



GENETIC VARIABILITY OF SORGHUM (*SORGHUM BICOLOR* L.) RECOMBINANT INBRED LINES UNDER STRIGA (*STRIGA HERMONTICA* (DEL.) BENTH) INFESTED AND STRIGA FREE ENVIRONMENTS

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ABSTRACT

Striga hermonthica is the most important biotic agent that causes significant loss in yield and productivity of sorghum in the savannas. This study objective was to assess the levels of Striga resistance in recombinant inbred populations of sorghum. Six hundred and sixty recombinant inbred populations of sorghum (parents and checks inclusive) obtained from F₄ generations of NRL-3 × SRN4841 F₄ and SAMSORG 39 × WADAHMED F₄ were evaluated in two *Striga* infested environments (Samaru and Birnin Kudu) and two *Striga* free environments (Samaru and Kano). Data collected on *Striga* characteristics, yield and yield related characteristics were subjected to statistical analyses using R statistical software. The result revealed great variability within recombinant inbred lines with the identification of eleven NRL-3 × SRN4841 F₄ and seven SAMSORG 49 × WADAHMED F₄ recombinant inbred populations having zero striga count indicating striga resistance. Large differences between phenotypic and genotypic coefficients of variation were obtained for striga characters and ranged from 0.00% to 68.53% for NRL-3 × SRN4841 F₄ and 25.97% to 91.10% for SAMSORG 49 × WADAHMED F₄ suggesting that environment contributed to the expression of striga characteristics. Low (< 30%) broad-sense heritability for striga count, striga vigour, ASNPC and ASVPC indicate small genetic variation implying that genetic gain after selection will be low due to the combined effects of genetic and environmental variations. Therefore, the highly *Striga* resistant recombinant inbred lines can readily be exploited in sorghum improvement as sources of favourable alleles to improve locally adapted germplasm.

Keywords: genotype x environment, recombinant, resistance, sorghum, striga, variation

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INTRODUCTION

Sorghum is a source of livelihood for over half a billion people in sub-Saharan Africa. It is grown in the tropical and subtropical regions in the continent with an average yield of less than 2 tonnes per hectare [1]. Several biotic and abiotic factors have been attributed to the low productivity of sorghum. However, the major biotic factor causing significant damage and impacting negatively on sorghum production in Africa is *Striga hermonthica* [2]. The harm caused by the obligate hemi root parasitic weed has worsen over decades due to drought and low soil fertility of the soils cultivated to sorghum [1, 3]. In response to chemical signals from its host, the weed produces a hook-like structure called haustoria with which it attaches itself to the xylem of the host and derives nourishment. The infested sorghum plant becomes malnourished expressing stunted growth [4]. The practice of monoculture and continuous cropping has in no small measure contributed to the spread and severity of the weed [1].

The average sorghum grain yield loss due to *Striga hermonthica* has been reported to be 65%. The

annual yield loss due to *Striga hermonthica* has been estimated to be over \$ 7 billion [1-5]. In Nigeria, 40 % sorghum yield loss has been reported [6]. Nigeria has been classified as one of the regions with heavy striga infestation in Africa [1]. The yield loss is more severe in the savannah agroecology due to intermittent drought and low organic matter [1].

Researchers and farmers have devised several management measures to forestall the striga problem. These include the augmenting marginal soils with organic matter and incorporating soil residues into the soil to suppress striga growth, intercropping sorghum with legumes and use of *Desmodium spp* and *Fusarium oxysporum* as biological control [7, 8]. Yet none of these practices have effectively managed *Striga hermonthica* on arable farmlands. The use of striga resistant cultivars is the most effective and efficient measure for controlling striga infestation [2]. Striga resistant cultivars when grown in striga infested environment will maximize metabolic pathways and out yield a susceptible cultivar. They have dual advantage of reducing striga seed production and germination [2, 1]. The aim of this study is to assess

the response of sorghum recombinant inbred populations to *Striga hermonthica*.

MATERIALS AND METHODS

Field experiments were conducted at the Institute for Agricultural Research (IAR) farm, Samaru (686 m above sea level, Lat 11° 11' N, Long 07° 38' E) during the 2022 growing season in the Northern Guinea Savanna agroecology, Bayero University Kano (BUK) research farm (437 m above sea level, Lat 11° 58' N, Long. 8°25' E) and Birnin Kudu, Jigawa state (439 m above sea level, Lat 9° 28' N, Long 11° 28' E) in the Sudan Savanna agroecology of Nigeria. The plant materials consisted of 640 recombinant inbred lines namely, 365 population of NRL-3 × SRN4841 F₄ and 275 population of SAMSORG 49 × WADAHMED F₄ obtained from two susceptible parents namely, NRL-3 and SAMSORG 49, and two resistant parents namely, SRN4841 and WADAHMED. Each cross was advanced to F₄ generation (Table 1) and evaluated separately along with the parents and six checks under *Striga* free environments in IAR farm Samaru and BUK research farm and under *Striga* infested environments in IAR farm Samaru and Birnin Kudu, Jigawa state in the 2022 growing season. The checks (Table 2) comprise 3 resistant lines (Ag-8×N13) BC3F5-27, (Ag-8×N13) BC3F5-37 and FRAMIDA, and 3 susceptible lines, SAMSORG 40, SAMSORG 46 and SAMSORG 48.

At IAR Farm Samaru, fine sand-striga mixture in a ratio of 9:1 was applied at 0.05 grams per hill [9] while Birnin Kudu was under natural striga plots. The experiments were laid in an incomplete block design, with 750 RILs of NRL-3 × SRN4841 F₄ arranged in a 15 × 50 lattice and 570 RILs of SAMSORG 49 × WADAHMED in a 15 × 38 lattice with two replications using one row plot of 3 m in length and an inter and intra row spacing of 0.75 m and 0.3 m, respectively at the three environments (Samaru, Birnin Kudu, and Kano). In the *Striga* infested field, sorghum cultivars were sown at four seeds per hill and later thinned to 2 plants per hill after emergence. A basal application of NPK 15-15-15 fertilizer at the rate of 50 kg/ha and hoe weeding were done once at 10 days after sowing to enable the production of strigolactone for stimulation of *Striga* growth [10-15]. Whereas for the *Striga* free plots, all the agronomic practices were observed including regular hoe weeding, spraying with insecticides, basal and split doses of NPK 15-15-15 fertilizer at the rate of 50 kg/ha and urea at the rate of 50 kg/ha.

Data were collected for seedling vigour; scored on the scale of 1 (least vigorous) to 5 (most vigorous), days to 50 heading (days from emergence to when 50% of the plants started heading or booting), days to 50% flowering (days from emergence to when 50% of plants started flowering), plant height (the distance from ground to the top of the main axis was measured using meter rule), panicle length (the

distance between the panicle node and panicle tip was measured using meter rule), threshing percentage (grain weight divided by the panicle weight expressed in percentage) and grain yield (the yield per plot were converted to yield per hectare). Striga count was done by counting the number of *Striga* plants within each plot, Striga vigour (based on the visual assessment of mean *Striga* height and number of branches suggested by Ezeaku & Gupta [16], Striga severity (based on emerged striga count multiplied by the respective striga vigour score on each plot). The area under striga number progress curve (ASNPC) and area under striga severity progress curve (ASVPC) were calculated to provide a quantitative measure of *Striga* infestation and severity over the entire season using the formula reported by Haussmann *et al.* [9] and Rodenburg *et al.* [17].

Statistical Analysis:

Analysis of variance

Analysis of variance for one location was first performed on the collected data to test the significant differences among the genotypes using the general linear model procedure in R statistical software version 4.1.2. [18]. The linear model for one environment used is shown below.

$$Y_{ijl} = \mu + \tau_i + \gamma_j + \rho_{i(j)} + \varepsilon_{ijl}$$

Where;

Y_{ijl} = Response of the i^{th} genotype in the l^{th} block of the j^{th} replication;

μ = Overall mean;

τ_i = Effect of the i^{th} genotype;

γ_j = Effect of the j^{th} replication;

$\rho_{i(j)}$ = Effect of the l^{th} block within j^{th} replication;

ε_{ijl} = Random error.

To generate means of individual genotypes across replications, a linear mixed-effect model using R lme4 package on meta-R was used and genetic variance components were generated.

Rank Summation Index

Rank Summation Index (RSI) was generated for the agronomic characters/ The index was obtained by ranking seedling vigour, plant height, panicle length, threshing percentage and grain yield in descending order, while days to 50% heading, days to 50% flowering, striga count, striga severity, striga vigour, area under striga number progress curve (ASNPC) and area under striga severity progress curve (ASVPC) were ranked in ascending order. The lesser the RSI of these characters the better their value. The values assigned to each character were summed up to obtain rank index for each genotype. Rank summation index was used to select the best thirty (20) genotypes and worst ten (5).

Phenotypic and genotypic coefficients of variation

Phenotypic (PCV) and genotypic (GCV) coefficients of variation were derived using the formula of Allard [19]:

$$PCV = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

$$GCV = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

Where,

σ_g^2 =genetic variance

σ_p^2 =phenotypic variance

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$\bar{x}$ = grand mean

PCV and GCV values were categorized into low (<10%), moderate (10-20%) and high (>20%) based on the classification of Sivasubramanian & Menon, [20].

Broad-sense heritability

Expected mean squares (EMS) from analysis of variance was estimated using phenotypic (σ_p^2) and genotypic (σ_g^2) variances according to Keneni & Jarso [21]. Broad-sense heritability was calculated according to Falconer & Mackay [22] as

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

H^2 = Broad sense heritability

σ_g^2 =genetic variance

σ_p^2 =phenotypic variance

The heritability percentage was categorized as high (> 50%), moderate (20 – 49%) and low (< 20%) as suggested by Stansfield, [23].

RESULTS

Genetic variability and heritability of sorghum RILs under striga infested environment

Non-significant mean squares were observed for striga count, striga severity, area under striga number progress curve and area under striga severity progress curve for both populations (Table 3). However, highly significant mean square was observed striga vigour for SAMSORG 49 x WADAHMED

NRL-3 x SRN4841 recorded low genotypic coefficient of variation (0.00) for striga count, striga severity, area under striga number progress curve and area under striga severity progress curve with the exception of striga vigour (38.72%) that had high genotypic coefficient of variation. Phenotypic coefficients of variation were high for striga severity

(135.23%), area under striga number progress curve (132.42%), striga count (117.41%), area under striga number progress curve (115.80%) and striga vigour (107.25%).

SAMSORG 49 x WADAHMED had significant genotypic coefficient of variation for area under striga number progress curve (31.54%) and striga count (30.94%) and moderate values were obtained for striga vigour (29.28%), striga severity (18.43%), and area under striga severity progress curve (15.83%). High phenotypic coefficients of variation were observed for striga severity (109.53%), area under striga severity progress curve (107.75%), striga count (85.71%), area under striga number progress curve (84.47%) and striga vigour (55.25%). Low heritability estimates were recorded for both populations for striga vigour, striga count, striga severity, area under striga number progress curve and area under striga severity progress curve with negative estimates equated to zero.

Genetic variability and heritability of yield and its attributes for NRL-3 × SRN4841 under striga infested and striga free environments

Under striga infested environments, significant mean squares were observed among the genotypes and genotype x location for grain yield, plant height, days to 50% heading, days to 50% flowering, panicle length and seedling vigour (Table 4).

There were moderate and with no statistical differences between genotypic and phenotypic coefficient of variation for days to 50% heading (17.00%, 18.39%) and days to 50% flowering (16.22%, 17.54%) Genotypic coefficient of variation was moderate estimates for plant height (23.42%) and panicle length (23.12%). Threshing percentage (6.97 %), seedling vigour (2.55%) and grain yield (2.37 %) had low estimate. As regards phenotypic coefficient of variation, grain yield (54.92%) showed had high value. Plant height (25.83%), panicle length (25.44%) and threshing percentage (10.81%) were moderate with seedling vigour (9.29%) having low phenotypic coefficient of variation.

Days to 50% heading (85.51%), days to 50% flowering (85.47%), panicle length (82.56%) and plant height (82.21%) had high broad-sense heritability values. Threshing percentage (41.59%), seedling vigour (7.55%) and grain yield (0.19%) had the least heritability estimate.

Under striga free environments, mean square estimates were highly significant for genotype and genotype x location for the characters studied while threshing percentage showed significance for genotype and genotype x location.

Moderate values of genotypic coefficient of variation were obtained for grain yield (16.67%), plant height (11.08%) and panicle length (10.11%). Low estimates were obtained for days to 50% heading (8.06%), days to 50% flowering (7.97%) and threshing percentage (1.08%). Plant height (15.64%),

panicle length (14.39%), days to 50% heading (11.37%) and days to 50% flowering (11.11%) had moderate phenotypic coefficient of variation. Grain yield (43.35%) showed high estimate. Seedling vigour (8.30%) and threshing percentage (6.95%) had low estimates.

Days to 50% flowering (51.48%), days to 50% heading (50.24%), plant height (50.19%), panicle length (49.32%) had high broad sense heritability. Moderate estimates were computed for grain yield (14.79%). While low estimates were obtained for threshing percentage (2.40%) and seedling vigour (0.00%).

Genetic variability and heritability of yield and its attributes for SAMSORG 49 × WADAHMED under striga infested and striga free environments

Under striga infested environments, mean squares due to location and genotype were highly significant for the characters studied (Table 5). Mean squares due to genotype × location were highly significant for days to 50% flowering, days to 50% heading, plant height, panicle length and grain yield but significant for threshing percentage.

Panicle length (10.75%), plant height (10.34%) and grain yield (10.04%) were moderate in terms of genotypic coefficient of correlation. While seedling vigour (6.14%), days to 50% heading (4.82%), days to 50% flowering (4.60%) and threshing percentage (3.45%) were low. Low estimates of phenotypic coefficients of variation were obtained for threshing percentage (8.94%), days to 50% heading (8.72%) and days to 50% flowering (8.55%). Moderate estimates were obtained for panicle length (19.03%), plant height (17.88%) and seedling vigour (10.64%). Grain yield (61.91%) had high phenotypic coefficients of variation. Broad sense heritability was low for days to 50% flowering (28.91%) and threshing percentage (14.88%) and grain yield (2.63%) but was moderate for plant height (33.43%), seedling vigour (33.33%), panicle length (31.93%), days to 50% heading (30.48%).

Under striga free environments, mean squares for location was highly significant for seeding vigour, days to 50% heading, days to 50% flowering, panicle length, threshing percentage and grain yield (Table 7). Highly significant genotype and genotype × location mean squares were obtained for days to 50% heading, days to 50% flowering, plant height, panicle length and grain yield.

Panicle length (20.69%) had high genotypic coefficients of variation. Low values were obtained for days to 50% heading (3.29%), days to 50% flowering (3.45%), plant height (2.40%), threshing percentage (1.84%) and grain yield (0.37%). Grain yield had high phenotypic coefficient of variation (52.88%). Moderate values were obtained for plant height (19.11%) and panicle length (15.87%) with low for seedling vigour (9.81%), days to 50% heading (8.90%), days to 50% flowering (8.64%), and

threshing percentage (7.78%). Panicle length (48.02%), plant height (31.45%) and grain yield (28.09%) had moderate heritability values. Days to 50% flowering (7.21%), days to 50% heading and threshing percentage (0.78%) showed low heritability estimate.

Mean performance of NRL-3 × SRN4841 for striga characteristics and yield under striga infested and striga free environments

Eleven lines namely, NRL-3 × SRN4841-1-11-1, NRL-3 × SRN4841-3-20-3, NRL-3 × SRN4841-6-21-2, NRL-3 × SRN4841-1-26-4, NRL-3 × SRN4841-1-28-1, NRL-3 × SRN4841-4-6-2, NRL-3 × SRN4841-6-21-1, NRL-3 × SRN4841-5-17-1, NRL-3 × SRN4841-5-15-2, NRL-3 × SRN4841-7-1-2, NRL-3 × SRN4841-5-16-3 had zero striga count, striga vigour, striga severity, area under striga number progress curve and area under striga severity progress curve (Table 6). There were three outstanding lines namely NRL-3 × SRN4841-1-11-1, NRL-3 × SRN4841-5-19-4 and NRL-3 × SRN4841-4-2-2 with rank summation index of 30, 43 and 58 respectively. The least vigorous (3) was NRL-3 × SRN4841-5-7-1. NRL-3 × SRN4841-6-2-3 was the earliest to reach days to 50% heading (80 days) and days to 50% flowering (84 days). The tallest plant (217 cm) with the longest panicle length (37 cm) was obtained from NRL-3 × SRN4841-1-28-1. Threshing percentage was highest for NRL-3 × SRN4841-7-1-2 (65.9%). NRL-3 × SRN4841-1-23-3 recorded the highest grain yield of 501.7 kg/ha.

Mean performance of SAMSORG 49 × WADAHMED for yield and yield component under striga infested and striga free environments

Seven lines namely, SAMSORG 49 × WADAHMED-1-2-3, SAMSORG 49 × WADAHMED-6-1-1, SAMSORG 49 × WADAHMED-1-10-1, SAMSORG 49 × WADAHMED-5-14-1, SAMSORG 49 × WADAHMED-3-16-2, SAMSORG 49 × WADAHMED-1-12-4 and SAMSORG 49 × WADAHMED-1-3-2 had zero striga count, striga vigour, striga severity, area under striga number progress curve and area under striga severity progress curve (Table 7). The best three lines were SAMSORG 49 × WADAHMED-2-14-5 (31), SAMSORG 49 × WADAHMED-1-2-3 (42) and SAMSORG 49 × WADAHMED-2-6-1 (43).

SAMSORG 49 × WADAHMED-3-11-2 was the most vigorous (5). The earliest to reach days to 50% heading (73 days) and days to flowering (78 days) was SAMSORG 49 × WADAHMED-6-1-1. SAMSORG 49 × WADAHMED-5-14-1 was the tallest (153 cm) while SAMSORG 49 × WADAHMED-2-6-1, SAMSORG 49 × WADAHMED-1-10-1 and SAMSORG 49 × WADAHMED-5-14-1 had the longest panicle length (25 cm). FRAMIDA (72.5%) had the highest threshing percentage yet the highest yielder was

SAMSORG 49 × WADAHMED-3-11-2 (581.3 kg/ha).

DISCUSSION

NRL-3 × SRN4841 and SAMSORG 49 × WADAHMED had non-significant differences for striga characteristics indicating that the populations were tolerant to *Striga hermonthica*. Few striga plants emerged during the experiment. Similar trend was reported by Afolayan et al. [4] in a trial to determine the response of 25 accessions of sorghum to *Striga hermonthica* and grain yield in Nigeria. The high phenotypic coefficient of variation with low broad sense heritability showed that the environment contributed largely to the differences in the expression of striga characteristics. Hence, selection of lines for improvement should be location specific.

Genetic variability and heritability of NRL-3 × SRN4841 and SAMSORG 49 × WADAHMED

Both populations had significant mean squares for genotype, environment and genotype x environment for the genotypes studied under striga infested environments for agronomic characters indicating useful variations for sorghum breeding programme. Among the mean squares, environment had the largest contribution for the expression of the measured characters. These genotypes will require multiple cycles of recurrent selection over expanded environment to exploit genetic gains. However, genotype x environmental interaction requires the selection of genotypes that are stable and adapted to each environment [24]. Although phenotypic coefficients of variations exceeded genotypic coefficients of variations, the characters were highly heritable. Hence, these genotypes should be selected and incorporated into a sorghum breeding programme for advancement [4].

Under striga free environments, the characters expressed variability across locations for the populations tested with the exception of seedling vigour and threshing percentage. Genotypes, environments and genotype x environmental interaction contributed significantly in the observed variations for most of the characters studied [24]. In both locations, high genotypic coefficients of variations were obtained for panicle length while high phenotypic coefficient of variation recorded for grain yield. These indicates that environment played a lesser role in the genetic expression of panicle length but played a greater role in the genetic expression of grain yield. However, moderate to low broad sense heritability was revealed for most of the traits studied for both populations across the two locations.

Mean performances of NRL-3 × SRN4841 and SAMSORG 49 × WADAHMED

The genotypes responded differently under striga infested condition due to the presence of wide genetic

differences. Among the recombinant inbred populations, lines such as NRL-3 × SRN4841-1-11-1, NRL-3 × SRN4841-3-20-3, NRL-3 × SRN4841-6-21-2, NRL-3 × SRN4841-1-26-4, NRL-3 × SRN4841-1-28-1, NRL-3 × SRN4841-4-6-2, NRL-3 × SRN4841-6-21-1, NRL-3 × SRN4841-5-17-1, NRL-3 × SRN4841-5-15-2, NRL-3 × SRN4841-7-1-2, NRL-3 × SRN4841-5-16-3, SAMSORG 49 × WADAHMED-1-2-3, SAMSORG 49 × WADAHMED-6-1-1, SAMSORG 49 × WADAHMED-1-10-1, SAMSORG 49 × WADAHMED-5-14-1, SAMSORG 49 × WADAHMED-3-16-2, SAMSORG 49 × WADAHMED-1-12-4 and SAMSORG 49 × WADAHMED-1-3-2 that showed minimal incidence of striga with zero striga scores are resistant to the noxious weed. Genotypes with low striga scores are resistant and should be used for sorghum improvement [25].

NRL-3 × SRN4841-1-23-3 and SAMSORG 49 × WADAHMED-3-11-2 had the highest grain yields of less than 600 kg/ha. The low grain yield compared to the average yield of 2.5 tonnes per hectare worldwide [26] was due to the devastating effect of *Striga hermonthica*. The recombinant inbred lines showing earliness in addition to yield characteristics have good genetic recombination that could be exploited to boost the genetic base of sorghum. Grain yield is a sum of the associations of the various plant components [27].

CONCLUSION

There was sufficient genetic variability in NRL-3 × SRN4841 and SAMSORG 49 × WADAHMED populations with the identification of eleven striga resistant recombinant inbred lines for the former and seven for the latter with zero striga count. The highly *Striga* resistant recombinant inbred lines can readily be exploited in sorghum breeding programmes as sources of favourable alleles to improve locally adapted germplasm. Large differences between phenotypic and genotypic coefficients of variation were obtained for striga characters and ranged from 0.00 % to 68.53 % for NRL-3 × SRN4841 and 25.97 % to 91.10 % for SAMSORG 49 × WADAHMED suggesting that environment played a major role in the expression of striga characteristics. Low (< 30 %) broad-sense heritability for striga count, striga vigour, ASNPC and ASVPC indicate small genetic variation implying that genetic gain after selection will be low due to the combined effects of genetic and environmental variations.

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Table 1: Information on the sorghum recombinant inbred populations of at Samaru in 2018-2020

Crosses	Parent(s) in the Cross	Description	F ₁ generation(s)	No. of panicles harvested at F ₂ generation(s)	No. of panicles harvested at F ₃ generation(s)	No. of panicles harvested at F ₄ generation(s)
1	SAMSORG 49 WADAHMED	Susceptible Resistant	SAMSORG 49 × WADAHMED	6	109	275
2	NRL-3 SRN4841	Susceptible Resistant	NRL-3 × SRN4841	6	142	365
	Total			12	251	640

Table 2: Status of sorghum lines used as checks along with the F₄ population

S/No.	Sorghum lines	Characteristics	Source
1	(Ag-8×N13) BC3F5-37	Resistant	ICRISAT, Sudan
2	FRAMIDA	Resistant	ICRISAT, Sudan
3	(Ag-8×N13) BC3F5-27	Resistant	ICRISAT, Sudan.
4	SAMSORG 40	Susceptible	IAR
5	SAMSORG 46	Susceptible	IAR
6	SAMSORG 48	Susceptible	IAR

IAR- Institute for Agricultural Research,

ICRISAT- International Crops Research Institute for the Semi-Arid Tropics

Table 3: Genetic variability and heritability of striga characters for NRL-3 × SRN4841 and SAMSORG 49 × WADAHMED under striga infested environment of Birnin Kudu in 2022 growing season

SOV	DF	STRIGA COUNT	STRIGA VIGOUR	STRIGA SEVERITY	ASNPC	ASVPC
NRL-3 × SRN4841						
REPLICATION	1	4.64	12.29	7712.03**	1499909.00	637175818.80**
REP(BLOCK)	24	7.88	7.30	1024.52	1243001.00	77147091.00
GENOTYPE	374	9.62	9.90	961.34	1468590.00	71550918.00
ERROR	350	10.35	8.61	991.99	1571983.00	73376611.00
MEAN		1.87	2.07	16.21	740.00	4516.76
GCV (%)		0.00 ^x	38.72	0.00 ^x	0.00 ^x	0.00 ^x
PCV (%)		117.41	107.25	135.23	115.80	132.42
H (%)		0.00 ^x	13.03	0.00 ^x	0.00 ^x	0.00 ^x
SAMSORG 49 × WADAHMED						
REPLICATION	1	13.59	81.47 **	313.91	120277.90	22062069.00
REP(BLOCK)	18	15.50	7.39	802.00	1971005.00	60019106.00
GENOTYPE	284	14.35	10.65 **	804.49	1838199.00	59211863.00
ERROR	266	12.48	7.66	781.71	1581903.00	57933039.00
MEAN		3.13	4.18	18.31	1134.95	5049.79
GCV (%)		30.94	29.28	18.43	31.54	15.83
PCV (%)		85.71	55.25	109.53	84.47	107.75
H (%)		13.03	28.08	2.83	13.94	2.16

ASNPC = area under striga number progress curve, ASVPC = area under striga severity progress curve, SOV =sources of variation, DF =degree of freedom, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, H=broad sense heritability, 0.00^x=negative estimate has been equated to zero.

Table 4: Genetic variability and heritability of yield and yield components for NRL-3 × SRN4841 under striga infested environments (Birnin Kudu and Samaru) and striga free environments (Kano and Samaru) in 2022 growing season

SOV	DF	SEEDLING VIGOUR	DAYS TO 50% HEADING	DAYS TO 50% FLOWERING	PLANT HEIGHT	PANICLE LENGTH	THRESHING %	GRAIN YIELD
STRIGA INFESTED ENVIRONMENTS								
LOCATION	1	74.15**	150120.02**	156121.21**	17743.52**	687.76**	2230.36**	104321162.07**
REP (LOC)	2	7.07**	823.00**	1064.22 **	299.80	3.66	2020.05**	256921.24*
BLOCK (LOC x REP)	48	0.38	114.64	124.37	358.33	15.08	68.56	61896.56
GENOTYPE	374	0.50*	480.39**	479.85**	1791.48**	59.63**	116.94**	103059.94**
GENOTYPE x LOC	374	0.49*	194.47**	193.88**	831.27**	27.31*	99.27	103011.73**
ERROR	700	0.41	104.57	104.00	546.66	22.80	92.41	58104.86
MEAN		3.92	99.46	104.28	132.31	24.59	60.27	292.49
GCV (%)		2.55	17.00	16.22	23.42	23.12	6.97	2.37
PCV (%)		9.29	18.39	17.54	25.83	25.44	10.81	54.92
H (%)		7.55	85.47	85.51	82.21	82.56	41.59	0.19
STRIGA FREE ENVIRONMENTS								
LOCATION	1	71.50**	1861.49**	1393.94**	223589.52**	4384.44**	1970.10**	6345128.96**
REP (LOC)	2	1.08*	84.85	77.27	1735.55*	81.49**	54.87	46050.78
BLOCK (LOC x REP)	48	0.27	57.14	60.80	434.34	13.04	50.82	33291.83
GENOTYPE	374	0.47**	435.42**	457.36**	2061.77**	62.12**	69.18*	85679.71**
GENOTYPE x LOC	374	0.47**	216.66**	221.90**	1026.87**	31.48**	67.52*	73006.14**
ERROR	700	0.35	67.81	71.36	503.09	17.22	57.54	37051.83
MEAN		4.13	91.76	96.27	145.19	27.38	59.88	337.64
GCV (%)		0.00	8.06	7.97	11.08	10.11	1.08	16.67
PCV (%)		8.30	11.37	11.11	15.64	14.39	6.95	43.35
H (%)		0.00	50.24	51.48	50.19	49.32	2.40	14.79

SOV =sources of variation, DF =degree of freedom, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, H=broad sense heritability

Table 5: Genetic variability and heritability of yield and yield components for SAMSORG 49 × WADAHMED under striga infested environments (Birnin Kudu and Samaru) and striga free environments (Kano and Samaru) in 2022 growing season

SOV	DF	SEEDLING VIGOUR	DAYS TO 50% HEADING	DAYS TO 50% FLOWERING	PLANT HEIGHT	PANICLE LENGTH	THRESHING %	GRAIN YIELD
STRIGA INFESTED ENVIRONMENTS								
LOCATION	1	41.50**	36087.19**	38966.86**	39594.95**	5765.40**	3821.70**	71034846.34**
REP(LOC)	2	35.31**	1676.86**	2003.06**	2684.87*	137.78**	17.19	2535979.91**
BLOCK (LOC x REP)	36	0.57	81.04	121.02	727.90	22.97	70.68	67492.26
GENOTYPE	284	0.69**	281.29**	296.95**	1739.82**	54.28**	129.99**	114104.50**
GENOTYPE x LOC	284	0.46	195.56**	211.11**	1158.26**	36.95**	110.65*	111104.64**
ERROR	532	0.50	110.64	120.10	598.17	19.02	89.05	62764.74
MEAN		3.90	96.11	100.77	116.64	19.36	63.74	272.80
GCV (%)		6.14	4.82	4.60	10.34	10.75	3.45	10.04
PCV (%)		10.64	8.72	8.55	17.88	19.03	8.94	61.91
H (%)		33.33	30.48	28.91	33.43	31.93	14.88	2.63
STRIGA FREE ENVIRONMENTS								
LOCATION	1	30.18**	6244.06**	7010.46**	14.17	408**	12463.57**	1843572.22**
REP(LOC)	2	0.58	127.01	83.09	1024.43	10.93	135.66	58961.85
BLOCK (LOC x REP)	36	0.54	93.38	92.74	919.56	12.45	100.89	27755.04
GENOTYPE	284	0.60*	233.31**	242.93**	2188.11**	44.86**	93.09	80779.74**
GENOTYPE x LOC	284	0.65**	218.59**	225.42**	1499.85**	23.32**	92.36	58086.91**
ERROR	532	0.50	92.15	96.01	1130.00	11.25	86.11	28952.90
MEAN		3.95	85.82	90.18	122.36	21.11	62.01	268.75
GCV (%)		0.00 ^x	3.29	3.45	2.40	20.69	1.84	0.37
PCV (%)		9.81	8.90	8.64	19.11	25.87	7.78	52.88
H (%)		0.00 ^x	6.31	7.21	31.45	48.02	0.78	28.09

Sov =sources of variation, df=degree of freedom, GCV=genotypic coefficient of variation, PCV=phenotypic coefficient of variation, H=broad sense heritability.

Table 6: Mean performance of some selected NRL-3 × SRN4841 population for striga characteristics and yield under striga infested and striga free environments in the 2022 growing season

Entry	Striga count	Striga severity	Striga vigour	ASNPC	ASVPC	Seedling vigour	Days to 50 % heading	Days to 50 % Flowering	Plant height (cm)	Panicle length (cm)	Threshing percentage	Grain yield (kg/ha)	RSI
NRL-3 × SRN4841-1-11-1	0.0	0.0	0.0	0.0	0.0	4	96	101	150	26	55.5	311.5	30
NRL-3 × SRN4841-5-19-4	0.2	1.5	1.5	75.0	450.0	4	87	91	143	27	58.4	410.9	43
NRL-3 × SRN4841-4-2-2	0.8	0.3	1.3	300.0	300.0	4	101	106	125	23	62.4	347.4	58
NRL-3 × SRN4841-3-20-3	0.0	0.0	0.0	0.0	0.0	4	102	107	146	24	63.4	356.7	64
NRL-3 × SRN4841-6-21-2	0.0	0.0	0.0	0.0	0.0	4	96	101	143	28	65.3	309.8	69
NRL-3 × SRN4841-1-26-4	0.0	0.0	0.0	0.0	0.0	4	104	109	153	27	54.2	301.9	84
NRL-3 × SRN4841-1-29-3	0.5	1.0	1.8	210	510.0	4	97	102	129	24	62.4	223.1	86
NRL-3 × SRN4841-1-28-1	0.0	0.0	0.0	0.0	0.0	4	88	93	237	37	60.1	263.9	89
NRL-3 × SRN4841-1-12-2	0.8	3.5	3.5	315.0	975.0	4	85	90	146	28	63.7	280.8	90
NRL-3 × SRN4841-4-14-2	0.5	1.5	1.5	195.0	450.0	4	90	95	145	27	62.5	243.9	94
NRL-3 × SRN4841-4-6-2	0.0	0.0	0.0	0.0	0.0	4	83	87	148	30	56.7	223.9	94
NRL-3 × SRN4841-1-23-3	0.7	2.5	4.3	240.0	1065.0	4	84	90	148	27	60.7	501.7	96
NRL-3 × SRN4841-6-21-1	0.0	0.0	0.0	0.0	0.0	4	95	100	113	21	57.7	168.9	97
NRL-3 × SRN4841-6-6-1	0.3	2.5	2.5	150.0	750.0	4	95	99	129	25	60.8	176.9	97
NRL-3 × SRN4841-5-17-1	0.0	0.0	0.0	0.0	0.0	4	101	105	143	30	59.2	471.1	98
NRL-3 × SRN4841-6-4-1	0.2	1.8	1.8	75.0	525.0	4	89	94	141	22	61.5	282.2	98
NRL-3 × SRN4841-5-15-2	0.0	0.0	0.0	0.0	0.0	4	85	89	132	31	62.8	412.4	101
NRL-3 × SRN4841-7-1-2	0.0	0.0	0.0	0.0	0.0	4	106	111	174	28	65.9	347.7	102
NRL-3 × SRN4841-6-22-5	0.5	0.3	0.8	180.0	180.0	4	100	105	139	32	62.6	303.6	105
NRL-3 × SRN4841-5-16-3	0.0	0.0	0.0	0.0	0.0	4	96	101	96	23	58.3	218.7	106
NRL-3 × SRN4841-6-2-3	7.8	7.8	80.0	3060.0	22440.0	4	80	84	142	27	59.6	400.8	383
NRL-3 × SRN4841-6-19-3	2.7	2.5	14.0	1005.0	3675.0	4	97	101	131	25	58.5	366.8	385
NRL-3 × SRN4841-1-10-1	2.5	3.8	15.0	1005.0	4500.0	4	101	106	111	23	58.8	270.4	388
NRL-3 × SRN4841-1-13-3	2.3	6.3	21.3	900.0	5835.0	4	111	116	126	24	58.8	352.5	399
NRL-3 × SRN4841-5-7-1	6.0	4.0	46.0	2550.0	13800.0	3	110	115	119	22	58.2	333.6	404
Mean	1.9	3.6	16.2	740.0	4516.8	4.	96	100	139	26	60.1	315.1	
SE	2.3	2.1	22.3	886.6	6057.1	0.	6.6	6.7	16.1	3.1	6.2	154.6	

ASNPC=area under striga number progress curve, ASVPC= area under striga severity progress curve, LSD=least significant difference, SE=standard errors=rank summation index

Table 7: Mean performance of some selected SAMSORG 49 × WADAHMED population for striga characteristics and yield in striga infested and striga free environments in the 2022 growing season

Entry	Striga count	Striga severity	Striga vigour	ASNPC	ASVPC	Seedling vigour	Days to 50% heading	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	Threshing %	Grain yield (kg/ha)	RSI
SAMSORG 49 × WADAHMED-2-14-5	0.3	0.3	0.5	150.0	150.0	4	88	92	129	20	63.2	262.3	31
SAMSORG 49 × WADAHMED-1-2-3	0.0	0.0	0.0	0.0	0.0	4	90	94	134	21	61.7	499.7	42
SAMSORG 49 × WADAHMED-2-6-1	0.8	0.0	0.0	225.0	0.0	4	94	98	110	25	63.3	408.1	43
SAMSORG 49 × WADAHMED-3-11-2	1.2	1.3	2.8	420.0	795.0	5	86	90	130	21	63.6	581.3	45
SAMSORG 49 × WADAHMED-2-1-1	0.8	2.0	4.3	360.0	1200.0	4	85	89	126	19	62.9	402.1	61
SAMSORG 49 × WADAHMED-6-1-1	0.0	0.0	0.0	0.0	0.0	4	73	78	131	20	59.5	195.6	62
SAMSORG 49 × WADAHMED-1-10-1	0.0	0.0	0.0	0.0	0.0	4	84	88	131	25	53.5	193.3	66
SAMSORG 49 × WADAHMED-2-4-1	0.7	2.8	2.8	225.0	720.0	4	88	92	124	21	65.8	412.9	71
SAMSORG 49 × WADAHMED-1-8-1	1.0	2.5	3.3	345.0	870.0	4	83	87	119	19	65.4	250.6	72
SAMSORG 49 × WADAHMED-5-13-1	1.5	1.3	5.8	675.0	1725.0	4	81	85	119	21	66.9	295.6	72
FRAMIDA	3.2	3.8	8.3	1140.0	2340.0	5	83	88	132	21	72.5	342.6	75
SAMSORG 49 × WADAHMED-5-14-1	0.0	0.0	0.0	0.0	0.0	4	74	78	153	25	54.7	222.2	78
SAMSORG 49 × WADAHMED-3-16-2	0.0	0.0	0.0	0.0	0.0	4	95	100	119	23	63.0	157.3	79
SAMSORG 49 × WADAHMED-5-3-3	3.0	5.0	12.0	1140.0	3390.0	4	95	99	115	20	63.8	361.8	87
SAMSORG 49 × WADAHMED-3-10-1	2.2	4.8	9.8	795.0	2790.0	4	89	93	112	18	66.2	348.6	87
SAMSORG 49 × WADAHMED-1-12-4	0.0	0.0	0.0	0.0	0.0	4	96	100	111	20	56.7	205.8	89
SAMSORG 49 × WADAHMED-3-11-3	1.2	3.8	4.8	420.0	1395.0	4	92	96	122	19	61.4	335.3	90
SAMSORG 49 × WADAHMED-1-3-2	0.0	0.0	0.0	0.0	0.0	4	92	96	122	19	61.4	335.3	91
SAMSORG 49 × WADAHMED-3-7-6	8.8	6.0	51.8	3315.0	14685.0	4	88	92	108	21	64.9	439.1	288
SAMSORG 49 × WADAHMED-1-11-1	5.2	7.5	24.0	1785.0	6975.0	4	93	98	98	17	66.2	210.5	291
SAMSORG 49 × WADAHMED-6-11-1	6.5	6.8	27.3	2370.0	7860.0	4	97	102	136	16	64.3	243.7	303
SAMSORG 49 × WADAHMED-1-6-2	5.0	5.8	29.3	1800.0	8235.0	4	101	106	93	17	64.2	173.3	311
SAMSORG 49 × WADAHMED-5-15-2	13.2	6.3	161.5	4980.0	40680.0	4	94	98	103	18	57.0	252.6	315
Mean	3.1	4.2	18.3	1134.9	5049.8	4	91	95	120	20	62.9	270.8	
SE	2.5	2.0	19.8	889.4	5382.1	1	7	7	21	3	6.6	155.3	

ASNPC=area under striga number progress curve, ASVPC= area under striga severity progress curve, LSD=least significant difference, SE=standard error, RSI=rank summation index