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Genetic variability and correlation analysis of rice (*Oryza sativa* L.) inbred lines based on agro-morphological traits

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In order to evaluate genetic variability of agro-morphological traits and also determine the correlation between grain yield with its components in rice lines, 17 recombinants inbred lines, their parents and a check variety were grown in research station of Africa rice center in Benin republic during two consecutive years 2013 and 2014. The experiments were laid out in a randomized complete block design with four replications. Phenotypic coefficients of variance were higher than genotypic coefficients of variance in all the characters across the two years. High heritability in broad sense (H^2) estimates were obtained for biomass (68.77%), date of 50% flowering (98.11%), plant height (81.94%), leaf area (82.90%), number of panicles (64.40%), leaf dry weight (72.91%), root weight (67.43%) and yield/plant (62.23%) suggesting that the traits were primarily under genetic control. A joint consideration of broad sense heritability (H^2) and genetic advance as per cent mean expected (GAM) revealed that leaves dries weight and roots weight combined high heritability and high GAM. Furthermore, high (H^2) and high GAM recorded in these characters could be explained by additive gene action. However, high estimates (H^2) combined with moderate GAM recorded for biomass, day to 50% flowering, leaf area, number of panicle and yield/plant could be due to non-additive gene effect. Grain yield/plant recorded positive and significant correlation with stem weight (r=0.5262) and biomass (r=0.9291). This result indicates that selection based on these two characters will be highly effective for yield improvement in rice.

Key words: Agro-morphological traits, correlation, genetic variability, heritability, rice.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important food crops in the world. It is a staple food crop for more than half of the world's human population. Rice grain contains 75 to 80% starch, 12% water and 7% protein (Oko et al., 2012; Hossain et al., 2015). Minerals like calcium,

magnesium and phosphorus are present along with some traces of iron, copper, zinc and manganese. In addition, rice is a good source of niacin, thiamine and riboflavin (Yousaf, 1992; Oko et al., 2012).

Rice is grown in 117 countries across all habitable

continents covering a total area of about 163 mha with a global production of about 740 mt and an average yield of about 4,539 kg / ha (FAOSTAT, 2014). The Asian continent ranks first with over 90.1% of world production, followed by the American continent (5.1%), African continent (4.2%), Europe (0.5%) and Oceania (0.1%). The major producing countries are China (206.5 million tons), India (157.2 million tons), Indonesia (70.8 million tons), Bangladesh (52.2 million tons) and Viet Nam with 44.9 million tons (FAOSTAT, 2014). In Africa, rice is grown and consumed in more than 40 countries. Its production has increased significantly from year 2000 to 2013. More than 20 million farmers in Africa are engaged on rice production in these countries and about 100 million people are dependent on it directly for their livelihood (Nwanze et al., 2006). For example in Burkina Faso, rice production has grown from 103,087 tons on year 2000 to 305,382 tons on 2013. It is no longer a luxury food but has become the cereal that constitutes a major source of calories for almost urban and rural people of Africa (Seck et al., 2013).

In a report published by United Nations the world population is going to cross the 8 billion mark by 2030 and 9.6 billion by the year 2050 and rice production must be increased by 50% in order to meet the growing demand. This demand in Sub-Saharan Africa is expected to grown substantially as the population is currently growing at the rate of 3 to 4% per annum (Ogunbayo et al., 2014). To meet the future demand resulting from population growth, development of news high yielding rice genotypes is therefore a necessity. Thus, to meet this demand and attend rice self-sufficiency, plant breeders have to develop high yielding cultivars with desirable agronomic traits for diverse ecosystems.

The development of new genotypes requires some knowledge about the genetic variability presents in the germplasm of the crop to build efficient breeding programme. The knowledge about genetic variability can help to know if these variations are heritable or non-heritable. The magnitude of variation due to heritable component is very important because, it would be a guide for selection of parents for crop improvement (Dutta et al., 2013). Therefore, selection for high yield requires knowledge about genetic variability and good understanding of correlation between yield and yield components regarding to the genetic material that is on hand. Genetic variability for agronomic traits is the key component of breeding programme for broadening the gene pool of rice (Dutta et al., 2013).

Heritability estimates provide authentic information about a particular genetic attribute which will be transmitted to the successive generations and constitute an efficient guide for breeders in the choice of parents for crop improvement programmes (Rafi and Nath, 2004). However, heritability in broad sense alone may not be helpful for selection based on phenotype, because it's influenced by environment. Thus, estimate heritability along with genetic advance conjointly are reliable helpful in predicting the gain under selection than heritability alone (Ogunbayo et al., 2014). Moosavi et al. (2015) reported that grain yield is a complex trait, quantitative in nature and a combined function of a number of constituent traits. Consequently, selection for yield may not be satisfying without taking into consideration yield component traits. Thus, positives correlated between yield and yield components are requires for effective yield component breeding increasing grain yield in rice (Ogunbayo et al., 2014). So, it is important for plant breeders to understand the degree of correlation between yield and its components.

Therefore, the objective of the present study was to assess and evaluate genetic variability of rice recombinant inbred lines based on agro-morphological traits and analyse the relationships between these traits.

MATERIALS AND METHODS

The experiment was conducted in the greenhouse of Africa rice center research station in Cotonou (Benin republic) from March to July 2013 and from February to June 2014. The site is located between 6°25.415N and 2°19.684E at an altitude of 21 m above sea level. Experiments were conducted in greenhouse using a randomized complete block design with four replications. Individual plant of each genotype was grown in 2 L pots containing natural field soil. Management practices such as irrigation and fertilization were performed by following the standard procedures (IRRI, 2002).

A total of 20 genotypes consisting of 17 F_5 inbred lines from the *indica*'s cross included their two parents and the *indica* variety APO were used in this study. The inbred lines were obtained from the *indica*'s cross IR64 X B6144F-MR-6-0-0.The parent, B6144F-MR-6-0-0, a drought resistant landrace was crossed with the variety IR64, a variety which possesses many agronomical superior traits. The variety APO, a popular variety known for its long term adaptation in drought prone ecosystem was used as a control.

Observations were recorded on one plant of each pot. Thus, morphological and agronomical data were collected for 11 quantitative characters at appropriate growth stage of rice plant following the standard evaluation system indicated by IRRI (IRRI, 2002). The characters that were evaluated included days to 50% flowering (50%DF, day), plant height (PH, cm), leaf area (LA, cm^2), number of tillers (NT), number of panicles (NP), number of fertile spikelets (NFS), leaf dry weight (LDW, g), roots weight (RW, g), panicles weight (PW, g), stem weight (SW, g), 1000 grains weight (1000GW, g), biomass (biom, g) and grain yield per plant (yield/plant, g/plant).

The data recorded on 12 morphological and agronomical traits from the genotypes used, were subjected to statistical analysis. Analysis of variance (ANOVA) was carried out to access the genotype effect and their interaction using R program package. The correlation analysis was performed using the same software to

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Table 1. Mean square of combined analysis of variance for all the characters studies of 20 rice genotypes.

Source	df	Biom	D50F	PH	LA	NT	NP	NFS	LDW	RW	PW	SW	1000GW	Yield/plant
Rep	3	31.6	4.126	49.06	95.51	1.22	48.35	75.88	8.32	15.47	3.26	20.73	9.68	24.95
Geno	19	89.1**	337.24**	66.37**	2992.44**	6.20**	11.66**	234.93**	4.72**	31.20**	1.03**	8.89**	11.35**	80.94**
Year	1	278.44**	120.16**	1863.36**	14.5ns	46.71**	30.11**	1956.69**	27.23**	38.43**	3.48**	1.52ns	47.91**	222.34**
G x Y	19	6ns	2.23ns	4.80ns	333.7**	0.22ns	0.20ns	53.25ns	0.49ns	2.59ns	0.21ns	2.40ns	6.21**	14.44ns
Error	117	10.58	1.4	2.923	71.56	1.26	2.04	65.6	0.36	3.74	0.33	2.38	2.57	8.64

1000 GW: 1000 grains weight; D50F: day to 50% flowering; LA: leaf area; LDW: leaf dry weight; NP: number of panicle; NFS: number of fertile spikelets; NT: number of tiller; PH: plant height; PW: panicle weight; RW: root weight; SW: stem weight; Yield/p: yield per plant; biom: biomass; ns: no significant; * : significant at 5% level probability; **: significant at 1% level probability.

determine the degree of correlation between yield and its components. In order to assess and quantify the genetic variability among the genotypes for the characters under study the variance components and values of heritability and genetic advance were estimated following the formula given by Burton and De Vane (1953); and Johnson et al. (1955) and applied by Tuhina-Khatun et al. (2015).

Phenotypic and genotypic variances were estimated using the following formula:

Vg = (MS$_g$ – MS$_{gxy}$) / ry

Vgxy = (MS$_{gxy}$ - MS$_e$) / r

Ve = MS$_e$

Vp = Vg + Vgxy / y + Ve / ry

Where, Vg = genotypic variance; Vgxy = genotype x year variance; Ve = environment variance; Vp= phenotypic variance; MS$_g$ = mean square of genotypes, MS$_{gxy}$= mean square of genotype x year; MS$_e$= mean square of error, r = number of replications and y = number of year.

Both genotypic and phenotypic coefficients of variability were estimated using the formula below:

$$GCV = \frac{\sqrt{Vg}}{X} 100$$

$$PCV = \frac{\sqrt{Vp}}{X} 100$$

Where GCV = genotypic coefficient of variability; PCV =

Phenotypic coefficient of variability; $\sqrt{Vg}$ = genotypic standard deviation; $\sqrt{Vp}$ = phenotypic standard deviation and X= general mean of the character.

Heritability in broad sense (H^2) was computed as the ratio of genetic (Vg) variance to the total phenotypic variance (Vp).

$$H^2 = \frac{Vg}{Vp} 100$$

The genetic advance (GA) and genetic advance as per cent of mean (GAM) were estimate using the formula given below:

$$GA = H^2 \, k\sqrt{Vp}$$

$$GAM = \frac{GA}{X} 100$$

Where H^2= heritability in broad sense; k = Selection differential which is equal to 2.06 at 5% intensity of selection; X= general mean of the character.

RESULTS

Analysis of variance

The results of combined analysis of variance for the all characters are shown in Table 1. Significant effects of genotype were observed for all the characters under study. High significant effect of

year for all the characters except the leaf area (LA) and stem weight (SW) were shown from this analysis. The genotype x year was highly significant only for the characters leaf area (LA) and 1000 grain weight (1000 GW). Environmental conditions were not similar in two years, meaning that climate changes were observed during the study suggesting that the differences among genotypes were not stable across years.

Estimate of genetic parameters

Estimates of genotypic (Vg) and phenotypic variances (Vp), genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV), broad sense heritability (H^2), genetic advance (GA) and genetic advance as percentage of the mean (GAM) are shown in Table 2.

High genotypic and phenotypic variances were recorded with leaf area, 332.34 and 400.89, respectively. High genotypic and phenotypic variances were equally observed for 50% flowering day (41.88 and 42.68) and the number of fertile spikelets 22.71 and 53.97, respectively. The low values of genotypic and phenotypic variances were observed with the characters panicle weight (0.10 and 0.26), stem weight (0.81 and 2.01) leaf dries weight (0.53 and 0.73), number

Table 2. Genotypic (Vp) and phenotypic variance (Vp), genotypic coefficient (GCV) and phenotypic coefficient of variance (PCV), broad sense heritability (H^2) , genetic advance (GA) and genetic advance as per cent of mean (GAM) for all the traits.

Characters	Min	Means	Max	Vg	Vp	GCV	PCV	H2 (%)	GA	GAM
Biomass (g)	39.79	50.34	62.85	10.39	15.11	6.40	7.72	68.77	5.51	10.94
Day to 50% flowering	81.60	92.67	118.30	41.88	42.68	6.98	7.05	98.11	13.20	14.25
Plant height (cm)	79.00	87.24	100.30	7.70	9.39	3.18	3.51	81.94	5.17	5.93
Leaf area (cm^2)	175.20	213.60	264.70	332.34	400.89	8.53	9.37	82.90	34.19	16.01
Number of tillers	10.00	13.43	16.89	0.75	1.25	6.44	8.33	59.79	1.38	10.26
Number of panicles	6.50	10.29	15.07	1.43	2.23	11.63	14.50	64.40	1.98	19.23
Number of fertile spikelets	8.81	86.39	101.30	22.71	53.97	5.52	8.50	42.08	6.37	7.37
Leaf dry weight (g)	3.02	5.09	9.35	0.53	0.73	14.31	16.75	72.91	1.28	25.16
Roots weight (g)	3.05	9.44	16.86	3.58	5.30	20.03	24.39	67.43	3.20	33.87
Panicle weight (g)	1.17	2.17	8.73	0.10	0.26	14.78	23.30	40.25	0.42	19.32
Stem weight (g)	3.48	8.00	13.78	0.81	2.01	11.27	17.71	40.49	1.18	14.77
1000 grains weight (g)	12.85	23.49	29.28	0.64	2.39	3.41	6.58	26.95	0.86	3.65
Yield/plant (g/plant)	22.79	36.04	45.79	8.31	13.36	8.00	10.14	62.23	4.69	13.00

number of tiller (0.75 and 1.25) and 1000 grains weight (0.64 and 2.39), respectively. In general, the phenotypic variances were higher than genotypic variances for all the characters.

Genotypic coefficients of variance (GCV) were ranged from 3.18% for plant height to 20.03% for root weight, whereas phenotypic coefficients of variance (PCV) were ranged from 3.51% for plant height to 24.39% for root weight. According to Sivasubramanian and Menon (1973) PCV and GCV values more than 20% are regarded as high, whereas values less than 10% are considered to be low and values between 10 and 20% to be moderate. Based on this delineation, GCV and PCV values were low for biomass, day to 50% flowering, plant height and 1000 grains weight; medium for number of panicle, leaf dry weight and stem weight; high for root weight. The panicle weight and plant height were recorded with low GCV and moderate PCV. In addition, PCV values were higher than theirs corresponding GCV values for all the characters considered. However, this difference was low for all the characters except the panicle weight and stem weight.

Heritability analyses estimate the relative contributions of differences in genetic and non-genetic factors to the total phenotypic variance in a population. It is an important concept in quantitative genetics, particularly in selective breeding. The heritability in broad sense (H^2) estimate varied from 26.95% to 98.11%, respectively for 1000 grains weight and day to 50% flowering. All the characters studies had high heritability (>60%) except the numbers of fertile spikelets, panicle weight, stem weight and 1000 grains weight. This result indicates that these characters could be easily improved by selection.

Genetic advance (GA) under selection refers to the improvement of characters in genotypic value for the new population compared with the base population under one cycle of selection at a given selection intensity (Wolie et

al., 2013). The high value of GA was recorded with leaves area (34.19) and the low (0.42) with panicle weight. Estimates of GA for yield/plant was 4.69 g/plant indicating that whenever we select the best, 5% high yielding genotypes as parents, average grain yield/plant of progenies could be improved by 4.69 g/plant.

Genetic advance as per cent mean expected (GAM) had a general range between 3.65% for 1000 grains weight and 33.87% for roots weight. Among the characters high values of GAM (>20%) were recorded only for roots weight and leaf dry weight (25.16%). It was moderate (10 to 20%) for biomass, day to 50% flowering, leaf area, number of tillers, number of panicle, panicle weight, stem weight and yield/plant; low (<10%) for plant height, number of fertile spikelets and 1000 grains weight. Leaf dry weight and roots weight had high heritability and high GAM, whereas biomass, day to 50% flowering, leaf area, number of panicle and yield/plant had high heritability but moderate GAM. Panicle weight and stem weight had both moderates heritability and GAM.

Correlation

The degree of correlation between the traits is important in plant breeding. It can be used as tool for indirect selection. Correlation studies help the plant breeder during selection and provide the understanding of yield components. The results of correlation analysis showed in Table 3 reveals that there was positive and highly significant correlation between day to 50% flowering (50%DF) with leaf dry weight (r=0.6223), number of panicle (r=0.7091) and stem weight (r=0.5566). The characters which had positive relationship with grain yield/ plant were day to 50% flowering (r=0.3997), leaf area (r = 0.0382), leaf dry weight (r=0.101), number of

Table 3. Correlation coefficients among agronomical and morphological characters in twenty recombinants inbreed rice lines.

Correlation	100GW	D50F	LA	LDW	NP	NFS	NT	PH	PW	RW	SW	Yield/p
100GW	-											
D50F	-0.0842^{ns}	-										
LA	0.119^{ns}	-0.3095^{ns}	-									
LDW	0.2171^{ns}	0.6223^{**}	-0.08^{ns}	-								
NP	-0.2698^{ns}	0.7091^{**}	-0.5265^{*}	0.4235^{ns}	-							
NFS	0.3861^{ns}	-0.2657^{ns}	-0.1247^{ns}	0.1743^{ns}	-0.1863^{ns}	-						
NT	-0.0061^{ns}	0.4241^{ns}	-0.0837^{ns}	0.1964^{ns}	0.5345^{*}	-0.3501^{ns}	0.1598^{ns}					
PH	0.0526^{ns}	0.4329^{ns}	-0.1598^{ns}	0.0653^{ns}	0.2572^{ns}	-0.4627^{*}	0.1598^{ns}	-				
PW	-0.207^{ns}	0.3297^{ns}	-0.4161^{ns}	0.039^{ns}	0.5134^{*}	-0.3552^{ns}	0.1554^{ns}	0.2856^{ns}	-			
RW	0.1602^{ns}	-0.0833^{ns}	0.0456^{ns}	0.1133^{ns}	0.0952^{ns}	-0.0023^{ns}	0.0906^{ns}	-0.064^{ns}	0.2736^{ns}	-		
SW	0.037^{ns}	0.5566^{*}	0.0116^{ns}	0.4164^{ns}	0.2989^{ns}	-0.3386^{ns}	0.1536^{ns}	0.255^{ns}	0.1883^{ns}	0.1161^{ns}	-	
Yield/p	-0.0241^{ns}	0.3997^{ns}	0.0382^{ns}	0.101^{ns}	0.1286^{ns}	-0.3007^{ns}	-0.1425^{ns}	0.2794^{ns}	0.112^{ns}	-0.1489^{ns}	0.5262^{*}	-
Biom	-0.0366^{ns}	0.3658^{ns}	0.1106^{ns}	0.0596^{ns}	0.1783^{ns}	-0.3813^{ns}	-0.1343^{ns}	0.2902^{ns}	0.1895^{ns}	-0.0332^{ns}	0.5556^{*}	0.9291^{**}

1000GW: 1000 grains weight; D50F: day to 50% flowering; LA: leaf area; LDW: leaf dry weight; NP: number of panicle; NFS: number of fertile spikelets; NT: number of tiller; PH: plant height; PW: panicle weight; RW: root weight; SW: stem weight; Yield/p: yield per plant; biom: biomass; ns: no significant; * : significant at 5% level probability; **: significant at 1% level probability.

panicle (0.1286), plant height (r=0.2794), panicle weight (r=0.112), stem weight (r=0.5262) and biomass (r=0.9291). Among these characters only stem weight and biomass showed significant positive correlation with grain yield per plant. On the contrary 1000 grains weight (r=-0.024), number of fertile spikelets (r=-0.3007), number of tiller (r=-0.1425) and root weight (r=-0.1489) were inversely but no significant correlated with grain yield per plant. Plant height had positive correlation with all the characters except leaves area, number of fertile spikelets and root weight. In the same time, number of fertile spikelets had negative correlation with almost the characters except 1000 grains weight and leaf dry weight. Positive and significant correlation were shown for biomass with root weigh (r=0.5556) and for number of panicle with number of tillers and panicle weight (r=0.5345 and r=0.5134, respectively). However, plant height and number of panicle showed significant negative correlation with number of fertile spikelets (r=-0.4627) and leaf (r=0.5265), respectively.

DISCUSSION

Genetic diversity in breeding is very important. It is the key of crop improvement. More variability is observed in the basic population more is the chance of improvement. In the present study, results from ANOVA showed highly significant difference among the genotypes for all the characters, indicating huge genetic variability existing among the genotypes. So, the parents used for crossing were genetically different. Significant year effects were observed for all the characters except leaf area and stem weight, meaning that climate change were observed during the study. Environmental conditions were not similar during the two years. The results are in accordance to those found by Ogunbayo et al., (2014). All the characters, except leaf area and 1000 grains weight, exhibited stability across the seasons since the significance of genotype x year interaction was not detected and the differences among genotypes were clear. This appears to show that further improvement through selection for these characters may be effective. On the other hand, the significant effect of genotype x year interaction for leaf area and 1000 grains weight, indicating that genotypic difference in these characters was greatly influenced by the environment.

The current study suggests that phenotypic variance (Vp) and phenotypic coefficient variance (PCV) were higher than theirs corresponding genotypic variance (Vg) and genotypic coefficient of variance (GCV) respectively for all the characters studies, indicating that the expression of these

characters 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 this difference was low for all the characters except panicle weight and stem weight, indicating that these characters were less influenced by environment. It also suggests that selection based on these characters would be effective for future crossing. Similar result was also found by Prajapati et al., (2011) and Singh et al., (2014) for these traits. However the other traits like panicle weight and stem weight which showed a higher difference between PCV and GCV indicated that environmental effect on the expression of those traits is higher.

The most important function of the heritability in the genetic study of quantitative characters is its predictive role to indicate the reliability of the phenotypic value as a guide to breeding value (Falconer and Mackay, 1996; Al-Tabbal et al., 2012). High heritability estimates for yield/plant, plant height, day to 50% flowering, biomass and number of tillers, indicated a high response to selection in these traits. Similar results were also reported by Al-Tabbal et al., 2012; Dutta et al., 2013; Rafii et al., 2014, which support the present findings. Heritability in broad sense and the genetic advance are also important selection parameters. It is more useful as a selection tool when considered jointly with heritability. The estimates of genetic advance can help to understand the type of gene action of various polygenic characters. Johnson et al. (1955) suggested that high heritability estimates along with the high genetic advance is more helpful in predicting gain under selection than heritability estimates alone. Thus, the heritability estimates will be reliable if accompanied by high genetic advance. The present study revealed high heritability accompanied with high genetic advance as percent of the mean for leaf dry weight and root weight; high heritability and moderate genetic advance as percent of the mean for biomass, day to 50% flowering, leaf area, number of panicle and yield/plant. These results could be explained by additive gene action and their selection may be done in early generations. Similar findings have been reported by Wolie et al. (2013), Ogunbayo et al. (2014) on rice and Reza et al. (2015) on wheat. However, panicle weight and stem weight had moderate heritability coupled with low to moderate genetic advance as percent of the mean indicates non-additive gene effects; suggesting that these characters could be improved by developing varieties through recurrent selection method (Ogunbayo et al., 2014).

Selection of traits contributing simultaneously to a character will improve it in subsequent segregation population (Nor et al., 2013). Hence, the correlation analysis is therefore necessary to determine the direction of selection and the numbers of characteristics need to be considered in improving any character such as grain yield. The present study showed that there was a highly significant correlation between grain yield per plant with biomass at the 1% level and stem weight at the 5% level indicating that simultaneous selection for these characters would result in improvement of yield. Similar findings were earlier reported by Gulzar and Subhasl (2012), Azarpour (2013) and Moosavi et al. (2015). Also, day to 50% flowering exhibits a significant positive correlation with leaf area, number of panicle and stem weight. The observed positive correlation of date to 50% flowering was supported by earlier researchers such as Zhou et al. (2010) and Khan et al. (2014) for number of panicle. Plant height has not significant correlated with yield per plant. This result is in accordance with those 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 presented the negative correlation between plant height and yield per plant. Positive and significant correlation was shown between plant height and number of fertile spikelets. Similar results were early reported by Aris et al. (2010) and Kohnaki et al. (2013). Azarpour (2013) also reported that plant height in rice had significant and positive correlated with spikelet fertility per plant.

Conclusion

The present study highlighted the existence of diversity among the 17 rice recombinant inbred lines, their parents and the check variety. High heritability in broad sense recorded for biomass, day to 50% flowering, plant height, leaf area, number of panicles, leaf dry weight, roots weight and grain yield per plant demonstrates that these characters could be successfully transferred to offsprings if their selection is performed in hybridization programme. The correlation analysis revealed that 8 agronomical traits such as day to 50% flowering, leaf area, leaf dry weight, number of panicle, plant height, panicle weight, stem weight and biomass have the positive contribution to grain yield. Among these characters, biomass and stem weight showed significant correlation with grain yield. So, these two traits may be considered as the selection criteria for the improvement of grain yield in rice.

Conflict of Interests

The authors have not declared any conflict of interest.

REFERENCES

Al-Tabbal JA, Al-Fraihat AH (2012). Genetic variation, heritability, phenotypic and genotypic correlation studies for yield and yield components in promising barley genotypes. J. Agric. Sci. 4:3.

Aris H, Bambang K, Supartopo S (2010). Correlation analysis of agronomic characters and grain yield of rice for tidal swamp areas. Indonesian J. Agric. Sci. 11(1):11-15

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

Burton G.W, De Van EH, (1953). Estimating heritability in Tall Fescue (*Fescuta arundinacea*) from replicated clonal material. Agron. J. 45:481-487.

Dutta P, Dutta P.N. and Borua P. K (2013). Morphological Traits as Selection Indices in Rice: A Statistical View. Univ. J. Agric. Res. 1(3):85-96.

Falconer DS, Mackay TFC (1996). Introduction to quantitative genetics. 4th Edn.,Benjamin Cummings, England, ISBN-10:0582243025.

FAOSTAT (2014). Statistical data base. Food and Agriculture Organizations of the United Nations. Rome, Italia.

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

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

Hossain S, Maksudu HMD, Jamilur RJ (2015). Genetic Variability, Correlation and Path Coefficient Analysis of Morphological Traits in some Extinct Local Aman Rice (Oryza sativa L). J. Rice Res. 3:158.

IRRI (2002). Standard evaluation system for rice. International Rice Research Institute, Manila.

Johnson HW, Robinson HF, Comstock RE (1955). Estimation of genetic and environmental variability in soybeans. Agron. J. 47:314-318.

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

Kohnaki ME, Kiani G, Nematzadeh G (2013). Relationship between morphological traits in rice restorer lines at F3 generation using multivariate analysis. Int. J. Adv. Biol. Biomed. Res. 1(6):2013:572-577

Moosavi M, Ranjbar G, Zarrini HN, Gilani A (2015). Correlation between morphological and physiological traits and path analysis of grain yield in rice genotypes under Khuzestan. Biol. Forum Int. J. 7(1):43-47.

Nor AH, Abdul RH, Mohd RY, Norain MN, NurIzzah J (2013). Correlation analysis on agronomic aharacters 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).

Nwanze KF, Mohapatra S, Kormawa P, Keya S, Bruce-Olivier S (2006). Rice developmentt in sub-saharanAfrica. J. Sci. Food Agric. 86:675-677;

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

Oko AO, Ubi BE, Efisue AA, Dambaba N (2012). Comparative analysis of the chemical nutrient composition of selected local and newly introduced rice varieties grown in Ebonyi State of Nigeria. Int. J. Agric. For. 2(2):16-23.

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

Rafi SA, Nath UK (2004). Variability, Heritability, Genetic advance and relationship of yield and yield contributing characters in dry Bean (*Phaselous vulgaris* L.). J. Biol. Sci. 4(2):157-159.

Rafii MY, Zakiah MZ, Asfaliza R, Iffah HMD, Latif MA, Malek MA (2014). Grain quality performance and heritability estimation in selected f$_1$ rice genotypes. Sains Malaysiana 43(1):1–7

Reza M, Pour F (2015). Investigation of genetic variation for agronomic traits among the recombinant inbred lines of wheat from the norstar × zagross cross under water stress condition. Int. J. Biol. Biomol. Agric. Food Biotechnol. Eng. 9:9.

Seck PA, Touré AA, Coulibaly JY, Diagne A, Wopereisv MCS (2013). Africa's rice economy before and after 2008 rice crisis. Africa rice center Cotonou, Benin and CABI International UK 480 p.

Singh A, Singh AK, Singh V, Singh N, Singh VN, Shamin M, Vikram P, Singh S (2014). Genetic variability among traits associated with grain yield of rice (*Oryza sativa* L.) exposed to drought at flowering stage. Afr. J. Res. 9(16):1252.

Sivasubramanian S, Menon M (1973). Heterosis and inbreeding depression in rice. Madras Agric. J. 60:1139.

Tuhina-Khatun M, Hanafi MM, Yusop MR, Wong MY, Salleh FM, Ferdous J (2015). Genetic variation, heritability, and diversity analysis of upland rice (*Oryza sativa* L.) genotypes based on quantitative traits. BioMed. Res. Inter. ID 290861.

Wolie A, Dessalegn T, Belete K (2013). 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. 12(36):5529-5534.

Yousaf M (1992). Study on some Physico-chemical characteristics affecting cooking and eating qualities of some Pakistani Rice Varieties, M.Sc. Thesis Department of Food Technology, University of Agriculture Faisalabad, Pakistan.

Zhou HK, Hayat Y, Fang LJ, Guo RF, He JM, Xu HM (2010). Analysis of genetic and genotype X environment interaction effects for agronomic traits of rice (*Oryza sativa* L.) in salt tolerance. Pak. J. Bot. 42:3239-3246.