reaction (ICRT-PCR) [35–37]. However, these techniques are labor intensive with many steps for target detection [38]. Nkere et al. [39]

reported a chromogenic detection method of YMV by closed-tube RT loop-mediated isothermal amplification (CT- RT-LAMP). Silva et al. [38] utilized a rapid YMV specific detection technique by reverse-transcription recombinase polymerase amplification (RT-RPA). This study assessed the effect of field and storage diseases and pests on the tuber yield and quality of exotic and local yam (*Dioscorea* spp.) genotypes using the biological diagnostic technique.

2. Materials and Methods

2.1. Description of the Study Area

The study was conducted at the Foya Wulleh Crop Site, Njala University. Njala is located at an elevation of 50 m above the sea level on 8°6′ N latitude and 12°6′ W longitude. The area is characterized by two distinct seasons, the wet season from May to October and the dry season from November to April. The mean annual precipitation is 2526 mm, and the mean monthly maximum ambient temperature ranges from 29 °C to 34 °C, while the mean minimum temperature ranges from 21 to 23 °C. For the greater part of both day and night, relative humidity is high, especially during the rainy season [40]. The potential evapotranspiration exceeds rainfall during the dry season, whereas the reverse happens during the rainy season as precipitation exceeds evapotranspiration.

2.2. Experimental Design and Cultural Practices

A total of 113 genotypes of yam consisting of 15 genotypes of *D. rotundata*, 4 genotypes of *D. prahensilis*, 7 genotypes of *D. esculenta*, 74 genotypes of *D. alata*, 7 genotypes of *D. bulbifera*, and 4 genotypes of *D. cayenensis* were investigated in this study (Table 1). The experiment was arranged in a randomized complete block design (RCBD) with three replications in a set of two seasons, 2020 and 2021. Each genotype was assigned to an individual plot measuring 20 m^2 (2 × 10 m). Each plot had 20 mounds except for *D. esculenta* and *D. bulbifera*, which were planted on two ridges of the same plot size as above. The different species were tested against two control checks.

Each plot comprised 20 plants resulting in a plant population of 10,000 plants ha^{-1}. However, *D. esculenta* and *D. bulbifera* were planted at 0.5 × 1 m, giving a population of 20,000 plants ha^{-1}. The differential spatial arrangement is due to the small size seed tuber materials of these species utilized and also based on the recommended practice in the crop production guidelines for Sierra Leone [41]. Each set weighing 250 g was cut from the ware yam of each genotype and used as planting material. Before planting, the sets were locally disinfected with wood ash and allowed to dry under shade for one to two hours. The sets were planted in holes 10 cm deep on the crest of mounds and ridges. No fertilizer or pesticide was applied to test their genetic potential under natural conditions. Weeds were controlled manually by hand weeding and stake when appropriate.

2.3. Data Collection

A total of three pre- and postharvest diseases and two storage pests were evaluated. The genotypes were visually evaluated for their response to yam mosaic virus and anthracnose severity using a 1–5 scale, where 1 = no visible symptom, 2 = very low or mild, 3 = low, 4 = intermediate and 5 = high at one, three, and five months after planting (MAP) [42]. At harvest (8 MAP), storage tubers were weighed. The genotypes were assessed for their response to nematodes, mealy bug and yam tuber dry rot severity using a 1–5 scale as described above at one, two and three months after harvesting (MAH). The various disease infections and pest infestations studied were assessed naturally based on symptom expressions. The biological reservoirs of these diseases and pests are the tubers, bulbils, vines and/or leaves.

Table 1. List of accession numbers (genotypes) of *D. alata*, *D. rotundata*, *D. bulbifera*, *D. esculenta*, *D. praehensilis* and *D. cayenensis* used in the study.

Species				
D. alata			***D. rotundata***	***D. esculenta***
TDa 00/00103	WUSLY079-13	WRSLY082-13	TDr 00/00080	PSLY077-13
TDa 00/00046	MOSLY049-12	BOSLY063-13	TDr 205	BMSLY086-13
TDa 95/00247	MOSLY053-13	PSLY075-13	TDr 746	MOSLY045-12
TDa 02/00012	MOSLY041-12	KESLY013-12	TDr 747	MOSLY034-12
TDa 98/01168	MOSLY029-12	BOSLY070-13	TDr 89/02565	MOSLY047-12
TDa 95/00005	MOSLY040-12	KESLY018-12	TDr 95/00184	BOSLY066-13
TDa 95/00307	WUSLY078-13	PSLY073-13	TDr 95/01969	WRSLY083-13
TDa 98/01166	KESLY016-12	BOSLY069-13	TDr 95/18544	KESLY011-12
TDa 291	BMSLY084-12	KESLY019-12	TDr 96/00587	MOSLY052-13
TDa 98/01176	BOSLY067-13	KESLY008-12	TDr 97/00793	
TDa 95/00826	KESLY017-12	BOSLY058-13	TDr 98/03015	***D. prahensilis***
TDa 00/00194	MOSLY031-12	MOSLY050-13	TDr 99/02310	BMSLY085-13
TDa 98/01174	MOSLY033-12	KESLY020-12	TDr 99/02789	KESLY007-12
KASLY003-12	BOSLY060-13	MOSYL030-12	TDr 99-13	PSLY074-13
MOSLY026-12	MOSLY032-12	BOSLY057-13	TDr 99-15	MOSLY036-12
MOSLY042-12	MOSLY038-12	MOSLY035-12		
BOSLY065-13	MOSLY046-12	MOSLY043-12	***D. bulbifera***	***D. cayenensis***
KESLY022-12	KASLY002-12	KESLY015-12	MOSLY023-12	MOSLY051-13
MOSLY048-12	MOSLY025-12	WRSLY081-13	BOSLY062-13	BOSYL056-12
PSLY076-13	MOSLY039-12	KESLY006-12	BOSLY059-13	BOSLY071-13
KESLY021-12	KASLY004-12	KESLY014-12	BOSLY061-13	KESLY010-12
KESLY005-12	BOSLY064-13	BOSLY068-13	MOSLY044-12	
WUSLY080-13	KASLY001-12	BOSLY072-13	MOSLY024-12	
MOSLY027-12	MOSLY037-12	MOSLY028-13	KESLY009-12	
KONOPLANE	PULLI			

WUSLY = Western Urban Sierra Leone yam; BOSLY = Bo Sierra Leone yam; MOSLY = Moyamba Sierra Leone yam; KASLY = Kailahun Sierra Leone yam; KESLY = Kenema Sierra Leone yam; PSLY = Pujehun Sierra Leone yam; BMSLY = Bombali Sierra Leone yam; WRSLY = Western Rural Sierra Leone yam; TDa = Tropical *Dioscorea alata*; TDr = Tropical *Dioscorea rotundata*. The TDa and TDr accessions are exotic genotypes from the International Institute of Tropical Agriculture (IITA); the remaining genotypes across species are local yams of Sierra Leone.

2.4. Statistical Analysis

Data were statistically analyzed using the ANOVA in randomized complete block design in the Genstat 12.1 for Windows statistical software package to test the hypothesis [43]. The statistical relationships between yield and major field diseases as well as between fresh tuber weight and storage diseases were determined through regression analysis. The total variation in yield and fresh tuber weight percentage explained by major field and storage diseases was evaluated through the coefficient of determination (R^2) [44].

3. Results and Discussion

3.1. Effect of Field Disease Severity on Yield

Field disease severity generally increased with time among all genotypes assessed. The fitted regression model [45] is

$$Y = 17.57 - 0.47X_1 - 0.87X_2 + 1.48X_3 - 3.15X_4,$$

where Y = response variable (yield); X = explanatory variables: X_1 and X_2 = anthracnose severity at 3 and 5 MAP; and X_3 and X_4 = yam mosaic virus severity at 3 and 5 MAP, respectively. There was a highly significant ($p < 0.001$) linear relationship between tuber yield and field disease severity among yam genotypes.

Field disease (YAD and YMV) infection accounted for 38% of the total variation observed in fresh tuber yield. The remaining variation may be due to genotype-environment interactions. Disease infection ($p < 0.05$) significantly reduced yield in the various genotypes assessed.

The regression equation for mean yield indicated that for every ton increase in yield of yams, YAD and YMV severities at 5 MAP decreased by 0.5 and 3.1 units, respectively (Table 2). The severity of YAD and YMV at 5 MAP significantly contributed to yield reduction among genotypes. However, the differences among genotypes regarding their response to YAD and YMV severities at 3 MAP were not significant. The results indicated that mild infection of YMV and anthracnose at 3 MAP did not negatively affect yield.

Table 2. Major diseases influencing yields of yam genotypes assessed at Foya, Southern Sierra Leone, in 2020 and 2021 growing.

	Estimate	Standard Error	t (108)	t pr.
Intercept	17.57	1.71	10.25	<0.001
YAD3MAP	−0.477	0.941	−0.51	0.613
YAD5MAP	−0.872	0.307	−2.84	0.005
YMV3MAP	1.48	1.52	0.97	0.332
YMV5MAP	−3.149	0.754	−4.18	<0.001

YAD = yam anthracnose disease, YMV = yam mosaic virus, MAP = months after planting.

At 3 MAP, about 100% of genotypes of both *D. rotundata* and *D. bulbifera* exhibited no symptom of YAD, whereas 22, 25, 25 and 57% of genotypes of *D. esculenta*, *D. prahensilis*, *D. cayenensis* and *D. alata* respectively had mild infection of the disease. The yam mosaic virus showed a similar trend with eight genotypes exhibiting no visible symptoms of disease, while the remaining genotypes had mild infection of YMV ranging between 1.2 and 2.0 (Figures 1–4).

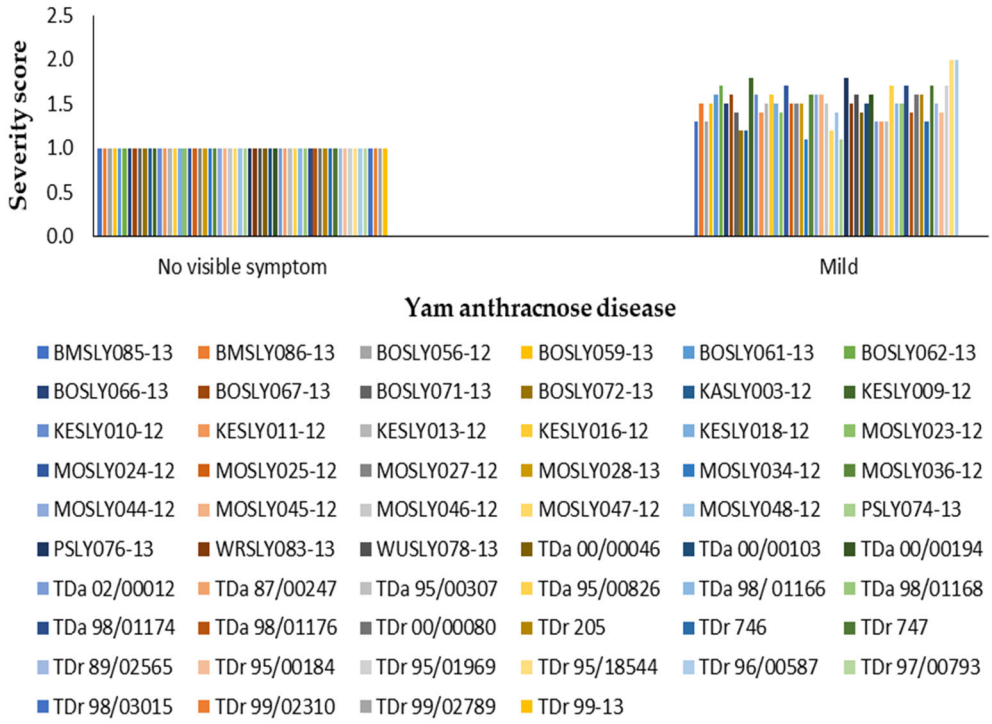

Figure 1. Anthracnose disease severity scores at three months after planting.

Three months after planting, the yam mosaic virus showed similar trends with eight genotypes of four species (two *D. prahensilis*, three *D. esculenta*, two *D. alata* and one *D. cayenensis*) exhibiting no visible symptom of disease, whilst the remaining 107 (including the control genotypes) exhibited mild infection of YMV ranging between 1.1 and 2.0 at three months after planting (Figure 2).

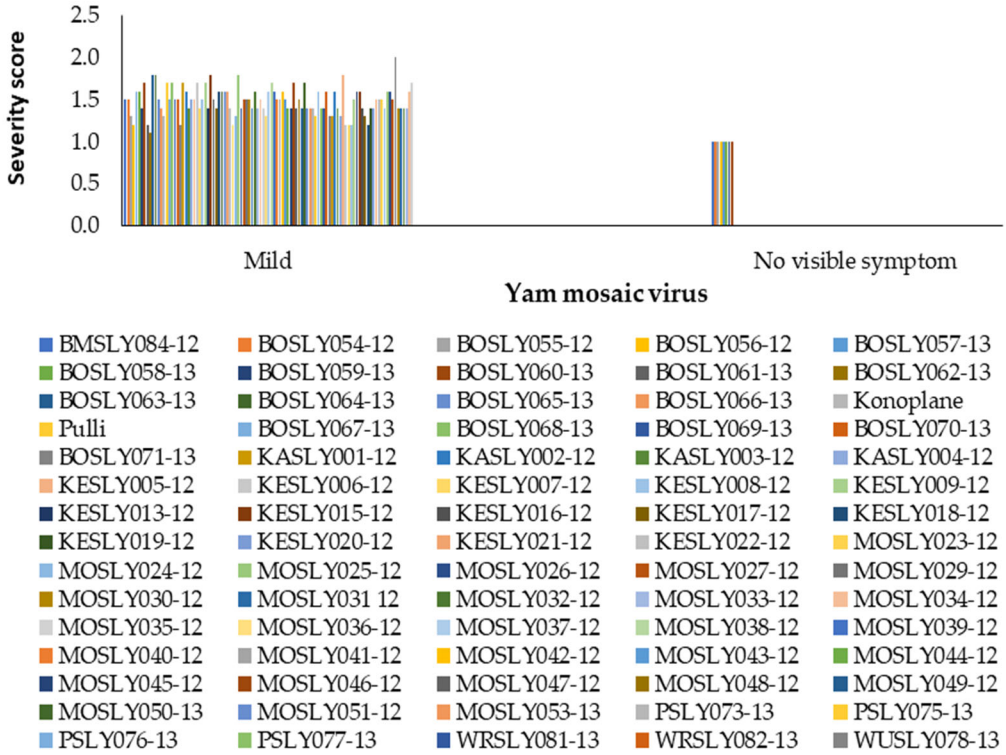

Figure 2. Yam mosaic virus disease severity scores at three months after planting.

Figure 3. Symptoms of anthracnose in different yam tissues. (**a**–**c**) Symptoms in leaves. (**d**) Symptoms in yam tubers. (**a**) Pale yellow margins surrounding the lesions. (**b**,**c**) Dark brown spot dotting the leaf lamina. (**d**) Dark brown lesions on tubers. Arrows indicates the lesions. Source: Ntui et al. [46].

At 5 MAP, 42 genotypes had mild infection of anthracnose, of which four belonged to *D. bulbifera*, seven belonged to *D. esculenta*, two belonged to *D. prahensilis*, four belonged to *D. cayenensis*, 11 belonged to *D. rotundata* (TDr 00/00080, TDr 746, TDr 747, TDr 89/02565, TDr 95/00184, TDr 95/01969, TDr 95/18544, TDr 97/00793, TDr 98/03015, TDr 99/02310, TDr 99-13) and 14 belonged to *D. alata*. About 30 genotypes had low infection of disease, of which two belonged to *D. rotundata* (TDr 205 and TDr 96/00587), two belonged to *D. prahensilis* (PSLY074-13 and BMSLY085-13), three belonged to *D. bulbifera* (MOSLY022-12, MOSLY024-12 and KESLY09-12), and one belonged to *D. esculenta* (WRSLY083-13), whilst the remaining 22 were *D. alata* species. About 27 genotypes of *D. alata* had intermediate infection and 14 genotypes of *D. alata* had the highest disease attack of anthracnose disease (Figure 5).

Figure 4. Symptom of yam mosaic virus on leaf.

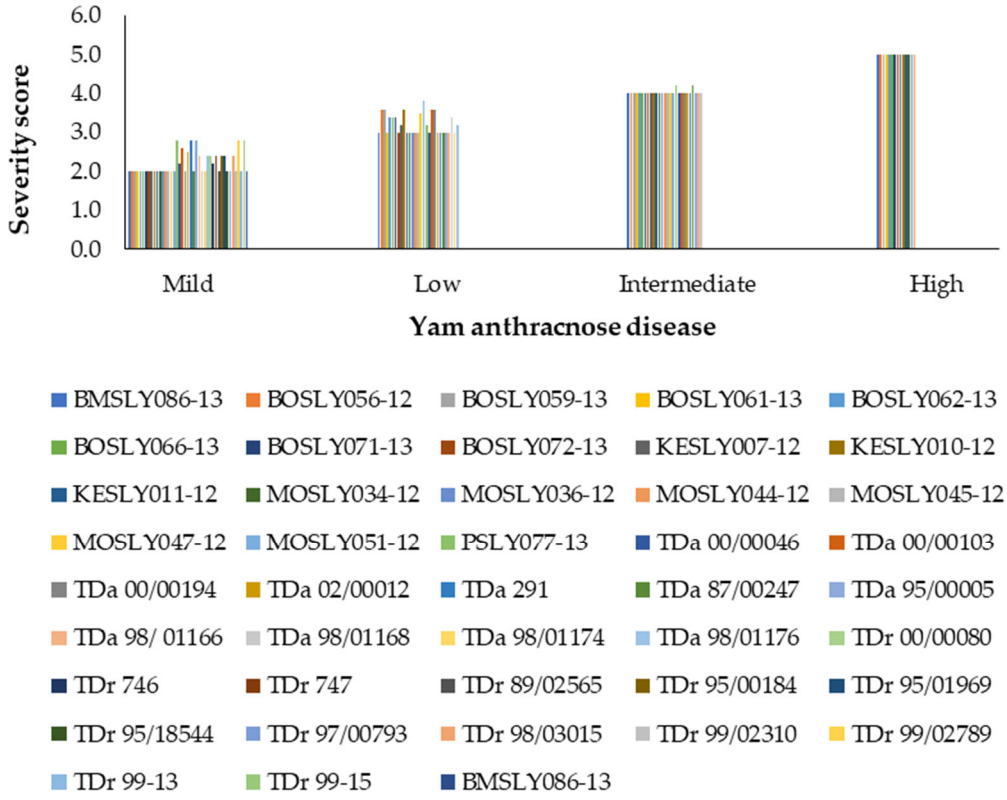

Figure 5. Anthracnose disease severity scores at five months after planting.

In a similar sampling regime, YMV attack was not as severe as anthracnose (Figure 6). About 100% of genotypes of both *D. prahensilis* and *D. cayenensis* had a mild attack of YMV. About 77% of genotypes of *D. rotundata* had mild attacks, whereas 23% had low severity of the disease. About 71% and 29% genotypes of *D. bulbifera* exhibited mild and low disease severity, respectively. For *D. esculenta*, 56% of the genotypes had mild infection, whilst 44% had low infection. About 45% of the genotypes (11 improved and 22 landraces) of *D. alata* had a mild attack of YMV, while 55% exhibited low infection of the disease. There was an observed wide variance of anthracnose severity compared to YMV disease infection, showing that the ranking of genotypes for anthracnose is more likely to change when tested in multiple locations (crossover interactions), thereby justifying the use of a site regression model (SREG). Gauch and Zobel [47] and Van Loon [48] also noted a severe

reduction in photosynthesis due to mosaic or chlorosis when calculated on a chlorophyll basis. The reduction in leaf area and shoot dry weight may have contributed to the reduced tuber yield in highly infected genotypes. The implication of these results is that it might be necessary for the selection of proper susceptible check varieties that are suitable to the mega-environments. The same genotypes observed to be resistant to anthracnose were also resistant to yam mosaic virus. These results show similar trends with little variation as those obtained by Egesi et al. [49]. These results have good implications for multiple disease resistance breeding as the different genes controlling these traits could be pyramided into developing a single ideotype. These genotypes can also be used to develop elite genotypes with stable resistance and supply a resource for further genetic studies.

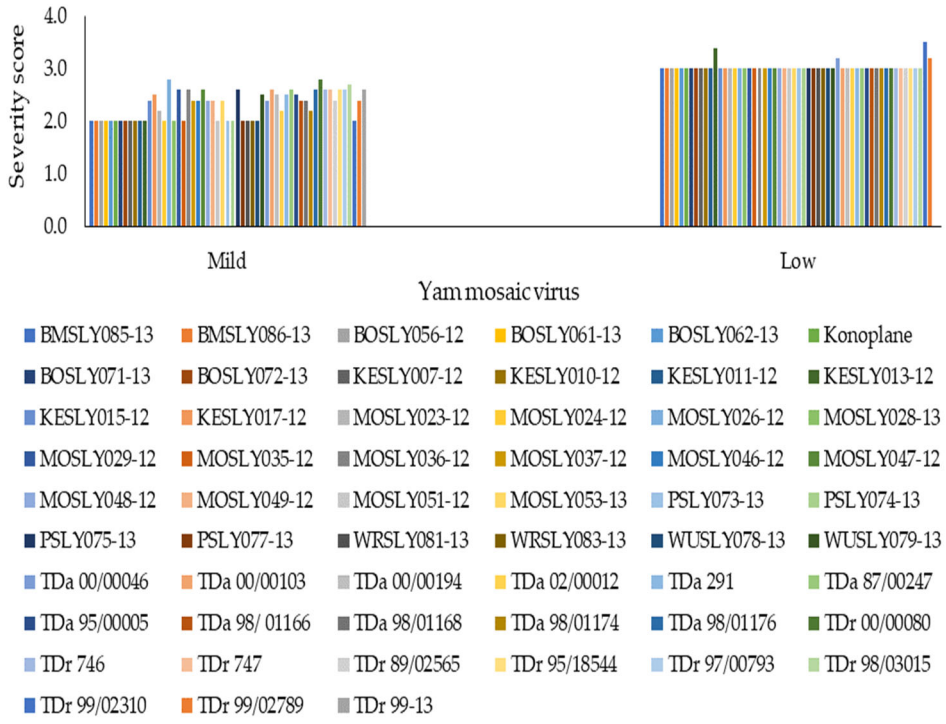

Figure 6. Yam mosaic virus disease severity scores at five months after planting.

3.2. Effect of Storage Disease Severity on Tuber Weight

Storage diseases also increased with time among genotypes. The fitted regression model follows: $y = -6.5 - 7.66X_1 - 0.84X_2 + 10.59X_3 + 3.21X_4 - 0.50X_5 - 0.44X_6 + 3.73X_7 - 5.21X_8 + 2.50X_9$. Here, y = response variable (percent tuber weight loss); X = explanatory variables: X_1 to X_3 = dry rot severity at 1, 2 and 3 MAH; X_4 to X_6 = mealy bug severity at 1, 2 and 3 MAH; and X_7 to X_9 = nematode severity at 1, 2 and 3 MAH, respectively. There was a highly significant ($p < 0.001$) linear relationship between percent tuber weight loss and dry rot severity assessed at 3 MAH among yam genotypes (Table 3). Dry rot severity accounted for 10.59% of the total variation observed in percent fresh tuber weight loss. The remaining variation may be due to environmental factors such as moisture stress and the genotype. Consequently, disease infection significantly ($p < 0.05$) contributed to fresh tuber weight loss in the various genotypes assessed.

The regression equation for mean fresh tuber weight loss indicated that for every kilogram decrease in the fresh tuber weight of yams, dry tuber rot severity at 3 MAH significantly contributes 10.59 units (Table 3). The pests, mealy bugs and nematodes, also contributed to yam fresh tuber deterioration over time among genotypes. However, the differences among genotypes regarding their response to mealy bug and nematode severities at 3 MAH were not statistically significant.

Table 3. Regression output of fresh yam tuber weight loss on major storage diseases assessed during 2020 and 2021 cropping seasons.

	Estimate	Standard Error	t (103)	t pr.
Intercept	−6.5	12.0	−0.54	0.591
DRYR1MAH	−7.66	3.89	−1.97	0.052
DRYR2MAH	−0.84	3.12	−0.27	0.788
DRYR3MAH	10.59	3.00	3.53	<0.001
MBUG1MAH	3.21	3.82	0.84	0.402
MBUG2MAH	−0.50	2.48	−0.20	0.839
MBUG3MAH	−0.44	1.99	−0.22	0.826
NEM1MAH	3.73	4.46	0.84	0.405
NEM2MAH	−5.21	3.64	−1.43	0.155
NEM3MAH	2.50	2.56	0.98	0.333

DRYR = dry rot, MBUG = mealy bug, NEM = nematode and MAH = months after harvesting.

Generally, the storage damage of fresh tubers of all species by dry rot, mealy bugs and nematodes was low within the first two months of storage. This was possibly due to storage in the modern yam barn at the Njala Agricultural Research Centre (NARC) where indoor temperature and relative humidity were slightly lower and higher, respectively, compared to the external ones (Table 4). However, at 3 MAH, severe damage by dry rot was observed mostly on genotypes of *D. esculenta* (Chinese yams) and *D. prahensilis* (bitter yams). The loss was partly due to the mechanical injury incurred during harvesting, storage beetles, mealy bugs, scale insects and harsher environmental conditions that favored disease development (Table 4). About 44% of the total genotypes assessed had ≤10% tuber weight loss, of which three belonged to *D. rotundata* (TDr 89/02565, TDr 98/03015 and TDr 99-15), three belonged to *D. esculenta* (MOSLY045-12, MOSLY047-12 and KESLY011-12), three belonged to *D. cayenensis* (BOSLY071-13, MOSLY051-12 and BOSLY056-12), four belonged to *D. bulbifera* (MOSLY023-12, MOSLY044-12, MOSLY024-12 and KESLY09-12) and 37 genotypes belonged to *D. alata* (comprising eight introduced and 29 landraces).

Table 4. Mean monthly temperature and relative humidity recorded during the storage period of fresh yam tubers.

Month	Time	Temperature (°C)		Relative Humidity (%)	
		Indoor	Outdoor	Indoor	Outdoor
January	09:00 a.m.	27.9	28.4	71.0	74.0
	12:00 p.m.	29.5	30.2	69.0	69.0
	15:00 p.m.	32.6	33.5	45.0	55.0
February	09:00 a.m.	27.6	29.4	59.0	63.0
	12:00 p.m.	29.3	32.5	57.0	59.0
	15:00 p.m.	34.1	33.6	37.0	74.0
March	09:00 a.m.	28.4	28.6	65.0	70.0
	12:00 p.m.	30.0	31.5	40.0	46.0
	15:00 p.m.	35.5	36.6	32.0	58.0

Our findings agree with Morse et al. [50], who reported that most of the yam rot induced by insect attacks is mainly due to storage beetles (*Coleoptera* sp.), mealy bug (*Planococcus citri*) and scale insects (*Aspidiella hartii*) during storage. Ansah et al. [51] also reported that about 24 to 25% of postharvest losses of yam in storage are due to fungal and bacterial pathogens infection and insect infestation.

4. Conclusions

This study established that field and storage diseases and pests significantly affect the tuber yield and quality of exotic and local yam (*Dioscorea* spp.) genotypes that could

be exploited for the genetic improvement of the crop. Field diseases (anthracnose and yam mosaic virus) infection accounted for 38% of the total variation observed in fresh tuber yield. The effect of disease attack on tuber yield reduction was higher at five months after planting with increasing attack as the plants approached maturity. About 37.2% of the total genotypes were identified to have a mild infection of anthracnose, of which four belonged to *D. bulbifera* (BOSLY062-13, BOSLY061-13, MOSLY044-12 and BOSLY059-13), seven belonged to *D. esculenta* (PSLY077-13, BMSLY086-13, MOSLY045-12, MOSLY034-12, MOSLY047-12, BOSLY066-13, WRSLY083-13 and KESLY011-12), two belonged to *D. prahensilis* (KESLY07-12 and MOSLY036-12), four belonged to *D. cayenensis* (MOSLY051-13, BOSLY056-12, BOSLY071-13 and KESLY010-12), 11 belonged to *D. rotundata* (TDr 00/00080, TDr 746, TDr 747, TDr 89/02565, TDr 95/00184, TDr 95/01969, TDr 95/18544, TDr 97/00793, TDr 98/03015, TDr 99/02310, TDr 99-13) and 14 belonged to *D. alata*. Storage disease (dry rot) and pest (mealy bug and nematode) infestation accounted for 15.1% of the total variation observed in fresh tuber weight loss. About 44% of the total genotypes were identified to have $\leq$10% tuber weight loss, of which three belonged to *D. rotundata* (TDr 89/02565, TDr 98/03015 and TDr 99-15), three belonged to *D. esculenta* (MOSLY045-12, MOSLY047-12 and KESLY011-12), three belonged to *D. cayenensis* (BOSLY071-13, MOSLY051-12 and BOSLY056-12), four belonged to *D. bulbifera* (MOSLY023-12, MOSLY044-12, MOSLY024-12 and KESLY09-12) and 37 genotypes belonged to *D. alata* (comprising eight exotic and 29 landraces). The study implies that genotypes identified with desired complementary traits can be used as parental materials for the genetic improvement of the crop. Genotypes TDa 00/00194, TDa 98/01168, TDa 98/01174, TDr 95/18544, TDr 89/02565, TDr 99-13, and TDr 99/02310, which combined $\leq$10% tuber weight loss with mild infection of field diseases and pests assessed, could be recommended for production.

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