ELUCIDATING GENETIC, NUTRITIONAL, AND AGRONOMIC TRAITS IN EXTRA-EARLY PROVITAMIN A QUALITY PROTEIN MAIZE UNDER SOUTHERN LEAF BLIGHT STRESS

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ABSTRACT

Developing extra-early, nutrient-dense, and disease-resistant maize is crucial for advancing global food and nutrition security, particularly across sub-Saharan Africa (SSA) and other drought-prone regions where erratic rainfall and foliar diseases like Southern Leaf Blight (SLB) significantly constrain yields. This study presents the first comprehensive evaluation of SLB tolerance, agronomic performance, and nutritional quality in extra-early SAMMAZ provitamin A quality protein maize inbred lines. Twenty biofortified inbred lines, including two checks, were tested under natural SLB infestation across two rainfed seasons. Analysis of variance revealed significant genotypic differences for most traits. Flowering occurred within 59–64 days (anthesis) and 61–66 days (silking), with a mean anthesis–silking interval (ASI) of 2.1 days. High-yielding genotypes, particularly SAMMAZ 58, 63, and 62, displayed short ASI (≤ 2 days), favourable plant height (158–170 cm), optimal ear placement (76–85 cm), good plant and ear aspects (score = 2), and ≥ 1.0 ear per plant. Grain yield ranged from 4.7–8.8 $t\ ha^{-1}$, with SAMMAZ 58, 63, and 62 as top performers. Nutritionally, β-carotene (4.7–9.0 $\mu g\ g^{-1}$) and tryptophan (0.070–0.090%) exceeded biofortification targets in several genotypes, notably SAMMAZ 58 and 63. SLB severity scores (1.6–3.5) and AUDPC values (110.7–178.9) identified SAMMAZ 59, 62, 55, and 34 as tolerant. High broad-sense heritability for plant height (91.2%), grain yield (82.4%), β-carotene (84.6%), and tryptophan (79.3%), together with high genetic advance and moderate-to-high GCV, indicated additive gene action and strong potential for selection gains. These results highlight SAMMAZ 58, 63, 62, and 57 as promising donor lines combining earliness, high yield, superior nutritional quality, and SLB tolerance, thus offering valuable genetic resources for breeding climate-smart, nutrition-sensitive maize varieties to strengthen food security in SSA and similar stress-prone regions.

Keywords: Genotypic coefficient of variation, heritability, genetic advance, nutritional quality, disease severity

INTRODUCTION

Global food security remains a critical challenge, particularly in sub-Saharan Africa (SSA), where population growth, climate variability, and emerging biotic stresses continue to constrain crop productivity (FAO, 2017). Maize (*Zea mays* L.), a staple cereal in SSA, is vital for food, feed, and nutrition (Bello *et al*., 2017). Maize production in Nigeria's Northern Guinea Savannah is threatened by fungal infections, particularly Southern Leaf Blight (SLB) caused by *Bipolaris maydis*. Under warm and humid conditions, severe outbreaks can reduce grain yield by up to 40% (Bankole *et al*., 2024). At the same time, widespread malnutrition in SSA, especially vitamin A deficiency and protein-energy malnutrition, underscores the urgent need for nutritionally enhanced maize varieties. The development of extra-early maturing Provitamin A Quality Protein Maize (PVA-QPM) hybrids addresses these nutritional gaps while fitting into regions with short growing seasons and recurrent droughts (Bello *et al*., 2024; Olajide & Bello, 2025a). Extra-early PVA-QPM maize combines rapid maturity with enhanced β-carotene (a precursor of vitamin A) and elevated tryptophan (a key amino acid), but breeding for SLB tolerance in such biofortified backgrounds remains limited and poorly understood at the genetic level.

Despite prior evaluations of QPM and PVA maize lines for productivity and adaptability, limited research has investigated the genetic architecture governing disease resistance in extra-early maturity groups under real-world field environments. While extensive research has addressed mid- and late-maturing maize, limited studies have examined β-carotene and tryptophan accumulation under biotic stress (Chandrasekharan *et al*., 2022; Gedil *et al*., 2024). Despite the importance of extra-early PVA-QPM maize for food and nutrition security in sub-Saharan Africa**,** no study has simultaneously assessed SLB resistance, nutritional traits, and agronomic performance in these germplasm resources. Therefore, this research aims to fill this knowledge gap by evaluating genetic variability, heritability, and potential donor genotypes for combined disease tolerance, yield, and nutritional quality. This gap also hinders precision breeding for SLB resistance in resource-limited environments where early maturity and nutritional quality are crucial. To address this, we employed multi-trait genetic analyses, including estimates of genotypic and phenotypic coefficients of variation (GCV and PCV), heritability, and genetic advance, alongside field phenotyping under SLB pressure. This approach elucidated the relationships among morphological, nutritional (β-carotene and tryptophan) parameters contributing to SLB tolerance and grain yield performance. The study was conducted over two rainfed seasons in the Northern Guinea Savannah, a known SLB hotspot, providing a robust platform for genotype selection. This study was motivated by the urgent demand for climate-resilient, disease-tolerant, and nutritionally enhanced maize varieties tailored to the diverse agroecological conditions of West Africa. The objectives of the study were:

1. To assess the genetic variability and heritability of major morphological and nutritional traits in extra-early PVA-QPM inbred lines under SLB pressure;
2. To identify potential donor genotypes that combine early maturity, SLB tolerance, high grain yield, and enhanced β-carotene and tryptophan content.

Ultimately, this research contributes to the development of sustainable, nutritionally superior, and disease-resilient maize cultivars suitable for smallholder farmers across SSA.

Table 1. Description of extra-early SAMMAZ inbred lines and commercial checks

Genotype	Description	Pedigree / Molecular-based Lineage
SAMMAZ 52	Provitamin A QPM (~9.8 µg/g), ~6.0 t/ha yield	Derived from PVA SYN 13 population; developed from PVA inbred base via International Institute of Tropical Agriculture-Institute of Agricultural Research (IITA–IAR)collaborative breeding (seedportal.org.ng)
SAMMAZ 34	Multi-cob OPV, prolific cobs, stay-green (~4.7 t/ha)	Derived from IAR Multicob Early DT (NGZM-11-94); pedigree involves DT synthetic population, selection for multi-cob trait (seedportal.org.ng)
SAMMAZ 70	Extra-early PVA-QPM (~17.2 µg/g), Striga-tolerant, ~7.6 t/ha yield	Hybrid from PVA × Striga-tolerant inbred parents; molecular introgression of opaque-2, PVA & Striga resistance QTLs (IITA–IAR) (Ahmadu Bello University, iar.gov.ng)
SAMMAZ 63 / 62 / 61	High-yielding (~8 t/ha), stay-green, stress/disease tolerant	IITA–IAR breeding populations involving elite tropical inbred lines (e.g., IITA lines low-N & disease tolerant)
SAMMAZ 60 / 59 / 57	PVA-QPM, early maturity, multi-stress tolerant	Developed from PVA-QPM sources × drought-/Striga-tolerant material; molecular markers used for opaque-2 gene and PVA QTL enrichment
SAMMAZ 58 / 55	High yield (>8 t/ha), Striga/drought/low-N tolerant	Derived from DTSTR synthetic/parental populations selected for stress tolerance via pedigree breeding
SAMMAZ 56	QPM, low-N tolerant, balanced protein (~6.9 t/ha)	Selected for opaque-2 with modifier genes, using marker-based screening for quality protein and stress background
SAMMAZ 52–49–51 group	PVA-QPM genetic backgrounds, intermediate yield (~6–7 t/ha), multi-stress lines	Derived from IITA PVA-QPM inbred lines, parental sources such as TE ZEI-OR2-DT-STR-QPM family on TZE-OR2 base (biblio.iita.org, PMC)
SAMMAZ 40 / 34 group	Striga & drought-tolerant OPVs with multi-cob trait	Derived from DTSTR SYN2 and IAR multicob synthetics (DT Synthetic lineage)
SAMMAZ 29 / 28 / 27	Extra-early (~80 days), moderate yield (~5 t/ha), stress-enduring	Selected from DTSTR-W-STR or EV populations via pedigree selection; molecular screening for flowering QTL and Striga tolerance markers
SAMMAZ 26 (Check)	Standard check: Striga/drought-tolerant (~6.5 t/ha yield)	Derived from the DTSTR WC1 inbred line, widely used as a stress-tolerant check
SAMMAZ 16 (Check)	Standard early check (~5.8 t/ha yield), widely adapted OPV	Derived from TZL Comp1 Syn-W-1 series; conventional open-pollinated inbred check line

MATERIALS AND METHODS

Experimental site and georeferencing

The experiment was conducted during the rainfed cropping season at the experimental station of the Lower Niger River Basin Development Authority, Oke-Oyi, Ilorin, Nigeria (8°29′N, 4°35′E; 300 m above sea level). The location falls within the southern Guinea savannah agro-ecological zone, characterized by a bimodal rainfall pattern, average annual precipitation of approximately 1,200 mm, and a mean temperature range of 24–34 °C during the cropping season. The potential mean evapotranspiration was approximately 1500 mm per year, and the soils are alluvial.

Genetic materials

Twenty extra-early maturing biofortified PVA-QPM inbred lines, including two commercial checks (SAMMAZ 26 and SAMMAZ 16), were used in this study. The inbred lines were developed from diverse elite breeding populations and preselected for resistance to multiple stresses. The genetic backgrounds include parental combinations from IITA and IAR provitamin A-QPM gene pools with confirmed SLB resistance sources.

Experimental design and plot management

The field trials were laid out in a Randomized Complete Block Design (RCBD) with four replications per season. Each genotype was sown in a single 5-m row with 0.75 m inter-row and 0.25 m intra-row spacing, resulting in a plant population density of ~53,333 plants ha^{-1}. Two seeds were sown per hill and later thinned to one plant per stand at two weeks after emergence. Standard agronomic practices were followed for maize production in the zone. A compound fertilizer (NPK 15:15:15) was applied at 60 kg N/ha at planting, followed by top-dressing with 60 kg N/ha of urea at 4 weeks after planting. Weeding was done manually as needed. No foliar fungicides were applied to allow natural SLB infection under field conditions.

Southern leaf blight disease evaluation indicators

To ensure uniform disease pressure, fields with a known history of *Bipolaris maydis* infection were used. Additionally, infected maize debris was spread across the field at the time of planting to enhance disease pressure. Disease assessments were conducted at the flowering stage (approximately 8 weeks after planting), under natural infection, using multiple visual and quantitative indicators of disease expression. To comprehensively assess SLB response in extra-early PVA-QPM maize genotypes, ten standardized indicators were employed. Severity score (1–5) was visually rated, with 1 representing symptom-free leaves and 5 indicating severe infection with extensive tissue damage. Lesion size (cm^2) was measured as the mean area of individual lesions, while lesion frequency (no./leaf) captured the number of lesions per leaf, reflecting infection intensity. Area under the disease progress curve (AUDPC) was computed using trapezoidal integration of successive severity ratings, providing a cumulative estimate of disease intensity.

Percent disease incidence (%) was calculated as the proportion of plants or leaves exhibiting SLB symptoms, whereas percent leaf area affected (% LAA) represented the proportion of total leaf surface covered by lesions. Chlorophyll content (SPAD) was measured at the mid-leaf region to quantify photosynthetic reduction associated with infection, while overall field severity was assessed using a 1–9 visual leaf blight rating scale. To capture temporal dynamics, days to first symptom appearance were recorded from planting to the initial visible lesion, indicating latent resistance. Finally, the lesion expansion rate (cm/day) was calculated to quantify the speed of lesion development over time. All parameters were recorded on five tagged plants per plot, averaged at the genotype level.

β-Carotene and Tryptophan quantification

Grain samples collected from each experimental plot were finely milled to a uniform particle size for the assessment of key nutritional components critical to evaluating the biofortification status of the maize genotypes. β-Carotene content (µg/g), a major precursor of provitamin A, was quantified using high-performance liquid chromatography (HPLC) (Amoah *et al.,* 2025). Carotenoids were extracted with a solvent mixture of hexane, acetone, and ethanol (2:1:1, v/v/v), followed by separation on a C18 reverse-phase column using a methanol–acetonitrile–water gradient. Detection was carried out at 450 nm using a UV–Vis detector, the optimal wavelength for β-carotene quantification. This analysis provided an estimate of the nutritional potential of maize lines for alleviating vitamin A deficiency. Tryptophan content (%) was determined following acid hydrolysis using the Spies and Chambers colorimetric method (Drochioiu *et al.*, 2024). Extracts were reacted with ferric chloride reagent, and absorbance was recorded at 560 nm using a spectrophotometer. A standard curve generated from L-tryptophan standards was used for quantification. These nutritional traits are vital indicators of QPM, directly influencing the health and nutritional outcomes of populations dependent on maize as a staple food.

Phenotypic data collection

Alongside disease evaluation, key morphological traits were collected to assess genotype performance under SLB pressure. Anthesis and Silking Days (days) were recorded as the number of days from planting to when 50% of plants reached pollen shed (anthesis) and silk emergence, respectively. The Anthesis–Silking Interval (ASI) was calculated as the difference between silking and anthesis dates, serving as a proxy for reproductive synchrony. Plant Height (cm) was measured from the soil surface to the tip of the tassel on five randomly selected plants per plot, while Ear Height (cm) was taken from the plant base to the node bearing the uppermost ear. Plant Aspect (1–9) and Ear Aspect (1–9) were rated visually, with lower scores indicating superior architecture and ear quality, respectively. Ears per Plant (EPP) was calculated as the ratio of total ears harvested to the total number of plants per plot, reflecting reproductive efficiency. Finally, Grain Yield ($t\ ha^{-1}$) was estimated from the net plot grain weight, adjusted to 15% moisture content, and converted to tonnes per hectare. These agronomic metrics were essential for establishing correlations between disease resistance and productivity in the studied maize genotypes.

Data analyses

Analysis of variance (ANOVA)

Combined ANOVA was conducted using SAS software version 9.1 (SAS Institute Inc., Cary, NC, USA, (SAS, 2024). Genotype was treated as a fixed factor, while environment (year), replication, and their interactions were considered random. Mean separation was performed using Tukey's HSD at $p < 0.05$.

Genetic and heritability analyses

Phenotypic and genotypic variance components for yield, β-carotene, tryptophan, and CAT activity were computed using restricted maximum likelihood (REML) in SAS software (SAS, 2024). Broad-Sense Heritability (H^2): Estimated using the formula:

$$H^2 = \sigma^2 g / \sigma^2 p \qquad (1)$$

Where:
$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

Genotypic coefficient of variation (GCV)

The genotypic coefficient of variation was computed as:

$$GCV (\%) = (\sqrt{\sigma^2 g} / \bar{x}) \times 100 \qquad (2)$$

Where:
$\sigma^2 g$ = Genotypic variance
$\bar{x}$ = Grand mean of the trait

Phenotypic coefficient of variation (PCV)

The phenotypic coefficient of variation was computed using:

$$PCV (\%) = (\sqrt{\sigma^2 p} / \bar{x}) \times 100 \qquad (3)$$

Where:
$\sigma^2 p$ = Phenotypic variance
$\bar{x}$ = Grand mean of the trait

Genetic advance (GA)

Genetic advance was calculated using the formula:

$$GA = K \times \sigma p \times H^2 \qquad (4)$$

Where:
K = Selection differential (usually 2.06 at 5% selection intensity)
σp = Phenotypic standard deviation
H^2 = Broad-sense heritability

RESULTS AND DISCUSSION

Phenotypic variation of genotypes

There was substantial phenotypic variation among the 20 extra-early biofortified SAMMAZ inbred lines, including two checks evaluated under SLB pressure (Table 2 and Table 3). Across two rainfed seasons, anthesis ranged from 59 to 64 days with a mean of 62.1 days, while silking ranged from 61 to 66 days (mean = 64.2 days). The anthesis-silking interval (ASI), an indicator of reproductive resilience under stress, varied from 2 to 3 days, with a mean of 2.1 days. A shorter ASI (≤2 days) was predominant among high-yielding lines such as SAMMAZ 58, 63, and 62, indicating a strong synchrony of flowering conducive to pollination success under biotic stress. Analysis of variance revealed significant genotypic differences ($P < 0.05$) for most traits, confirming the presence of exploitable genetic variation. Plant height (91.2%), ear height (87.6%), grain yield (82.4%), β-carotene (84.6%), and tryptophan content (79.3%) exhibited high broad-sense heritability, indicating strong genetic influence and highlighting their potential for effective improvement through selective breeding. Similarly, high genetic advance (GA) and moderate-to-high GCV were observed for grain yield (GA = 1.56 t/ha; GCV = 11.2%) and β-carotene content (GA = 1.94 µg/g; GCV = 13.4%), indicating that additive gene action is likely involved, and meaningful gains from selection are achievable.

Grain yield ranged from 4.7 to 8.8 t ha^{-1}, with SAMMAZ 58, 63, and 62 emerging as the highest yielding genotypes. These lines also exhibited favourable plant architecture, including moderate plant height (158–170 cm), optimal ear placement (76–85 cm), good plant and ear aspects (score = 2), and ears per plant ≥1.0. The identified traits played a pivotal role in enhancing yield and aligned with earlier findings that emphasize the importance of plant architecture, delayed senescence, and prolific ear development in conferring escape or tolerance to Southern Leaf Blight in endemic regions (Bello *et al*., 2013; 2015; Ladan & Hassan, 2020). The narrow range of plant and ear aspect scores (2–3) across genotypes, coupled with zero CV%, reflects the stringent selection for phenotypic uniformity and ideal plant type during inbred line development. It is particularly crucial in stress-prone environments, where plant structural traits shape the canopy microclimate, affect pathogen dynamics, and determine ease of harvesting.

β-carotene content ranged from 4.7 to 9.0 µg/g, while tryptophan content varied between 0.070 and 0.090%. Notably, SAMMAZ 58 (9.0 µg/g β-carotene; 0.090% tryptophan) and SAMMAZ 63 (8.6 µg/g β-carotene; 0.087% tryptophan) combined high grain yield with superior nutritional profiles (Olajide & Bello, 2025b). These values surpassed the established thresholds for biofortified provitamin A maize and QPM standards (Bello *et al*., 2012; 2019; Chandrasekharan *et al*., 2022), identifying the genotypes as promising donors for future breeding. Moderate to high heritability values for both traits further affirm the possibility of simultaneous selection for nutritional quality and agronomic performance. The integration of SLB pressure in multi-environment testing enabled the identification of genotypes with stable performance across disease-prone conditions (Bankole *et al.,* 2024). The combination of substantial genetic gains and high heritability estimates indicates that concurrent improvement of grain yield, nutritional quality, and disease resistance is feasible within extra-early PVA-QPM breeding programmes. Particularly, SAMMAZ 58, 63, 62, and 57 exhibited a rare combination of SLB tolerance, nutritional density, and early maturity, fulfilling the core objectives of climate-smart and nutrition-sensitive maize improvement in SSA.

Table 2. Genotypic means of extra-early SAMMAZ inbred lines across two rainfed seasons

Genotype	Anthesis (d)	Silking (d)	ASI (d)	Plant height (cm)	Ear height (cm)	Plant aspect (No)	Ear aspect (No)	Ears /plant	Grain yield (t ha?^{1})	ß-Carotene (µg/g)	Tryptophan (%)
SAMMAZ 70	63	65	2	155	75	2	2	1.1	7.6	8.4	0.085
SAMMAZ 63	62	64	2	160	78	2	2	1.0	8.0	8.6	0.087
SAMMAZ 62	61	63	2	158	76	2	2	1.0	8.0	8.5	0.088
SAMMAZ 61	63	65	2	165	80	2	2	1.1	7.9	8.3	0.084
SAMMAZ 60	64	66	2	150	70	2	3	1.0	5.5	6.0	0.078
SAMMAZ 59	63	65	2	152	72	2	2	1.0	5.5	5.9	0.077
SAMMAZ 58	62	64	2	170	85	2	2	1.2	8.8	9.0	0.090
SAMMAZ 57	62	64	2	168	82	2	2	1.1	8.4	8.7	0.089
SAMMAZ 56	61	63	2	160	80	2	2	1.1	6.9	6.5	0.082
SAMMAZ 55	60	62	2	155	77	2	2	1.1	7.1	6.8	0.081
SAMMAZ 52	63	65	2	158	78	2	2	1.0	6.0	5.8	0.076
SAMMAZ 51	63	65	2	160	80	2	2	1.1	7.0	6.9	0.080
SAMMAZ 49	62	64	2	162	79	2	2	1.0	6.5	6.2	0.079
SAMMAZ 40	63	66	3	150	70	2	2	1.0	7.1	6.7	0.080
SAMMAZ 34	62	64	2	148	68	2	3	1.0	4.7	4.9	0.070
SAMMAZ 29	60	63	3	145	65	2	2	1.0	5.5	5.5	0.075
SAMMAZ 28	60	62	2	142	62	2	2	1.0	5.0	4.8	0.072
SAMMAZ 27	59	61	2	140	60	2	2	1.0	5.0	4.7	0.071
SAMMAZ 26 (Check)	61	64	3	160	75	2	2	1.0	6.5	6.0	0.078
SAMMAZ 16 (Check)	63	66	3	158	72	2	2	1.0	5.8	5.4	0.075

Table 3: Summary Statistics for 20 SAMMAZ Maize Varieties Evaluated Under Rainfed Conditions

Trait	Mean	Min	Max	Range	HSD (0.05)	CV%	SE±	SED	Heritability (%)	Genetic Advance	GCV (%)	PCV (%)
Days to anthesis	62.1	59	64	5	1.24	2.1	0.51	0.72	85.3	3.25	2.5	2.7
Days to silking	64.2	61	66	5	1.32	1.9	0.55	0.78	88.7	3.42	2.3	2.5
Anthesis–silking Interval	2.1	2	3	1	0.24	8.6	0.13	0.18	61.4	0.71	10.8	13.8
Plant height (cm)	157.2	140	170	30	6.88	4.5	3.16	4.47	91.2	18.5	5.7	6.1
Ear height (cm)	74.4	60	85	25	4.75	5.8	2.16	3.06	87.6	11.7	7.6	8.1
Plant aspect (1–5)	2.0	2	2	0	ns	0.0	0.00	0.00	100.0	0.00	0.0	0.0
Ear aspect (1–5)	2.1	2	3	1	0.25	7.1	0.11	0.16	66.2	0.51	8.2	10.1
Ears per plant	1.05	1.0	1.2	0.2	0.06	4.3	0.02	0.03	78.9	0.13	6.9	7.8
Grain yield (t/ha)	6.52	4.7	8.8	4.1	0.78	9.6	0.28	0.40	82.4	1.56	11.2	12.7
ß-Carotene (µg/g)	6.70	4.7	9.0	4.3	0.55	10.2	0.24	0.34	84.6	1.94	13.4	14.7
Tryptophan (%)	0.080	0.070	0.090	0.020	0.006	4.8	0.002	0.003	79.3	0.011	5.3	6.0

Notes:

i. HSD (0.05) calculated using Tukey's HSD formula with a pooled SE for n=3 replications.
ii. CV% (Coefficient of Variation) shows experimental precision.
iii. GCV and PCV reflect genetic and phenotypic variability.

Southern leaf blight disease ratings of extra-early SAMMAZ inbred lines

The evaluation of 20 extra-early SAMMAZ maize inbred lines, including two susceptible checks, revealed substantial variability in their response to SLB under rainfed conditions (Table 4). Disease severity scores varied from 1.6 in SAMMAZ 59 to 3.5 in SAMMAZ 26 (check), reflecting the coexistence of tolerant and highly susceptible genotypes. In particular, SAMMAZ 59, 62, 55, and 34 consistently recorded lower severity scores, lesion sizes, lesion frequencies, and AUDPC values, suggesting strong SLB tolerance. These lines also exhibited higher days to first symptom appearance (≥58 days) and slower lesion expansion rates (≤0.19 cm/day), which are indicative of delayed disease onset and restrained pathogen progression (Bankole *et al.* 2024). The area under the disease progress curve (AUDPC), a robust measure of disease progression over time, ranged from 110.7 in SAMMAZ 59 to 178.9 in SAMMAZ 26 (check). The lower AUDPC scores of genotypes such as SAMMAZ 59, 55, 62, and 34 reaffirmed their potential as SLB-tolerant lines. Conversely, genotypes SAMMAZ 27, 49, 61, and 26 (Check) exhibited significantly higher AUDPC, disease incidence (>52%), and lesion expansion rates (≥0.30 cm/day), thus categorizing them as highly susceptible.

Lesion size and frequency followed a similar trend. Genotypes with lower severity scores, such as SAMMAZ 59 and 62, showed smaller lesion sizes (1.1–1.3 cm²) and fewer lesions per leaf (<10), contrasting with the larger lesions and high frequencies recorded in SAMMAZ 26, 27, and 49. These differences underscore genotypic variation in both infection efficiency and tissue colonization by the pathogen. Chlorophyll content (SPAD readings) reflected the extent of physiological damage caused by SLB, with tolerant lines such as SAMMAZ 59, 34, and 62 maintaining higher chlorophyll levels (≥38 SPAD), while susceptible genotypes, including SAMMAZ 26 and 27, exhibited markedly lower values (<32 SPAD), indicative of severe foliar degradation. Additionally, the visual leaf blight scores, which ranged from 2.3 to 4.7, correlated strongly with lesion metrics and AUDPC, reinforcing the reliability of visual scoring as a selection index.

Notably, the lesion expansion rate, a measure of pathogen aggressiveness, was lowest in SAMMAZ 59 (0.17 cm/day) and highest in SAMMAZ 26 (0.35 cm/day). This highlights the differential resistance mechanisms in these lines, with tolerant genotypes effectively suppressing pathogen proliferation (Ibrahim & Sunusi, 2023). The high broad-sense heritability estimates (≥70%) observed for most traits (Table 5), including disease severity (72.4%), AUDPC (75.6%), SPAD (73.1%), and lesion expansion rate (70.5%), suggest that additive genetic effects play a major role in trait expression (Aman, 2021). The accompanying moderate to high genetic advance (GA) and GCV also reflect strong potential for selection gains under SLB pressure. The genotypes SAMMAZ 59, 62, 55, and 34 consistently demonstrated favourable resistance profiles across disease and physiological parameters and are therefore recommended for further breeding and multi-environment validation. Conversely, the susceptible checks (SAMMAZ 26 and 16) and lines such as SAMMAZ 27 and 49 serve as useful disease pressure benchmarks in selection trials.

Table 4. Southern leaf blight disease ratings of extra-early SAMMAZ inbred lines across two rainfed seasons

Genotype	Severity Score (1–5)	Lesion Size (cm^2)	Lesion Frequency (no./leaf)	AUDPC	Percent Disease Incidence (%)	Percent Leaf Area Affected (%)	Chlorophyll Content (SPAD)	Visual Leaf Blight Score (1–9)	Days to First Symptom Appearance	Lesion Expansion Rate (cm/day)
SAMMAZ 70	2.1	1.5	10.2	132.5	40.6	18.4	37.2	3.0	56.2	0.22
SAMMAZ 63	2.5	1.8	11.4	148.7	44.3	20.2	35.6	3.3	55.0	0.25
SAMMAZ 62	1.9	1.3	9.1	120.3	35.5	16.0	38.4	2.7	58.0	0.19
SAMMAZ 61	3.0	2.2	13.7	165.4	52.7	23.6	33.2	4.0	53.4	0.30
SAMMAZ 60	2.8	2.0	12.5	159.0	49.9	22.0	34.0	3.8	54.1	0.28
SAMMAZ 59	1.6	1.1	8.4	110.7	32.8	14.2	39.1	2.3	59.2	0.17
SAMMAZ 58	2.3	1.7	10.8	140.2	42.2	19.3	36.1	3.1	56.6	0.23
SAMMAZ 57	2.9	2.1	12.9	162.3	51.1	22.7	33.7	3.9	54.0	0.29
SAMMAZ 56	2.0	1.4	9.7	126.4	38.0	17.1	37.8	2.9	57.2	0.20
SAMMAZ 55	1.8	1.2	8.9	117.3	34.4	15.5	38.9	2.5	58.4	0.18
SAMMAZ 52	2.6	1.9	11.9	151.6	46.0	20.8	35.0	3.4	55.3	0.26
SAMMAZ 51	2.2	1.6	10.4	136.7	41.0	18.0	36.8	3.0	56.5	0.22
SAMMAZ 49	3.2	2.4	14.6	170.1	54.8	25.1	32.0	4.3	52.8	0.32
SAMMAZ 40	2.7	2.0	12.3	157.9	48.5	21.5	34.3	3.7	54.3	0.27
SAMMAZ 34	1.7	1.2	8.6	112.4	33.6	14.8	39.4	2.4	59.0	0.18
SAMMAZ 29	2.4	1.8	11.2	145.2	43.3	19.9	35.8	3.2	55.6	0.24
SAMMAZ 28	2.1	1.5	10.0	133.6	39.2	17.7	37.0	2.8	56.8	0.21
SAMMAZ 27	3.3	2.5	15.2	174.6	56.1	26.0	31.6	4.5	52.3	0.33
SAMMAZ 26 (Check)	3.5	2.7	16.1	178.9	58.3	27.5	30.9	4.7	51.7	0.35
SAMMAZ 16 (Check)	3.1	2.3	13.5	167.0	53.0	24.0	32.7	4.1	53.1	0.31

Table 5. Summary statistics for southern leaf blight disease rating of extra-early PVA-QPM maize inbred lines evaluated under rainfed conditions

Indicator	Mean	Min	Max	Range	HSD (0.05)	CV (%)	SE ±	SED	Heritability (%)	Genetic Advance	GCV (%)	PCV (%)
Disease Severity Score (1–5)	2.73	1.50	4.20	2.70	0.42	13.8	0.21	0.29	72.4	0.89	18.9	22.3
Lesion Size (cm)	1.86	0.80	3.70	2.90	0.47	15.2	0.26	0.36	68.1	0.76	17.2	21.0
Lesion Frequency (no./leaf)	3.51	1.10	6.80	5.70	0.66	18.5	0.34	0.48	70.7	1.31	19.6	24.3
AUDPC	92.5	40.3	160.1	119.8	9.71	14.6	4.51	6.38	75.6	28.2	21.4	25.0
Percent Disease Incidence (%)	47.8	20.0	88.0	68.0	6.15	12.1	2.72	3.85	77.2	15.9	18.3	21.1
Disease Severity Index (DSI %)	38.7	15.4	72.6	57.2	4.83	13.6	2.22	3.13	76.4	12.3	19.1	22.6
Leaf Area Affected (LAA %)	32.1	10.2	64.9	54.7	5.20	16.9	2.60	3.66	69.9	10.6	20.7	24.0
Chlorophyll Content (SPAD)	35.6	30.9	39.4	8.5	0.38	11.3	0.72	1.02	73.1	2.10	16.5	19.4
Visual Leaf Blight Score (1–9)	3.30	2.3	4.7	2.4	0.40	14.2	0.22	0.31	74.8	0.88	19.0	22.8
Lesion Expansion Rate (cm/day)	0.25	0.17	0.35	0.18	0.036	12.6	0.014	0.020	70.5	0.06	15.3	18.2

Notes:

i. AUDPC: Area Under Disease Progress Curve; DSI: Disease Severity Index; LAA: Leaf Area Affected.
ii. Traits 9 and 10 (NLB, Rust/MSV) were excluded from evaluation.
iii. HSD: Tukey's Honest Significant Difference; CV: Coefficient of Variation; SE: Standard Error; SED: Standard Error of Difference; GCV: Genotypic Coefficient of Variation; PCV: Phenotypic Coefficient of Variation.

CONCLUSION

To the best of our knowledge, this study is the first to simultaneously assess SLB tolerance, agronomic performance, and nutritional quality in extra-early PVA-QPM maize inbred lines. The findings highlight the genetic potential for concurrent improvement of disease resistance, yield, and nutritional quality, providing a solid foundation for future breeding programs aimed at developing climate-resilient, nutrient-dense maize varieties. This study demonstrated substantial genetic variation among 20 extra-early SAMMAZ PVA-QPM maize inbred lines evaluated under SLB pressure in rainfed environments. Key morphological traits, including grain yield, flowering time, plant architecture, and ears per plant, showed significant genotypic differences, high heritability estimates, and moderate-to-high genetic advance, underscoring their potential for genetic improvement through selection. Genotypes SAMMAZ 58, 63, 62, and 57 stood out by integrating superior grain yield with optimal plant architecture and elevated nutritional profiles, surpassing established benchmarks for provitamin A and tryptophan content in biofortified maize. In terms of disease resistance, there was significant variation in SLB-related traits, severity score, lesion metrics, chlorophyll retention, and AUDPC. Genotypes SAMMAZ 59, 62, 55, and 34 consistently exhibited lower disease scores, delayed symptom expression, and reduced lesion expansion rates, traits strongly associated with SLB tolerance. These genotypes also exhibited elevated SPAD values, reflecting sustained chlorophyll content and minimized physiological stress under disease pressure.

The high heritability estimates for morphological and disease-related traits suggest a strong genetic basis, enabling reliable selection for SLB resistance alongside yield and nutritional parameters. The results confirm the potential for concurrent selection of early maturity, enhanced nutrition traits, and disease resistance within extra-early maize breeding strategies tailored for sub-Saharan Africa. The identified genotypes, particularly SAMMAZ 58, 63, 59, and 62, offer valuable germplasm for breeding climate-resilient and nutrition-sensitive maize cultivars suited to low-input, disease-prone environments. Future multi-environment trials and molecular validation will further consolidate their utility in breeding pipelines aimed at achieving food and nutritional security under biotic stress conditions.

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