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Multi-variate analysis for yield evaluation in rice (*Oryza sativa* L.) genotypes

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Abstract

Field experiment was carried out at the experimental field of the Department of Plant Science and Biotechnology beside the screen house, to study yield evaluation in rice genotypes. The plot was laid out in a randomized complete block design (RCBD) and the treatments replicated three times. Seven rice genotypes sourced from the department crop improvement unit were sowed in a plot size of 5×1m. The study was conducted in 2016/2017 planting seasons. Data were collected on yield component traits i.e. number of tillers, plant height, number of days to panicle initiation, number of days to maturity, panicle length, panicle weight, number of spikelet per panicle, number of grain per panicle, 1000 grain weight, grain yield per hill and flag leaf length. The result of factor analysis indicated that the first factor was positively loaded for yield component trait however; the first six principal components jointly accounted for 98.99% of the total variation among the genotype studied. High levels of variability expressed among the varieties suggested that further improvement in the varieties is possible.

Keywords: Variation; Principal component; Rice, Variety

1. Introduction

Rice, Oryza species is a grass belonging to the family of Poaceae. As an annual plant the height ranges between 36 – 150 cm. It is the most consumed cereal grain after wheat globally (FAO, 2004) and are cultivated in most countries of the world. It has about 20 different species, of which the cultivated varieties are Oryza sativa belonging to Asia and Oryza glaberrima Africa (Vaughan and Morishima, 2003). The major resource of plant breeders is the genetic variability in gene pool accessible to the crop of interest without which improvement may not be possible (Thottappily et al., 1996). The success of crop improvement programs is highly dependent on the efficient manipulation of the germplasm that results in sufficient genetic variability. Morphological markers have played a major role in crop improvement since the beginning of modern breeding programs (Mignouna et al., 1996). When more sophisticated attributes are required, isozyme, restriction fragment length polymorphism (RFRP) and other molecular level analysis are used (Ng and Padulosi, 1992; Flavel, 1991). Information from the use of these morphological makers is used by breeders and taxonomists to study genetic diversity with the aim of identifying variations and correlations among living organisms (Ng and Padulosi, 1992). The evaluation of germplasm frequently includes recording traits of agronomic interests, such as resistance to pests and diseases and tolerance to physiological stresses that are influenced by environment. These data are most sought after by plant breeders according to (Ng and Padulosi (1992); Peters and Williams, 1984). Continuous evaluation of germplasm contributed to variation in the rice populations. Therefore this study is conducted to identify traits that contribute to variability and for their possible exploitation in breeding programs.

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2. Material and methods

The location of the experiment was Akungba Akoko, longitude 50 501E and latitude 9° 051 N, at the experimental fields of the Department of Plant Science and Biotechnology, to assess genetic variations that exist among 7 improved rice varieties. The experiment was conducted during the rainy seasons of 2017 in an upland agro-ecology. The improved varieties were obtained from the Crop improvement section, of the Department of Plant Science and Biotechnology, Adekunle Ajasin University, Akungba Akoko. The plot was laid out in a randomized complete block design (RCBD) and replicated 3 times. Each entry was planted in a plot size of 5 × 1 m and the spacing adopted was 0.2 m × 0.2 m. Cultural operations were carried out such as weeding, and NPK 15:15:15 fertilizer was applied. Data were collected on yield component traits i.e. number of tillers per hill, plant height, number of days to panicle initiation, number of days to maturity, panicle length, panicle weight, number of spikelets per panicle, number of grains per panicle, 1000 grain weight, grain yield per hill, flag leaf length. The data was analyzed using Genstat version 2004.

3. Results

The analysis of variance (ANOVA) for all the traits is shown in Table 1. Significant effects of genotypes were observed for all the studied traits. Number of tillers per hill, plant height, number of days to maturity, number of days to flowering, panicle length, panicle weight, number of spikelets per panicle, number of grains per panicle, 1000 gain weight, yield per hill and flag leaf length were significantly different at p≤ 0.05.

Table 1 Mean squares for the yield component traits.

Source of variation	**Treatment**	**Error**	**C.V**
Degree of freedom	6	14	
NOT	14.73*	2.22	28.74
PH	295.63**	15.42	11.81
1000GW	217.95**	0.17	0.95
FL	367.44*	220.73	39.78
PL	769.33**	30.96	24.29
PW	2.51*	0.63	24.3
NSPP	15.03*	2.43	16.99
NGPP	6068.10**	830.8	22.08
DTM	1173.62*	0.17	0.95
YPH	280.52**	5.74	16.4
DTF	367.44**	2.86	2.1

NOTE: NOT: number of tillers/hill; PH: plant height (cm); DTM: number of days to maturity; DTF: number of days to flowering; PL: panicle length (cm); PW: panicle weight (g); NSPP: number of spikelet's per panicle; NGPP: number of grains per panicle;1000GW: 1000 grains weight (g); YPH: grain yield per hill (g); FL: flag leaf (cm); * : significant at p≤ 0.05; **: significant at p≤ 0.01.

The mean performance of rice genotype in eleven quantitative traits was presented in Table 2. Nerica8 (2.53) has the lowest number of tiller whereas Lady's finger (8.73) has the most numerous number of tillers. NERICA8 was the tallest (51.99cm) whereas IWA10(24.82) the shortest. In yield per hill, LADY'S FINGER has the highest yield whereas IRO 6A has the shortest yield. LADY FINGER (97.00 days) has the longest life span in days to flowering while NERICA8 has the shortest life span (59.67) to flowering. For panicle length, NERICA8 (27.35cm) has the highest panicle length whereas IRO6A (6.64cm) has the shortest panicle length. For panicle weight IRO7A and NERICA8 are significantly different. IRO7A (4.47) has the highest panicle weight whereas IRO6A (1.95) has the shortest panicle weight. NERICA8 (11.60) has the highest number of spikelet per panicle whereas IRO6A (6.13) has the lowest number of spikelet per panicle. In number of grain per panicle, LADY's FINGER (194.60) has the highest number whereas NERICA8 (156.67) has the lowest number mean value. In one thousand gain weight, IRO6A (61.27) has the highest of mean whereas IRO7A (15.67) has the lowest mean number. In days to maturity, LADY'S FINGER has the longest life span of (128days) whereas NERICA 8 has the shortest life span (81.67 days). In flag leaf length, LADY'S FINGER (49.01) has the highest length while IWA 8 has the shortest length.

Table 2 Mean performance of rice genotypes on eleven quantitative traits.

VARIETY	IRO 6A	IWA 8	IWA 10	N8	IRO 6N	LF	IRO 7A
NOT	3.27 ±0.87^{ab}	5.73±0.67^{bc}	7±0.48^{ab}	2.53±0.35^{a}	4.93±1.29^{abc}	8.73±0.44^{cd}	7.20±1.33^{d}
PH	32.41±2.77^{b}	31.61±3.35^{ab}	24.82±3.07^{a}	51.99±2.28^{d}	40.45±0.54^{c}	26.02±0.88^{ab}	25.41±1.21^{ab}
YPH	5.76±2.84^{a}	9.61±0.53^{abc}	11.16±2.13^{bc}	6.82±0.02^{ab}	12.14±0.24^{c}	28.45±0.33^{d}	28.30±0.33^{d}
DTF	78.33±1.33^{b}	85.33±1.45^{c}	81.00±0.58^{b}	59.67±0.33^{a}	80.00±0.00^{b}	97.00±1.16^{d}	81.00±1.00^{b}
PL	6.64±3.59^{a}	18.92±1.16^{b}	17.83±1.06^{b}	27.35±6.616^{c}	17.63±0.63^{b}	23.34±0.89^{b}	18.64±3.46^{b}
PW	1.95±0.48^{a}	2.76±0.55^{a}	3.31±0.27^{ab}	2.92±0.45a	2.94±0.68a	4.43±0.37^{b}	4.47±0.22^{b}
NSPP	6.13±0.77^{a}	6.80±0.31^{a}	8.87±1.04^{abc}	11.60±1.71^{c}	8.37±0.32^{ab}	11.40±0.61^{c}	11.06±0.82^{c}
NGPP	61.73±4.10^{a}	86.93±13.13^{ab}	119.20±24.58^{bc}	156.67±13.22^{cd}	143.77±11.29^{cd}	194.60±24.12^{d}	150.80±16.16^{cd}
1000 GW	21.27±0.15^{f}	21.90±0.06^{b}	25.70±0.38^{f}	25.17±0.27^{c}	18.73±0.15^{a}	26.87±0.88^{e}	15.67±0.33^{d}
DTM	99.33±1.33^{b}	108.33±2.08^{c}	103.33±0.88^{b}	81.67±0.67^{a}	100.00±0.00^{b}	123.33±2.03^{d}	101.33±1.33^{b}
FL	32.27±4.54 a	26.11±0.13^{a}	45.65±20.75^{a}	32.01±1.46^{a}	33.2±4.274^{a}	49.01±1.38^{a}	43.15±6.45^{a}

Note: Mean values with the same alphabet along the same column are not significantly different from each other.
NOT: number of tillers/hill; PH: plant height (cm); DTM: number of days to maturity; DTF: number of days to flowering; PL: panicle length (cm); PW: panicle weight (g); NSPP: number of spikelets per panicle; NGPP: number of grains per panicle; 1000GW: 1000 grains weight (g); YPH: grain yield per hill (g); FL: flag leaf (cm); significant at p≤ 0.05.

Table 3 Estimate of genetic parameters for all the measured traits.

TRAITS	**Vg**	**Vp**	**GCV**	**PCV**	**H_2 (%)**	**GA**	**GAM**
No of tillers	4.17	6.40	39.41	48	55.16	2.87	55.33
Plant height (cm)	93.47	108.9	29.03	31.33	85.83	13.27	39.32
Yield per hill	91.53	97.27	65.44	67.52	94.03	19.37	132.51
No of days to flowering	121.53	124.39	13.72	13.83	97.77	22.52	28.03
Panicle length (cm)	246.12	277.08	68.44	72.66	88.83	30.18	131.75
Panicle weight (g)	0.63	1.26	24.39	34.57	50.00	1.16	35.66
No of spikelet/panicle	4.2	6.63	22.33	28.05	63.35	3.34	36.34
No of grains /panicle	1745.77	2576.53	38.84	38.84	67.76	71.17	54.52
1000 grains weight (g)	391.15	391.32	46.13	46.13	99.96	40.34	94.07
No of days to maturity	151.55	157.12	12.01	12.23	96.45	24.74	24.14
Flag leaf length (cm)	0.93	219.8	2.58	39.63	0.42	0.12	0.32

Note: Genotypic (vg) and phenotypic variance (Vp), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (h2) , genetic advance (GA) and genetic advance as per cent of mean (GAM)

Estimates of genetic parameters for the yield component traits were presented in Table 3. High genotypic and phenotypic variance were obtained for number of grain (1745.77 and 2576.53), 1000 grain weight (391.15 and 391.32), panicle length (246.12 and 277.08), number of days to maturity (121.53 and 157.12), number of days to flowering (121.53 and 124.39), plant height (93.47 and 108.90) and yield per hill (91.53 and 97.27). Low estimates of genetic and phenotypic variance were obtained for number of tillers (4.17 and 6.40), panicle weight (0.63 and 1.26), and number of spikelets per panicle (4.20 and 6.63). In general, the phenotypic variance was higher than genotypic variance for all the traits.

Genotypic coefficient of variation (GCV) ranged from (2.58%) for flag leaf length to (68.44%) panicle length whereas phenotypic coefficients of variation (PCV) ranged from 12.23% for number of days to maturity of 77.66% in panicle length. GCV was low for flag leaf length (2.58), whereas number of days to maturity (12.01) and number of days to flowering (13.72) had moderate GCV, also number of tillers (39.41%), plant height (29.03%), panicle length (68.44%), panicle weight (24.39), number of spikelet per panicle (22.33%), number of grains per panicle (38.84%), 1000 grain weight (46.13%), yield per hill (65.44%) had high GCV. PCV was moderate for number of days to maturity and number of days to flowering, whereas number of tillers, plant height, panicle length, panicle weight, number of spikelets per panicle, number of grains per panicle, one thousand grain weight, yield per hill and flag leaf had high PCV.

Heritability estimates the relative contributions of differences in heritable and non-heritable factors to the total phenotypic variance in a population. It is an important concept in quantitative genetics, particularly in selective breeding. Heritability in broad sense (h2) varied from 0.42% to 99.96% for flag leaf length and1000 grain weight respectively. All the traits studied had high heritability (greater than60%) exceptfor panicle weight, flag leaf length and number of tillers. The high value of genetic advance (GA) was recorded in number of grains per panicle (71.17) and low (0.12) for flag leaf length. Genetic advance as per cent mean (GAM) range from 0.32% for flag leaf length and132.51%for yield per hill.

Table 4 Simple correlation coefficient among quantitative traits in rice.

CHARATERS	**PH**	**DTM**	**DTF**	**PL**	**PW**	**NSPP**	**NGPP**	**1000GW**	**YPH**	**FL**
No of tillers	-0.42	0.674**	0.685**	-0.20	0.486*	0.31	0.38	0.19	0.818**	0.20
Plant height		-0.717**	-0.750**	0.664**	-0.348	0.094	0.020	-0.672**	-0.498*	-0.246
Days to maturity			0.987**	-0.536*	0.354	-0.065	0.183	0.362	0.573**	0.299
Days to flowering				-0.637**	0.339	-0.106	0.125	0.366	0.580**	0.282
Panicle length					0.090	0.553**	0.447*	-0.420	-0.101	-0.122
Panicle weight						0.541*	0.675**	0.241	0.771**	0.195
No of spikelet's/panicle							0.699**	0.064	0.561**	0.045
No of grains/ panicle								-0.024	0.616**	0.089
1000 grain weight									0.087	0.088
Yield per hill										0.284
Flag leaf										-

NOTE: NOT: number of tillers; PH: plant height (cm); DTM: number of days to maturity; DTF: number of days to flowering; PL: panicle length (cm); PW: panicle weight (g); NSPP: number of spikelets per panicle; NGPP: number of grain per panicle: 1000 GW: one thousand grain weight; YPH: yield per hill (g); FL: flag leaf length (cm); ns: no significant; *: significant at 5% level probability; **: significant at 1% level probability.

Results of simple correlation analysis among eleven quantitative traits were presented in Table 4. Number of tiller had highly significant positive correlation with number of days to maturity (0.674), number of days to flowering (0.625) and yield per hill (0.818). Plant height had highly significant negative correlation with days to maturity (-0.717), days to flowering (-0.750) and one thousand grain weight (-0.672). There was highly significant positive correlation with yield per hill (0.498) and panicle length (0.664). Number of days to maturity had positive and highly significant correlation with number of days to flowering (0.977) and yield per hill (0.573). It only showed highly significant negative correlation with panicle length (-0.536). Number of days to flowering had negative and highly significant correlation with panicle length (-0.637), but was positive and correlate significantly with yield per hill (0.580). Panicle length had positive and highly significant correlation with number of spikelets per panicle (0.553) and number of grains per panicle (0.447). Panicle weight had highly significant positive correlation with number of spikelets per panicle (0.541), number of grains per panicle (0.675) and yield per hill (0.771). Number of spikelets per panicle had positive and highly significant correlation with number of grains per panicle (0.699) and yield per hill (0.501). Number of grain per panicle had positive and highly significant correlation with yield per hill (0.616) only.

Table 5 Eigen value, percentage of variance accounted for and cumulative percentage of factor analysis for six factor in rice.

Factor of 7 traits	Eigen value	proportion of variance accounted for %	Cumulative of variance accounted for %
1	6.68	95.36	95.36
2	0.22	3.18	98.54
3	0.06	0.86	99.43
4	0.03	0.47	99.9
5	0.005	0.07	99.97
6	0.002	0.003	100

Table 5 showed Eigen value, percentage of variance accounted for and cumulative percentage of factor analysis of six factors in rice. Six factors were identified, of which only four were considered important. These four factors accounted for 99.9% of total variance. The first factor with Eigen value of 6.68 accounted for 95.36% of the variance, second factor with Eigen value of 0.22 explained 3.18% of the variance whereas the third and fourth factors with 0.03 and 0.005 Eigen value explained 0.89% and 0.47% of the variance respectively.

Table 6 Factor scores and communality of eleven traits of rice factor analysis.

	Factor			
Traits	**1**	**2**	**3**	**4**
NOT	0.00	-0.04	0.22	0.22
PH	0.77	-0.55	-1.92	-0.23
DTM	0.29	-2.17	-0.23	1.20
DTF	0.12	-1.72	0.09	1.15
PL	1.23	0.15	-1.82	-0.89
PW	0.04	-0.02	0.07	0.02
NOS	0.19	-0.07	-0.05	-0.13
NOG	2.93	0.29	1.28	0.08
GW	-0.27	-1.60	0.80	-2.62
YPH	0.08	0.08	1.18	0.29
FLL	0.29	-0.60	0.49	-0.61

NOTE: NOT: number of tillers; PH: plant height (cm); DTM: number of days to maturity; DTF: number of days to flowering; PL: panicle length (cm); PW: panicle weight (g); NSPP: number of spikelets per panicle; NGPP: number of grains per panicle; 1000GW: one thousand grain weight (g); YPH: yield per hill (g); FL: flag leaf (cm).

Factor scores on eleven traits of rice were presented in table 6. The first factor was positively loaded with plant height (0.77), panicle length (1.23) and number of grain per panicle (2.93). The second factor was negatively loaded with plant height (-0.55), number of days to maturity (-2.17), number of days to flowering (-1.72), one thousand grain weight (-1.60), and flag leaf length (-0.60). the third factor was positivity loaded with one thousand grain weight (0.80), yield per hill (1.18) and flag leaf length (0.49) while it was negatively loaded with plant height (-1.92) and (-1.82) per panicle length. Factor four was loaded with number of days to maturity (1.20) and number of days to flowering (1.15) while it was negatively loaded with panicle length (-0.89), one thousand grain weight (-2.62) and flag leaf length (-0.61).

Table 7 Eigen vectors for agronomic traits of the first six principal components.

	PC 1	**PC 2**	**PC 3**	**PC 4**	**PC 5**	**PC 6**
NOT	0.37	0.00	0.36	-0.22	0.19	0.27
PH	-0.31	0.31	0.18	0.21	-0.22	0.59
DTM	0.33	-0.23	0.28	0.48	0.25	0.03
DTF	0.33	-0.26	0.28	0.32	0.02	0.02
PL	-0.14	0.49	0.02	0.26	0.68	-0.20
PW	0.36	0.25	0.01	-0.33	0.03	-0.37
NOS	0.18	0.49	-0.13	-0.02	0.12	0.05
NOG	0.23	0.43	0.12	0.30	-0.41	0.09
GW	0.23	-0.17	-0.69	0.08	0.29	0.49
YPH	0.38	0.13	0.07	-0.43	-0.05	0.32
FL	0.34	0.11	-0.41	0.34	-0.36	-0.25
Eigen value	5.93	3.29	1.18	0.32	0.16	0.12
% variance	53.94	29.90	10.72	2.88	1.46	1.09
Commutative variance	53.49	83.84	93.56	96.44	97.99	98.99

NOTE: NOT: number of tillers; PH: plant height (cm); DTM: number of days to maturity; DTF: number of days to flowering; PL: panicle length (cm); PW: panicle weight (g); NSPP: number of spikelet per panicle; NGPP: number of grains per panicle; 1000GW: one thousand grains weight (g); YPH: yield per hill (g); FL: flag leaf (cm).

Table 7 showed result of Eigen vectors for agronomic traits on the first six principal component axes. Two out of the six principal components had Eigen value greater than 2.0. The six principal components jointly accounted for 98.99% of the total variation in the studied genotypes. Traits that contributed to the total variation and positively loaded includes yield per hill (0.36), flag leaf (0.34), number of days to maturity (0.33), number of days to flowering (0.33), number of grains per panicle (0.23), one thousand grains weight (0.23). Whereas plant height had (-0.31) was negatively loaded. PC 2 accounted for 29.90% of the total variation and was loaded with Panicle length (0.49) and number of spikelets per panicle (0.49), and negatively loaded with number of days to flowering (-0.26) and number of days to maturity (-0.23).The third PC accounted for 10.72% of the total variation and positively loaded with number of tillers (0.36) but negatively loaded with grain weight (-0.69) and flag leaf length (-0.41). At the second principal components the commutative percentage variance had reached 83.54% of the total variation with an Eigen value of 3.29.

4. Discussion

The study of genetic variance and other genetic parameters had help in no small measure in formulating a suitable breeding program for improvement of the crop especially in rice. It is a prerequisite for successful crop improvement programs. A genetic diversity study is an important component in characterization of breeding materials which is very key in crop improvement. More variability observed in the base population is a veritable effort in the choice of parent for hybridization in the improvement of crops.

Based on above understanding, variance analysis revealed high significant differences among the genotypes for all the traits indicating huge genetic variability that existed among the genotypes, this appears that further improvement through selection for these traits may be effective, this results are in agreement with those found by Ogunbayo et al., (2014). The sufficient amount of variability observed for all the traits studied indicate that the expression of these traits was influenced by environment. Similar results were reported by Dutta et al., (2013), Singh et al., (2014) and Tuhina-Khatun et al., (2015) in rice. It is interesting to note that some traits showed low differences in panicle length, panicle weight, number of grains per panicle and flag leaf length indicating that influence of the environment on them were minimal. It also suggests that selection based on these traits would not be effective for future breeding program. These were corroborated by Prajapati et al., (2011) and Singh et al., (2014). However, other traits like panicle length, panicle weight, number of spikelet per panicle and flag leaf length which showed higher difference both in PCV and GCV indicated that selection for those traits for further breeding program is sure.

The most important function of the heritability in the genetic study of quantitative traits is its predictive role in the selection process and as a guide to breeding value (Falconer and Mackay, 1996; Al-Tabbal et al., 2012). Heritability in broad sense and genetic advance are important selection parameters. Genetic advance is more useful as a selection tool when considered jointly with heritability. The present study revealed high heritability accompanied with high genetic advance as percent of the mean for number of tillers, plant height, panicle length, number of spikelets per panicle, number of grains per panicle, one thousand grains weight and yield per hill; hence, high heritability and moderate genetic advance as percent of the mean for number of days to maturity and number of days to flowering suggest high genetic variability and transmissibility of hereditary factors. Similar findings has been reported by Wolie et al., (2013), Ogunbayo et al., (2014) in rice and wheat by Reza et al., (2015).Correlation analysis measures the extent of association between two traits or the extent to which they vary together; it is an important tool that can be used to determine the direction of selection in a breeding program. Based on the above understanding significant and positive correlation between two traits suggests that the traits can be improved simultaneously in a selection program, the present study showed that number of tillers exhibits a highly significant positive correlation between number of days to maturity, number of days to flowering and yield per hill indicating that simultaneous selection for these traits would result in the improvement of yield. Similar findings were earlier reported by Gulzar and Subhasl (2012), Azarpour (2013) and Moosavi et al., (2015). Plant height exhibited a negative and highly significant correlation with number of days to maturity, number of days to flowering and one thousand grains weight. The result is in agreement with the reports of Golam et al. (2011) and Nor et al., (2013). However, this is in contrast with the previous study of Khan et al., (2014) and Moosavi et al., (2015) that reported negative correlation between plant height and yield per hill.

Factor analysis and principal component analysis identified some similar traits as the most important for grouping the variation that existed among the studied rice genotypes and these includes, plant height, number of grains per panicle, one thousand grains weight, flag leaf length, number of days to flowering, panicle length, number of days to maturity and yield per hill. The similarity between the two techniques had been reported earlier in okra by Ariyo (1993), rice by Nassir and Ariyo (2007). Meanwhile, the two techniques produced similar result, but their underlying principles are different from each other. Principal component analysis does not rely on any statistical model and assumptions but factor analysis does. It is also important to note that factor analyses suffer from some disadvantages such as absence of error term and the dependence upon scale used to measure the variables (Bartual et al., 1985). A combination of the identified traits will give a good description of the variability and hence discriminate among the genotypes.

5. Conclusion

Principal component analysis was utilized to examine the variation and to estimate the relative contribution of various traits for total variability. The PCI showed 53.94%, while, PC2 and PC3 exhibited 29.90% and 10.72% variability. It can be concluded that principal component analysis highlights the characters with maximum variability. The varieties that are higher yielding and stable are selected for farmers in the location for enhance productivity. In the experiment carried out, NERICA 8 can be recommended to farmers because it has a greater yield, has faster date of maturity and more grain per panicle than the other genotype.

Compliance with ethical standards

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Disclosure of conflict of interest

No disclosure of conflict interest

References

[1] Aliyu B, Akoroda MO, Padulosi S. Variation within Vigna reticulata Hooke FII Nig. J.Gene. 2000; 1-8.

[2] Anonymous. Rice Consumption. In IRRI rice facts, 1994 IOS Banos, the Philippines. 1994.

[3] Anonymous. Foreign Traded Statistics. Abuja, Nigeria Federal Office of Statistics. 1998.

[4] Ariyo OJ. Genetic diversity in west Africa okra (Abelmorschus exculentum L. (chev.)Stevel- Multivariate analysis of morphological and agronomical characteristics. GeneticRes. Crop Evolution. 1993; 40: 25-32.

[5] Azarpour E. Path coefficient analysis for the yield components of rice cultivars in Iran under different nitrogen levels. J. Biodivers. Environ. Sci. (JBES). 2013; 3(10): 24-30.

[6] Bartual RE, A. Carbonell, Green DE. Multivariate analysis of a collection of soya bean cultivars from South-eastern Spain. Euphytio. 1985; 34: 113-123.

[7] Damola AA. Sector strategies and policies related to rice development in Nigeria. 2010.

[8] Dutta P, Dutta PN, Borua PK. Morphological Traits as Selection Indices in Rice: A Statistical View. Univ. J. Agric. Res. 2013; 1(3): 85-96.

[9] Falconer DS, Mackay TFC. Introduction to quantitative genetics. 4th Edn., Benjamin Cummings, England. 1996.

[10] FAO. Species description Oryza sativa. 2004.

[11] FAOSTAT Data. 2010.

[12] Flavel RB. Molecular biology and genetic conservation programs. Biol. J. Linnean Soc. 1991; 43: 73-80.

[13] FMARD. Agricultural export potential in Nigeria. 1996.

[14] Golam F, Yin YH, Masitah A, Afnierna N, Majid NA, Khalid N, Osman M. Analysis of aroma and yield components of aromatic rice in Malaysian tropical environment. AJCS. 2011; 5(11): 1318-1325.

[15] Grist DH. Rice. 3rd ed. 466 pp. Longmans, London. 1959.

[16] Gulzar SS, Subhash KC. Genetic Parameters and Selection Indicesin F3 Progenies of Hill Rice Genotypes. Not. Sci. Biol. 2012; 4(4): 110-114.

[17] Imolehin ED, Wada AC. Meeting the Rice Production and Consumption demand of Nigeria with improved Technologies. National Cereal Research Institute, Badeggi, PMB 8, Niger State, Nigeria. 2000; 1-11.

[18] Khan MSK, Iqbal J, Saeed M. Comparative study of agronomic traits of different rice varieties grown under saline and normal conditions. J. Anim. Plant Sci. 2014; 24(2): 634-642.

[19] Lenis SO, Gbolagade BA, Oyeleke RO. Enhancing the competiveness of agricultural commodity chains in Nigeria: Identifying opportunities with cassava, Mapping of poverty reduction strategies papers (PRSP). 2009; 1–66.

[20] Mignouna HD, Fatokun CA, Thottappily G. Choice of DNA marker system In DNA assisted improvement of the stable crops of sub-Saharan Africa. Proceedings of the workshop on DNA markers at IITA. Ibadan. 1996; 9-15.

[21] Nassir AL, Ariyo OJ. Multivariate analysis of variation of field planted upland rice Oryza sativa L.) in tropical habitat. Malays. Appl. Boil. 2007; 36(1): 47-57.

[22] Ng NQ, Padulosi S. Constraints in the accessibility and use of germplasm collection. In Biotechnology enhances research on tropical crops in Africa edited by Thottappily, L. M. Monti D. R. Mohan Raj. A. W. Moore IITA Ibadan. 1992.

[23] Nor AH, Abdul RH, Mohd RY, Norain MN, NurIzzah J. Correlation analysis on agronomic characters in F1 population derived from a cross of PongsuSeribu 2 and MR 264. ScFund MOSTI (06-03-01-SF0110) and RAGS (600RMI/RAGS 5/3). 2013.

[24] Ogunbayo SA, Sié M, Ojo DK, Sanni KA, Akinwale MG, Toulou B, Shittu A, Idehen EO, Popoola AR, Daniel IO, Gregoria GB. Genetic variation and heritability of yield and related traits in promising rice genotypes (Oryza sativa L.). J. Plant Breed. Crop Sci. 2014; 6(11): 153-159.

[25] Ogundele OO, Okoruwa V. Technical efficiency differentials in rice. 2006.

[26] Oyeleke BO. Management of major pest of rice in Tanzania. Department of crop. 2009.

[27] Prajapati MK, Singh CM, Suresh BG, Roopa LG, Jadhav P. Genetic parameters for grain yield and its component characters in rice. Electron. J. Plant Breed. 2011; 2(2): 235-238.

[28] Santos JK. Morphology of the flower and mature grain of Philippine rice. Philippine J. Sci. 1933; 52: 475-503.

[29] Thottappily G, Crouch JH, Quin FM. Overview of DNA marker research at IITA: Proceedings of the workshop on DNA markers at IITA. Ibadan Ed by J.H. Crouch and Tenkuoano A. 1996; 3-8.

[30] Vaughan DA, Morishima H. Biosystematics of the genus Oryza. Chapter 1.2. In: CW Smith, RH Dilday, eds. Rice. Origin. History. 2003.

[31] WARDA. Rice Trends in sub-Sahara Africa: A Synthesis of Statistics on Rice. 1996.

[32] Wolie A, Dessalegn T, Belete K. Heritability, variance components and genetic advance of some yield and yield related traits in Ethiopian collections of finger millet (Eleusinecoracana (L.) Gaertn.) genotypes. Afr. J. Biotechnol. 2013; 12(36): 5529-5534.