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SCREENING OF RICE GENOTYPES FOR AFRICAN RICE GALL MIDGE RESISTANCE IN SOUTHERN GUINEA SAVANAH AGRO-ECOLOGICAL ZONE OF NIGERIA.

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Abstract

*The major biotic constraint related with lowland rice production is African rice gall midge (AfRGM), and one way which has proved successful in management of this pest is varietal resistance or tolerance. In this study, Screening of genotypes was conducted to identify the resistant/tolerant cultivars of low-land rice under AfRGM infestation. Field experiments were conducted in 2017 cropping season at Badeggi and Edozhigi to screen 81 rice genotypes. The field was laid out in an Alpha Lattice Design, comprising of 5 blocks with 17 plots in each block and replicated three times. Gall midge was scored at 42 and 63 days after transplanting, while other parameters include, days to 50% flowering and grain yield were also recorded. All genotypes exhibited a wide-and significant (p<0.05) variation. The highest phenotypic and genotypic coefficient of variation was recorded for the panicle exertion and the highest heritability was found for panicle length, grain yield and panicle exertion. Correlation analysis revealed that days to 50 % flowering was highly significant (p<0.05) and correlated positively (0.559**) with African rice gall midge. Grain yield did not correlate significantly (p>0.05) with AfRGM while there were strong, positive and significant correlation between tiller counts and panicle (0.961**) counts. However, genotype G007 (HK71-NCRIJ-3-1) which was the only one found to be moderately resistance with (5.34 %) tiller infestation, all others genotypes ranged from susceptible to highly susceptible. Genotypes G015, G030, G045, G046, G051, and G068 gave better yield under Gall midge infestation compared with the checks and it could be recommended for crop improvement.*

Keywords: African Rice Gall Midge, Genotypes and Grain Yield.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the major crops cultivated by farmers in all agro-ecological zones of Nigeria. It is an important cereal crop, not only widely consumed by a large proportion of the population in Nigeria, but all around the world in various forms (Shehu *et al.*, 2013). Annual production of rice globally was 741 million metric tonnes (MMT) in 2015 (Fakayode *et al.*, 2010). In Nigeria, total consumption stands at 4.4 million tonnes of milled rice. Nigeria produces only about 2.8 million metric tonnes with a deficit of 1.6 million metric tonnes excluding the large quantity smuggled through the porous borders (USAID, 2010). FAO in 2000 classified the crop as the most important food crop depended by over 50 percent of the world population for about 80 percent of their food need, especially in Asia, West and Central Africa (Conteh *et al.*, 2012).

However, according to Abdul-Gafar *et al.* (2016), factors militating against the level of rice production in Nigeria are biotic and abiotic. One of the major biotic constraint in low-land rice production is the rice gall midge. Is the related insect known to exist on rice in Africa was titled as a new species by Harris and Gagné (1982) and was named as African rice gall midge, *Orseolia oryzivora* (AfRGM), the major insect pest of rainfed rice ecosystem among other insects. AfRGM damage the crop during early stage and the young larvae cause maximum damage. It destroys lowland rice in Africa (Omoloye, 2000), causing yield losses between 45 and 80 percent in farmers' fields (Nwilene *et al.*, 2006). Several control measures have been recommended for the management of AfRGM. Of these, varietal resistance and tolerance is seen as the most farmer friendly option. Other screenings have identified AfRGM moderately resistant varieties of O. *sativa* (Bashir *et al.*, 2013). With regard to mean susceptibility in farmers' fields, Cisadane from Indonesia is a tolerant variety released in Nigeria as FARO 51 (Omoloye *et al.*, 2002). This variety of *O. sativa* subsp. *indica* produces an acceptable yield for farmers (Williams *et al.*, 1999). Therefore, this evaluation will allow management interpolations intended at increasing productivity in gall midge prevalent areas.

MATERIALS AND METHODS

Experimental Site

Two field evaluations were conducted in 2018 cropping season at the National Cereals Research Institute (NCRI) experimental field Badeggi and Edozhigi, all in southern Guinea Savanna agro-ecological zone of Nigeria. Both locations are lowland ecology and are known to be prone to gall midge infestation.

Experimental Materials:

The 81 rice genotypes that were used for this study included four susceptible checks (WITA-4, NERICA L-34, FARO 44 and FARO 57). They were all collected from rice breeding Unit of National Cereals Research Institute, Badeggi, Bida, Nigeria. The treatments were laid out using Alpha Lattice Design (a resolvable incomplete block design) and the plots size was 5 × 1 m^2 replicated three times in gross experimental plot which measured 27 × 53 m^2. Rice seedlings at 21 days old were transplanted at 2 seedlings per stand at a spacing of 20 × 20 cm inter and intra rows and supply of missing stands was done at 7 days after transplanting (DAT). Manual weedings were carried out at 21 and 42 (DAT). NPK 15:15:15 fertiliser was applied as basal application at the rate of 150 kg/ha during land preparation. Urea was applied at the rate of 50kg /ha as top dressing first at tillering and second at booting stage by broadcasting. Tiller damage by gall midge was scored according to the standard evaluation system for rice (SES) (IRRI, 2013) as shown in (Table 1). Tiller infestation was computed using the following formula as described by Nwilene *et al.* (2002).

$$\text{Infested tiller percentage} = \frac{\text{Number of infested tillers}}{\text{Total number of tiller}} \times 100$$

Data were collected on the following parameters:

Number of tillers counted at 42 and 63 DAT; number of panicle m^2, days to 50 % flowering, plant height, 1000 grain weight, panicle length and panicle exertion.

Statistical Analysis

Data collected were subjected to statistical analysis using MSTAT package 1.3 version. Analysis of variance and correlation were done as described by Muhammad *et al.* (2015). Estimate of variance component were estimated according to Shivanna (2008).

Table 1: Assessments of damage by AfRGM according to IRRI's SES (IRRI, 2013)

Score	Percentage tiller damage	Rating (reaction)
0	No Injury	Highly Resistance or Immune
1	less than 1%	Resistance
3	1-5%	Moderately Resistance
5	6-10%	Moderately Susceptible
7	11-25%	Susceptible
9	above 25%	Highly Susceptible

RESULTS

Highly significant genotypes effects were observed for all the traits (Table 2). The genotype by location interaction effects were significant to all the traits except for panicle length, 1000 grain weight and grain yield. Environmental effect was highly significant on days to 50 % flowering, tiller count m^2, panicle count m^2 and gall midge at 63 DAT and non-significant effects were observed for panicle exertion, panicle length, 1000 grain weight, grain yield and gall midge at 42 DAT. However, there was significant effect on plant height

Means, estimate of genotypic and phenotypic variance, genotypic coefficients of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability and genetic advance expressed as percentage of means over two environments are presented in (Table 3). Phenotypic variances were generally higher than the genotypic variances in all the characters studied. The highest phenotypic and genotypic variances in all the characters considered were recorded in yield (194206.19 and 106462.20), respectively. Similarly, high phenotypic and genotypic variances were observed in number of tillers per square metre (3268.54 and 189.16). The phenotypic coefficient of variance (PCV) generally ranged between 8.68 % for days to 50 % flowering and 26.57 % for percentage tiller infestation, respectively. Equally, the genotypic coefficient of variance (GCV) ranged between 0.41 % for days to 50% flowering and 21.29 % for panicle exertion. However, heritability in broad sense (H^2) estimate varied from 0.23 % for days to 50 % flowering and 68.61 for panicle exertion respectively. In the same vain, genetic advance as per mean (GAM) had a general range between 0.03 % for days to 50 % flowering and 31.04 % for panicle exertion. A joint consideration of PCV, GCV, H^2 and GAM revealed panicle exertion (25.71, 21.29, 68.61 and 31.04 %) combined high PCV, GCV, broad sense heritability and genetic advance, whereas percentage tiller infestation at 42 DAT (20.41 and 10.19 %), percentage tiller infestation at 63 DAT (26.57 and 11.53 %) combined high PCV and moderate GCV. Also, panicle length (9.51 and 68.45 %), 1000 grain weight (10.41 and 42.55 %), and grain yield (10.07 and 54.82 %) combined moderate PCV and high broad sense heritability.

The individual performance in terms of grain yield of some rice genotypes are significantly ($p<0.05$) different over checks in this study (Table 4). Fourty one (41) genotypes out of eighty one (81) genotypes evaluated had high mean value than the population mean (4375.44 kg/ha). With the exception of G015 (5309.30 kg/ha), G003 (5112.57 kg/ha), G045 (5621.49 kg/ha), G046 (5479.94 kg/ha), G051 (5379.10 kg/ha), and G068 (5083.40 kg/ha) that gave significantly ($p<0.05$) different mean grain yield over the checks. FARO 52 (4201.92 kg/ha) and FARO 44 (4139.11 kg/ha) which were the susceptible checks performed less compared with FARO 57 (5275.41 kg/ha) and FARO 61 (4433.34 kg/ha). The grain yield of all other genotypes were not statistically significant over the checks.

Days to 50 % flowering revealed highly significant positive correlation with gall midge (0.559**), number of tiller per square metre was positively and highly significantly correlated with panicle count per meter square (0.961**) (Table 5). However, tiller count m^2 and panicle count m^2 had highly significant negative correlation with grain yield (-0.146** and -0.131**) and gall midge infestation (-0.474** and -0.489**) respectively. Grain yield was not significant correlated with gall midge infestation whereas panicle length was highly significant and positive correlated with grain yield. 1000 grain weight were highly significant negative correlation with grain yield (-0.212**).

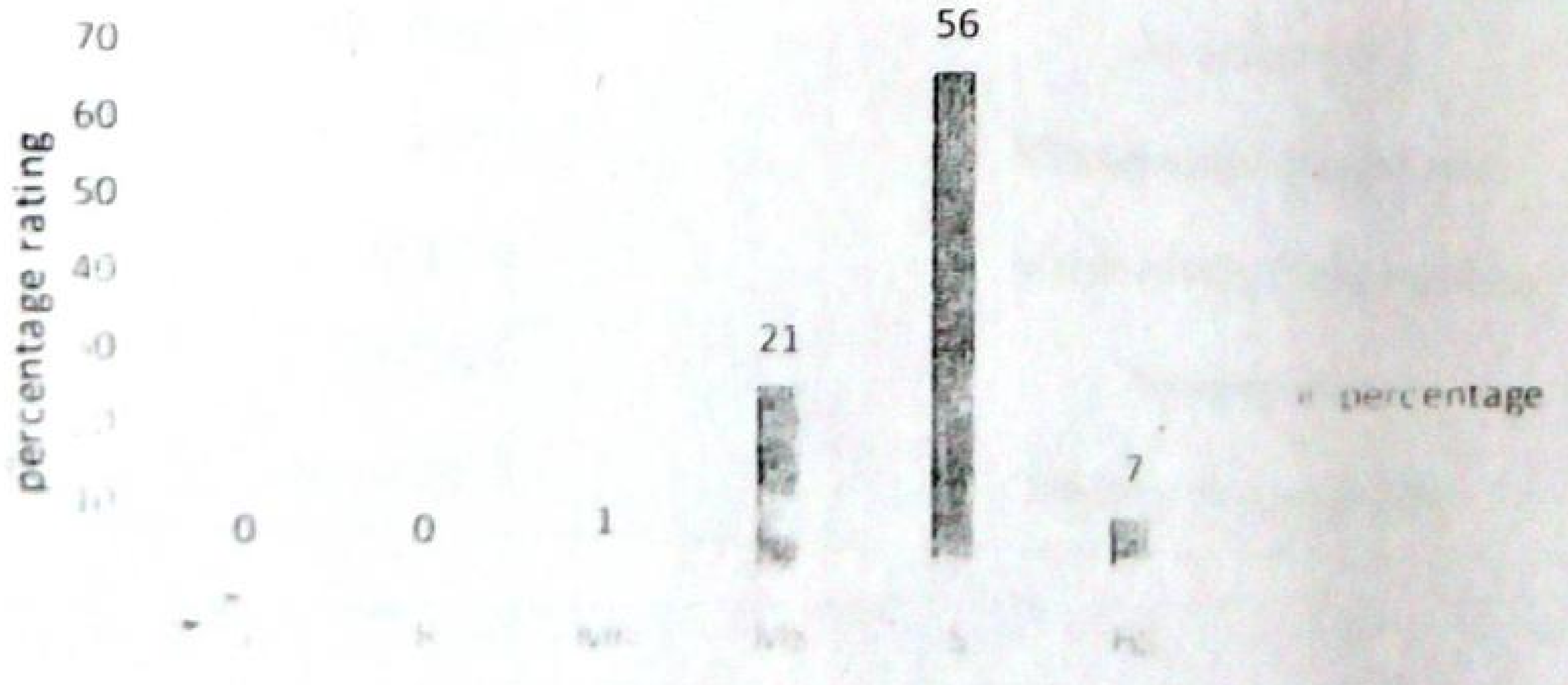

Figure I. Showing combined percentage rating of tiller infestation.

Result of the gall midge screening done is shown in fig 1. 1.2 % of the genotypes showed a score of 3 (moderately resistant reaction) while 24.7 % showed a score of 5 (moderately susceptible reaction). [illegible] of the genotypes were susceptible to AfRGM (score of 7) and only [illegible]

Table 2. Combined Analysis ANOVA for the two location

Parameter	Sources of variation	Sum Sq	Mean Sq	F value	Pr(>F)
Paniext	Location	2.83	2.83	1.63	0.27 ns
	Genotype	934.93	11.13	23.32	0.00**
	Location X Genotype	53.84	0.64	1.34	0.04*
Flowering	Location	79912.66	79912.66	25204.36	0.00**
	Genotype	12733.54	151.59	46.70	0.00**
	Location X Genotype	12825.01	152.68	47.04	0.00**
Plant Height	Location	9606.16	9606.16	9.53	0.04*
	Genotype	136909.37	1629.87	1.59	0.00**
	Location X Genotype	129018.46	1535.93	1.50	0.01*
Tiller Count	Location	3013480.80	3013480.80	3421.27	0.00**
	Genotype	870456.05	10362.57	35.86	0.00**
	Location X Genotype	727453.03	8660.16	29.97	0.00**
Panicle Count	Location	3090061.18	3090061.18	1619.88	0.00**
	Genotype	645632.17	7686.10	19.73	0.00**
	Location X Genotype	630461.82	7505.50	19.27	0.00**
Panicle Length	Location	1.81	1.81	5.06	0.09ns
	Genotype	2752.32	32.77	24.00	0.00**
	Location X Genotype	42.21	0.50	0.37	1.00ns
TGW	Location	2.54	2.54	0.49	0.52ns
	Genotype	3336.24	39.72	8.62	0.00**
	Location X Genotype	85.46	1.02	0.22	1.00ns
Grain Yield	Location	19472.88	19472.88	0.18	0.69ns
	Genotype	812505327.1	9672682.47	142.07	0.00**
	Location X Genotype	765113.29	9108.49	0.13	1.00ns
Afrgm42	Location	99.18	99.18	2.37	0.20ns
	Genotype	3561.66	42.40	5.88	0.00**
	Location X Genotype	1178.63	14.03	1.94	0.00**
Afrgm63	Location	5748.96	5748.96	119.31	0.00**
	Genotype	4773.12	56.82	10.42	0.00**
	Location X Genotype	2439.29	29.04	5.33	0.00**

Ns = not significant, *= significant at 5 %, **= highly significant at 1 % level of probability

Table: 3: Genetic Parameters for 10 Agronomic Traits of 85 Lowland Rice Genotypes

Parameters	mean	^{2}ph	^{2}g	PCV%	GCV%	H^2 %	GA %

Scanned by TapScanner

PE	5.00	1.70	1.17	25.71	21.29	68.61	31.04
DTF	84.01	53.18	0.12	8.68	0.14	0.23	0.03
PHT	94.64	1206.25	10.44	36.70	3.41	0.87	0.56
TC	426.95	3268.54	189.16	13.39	3.22	5.79	1.36
PC	397.84	2781.60	20.07	13.26	1.13	0.72	0.17
PL	24.06	5.24	3.58	9.51	7.87	68.45	11.46
TGW	30.37	10.11	4.30	10.47	6.83	42.55	7.84
GM42	17.43	12.64	3.15	20.41	10.19	24.94	8.96
GM63	15.24	16.40	3.09	26.57	11.53	18.82	8.80
GY	4375.44	194206.19	106462.20	10.07	7.46	54.82	9.72

σ^2g = Genotypic Variance, σ^2p = Phenotypic Variance, GCV = Genetic Coefficient of Variance, PCV = Phenotypic Coefficient of Variance H^2 = Heritability, GA = Genetic Gain, PC = Principal Component, PE = Panicle Exertion (score), DTF = Days to 50% Flowering, PHT = Plant Height (cm), TC = Tiller Count (per m^2), PC = Panicle Count (per m^2), PL = Panicle Length (cm), TGW = Thousand Grain Weight (g), GY = Grain Yield (kg/ha), GM = Gall Midge (score)

Table: 4. Grain Yield Performance of 81 Low-land Rice Lines under AfRGM infestation

S/N	Entries code	Grain Yield (Kg/ha)	% YA Over Check 1	% YA Over Check 2
1	G1	3804.17		
2	G10	4172.88		
3	G11	4370.40		
4	G12	4064.67		
5	G13	4344.70		
6	G14	4201.04		
7	G15	5309.30	0.64	19.76*
8	G16	4046.88		
9	G17	4905.16		10.64
10	G18	3617.61		
11	G19	4200.33		
12	G2	4559.47		2.85
13	G20	4180.46		
14	G21	4877.49		10.02
15	G22	4809.22		8.48
16	G23	4592.23		3.58
17	G24	4402.52		
18	G25	3769.28		
19	G26	4975.13		12.22
20	G27	4178.49		
21	G28	4679.32		5.55
22	G29	4396.37		
23	G3	5112.57		15.32*
24	G30	4202.22		
25	G31	3971.95		
26	G32	4489.23		1.26
27	G33	4275.58		
28	G34	4543.86		2.49
29	G35	4698.58		5.98
30	G36	3811.27		
31	G37	3969.79		
32	G38	3424.88		
33	G39	4505.12		1.62
34	G4	4400.33		
35	G40	4387.83		
36	G41	4485.18		1.17
37	G42	4416.27		
38	G43	4532.79		2.24
39	G44	4043.79		
40	G45	5621.49	6.56	26.80*
41	G46	5479.94	3.88	23.61*
42	G47	4278.26		
43	G48	4695.60		5.92
44	G49	3239.43		
45	G5	4322.87		
46	G50	4460.09		0.60
47	G51	5379.10	1.97	21.33*
49	G53	4561.96		2.90
50	G54	4558.37		2.82
51	G55	4476.17		0.97
52	G56	4791.63		8.08
53	G57	4104.97		
54	G58	4893.53		10.38
55	G59	4073.01		
56	G6	3807.71		
57	G60	4504.45		1.60
58	G61	4511.27		1.76
59	G62	4261.48		
60	G63	4460.92		0.62
61	G64	4073.08		
62	G65	3816.05		
63	G66	4287.57		
64	G67	3676.36		
65	G68	5083.40		14.66*
66	G69	3690.06		
67	G7	4837.16		9.11
68	G70	4571.27		3.11
69	G71	4680.15		5.57
70	G72	4177.26		
71	G73	4063.13		
72	G74	3671.55		
73	G75	4779.51		7.81
74	G76	4453.89		0.46
75	G77	3659.50		
76	G78	4167.26		
77	G79	4071.01		
78	G8	4499.93		1.50
79	G80	4649.82		4.88
80	G81	3911.73		
81	G82	4139.11		
82	G83	4201.92		
83	G84	5275.41		
84	G85	4433.34		
85	G9	4735.56		6.82
Mean		4375.44		
Minimum		1525.86		
Maximum		7762.50		
LSD		644.46		

% YA Over Check = Percentage Yield Advantage over Resistance Check, * = Significant at $p < 0.05$

Table 5. Correlation coefficient between yield component, yield, African rice gall midge and morphological characters of rice

Variable	PE	DTF	PHT	TC	PC	PL	TGW	GY	GM
PE	1.000								
DTF	-0.014	1.000							
PHT	-0.049	-0.083	1.000						
TC	0.086*	-0.724**	0.046	1.000					
PC	0.081	-0.756**	0.054	0.961**	1.000				
PL	0.022	0.121**	0.064	-0.085	-0.059	1.000			
TGW	0.095*	-0.022	0.052	0.151**	0.109	-0.114**	1.000		
GY	-0.017	0.051	0.049	-0.146**	-0.131**	0.179**	-0.212**	1.000	
GM	-0.039	0.559**	-0.108*	-0.474**	-0.489**	-0.019	-0.024	0.057	1.000

*= Significant, **=Highly Significant, PC = Principal Component, PE = Panicle Exertion (score), DTF = Days to 50% Flowering, PHT = Plant Height (cm), TC = Tiller Count (per m^2), PC = Panicle Count (per m^2), PL = Panicle Length (cm), TGW = Thousand Grain Weight (g), GY = Grain Yield (kg/ha), GM = Gall Midge (score)

DISCUSSION

The results of the field evaluation at Edozhigi and Badeggi locations revealed that the genotypes reactions to AfRGM infestation at 42 DAT in both locations 79 were found to be susceptible with the exception of genotypes G014 (9.97 %) and G079 (10.86 %) which were moderately susceptible at Edozhigi. However, seven genotypes reverted from the score of 7 (susceptible) to 9 (highly susceptible). These situation can be explained thus, genotypes that were less infested at 63 DAT than they were at 42 DAT implied that they had more tolerance than the others, but those that were susceptible at 42 DAT but reverted to highly susceptible suggest that they were more susceptible compared to the check. However, only genotype G007 exhibited moderate resistance with percentage tiller infestation of 5.34 %. Yao *et al* (2012) reported similar trend in their studied but instead of the progenies to be susceptible, they were reverting to resistance.

Grain yield performance of the test entries over their corresponding checks under high infestation level of AfRGM showed that genotypes G003, G015, G045, G046, G051 and G068 performed significantly ($p<0.05$) better than the check cultivars. In the same vain, 31 genotypes had similar or higher grain yield than the checks though statistically there was no significant difference. These could be due to their genetic in-build and the ability to produced extra tillers to compensate and nullify the effect of gall midge and it is an indication that they are tolerant cultivars. Similar result was reported by Ogah *et al* (2012) and Omoloye *et al* (2002) who reported high yielding *Sativa* lines that were tolerant to AfRGM. However, Nwilene *et al* (2009) observed that as gall midge infestation increased, extra tillers were produced and if not infested by the pest, can contribute effectively to grain yield.

The present study results indicated that there is adequate genetic variability present in the materials studied. The PCV was higher than the GCV in all the characters across the 2 locations. The difference between PCV and GCV was probably accounted for by the environmental effects. There was high heritability estimates for panicle exertion, panicle length, 1000 grain weight, gall midge at 42 DAT and grain yield suggesting that environmental factors did not affect greatly the phenotypic performance of these traits. Thus, high estimates of heritability GCV and GA may be good predictors of seed yield in rice. Hence, selection based on the phenotypic performance of these characters will be reliable and effective. The result of Tuhina-Khatun *et al* (2015) and Ogunbayo *et al* (2014) suggested that traits with high broad sense heritability estimates, GCV and GA value could be good predictors of seed yield. However, non-additive gene effect could be the explanation for the low values of heritability, GCV and GA for days to 50 % flowering, plant height, tiller count and panicle count per meter square indicates that selection on the basis of genotypes would offer greater genetic gain for the trait than single plant selection. These is in agreement with the findings of Yao *et al.* (2012), Salihu *et al.* (2017), and Ogunbayo *et al.* (2014).

The positive and highly significant correlations between days to 50 % flowering and gall midge, number of tiller count per square metre and number of panicle count per square metre is a strong indication that these traits are major factors in relation to seed yield. This suggests that selection directed towards these characters will be effective in ensuring seed yield in rice. Similarly, grain yield was highly and positively significant correlated with panicle length. These suggest that selection to improve rice yield directed by phenotype of these trait may be effective (Ogunbayo *et al.*, 2014). AfRGM score significantly and negatively correlated with number of tillers and panicles, this might be due to inability of damage tillers to produce panicles. The result is in agreement with Basiru *et al* (2017) but contrary to the findings of Ogunbayo *et al.* (2010) which indicated that AfRGM was highly significantly associated with panicle m^2.

CONCLUSION

[illegible] variability present in the materials studied. PCV was greater than GCV in all traits and there was high heritability estimate recorded. It can be concluded that for increasing rice grain yield and tolerance to AfRGM, characters such as days to 50 % flowering, tillers count m², panicle count m², 1000 grain weight, panicle exertion and panicle length should be selected for improvement. The results suggested that these characters are important yield contributing traits and selection on these traits would be most effective. However, genotype G003, G015, G045, G046, G051 and G068 gave the highest grain yield while genotype G007 exhibited moderate resistance to AfRGM. These lines are recommended for further evaluation across different environments.

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