

Yield Evaluation and Stability of Interspecific Rice (*Oryza* species) Progenies under three Ecologies in Ibadan, Nigeria

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Abstract: Rice (*Oryza sativa*) is an important staple cereal that accounts for 20% of total food calories for more than half of the world's population. Its cultivation is adversely affected by several constraints, among which are drought and low adaptive capabilities. *Oryza barthii* is the immediate ancestor of African rice (*Oryza glaberrima*). However, it has not been widely used in varietal development, despite the wide recognition of wild species for improving crops. Hereby, we investigated the adaptability and stability of interspecific *Oryza* species progenies under three rice ecologies in Ibadan. An advanced interspecific populations of twenty-seven progenies (G3 to G29), and their two parents (IRGC 104084 [G1] (*O. barthii*) and TGS 25 [G2] (*O. glaberrima* x *O. sativa*) x *O. sativa*) were evaluated using augmented randomized block design. The trials were done under upland, hydromorphic and lowland rice ecologies at the Africa Rice Center, Nigeria station, in International Institute of Tropical Agriculture campus, Ibadan. The progenies were evaluated for grain yield. Data were analysed using ANOVA at $\alpha_{0.05}$. Stability and adaptability of the progenies were analysed using GGE biplot. The highest grain yield of 4670±17.5 kg/ha (G11) was observed in upland, 5902.7±45.96 kg/ha and 6866.7±79.94 kg/ha (G2) in hydromorphic and lowland ecologies, respectively. Progenies G13 and G29 had stable grain yield across all ecologies. The genotype G2 performed better and adapted well to hydromorphic and lowland ecologies while G11 had the best performance in upland ecology. The stable grain yield of genotypes G13 and G29 across ecologies could also be explored for increasing rice production in Nigeria.

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Keywords: Genotypic adaptability, Rice ecologies, progenies, *Oryza barthii*

1. Introduction

Rice is a global staple food, accounting for the nourishment of over half of the world's population and supplying 20% of the total food calories in the world (IRRI, 2005). Therefore, it is one of the most important commercial food crops of the world. It is adaptable to numerous climates, terrains and cultures and it is cultivated on every continent except Antarctica (Rice almanac, 2013). Rice production is adversely affected by climate change, variabilities such as fluctuations in rainfall causing drought or flood, temperature and low adaptive capacity (Zoellick, 2009 and Rice almanac, 2013).

The demand for rice in Sub Saharan Africa is increasing at an annual rate of 6 % over the past three decades and the total rain-fed rice area accounts for about 85 % of the total rice lands in Sub-Saharan African (Ikeda, 2004).

Rice is becoming a major staple food crop in West Africa. Although its production increased up to 170% between 1970s to early 2000s, but production has never catch up with consumer demand (Africa Rice Center, 2007); only about 40% of current rice consumption is satisfied by domestic production.

Oryza barthii is the immediate ancestor of the cultivated African rice (*Oryza glaberrima*). However, it has not been in the focus of research as deserved, despite the wide recognition of wild species for improving crops (Li, 2011). *O. barthii* has long panicles, diverse grain sizes and weight which might be considered a prerequisite for high yield; the long flag leaf and awns may both offer protection against bird damage. AfricaRice (2012) reported that the flag leaf shields the panicles from the sight of flying birds while the long awns could make access to the grains difficult. *O. barthii* hosts a lot of diversity that is not available in *O. glaberrima* (Orjuela et al., 2014).

African rice originated about 3,500 years ago from the Niger River Delta, with *O. barthii* as its progenitor (Linares 2002; Sarla and Swamy 2005). The survival of *O. barthii* for over 3,500 years could be due to its unique adaptive features capable of withstanding wide climatic changes.

Breeding for stable yield under changing environmental condition is of paramount necessity. Genotype by environment interaction (GEI) implies differential behavior of genotypes under different environments. This is observable in changes of the phenotypic expression for any trait, and yield is

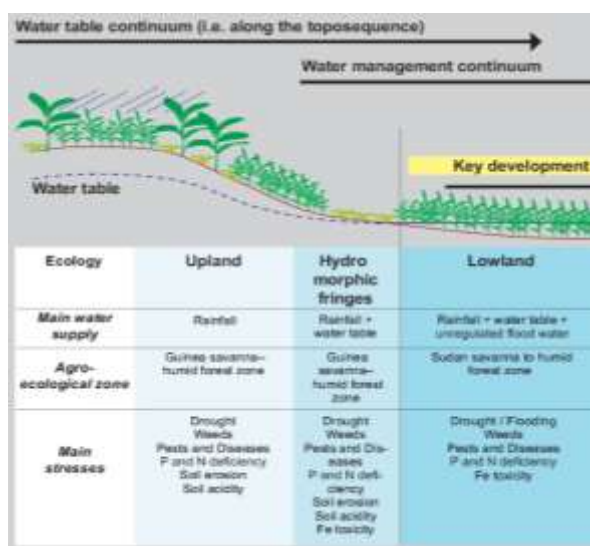
generally more affected in crop breeding. According to Kaya *et al.* (2006), a significant GEI may either be crossover or non-crossover. In the non-crossover situation, genotypes have wide adaptation for many environments; a crossover case limits the adaptation of genotypes to specific environment. Genotype and environmental conditions are the two main components that determine a phenotype. Gene expression is, in part, environmentally induced and regulated (Yan and Kang, 2003).

Multi-environment evaluation of interspecific lines generated from wild crosses is necessary to determine their adaptation as well as stability for specific environment

In this study, the F_8 generations, of a cross between *O. barthii* (IRGC 104084) and interspecific *O. glaberrima/O. sativa* (TGS 25) were evaluated for grain yield in three environments (ecologies). The objective of this study was to understand the grain yield differential responses of the 29 genotypes to three specific rice growing ecologies in Nigeria.

2. Material and Methods

The 29 genotypes; including the two parents-IRGC 104084 (*O.barthii*) and TGS 25(*O. glaberrima/O. sativa/sativa*) used in this experiment are breeding populations developed by Upland Breeding Unit of Africa Rice Center, Nigeria Station, Ibadan. The material and their pedigree used in the field experiments were presented in Table 1. The experiments were conducted in three rice ecologies in Nigeria. These ecologies included, upland (rice plant grown on dry soil), hydromorphic (rice plant grown on moist soil) and lowland (rice plant grown in wet soil) Figure 1.



Source: AfricaRice 2010

Figure 1: Rice Ecologies used in the experiment

The experiment was laid out in Augmented randomized block design at the Africa Rice Centre, Nigeria station Ibadan (latitude 7°3'N and longitude 3°45' E), Nigeria. The 29 test entries were evaluated in single plots of 5 rows and 5 meters long. Seeds were direct seeded, hand-dibbled at even depth and uniform spacing of 20 x 20 cm apart in the upland ecology. Seedlings were transplanted at 21days after planting in the case of the hydromorphic and lowland ecology also at uniform spacing of 20 x 20 cm. NPK (15-15-15) fertilizer were applied at the rate of 200 Kg/ha as basal application. Subsequently, 100 Kg/ha urea (46% N) were applied in two equal split at 21-30 and 42-50 days after sowing (DAS). Weeding and other agronomic practices were carried out as at when due.

The Standard Evaluation system for Rice (SES 2002) guided the data collection process. Data were collected on the following: Days to 50% flowering, Days to 85% maturity, Plant height, Panicle length, One thousand (1000) grain weight, Panicles per plant Spikelets per panicle and Grain yield.

Data Analysis

Data were analyzed using PROC GLM in Statistical Analysis System (SAS, version 9.2 software (SAS, 2009). The analysis of variance was carried out following the procedure of Scott and Milliken (1993), a SAS program for analyzing Augmented Randomized Block Designs using the model below:

$$Y_{ij} = \mu + b_j + C_i + X_i(C_i) + \sum_{ij}$$

Where b_j denotes the block effect, C_i the check effect and $X_i(C_i)$ denotes the entry effect.

The phenotypic variation for each trait was partitioned into genetic and non-genetic components and estimated following Johnson *et al.* (1955) and Wricke and Weber (1996) as:

$$VG = (MSG - MSE)/r$$

$$VP = MSG/r \text{ and}$$

$$VE = MSE/r$$

Where, VG = Genotypic variance VP = phenotypic variance, MSG = mean square genotype, MSE = mean square error and r = number of replication

The phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and environmental coefficient of variation (ECV) were computed according to the method suggested by Burton (1952) and Allard (1960):

$$GCV (\%) = (\sigma_g^2)^{0.5} / \text{Mean} \times 100$$

$$PCV (\%) = (\sigma_p^2)^{0.5} / \text{Mean} \times 100$$

Broad sense heritability (H^2) was calculated according to the procedure by Falconer and Mackay (1996) as the ratio of the genotypic variance (V_g) to the phenotypic variance (V_p) using the relationship as follows:

$$H^2 = \sigma_g^2 / \sigma_p^2$$

The genetic advance (G.A) as percentage of the mean was estimated as follows

$$G.A = (\sigma_g^2 / \sigma_p^2) k$$

Where σ_g^2 is the genotypic variance and σ_p^2 is the phenotypic variance and (k is the selection index at 5% = 2.06).

The yield stability of the variables with significant GEI from the ANOVA was analyzed using GGE Biplot (Yan and Kang 2003) and Pearson correlation coefficient was also estimated for all the traits evaluated in each of the three ecologies.

3. Result and Discussions

Genetic advance of traits evaluated under upland condition ranged from 2.10% for 1000 grain weight and 52.67% for grain yield. Broad sense heritability ranged from 2.45% for tiller number and 96.25% for plant height. Phenotypic Coefficient of Variation (PCV) ranged from 9.68% for panicle length and 43.43% for panicle exertion while Genotypic Coefficient of Variation (GCV) ranged from 3.23% for 1000 grain weight and 42.43% for panicle exertion. In hydromorphic ecology, heritability ranged from 0.79% for grain per panicle and 97.48% fertility, PCV ranged between 3.23% (1000 grain weight) and 37.90% (panicle exertion), GCV ranged between 3.09% for 1000 grain weight and 36.84% (panicle exertion) and genetic advance ranged from 0.53% (spikelets per panicle) and 73.8% (panicle exertion) however evaluated traits in the Lowland ecology (Table 2.) had broad sense Heritability ranging from 0.57 for tiller number and 99.2% for days to 85% maturity. PCV ranged from 4.32% for panicle length and 65.03% (Tiller number). GCV ranged from 4.90% for tiller number and 54.78% for shattering and genetic advance ranged from 0.76% for tiller number and 109.75% for shattering score. High phenotypic variance observed for all the traits studied indicate substantial influence of environment for the expression of these traits. Similar findings were earlier reported by Singh and Chakraborty (1996), Prajapati *et al.* (2011) and Singh *et al.* (2011).

Heritability and genetic advance are important selection parameters. High broad sense heritability estimates along with high genetic advance indicates a predominance of additive gene effect. They are helpful in predicting gain under selection rather than heritability estimates alone (Johnson *et al.*, 1955, Ali *et al.*, 2002, Yadav *et al.*, 2007 and Vange, 2009). However, Johnson *et al.*, (1955) remarked that it may not be necessary that a character showing high heritability will also exhibit high genetic advance.

Genetic advance of evaluated traits in the Upland ecology revealed that further improvement could be achieved in yielding ability, 1000 grain

weight, fertility, panicles per square meter, panicles per plant and panicle length through breeding by backcrossing some of the progenies; G11, G13, G16, G18 G28 and G29 to the TGS 25 parent since TGS 25 has the best yield in both hydromorphic and lowland ecologies (Johnson *et al.*, 1955, Ali *et al.*, 2002, Yadav *et al.*, 2007 and Vange, 2009).

Identification of best genotypes for different ecologies

The best environment for the genotypes studied is presented in figure 2. G28, G16 and G10 were most suitably adapted to the upland ecology, although G11 was the highest yielding genotype, G28, G16 and G10 were more stable and adaptable to the upland ecology.

The most stable genotype for lowland ecology was G18; while G13 and G29 were most suitable to hydromorphic ecology. G11 had the highest yield of 4670kg/ha (Table 1) in the upland ecology, while TGS 25 gave the highest yield of 5907 and 6866 kg/ha in both the hydromorphic and lowland ecologies respectively (Figure 2). Among the three ecologies, the lowland ecology produced the highest yield of 6866 kg/ha for TGS 25, hence the best environment for the genotype. Yield evaluation in the upland, lowland and hydromorphic ecologies showed an indication that the closest genotype to the ideal genotype is G29 and the most stable genotypes were G13 and G29 (Figure 3).

Polygon View of the genotype by environment interaction in the GGE biplot depicting "Which win Where" or which genotype is best for which environment was displayed in Figure 4. Within the Figure, hydromorphic and lowland ecologies fall in the same sector. Notable genotypes within the sector were: G2, G4, G5, G6, G8, G12, G13, G14, G15, G18, G26 and G29. The best genotype for the two ecologies was G2. Upland ecology was captured in another sector and the best genotype for the upland environment was G11. Other genotypes within the upland sector were G19, G27, G28, G16 and G10.

Highest yield was obtained in the lowland ecology for most of the rice genotypes.

Hence the lowland ecology may be regarded as the best ecology for the evaluated rice genotypes. The high variability observed in yield and ecological adaptation within the population of IRGC 104084 and TGS 25 might be due to ecological heterogeneity. This is similar to the findings of Sanni *et al.* (2008).

The stable yield of genotype 13 and 29 across the three ecologies indicated that the two genotypes could adapt well to multiple ecologies (upland, hydromorphic and lowland). This is in support of the observations of Montcho *et al.* (2013) in their efforts to breed for phenological plasticity in any rice growing environment. The least yielding genotype

was G1 (i.e. the *O. barthii* parent) while the highest yielding genotype was G2 (the TGS 25 parent).

Table 1. List of genotypes and yield (kg) per hectares in each ecology

Genotypes	F8	upland	hydromorphic	lowland	Mean
G1	IRGC 104084	1640.0	1320.0	1123.3	1361.1
G2	TGS 25	3340.0	5906.7	6866.7	5371.1
G3	ART31-1-1-1-1-1-B	1380.0	3350.0	5450.0	3393.3
G4	ART31-1-2-1-1-1-1-B	1760.0	3230.0	5130.0	3373.3
G5	ART31-1-3-1-1-1-1-B	1900.0	3580.0	4970.0	3483.3
G6	ART31-38-2-1-1-1-3-B	2210.0	2050.0	5590.0	3283.3
G7	ART31-5-2-1-1-1-1-B	1470.0	2750.0	4390.0	2870.0
G8	ART31-6-2-1-1-1-1-B	1560.0	3460.0	4290.0	3103.3
G9	ART31-7-2-1-1-1-1-B	1340.0	2160.0	3630.0	2376.7
G10	ART31-38-2-1-1-1-5-B	3750.0	4980.0	4110.0	4280.0
G11	ART31-13-1-1-1-1-1-B	4670.0	3790.0	4350.0	4270.0
G12	ART31-17-2-1-1-1-1-B	2600.0	5500.0	3830.0	3976.7
G13	ART31-17-3-1-1-1-1-B	2490.0	3250.0	4300.0	3346.7
G14	ART31-19-1-1-1-1-1-B	2100.0	3540.0	4540.0	3393.3
G15	ART31-19-2-1-1-1-1-B	1990.0	2720.0	4950.0	3220.0
G16	ART31-38-2-1-1-1-7-B	3430.0	4310.0	4150.0	3963.3
G17	ART31-23-1-1-1-1-1-B	1020.0	1870.0	4400.0	2430.0
G18	ART31-23-2-1-1-1-1-B	2400.0	3860.0	5420.0	3893.3
G19	ART31-26-3-1-1-1-1-B	2980.0	3210.0	2780.0	2990.0
G20	ART31-27-1-1-1-1-1-B	3730.0	1710.0	2070.0	2503.3
G21	ART31-27-2-1-1-1-1-B	1470.0	2470.0	2000.0	1980.0
G22	ART31-28-3-1-1-1-1-B	2140.0	2490.0	2270.0	2300.0
G23	ART31-29-1-1-1-1-1-B	1150.0	2740.0	1420.0	1770.0
G24	ART31-29-2-1-1-1-1-B	1250.0	3680.0	1360.0	2096.7
G25	ART31-30-1-1-1-1-1-B	1330.0	2020.0	1010.0	1453.3
G26	ART31-32-1-1-1-1-1-B	2480.0	2730.0	5090.0	3433.3
G27	ART31-36-2-1-1-1-1-B	2380.0	3990.0	2670.0	3013.3
G28	ART31-40-2-1-1-1-1-B	2480.0	4900.0	3350.0	3576.7
G29	ART31-41-1-1-1-1-1-B	2290.0	5170.0	4270.0	3910.0
	Mean	2232.1	3335.7	3820.0	3129.3
	CV	22.5	9.1	27.0	
	LSD	1741.7	2175.2	3593.9	

Table 2. Genetic estimates of some measured agronomic parameters in the three ecologies

Variables	Upland				Hydromorphic				Lowland			
	HB (%)	PCV (%)	GCV (%)	GA (%)	HB (%)	PCV (%)	GCV (%)	GA (%)	HB (%)	PCV (%)	GCV (%)	GA (%)
PLHT	96.25	20.46	20.08	40.57	76.29	17.93	15.66	28.18	88.03	28.58	26.81	51.83
TILNO	2.45	16.07	2.52	0.81	18.40	14.97	6.42	5.67	0.57	65.03	4.90	0.76
PAM	16.24	23.30	9.39	7.80	38.91	21.11	13.17	16.92	92.33	25.17	24.18	47.87
PANPL	16.28	23.29	9.40	7.81	92.08	14.87	14.27	28.21	92.36	25.19	24.20	47.92
PANO	47.41	9.68	6.67	9.46	39.04	21.10	13.18	16.97	43.57	4.32	2.85	3.88
FERT	95.68	13.63	13.33	26.86	97.48	16.35	16.14	32.83	98.89	15.07	14.98	30.69
SPKPAN	82.11	23.60	21.39	39.93	0.79	32.25	2.87	0.53	34.78	26.37	15.55	18.89
FLW	84.40	17.22	15.82	29.93	96.10	16.65	16.33	32.97	90.79	13.02	12.41	24.36
MAT	93.11	10.67	10.30	20.47	90.02	10.52	9.98	19.51	99.24	8.37	8.33	17.10
TGRNWT	9.97	10.23	3.23	2.10	91.67	3.23	3.09	6.09	71.73	8.17	6.92	12.07
SHATT	96.17	30.12	29.54	59.67	93.75	37.38	36.20	72.20	94.59	56.32	54.78	109.75
PA	88.50	12.50	11.76	22.79	88.18	23.86	22.41	43.34	33.33	11.70	6.76	8.04
PE	95.45	43.43	42.43	85.40	94.50	37.90	36.84	73.78	92.31	37.95	36.46	72.17
Yld	66.11	38.68	31.45	52.67	62.61	31.57	24.98	40.72	16.10	29.42	11.80	9.75

Plht - Plant height, Tilno- Tiller number, PAM- Panicle per meter square, Pano- Panicle per plant, Panlt- Panicle length, Fert- Fertility %, Spkpan- Spikelets per panicle, Flw- Days to 50% Flowering, Mat- Days to 85% maturity, TGRNWT- 1000 grain weight, Shatt- Shattering score, PA- Phenotypic Acceptability, PE- Panicle exertion, Yld- Yield kg/ha

Pearson correlation coefficient for evaluated traits in the three rice ecologies

The Pearson correlation coefficient for the upland ecology (Table 3) revealed that the following traits were significantly correlated with grain yield: days to 50% flowering, tiller number per plant, panicles per meter square, number of panicles per plant, panicle length, fertility percent, grains per panicle, lodging percent and panicle exertion.. However, in the hydromorphic ecology only four

variables were significantly correlated with grain yield; panicles per square meter, panicle length, lodging percent and panicle exertion. whereas in the lowland ecology, panicles per meter square, number of panicles per plant, panicle length, fertility percent, grains per panicle and shattering score were significantly correlated with grain yield.

Therefore these traits could be used as selection criteria for each ecology.

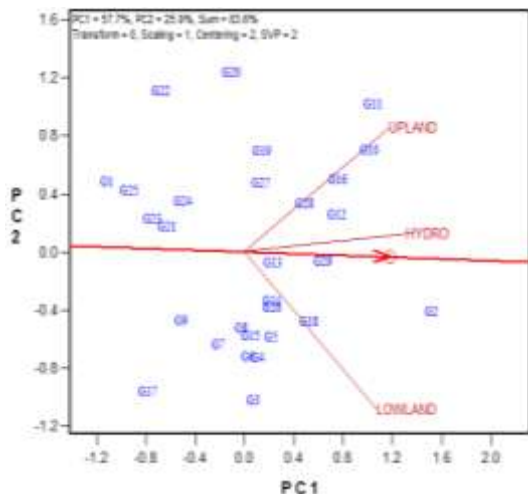


Figure 2. The mean yield and adaptation for each genotype to the three ecologies

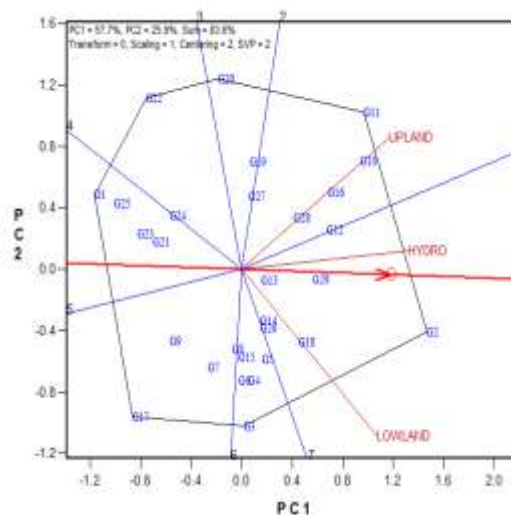


Figure 4. Polygon View of GGE biplot for the ‘Which wins Where or which is best for what’ Pattern of Yield in combined ecology (Upland, hydromorphic and lowland ecology) showing which genotypes yielded best in which environment

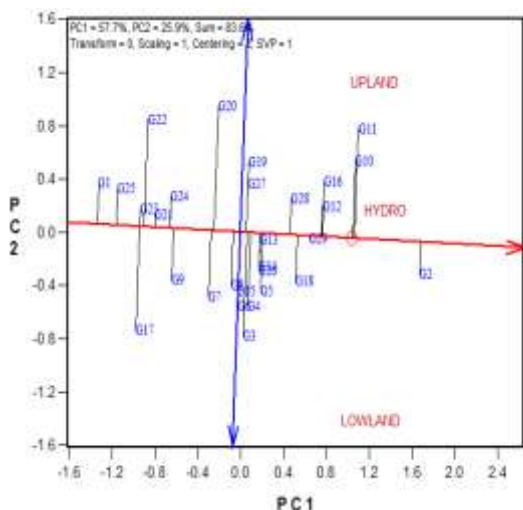


Figure 3. Mean Yield Performances and Stability of Genotypes Polygon View of GGE biplot for the ‘Which wins Where or which is best for what’ Pattern of Yield in combined ecology (Upland, hydromorphic and lowland ecology) showing which genotypes yielded best in which environment

4. Conclusion

Only four genotypes (G10, G11, G16 and G 20) had yield increase over TGS 25 in the Upland Ecology. Outstanding genotypes for each ecology were; G10, G11, G16, and G28 for the upland ecology; G13 and G29 for the hydromorphic and G18 for the lowland ecology. G13 and G29 were the most stable across the three ecologies. Significantly higher grain yields above both parents were observed only in the Upland ecology. Further studies are recommended for this population as the best yielding genotype in the hydromorphic and lowland ecologies is still the TGS 25 parent (G2).

Backcrossing G10, G11, G13, G16, G18, G28, and G29 to TGS 25 could give higher yielding progeny than the TGS 25 parent.

Table 3. Pearson correlation coefficients for evaluated traits to grain yield in the three studied rice ecologies

Traits	Upland Yld (kg/ha)	Hydromorphic Yld (kg/ha)	Lowland yld (kg/ha)
FLW	-0.33*	0.10 ^{NS}	-0.08 ^{NS}
MAT	-0.27 ^{NS}	0.17 ^{NS}	0.11 ^{NS}
PLHT	0.24 ^{NS}	0.09 ^{NS}	-0.21 ^{NS}
TILNO	0.39*	0.31 ^{NS}	0.26 ^{NS}
PAM	0.39*	0.47**	0.46**
PANO	0.39*	0.01 ^{NS}	0.46**
PANLT	0.46**	0.47**	0.35*
FERT	0.49**	-0.06 ^{NS}	0.33*
GRNPAN	0.42*	0.32 ^{NS}	0.50**
SHATT	-0.24 ^{NS}	-0.17 ^{NS}	-0.52**
PA	-0.37*	-0.46**	-0.25 ^{NS}
PE	-0.45**	-0.58**	0.07 ^{NS}
LOG	0.15 ^{NS}	-0.24 ^{NS}	-0.21 ^{NS}

Flw- Days to 50% flowering, Mat- days to 85% maturity, Plht @ mat- Plant height, Tilno- Tiller number/ plant, Pano- number of Panicle/plant, Pam- number of panicle/m², Panlt- panicle length, Fert- fertility, Grnpan- grain per panicle, Shatt- shattering score, PE- Panicle exertion, PA- Phenotypic acceptability, log- lodging score, and Yld- yield in kg/ha.

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