



# Genotypic Variation and Seed Morphological Determinants of Maize (*Zea mays* L.) Performance and Resistance to Bacterial Streak in a Naturally Infected Field

Bukola Ojo Adediran<sup>\*1</sup>  Oluwafemi Michael Adedire<sup>2</sup>  and Olufemi Stephen Olaoye<sup>3</sup> 

<sup>1</sup>Department of Crop Production Technology, School of Agriculture, Federal College of Agriculture, Ibadan, Nigeria

<sup>2</sup>Department of Microbiology, School of Applied Sciences, Federal College of Agriculture, Ibadan, Nigeria

<sup>3</sup>Department of Animal Production Technology, School of Agriculture, Federal College of Agriculture, Ibadan, Nigeria

## Abstract

Bacterial Leaf Streak (BLS), caused by *Xanthomonas vasicola* pv. *Vasculorum* is an emerging disease threatening maize (*Zea mays* L.) production worldwide. The limited efficacy of chemical and cultural control methods necessitates the development of host-plant resistance as a sustainable management strategy. This study evaluated the agronomic performance and bacterial streak tolerance of eight maize genotypes released by the Institute of Agricultural Research and Training (IAR&T), Ibadan, under naturally infected field conditions. Maize seeds of each genotype were sorted into three size categories (large, medium, and small) and planted in a randomized complete block design. Data were collected on key growth and yield parameters, including plant height, leaf area, cob traits, yield components, and disease severity. Results revealed that all genotypes exhibited tolerance to BLS, with disease severity ranging from 0.80 to 1.60 and incidence between 2.33% and 6.67%. Large-seeded genotypes of ART-98-SW6, PRD-VIT-A, and ART-98-SW1 showed the lowest severity (<1.0), suggesting enhanced resistance, while small-grained variants were more susceptible. Yield performance varied among genotypes and seed sizes, with LNTP showing the highest total grain weight. Overall, seed size influenced both disease tolerance and yield potential, with larger grains conferring greater resistance to BLS. These findings highlight the importance of genotype and seed morphology in breeding strategies aimed at improving maize tolerance to bacterial streak under endemic conditions.

**Keywords:** Bacterial leaf streak, Maize genotypes, Performance, Seed morphology, Tolerance.

## Introduction

Maize (*Zea mays* L.) is one of the world's most important cereal crops, serving as a primary source of food, feed, and industrial raw material. Maize (*Zea mays*) cultivation and exploration have been at their all-time high in Nigeria and indeed, all parts of the globe [2]. In many maize-growing regions, particularly in tropical and subtropical environments, productivity is constrained by a wide range of biotic stresses, among which bacterial diseases have gained increasing importance [19]. One of the emerging bacterial diseases affecting maize is Bacterial Leaf Streak (BLS), caused by *Xanthomonas vasicola* pv. *vasculorum* (Xvv) [14]. The disease is characterized by elongated, water-soaked lesions on leaves that coalesce to form streaks, leading to reduced photosynthetic area, premature senescence, and ultimately yield losses. In endemic areas, especially where climatic conditions favor disease development, bacterial streak has become a major challenge to sustainable maize production [20].

Chemical and cultural management strategies for bacterial streak are largely ineffective or uneconomical due to the limited availability of effective bactericides and the polycyclic nature of the pathogen [12]. Consequently, host-plant resistance remains the most viable and environmentally friendly approach for disease management [7].

However, the genetic basis of tolerance to bacterial streak in maize is complex, and resistance levels among available germplasm are variable [13]. Identifying and selecting genotypes that combine superior agronomic performance with tolerance to bacterial streak is therefore critical for breeding programs targeting disease-prone environments.

Field evaluation of maize genotypes under natural disease pressure provides an opportunity to assess both yield performance and resistance stability under realistic agronomic conditions [9]. Such assessments help distinguish genotypes that can maintain acceptable productivity despite infection pressure, making them valuable candidates for further breeding and deployment in endemic regions [6]. Furthermore, understanding the interaction between the performance of released maize genotypes from research institutes like the Institute of Agricultural Research and Training (IAR&T) and disease intensity contributes to the development of selection indices that integrate yield potential, seed morphology, and disease tolerance [8]. The present study was therefore undertaken to evaluate the agronomic performance of eight (8) maize genotypes released by IAR&T, Ibadan, in a bacterial streak endemic field in order to identify promising genotypes and grain size that combine high yield potential with stable tolerance.

10 October 2025: Received | 09 November 2025: Revised | 10 December 2025: Accepted | 07 January 2026: Available Online

**Citation:** Bukola Ojo Adediran Oluwafemi Michael Adedire and Olufemi Stephen Olaoye (2026). Genotypic Variation and Seed Morphological Determinants of Maize (*Zea mays* L.) Performance and Resistance to Bacterial Streak in a Naturally Infected Field. *Journal of Plant Biota*. 11 to 15. DOI: <https://doi.org/10.51470/JPB.2026.5.1.11>

Bukola Ojo Adediran | [bukoladoriginal@gmail.com](mailto:bukoladoriginal@gmail.com)

**Copyright:** © 2026 by the authors. The license of Journal of Plant Biota. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

## Materials and Methods

The experiment was conducted at the Teaching and Research Farm of Cocoa Research Institute of Nigeria (CRIN), Ibadan, Oyo State. Seeds of eight genotypes of maize used for the experiment were obtained at the seed store of IAR&T, Ibadan, Oyo State (Table 1). The experiment was carried out during the early cropping season of 2023 (May - August) on a bacterial streak endemic field [3]. Maize seeds (500 g) of each cultivar were sorted into three different sizes (big, medium, and small) [24][17]. One hundred seeds were randomly selected from each category to determine seed morphometrics through the use of a digital variety caliper (Table 2).

The experiment was laid out in a randomized complete block design (RCBD), replicated three times. The experimental field was laid out in three blocks, and each block comprised three replicates. Inter-block spacing was 2.0 m, inter-row spacing was 0.75 m while intra-row spacing was 0.50 m and seeds were sown at 2 cm depth.

**Table 1: Maize seed varieties used for the experiment**

Variety	Maturity Stage
V1 = ART 98 SW6	2 months
V2 = PRO-VIT-A	2.5 months (pro vitamin A)
V3 = ART 98 SW1	2.5 months
V4 = ESR	2 months
V5 = DMR-LSR-1	3 months
V6 = BR 9928	2.5 months
V7 = LNTP	2.5 months
V8 = Suwan-1	2.5 months

**Source:** Institute of Agricultural Research and Training (IAR&T) Moor Plantation Ibadan.

**Table 2: Grouping of maize seeds based on their 100-seed weight (g)**

Variety	Small seed size	Medium seed size	Large seed size
ART 98 SW6	24.15	25.56	28.17
PRO-VIT-A	20.11	25.81	26.11
ART 98 SW1	24	25.47	28.8
ESR	23.13	25.11	28.21
DMR-LSR-1	22.57	25.5	26
BR 9928	24.11	25.91	27.71
LNTP	23.11	25.54	27.33
Suwan-1	22.11	25.49	27.37

Data were collected on five randomly selected plants to study the agronomic traits: Plant height at 95% maturity (cm), leaf area (cm<sup>2</sup>), stem girth (cm), cob length (cm), cob girth (cm), total grain weight (kg), cob weight/fruit (kg), grain yield per hectare (kg), harvest index (calculated as percentage of grain weight divided by total biomass), shelling percentage was calculated as percentage of grain weight divided by cob weight (%), 1000-seed was the average weight of 1000 seeds obtained from five shelled cobs (kg). The data collected were subjected to analysis of variance (ANOVA) using statistical analysis software [22]. Means were separated using Duncan's multiple range test (DMRT) at 5% probability.

## Isolation of *Xanthomonas vasicola* and characterization of bacterial streak

Affected portions (5 mm sections) of infected leaves were inoculated on Nutrient Agar for isolation of the streak pathogen (*X. vasicola*). Samples were surface-sterilised with 2% sodium hypochlorite, rinsed thrice with sterile water, drained, and inoculated on prepared agar plates [2]. Microbial strains were isolated from infected tissue samples on Nutrient Agar, and bacterial streak disease was eventually characterized in the maize genotypes as reported by Malvick *et al.*, 2024 [15].

A modified disease severity scale (0-5) for maize streak was used Mushayi *et al.*, 2025 [16], while percentage incidence [18] of the disease was determined as described below:

$$\% \text{ Incidence} = \frac{\text{Number of soil samples infected by a genus}}{\text{Total number of soil samples collected from the field}} \times 100$$

Resistance and tolerance to bacterial wilt were determined according to the rating class described by Borisade *et al.*, 2017 [5] as < 1% and ≤ 25% severity measures, respectively.

## Results and Discussion

### Performance of maize genotypes

The mean performance of growth characters evaluated in the eight varieties of maize is presented in Table 3. There was no significant difference among the varieties in terms of their stem girth and seed sizes, although variety ART-98-SW1 (Small) recorded the highest mean of 6.26 cm. There was no significant difference in the plant height of maize; however, plant height for small seed size was lower, considering seed size. This was in concordance with the result observed in a collection of soybean varieties [27]. Mean performance of yield and yield components evaluated in the eight (8) varieties of maize is presented in Table 4. With reference to cob length, there was no significant difference in the varieties and seed sizes. However, variety Suwan-1 (Large) recorded the longest cob length (28.20 cm) while ALT-98-SW6 (Small) recorded the least cob length (23.49 cm). For cob girth, there were significant differences among the varieties; variety ALT-98-SW6 (Large) recorded the widest average cob (17.83 cm), while the shortest cob girth was recorded for variety LNTP (Small).

For 1000-seed weight, a significant difference was observed among the varieties and their seed sizes. Variety DMR-LSR-Y (Small) recorded the heaviest weight (0.38 kg). Variety LNTP (Medium) recorded the heaviest/largest total grain yield (0.23 kg). PRO-VIT-A (Medium) recorded the largest grain yield/hectare (99.749 tonnes). Variety PRO-VIT-A (Small) expressed a superior performance in harvest index (73.83%) and biomass measurement (0.13%). Both medium and small seed size PRO-VIT-A had the highest shelling percentage (78.01%) when variety BR-9928 (Large) recorded the least performance (55.52%). Small and medium maize seed fractionation performed significantly better than the large seed size [24]. Contrary results by Wang *et al.*, 2025 [27] were obtained in soybean, where larger seed size performed better in pod yield and 100-seed weight than the smaller sizes.

The significant variety effect on 1000-seed weight, total grain weight, shelling percentage, harvest index, biomass measurement, and grain yield/hectare suggests that differences in varieties and seed sizes were responsible for variation in these characters. The result indicates that dissimilar maize cultivars exhibited significantly different yield characteristics. It is in agreement with the study carried out by Adediran *et al.*, 2025 [1] on okra genotypes. Differences in evaluated yield and yield components for seed sizes (Large, Medium, and Small) showed that different fractions of seed size did influence the yield of the maize plant [24].

A similar trend of outcome was obtained by Sulewska and Kaziora 2006 [23] in an experiment with maize cv. Clarica, in which grain yield from plants grown from a large fraction declined when compared with that of plants grown from the small and medium sizes. Graven and Carter (1990) [11] showed a downward trend in large maize seeds compared to plants grown from smaller seeds.

Royo *et al.*, 2006 [21] revealed that the effect of durum wheat plants grown from large grains was higher (16% increment) compared with plants grown from small seeds. Contrary to the study, however, EmayatGholizadeh *et al.*, 2012 [10] showed that by increasing maize seed size, commercial yield increased and the seed with higher vigour and size produced stronger seedlings, thus increasing the establishment.

**Table 3: Mean performance for growth components of eight varieties of maize**

Variety	Seed size	leaf Area (cm <sup>2</sup> )	stem girth (cm)	plant height at 95% maturity (cm)
ART98 SW6	Large	534.66a	5.15ab	164.05ab
	Medium	422.61abc	5.52ab	159.89ab
	Small	525.20ab	6.26a	174.32a
PRO-VIT-A	Large	518.21ab	5.58ab	158.48ab
	Medium	384.99c	5.09ab	161.53ab
	Small	453.08abc	5.65ab	161.35ab
ART-98- SW1	Large	457.82abc	5.00b	166.41ab
	Medium	464.82abc	5.56ab	159.70ab
	Small	475.60abc	5.38ab	156.55b
ESR	Large	414.41bc	5.31ab	168.58ab
	Medium	527.62ab	5.31ab	157.22ab
	Small	501.36ab	5.50ab	158.94ab
DMR-LSR-1	Large	483.89abc	5.12ab	158.55ab
	Medium	437.20abc	5.76ab	160.76ab
	Small	427.59abc	5.79ab	162.36ab
BR-9928	Large	483.89abc	5.07ab	162.68ab
	Medium	458.80abc	5.68ab	160.61ab
	Small	456.26abc	5.27ab	168.74ab
LNTP	Large	422.88abc	5.82ab	163.22ab
	Medium	458.72abc	5.26ab	163.83ab
	Small	457.29abc	5.38ab	157.61ab
Suwan-1	Large	497.73abc	5.63ab	162.02ab
	Medium	433.36abc	5.52ab	163.22ab
	Small	422.86abc	5.59ab	165.81ab
Variety x Seed size		Ns	Ns	Ns

Ns: not significant

Mean values with similar letter(s) along the column are not significantly different at 5% level of significance using Duncan's multiple range test (DMRT).

**Table 4: Means Performance for yield and yield components of eight varieties of maize**

Variety	Seed size	Cob length (cm)	Cob girth (cm)	Cob weight (kg)	1000-seed weight (kg)	Total grain weight (kg)	Shelling percentage (%)	Harvest index (%)	Biomass measurement (kg)	Grain yield/ hectare (tonne)
V1	L	24.61ab	17.83a	0.11c	0.11ef	0.07b	62.49abc	59.91ab	0.11abc	73.20ab
	M	24.20ab	15.65abcd	0.10c	0.17bcdef	0.06b	61.05bc	57.82ab	0.11abc	87.04ab
	S	23.49b	14.13cde	0.12c	0.31abcd	0.08b	66.08abc	65.21ab	0.12abc	81.43ab
V2	L	24.32ab	14.62bcde	2.43a	0.13def	0.07b	66.46abc	63.97ab	0.10bc	72.56ab
	M	24.88ab	14.21cde	0.09c	0.13cdef	0.06b	78.01a	58.30ab	0.10bc	99.75a
	S	24.60ab	13.46cde	0.12c	0.29abcde	0.09b	78.01a	73.93a	0.13a	79.040ab
V3	L	25.67ab	13.88cde	0.10c	0.03f	0.07b	67.87abc	65.68ab	0.11abc	71.36b
	M	25.03ab	15.14abcde	0.11c	0.12def	0.06b	56.43c	61.19ab	0.01c	81.29ab
	S	24.58ab	15.04abcd	0.11c	0.32abc	0.07b	65.54abc	60.53ab	0.12abc	89.44ab
V4	L	25.55ab	15.47abcd	0.30c	0.03f	0.07b	68.78abc	64.34ab	0.11abc	74.64ab
	M	25.39ab	13.80cde	0.11c	0.14cdef	0.06b	56.05c	53.35b	0.12abc	86.77ab
	S	25.55ab	13.99cde	0.12c	0.30abcd	0.08b	71.65abc	69.99ab	0.12abc	88.13ab
V5	L	24.96ab	15.82abc	1.59b	0.03f	0.07b	67.59abc	64.82ab	0.11abc	72.40ab
	M	25.51ab	14.62bcde	0.10c	0.04f	0.06b	59.30bc	55.83ab	0.11abc	93.68ab
	S	24.80ab	12.75de	0.11c	0.38a	0.08b	68.82abc	66.24ab	0.12abc	84.48ab
V6	L	26.05ab	14.67bcde	0.11c	0.03f	0.07b	55.52c	60.89ab	0.11abc	69.28ab
	M	24.83ab	14.87bcde	0.10c	0.04f	0.06b	59.51bc	56.37ab	0.10abc	77.04ab
	S	25.77ab	14.65bcde	0.10c	0.30abcde	0.06b	66.57abc	59.68ab	0.11abc	86.88ab
V7	L	26.05ab	15.93abc	0.10c	0.03f	0.11b	67.71abc	66.91ab	0.11abc	68.00b
	M	23.55ab	13.99cde	0.10c	0.04f	0.23a	64.24abc	59.27ab	0.11abc	88.00ab
	S	25.63ab	12.25e	0.12c	0.29abcde	0.08b	61.82abc7	67.08ab	0.11abc	89.04ab
V8	L	28.20a	13.29cde	0.11c	0.03f	0.08b	74.67ab	67.85ab	0.12abc	84.48ab
	M	25.09ab	14.66bcde	0.12c	0.04f	0.07b	59.51bc	56.61ab	0.12abc	87.36ab
	S	25.25ab	17.29ab	0.10c	0.34ab	0.07b	70.69abc	63.23ab	0.12abc	88.08ab
V x S		ns	*	*	Ns	Ns	ns	Ns	ns	ns

Ns: not significant; V1: ART98-SW6, V2: PRO-VIT-A, V3: ART-98-SW1, V4: ESR, V5: DMR-LSR-1, V6: BR-9928, V7: LNTP, V8: Suwan-1, Variety: Variety; S: Seed size. Mean values with similar letter(s) along the column are not significantly different ( $p > 0.05$ ) using Duncan's multiple range test.



### Incidence and severity of bacterial streak disease among maize genotypes

All the selected genotypes of maize were tolerant to bacterial streak, disease severity varied significantly among the eight maize genotypes evaluated under endemic field conditions, with severity scores (on a 0–5 scale) ranging from 0.80 to 1.60 (Table 5). However, large grain sizes of ART-98-SW6, PRO-VIT-A, and ART-98-SW1 with severity measures less than 1 (0.80, 0.93, and 0.93, respectively) appeared more resistant to the disease than other genotypes, but their symptom were not significantly better compared to other varieties. ART-98-SW6 large grain size was less susceptible to bacterial streak, as it manifested a significantly lower severity than the small and medium grain plants. Leaves infected with *X. vasicola* were characterised with brown to light brown streak lesions, manifesting between the leafveins.

Disease incidence ranged from 2.33% to 6.67%, indicating generally low infection levels across the genotypes. Among the genotypes, BR-9928 and LNTP consistently exhibited the lowest mean disease incidence (2.33%) in large-grained plants; however, infected plants expressed severity higher than 1.00. In contrast, ART-98-SW6 (medium grain) recorded the highest disease incidence (6.67%); it equally exhibited a corresponding higher severity score (1.27), indicating worse susceptibility to *X. vasicola*. Similarly, small-grained variants of ART-98-SW6 and PRO-VIT-A recorded the highest severity values (1.60), signifying that grain size may influence the plant's response to bacterial streak infection.

Across genotypes, large-grained plants generally showed lower incidence and severity compared to medium and small-grained forms. This observation suggests that grain size may be associated with physiological or structural factors conferring partial resistance, possibly due to better resource allocation or stronger cell wall composition that limits bacterial penetration. These findings align with previous studies that reported genotypic and morphological influences on disease tolerance in maize and other cereals under bacterial and fungal stress.

Tasnim *et al.*, 2025 [26] investigated the influence of morphological properties of maize genotypes on drought tolerance. This study identified BHM-7, BHM-14, and BHM-15 as genotypes with superior drought tolerance at the reproductive stage, while Black, Violet, and White Vutta showed resilience at the seedling stage, exhibiting greater plant vigor under drought stress. A similar relationship was observed between bacterial streak tolerance and seed size of maize in the current study. Recognizing the relationship between phenotypic classifications of maize genotypes and their resistance to biotic and abiotic stressors was therefore proposed as a significant step toward breeding programmes for food security and sustainable agriculture [26].

In a similar study, genotypic differences in maize root morphology were associated with their response to low-nitrogen stress [25]. Advancements in breeding have led to modern hybrid maize genotypes characterized by smaller yet more responsive root systems under low-nitrogen (low-N) conditions. For instance, the root phenotypes of *Zhengdan958* and *Xianyu335* maize genotypes were determined by distinct genetic architectures, while in the *B73* genotype, crown roots, rather than embryonic roots, exhibit greater functional activity in adapting to low-N stress [25]. Furthermore, shoot nitrogen concentration serves as an indicator of the plant's internal nitrogen status, which exerts a regulatory influence on root morphogenesis, disease tolerance, and developmental plasticity [4].

Overall, while variations existed among grain sizes within genotypes, the differences were not statistically significant ( $p > 0.05$ ) for most comparisons. Nevertheless, the consistently low incidence and severity observed in large-grained genotypes (especially, ART-98-SW6, PRO-VIT-A, and ART-98-SW1) highlight these plants as promising candidates for further evaluation and possible use in resistance breeding programs against bacterial streak disease.

### Conclusion

Evaluation of agronomic performance of maize genotypes in disease-endemic fields is imperative in order to identify promising genotypes and grain size that combine high yield potential with stable tolerance. This study established the performance and tolerance of 8 maize genotypes, further classified into different grain sizes (large, medium, and small), to bacterial streak disease. The yield of maize genotypes was dependent on the seed fraction used, and it decreased with an increase in the size of the seeds. However, variety LNTP performed best in total grain weight. The genotypes were all tolerant to streak disease, while large grain size genotypes manifested more tolerance than medium and small grain-plants, particularly in ART-98-SW6, PRO-VIT-A, and ART-98-SW1. These findings provide useful insights for maize improvement programs and inform the influence of grain size in strategies for managing bacterial streak through host resistance, especially in endemic fields.

### Recommendation

The released maize hybrids by IAR&T, Ibadan appeared to be tolerant to bacterial streak disease.

However, genotypes PRO-VIT-A and ART-98-SW1 (large grains) should be selected for subsequent breeding programmes for disease resistance and screening for resistance genes. Furthermore, LNTP with outstanding performance can be recommended for maize researchers and farmers to obtain optimum yield, especially in a bacterial streak-free environment.

**Table 5: Percentage incidence and severity (0-5) of bacterial streak phenotypes in selected genotypes of maize**

Genotypes	Grain size	Incidence (%)	Severity
ART-98-SW6	Large	4.33ab	0.80c
	Medium	6.67a	1.27ab
	Small	4.67ab	1.60a
PRO-VIT- A	Large	3.67bc	0.93bc
	Medium	5.67ab	1.33ab
	Small	4.00ab	1.60a
ART -98-SW1	Large	3.00bc	0.93bc
	Medium	6.00ab	1.33ab
	Small	4.33ab	1.00ab
ESR	Large	2.67bc	1.20ab
	Medium	5.00ab	1.07ab
	Small	6.00ab	1.00ab
DMR-LSR-1	Large	3.67bc	1.27ab
	Medium	5.00ab	1.13ab
	Small	5.00ab	1.00ab
BR-9928	Large	2.33c	1.00ab
	Medium	6.00ab	1.20ab
	Small	5.00ab	1.07ab
LNTP	Large	2.33c	1.13ab
	Medium	4.67ab	1.00ab
	Small	6.33ab	1.13ab
Suwan-1	Large	3.67bc	1.27ab
	Medium	5.67ab	1.40ab
	Small	5.00ab	1.00ab

Mean values with similar letter(s) down the column are not significantly different at 5 % level of significance using Duncan's Multiple Range Test (DMRT).

## REFERENCES

1. Adediran, B. O., Adedire, O. M. and Aina, A. (2025). Selection and Genetic Variation in Okra (*Abelmoschus esculentus* L.) Genotypes in a Rainforest Agroecology. *Chemical & Pharmaceutical Research*, 7 (1): 1-5.
2. Adedire, D. E., Owoeye, T. E., Farinu, O. M., Ogundipe, W. F. and Adedire, O. M. (2023). Management of fusarium wilt disease of maize (*Zea mays* L.) with selected antimycotic plant extracts and inhibitory *Bacillus* strains. *Current Microbiology*, 80: 204.
3. Adekeye, A. O. (2023). Characterization of bacterial streak caused by *Xanthomonas vasicola* on selected maize genotypes (*Zea mays* L.). *FCAIB Library*.
4. Aluko, O. O., Kant, S., Adedire, O. M., Li, C., Yuan, G., Liu, H. and Wang, Q. (2023). Unlocking the potentials of nitrate transporters at improving plant nitrogen use efficiency. *Frontiers in Plant Science*, 14:1074839.
5. Borisade, O. A., Uwaidem, Y. I. and Salami, A. E. (2017). Preliminary report on *Fusarium oxysporum* f. sp. *lycopersici* (*Sensu lato*) from some tomato producing agroecological areas in southwestern Nigeria and susceptibility of F1-resistant tomato hybrid (F1-Lindo) to infection. *Annual Research and Review in Biology*, 18(2): 1-9.
6. Canale, M. C., Nesi, C. N. and Castilhos, R. V. (2023). Abundance of *Dalbulus maidis* and impact of maize rayado fino disease on different genotypes in field conditions in Santa Catarina, Brazil. *Tropical Plant Pathology*, 48: 675-684.
7. Chang, J., Wei, S., Liu, Y., Zhao, Z. and Shi, J. (2025). Harnessing genetic resistance in maize and integrated rust management strategies to combat southern corn rust. *Journal of Fungi*, 11(1): 41.
8. Derbyshire, M. C., Newman, T. E., Thomas, W. J. W., Batley, J. and Edwards, D. (2024). The complex relationship between disease resistance and yield in crops. *Plant Biotechnol. J.*, 22: 2612-2623.
9. Dudek, G., Molin, L. M. D., Missio, V. C., Luchese, A. V. and Missio, R. F. (2024). Understanding maize genotype behavior under stunt complex pressure. *Agricultural Sciences*, 48: e009024.
10. EmayatGholizadeh, M. R., Bakhshandeh, A. M., Shoar, D. M., Ghaine, M. H., Saeid, A. K. H. and Sharafizadeh, M. (2012). Effect of source and seed size on yield component of corn S.C704 in Khuzestan, *African Journal of Biotechnology*. 11 (12): 2938-2944.
11. Graven, L. M., Carter, P. R. (1990). Seed size and tillage system on corn growth and grain yield. *Journal of Agriculture Production*, 3 (4): 445-452.
12. Heiden, N., Broders, K. A., Hutin, M., Castro, M. O., Roman-Reyna, V., Toth, H. and Jacobs, J. M. (2023). Bacterial leaf streak diseases of plants: symptom convergence in monocot plants by distant pathogenic *Xanthomonas* species. *Phytopathology* 113(11): 2048-2055.
13. Li, S., Zhu, L., Li, Y., Guo, Y., Zhang, Y., Huang, C., Wu, W., Sun, S., Cheng, Z. and Duan, C. (2025). Precise identification and analysis of maize germplasm resistance to Ear Rot caused by six *Fusarium* species. *Plants*, 14(15): 2280.
14. Longhi, T. V., Robaina, R. R., de Carvalho, D. U., de Oliveira, A. G., Leite Junior, R. P. and Balbi-Peña, M. I. (2023). New insights on alternative hosts of *Xanthomonas vasicola* pv. *vasculorum*, the causal agent of bacterial leaf streak of maize. *Agronomy*, 13(4): 1073.
15. Malvick, D. K., Rohwer, C. L. and Floyd, C. M. (2024). Effects of hybrids, foliar treatments, and infection conditions on bacterial leaf streak of sweet corn. *Plant Disease*, 108(9): 2906-2912.
16. Mushayi, M., Shimelis, H., Derera, J. and Tesfamariam, S. A. (2025) Breeding for resistance to maize streak virus: challenges, progress and future directions: a review. *Front. Plant Sci.* 16:1590870.
17. Panasiewicz, K., Sobieszcza, R., Ratajczak, K., Faligowska, A., Szyma, G., Bocianowski, J., Kolanos, A. and Pretkowski, R. (2025). Effects of Seed Fraction on Sowing Quality and Yield of Three-Line Hybrid Maize. *Agriculture*, 15, 972.
18. Pärnänen, K. M. M., Hultman, J., Markkanen, M., Satokari, R., Rautava, S., Lamendella, R., Wright, J., McLimans, C. J., Kelleher, S. L. and Virta, M. P. (2021). Early-life formula feeding is associated with infant gut microbiota alterations and an increased antibiotic resistance load, *The American Journal of Clinical Nutrition*, 115(2): 407–421.
19. Pfordt, A. and Paulus, S. (2025). A review on detection and differentiation of maize diseases and pests by imaging sensors. *J. Plant Dis. Prot.* 132: 40.
20. Robaina, R. R., Longhi, T. V., Zeffa, D. M., Gonçalves, L. S. A. and Leite, R. P. Jr. (2020). Development of a protocol and a diagrammatic scale for quantification of bacterial leaf streak disease on young plants of maize. *Plant Dis.*, 104: 2921–2927.
21. Royo, C., Ramdani, A., Moragues, M. and Villegas, D. (2006). Durum wheat under Mediterranean conditions as affected by seed size. *Journal of Agronomy and Crop Science*, 192 (4): 257-266.
22. SAS Institute (2002). Procedures Guide. Cary: SAS Institute.
23. Scully B. T., Wallace D. H. Variation in and Relationship of Biomass, Growth Rate, Harvest index, and Phenology to Yield of Common Bean. *Journal of the American Society for Horticultural Science*, 115: 218-225.
24. Sulewska, H. and Kaziora, W. (2006). Evaluation of sowing value and yielding potentials of three fractions of maize seeds treated with Biocuikol c20 PC. *Journal of Research and applications in Agricultural Engineering*. 51 (2): 178-182.
25. Sulewska, H., Śmiatacz, K., Szymańska, G., Panasiewicz, K., Bandurska, H. and Głowicka-wołoszyn, R. (2014). Seed size effect on yield quantity and quality of maize (*Zea mays* L.) cultivated in South East Baltic region. *Zemdirbyste-Agriculture*, 101: (1), Pp. 35-40.
26. Sun, X., Wang, P. and Mi, G. (2025). Genotypic differences in maize root morphology in response to low-nitrogen stress. *Agronomy*, 15(2): 332.
27. Tasnim, F., Ahmed, M. S., Rahaman, M. A. and Sagor, G. H. M. (2025). Morphological characterization of maize (*Zea mays* L.) genotypes for drought tolerance. *Journal of Phytology*, 17: 46–54.
28. Wang, X., Sun, J., Yi, Z. and Dong, S. (2025). Effect of seed size on soybean performance: germination, growth, stress resistance, photosynthesis, and yield. *BMC Plant Biology*. 219: 2393.