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Genetic Varability, Heritability and Genetic Advance for Local Rice Cultivated In Abakaliki, Ebonyi State, Nigeria.

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ABSTRACT

Genetic variability studies are of a supreme importance for the success of any plant-breeding program. Hence, this experiment was conducted to assess the extent of genetic variability among agro-morphological characteristics of rice cultivars from various localities of Ebonyi State, Nigeria. Fourty (40) different rice cultivars were collected from diifernt local Government Area in Ebonyi State in 2016 harvesting season. They were planted in a complete radomised complete block design during 2017 and 2018 farming seasons. Agro-morphological characteristics including Number of Primary Tillers (NPT), Number of Secondary Tillers (NST), Plant Height (PH), Flag Leaf Length (FL), Number of Primary Panicles (NPP), Number of Secondary Panicles (NSP), Panicle Length (PanL), Panicle Exsertion (PanEx), Grain Length (Grain L), GrainWidth (Grain W), Panicle Thresh-ability (Pthresh) and 1000grain/weight (1000G/W) were measured using standard rice evaluation methods. The results of the genetic varabilities revealed highly significant differences among the genotypes for most of the traits. High values PCV, GCV, heritability and genetic advances were recorded for Plant height, Number of primary tillers, Flag leaf length and Panicle thresh-ability. phenotypic coefficient of variation (PCV) were all higher than the genotypic coefficient of variation (GCV) with values that ranged from 123 to 827.3 for PanL and Pthresh respectively while GCV ranged from 99.1 to 666.8 for grain length and panicle thresh-ability respectively. Broad sense heritability (h2B) had values ranged from 55 to 67.0 for NPT and PanL respectively. Genetic variance (GA) ranged from 6.036 to 40.589 for 1000G/W and PH respectively while GA as percent of mean ranged from 8.006 to 45.892 for 1000 and PH respectively sugessting that improvement of these characters could be effective through phenotypic selection.

Keywords: Rice, Genetic variability,, heritability, genetic advance, agro-morphologic characters

INTRODUCTION

Rice is the staple food of more than half of the world's population. Asia accounts for more than 90 percent of the world's total rice production; the balance is divided almost equally between Africa and Latin America, where the demand for rice is increasing [1]. Rice has been cultivated in Asia since ancient times and for generations farmers have maintained thousands of different varieties [2]. These landraces, together with the 22 pan tropical, wild species of *Oryza*, are the genetic foundation for the breeding efforts needed to sustain the productivity of rice cultivation. Besides the landrace varieties and wild species already mentioned, the genetic resources of rice also encompass natural hybrids, commercial and obsolete varieties, breeding lines and a range of different genetic stocks [3].

In Nigeria, two types of rice have been mainly cultivated: the African rice *(Oryza glaberrima)* and the Asian rice (*Oryza sativa).* In recent times, however, new rice varieties have also been introduced including the West African Rice Development Association's (WARDA) hybrid rice varieties referred to as NERICA i.e. New Rice for Africa, which are inter specific hybrids between the African and Asian rice. In Ebonyi State, rice is rich in genetic diversity, with the varieties grown throughout the area and its economic importance related to agro-ecological adaptation, household food security, ceremonies, nutritional diversification, income generation and employment [4].

As world population growth and climate change are undeniable, demands for higher yield and better quality rice have become a critical issue [5]. Therefore, breeding new rice varieties with high adaptability to the environment and productivity is an unprecedented challenge [6]. With assistance from biotechnology, rice-breeding targets are not only improving crop productivity, but also upgrading quality characteristics through alterations in heredity [7]. Many tremendous efforts and rapid progresses in rice breeding programs have been carried out and received remarkable achievements [8]. As a result, new rice varieties have been developed and released with higher yield and quality. The amount of genetic diversity within species is essential for the survival of species and their adaptation to changing environments. Understanding the genotype × environment interaction has long been a key issue for plant breeders and geneticists. In crop performance, the observed phenotype is a function of genotype (G), environment (E) and genotype × environment interaction (GEI). GEI is said to occur when different cultivars or genotypes respond differently to diverse environments. Researchers agree that GEI is important only when it is significant and causes considerable changes in genotype ranks in different environments [9]. Thus, identifying varieties of Abakaliki rice cultivars with stable expression of some desirable traits across diverse environment that may likely be used in breeding programme is necessary.

MATERIALS AND METHODS

Collection of plant materials

A total of forty rice cultivars were collected from Ebonyi State rice farmers at their farm sites during harvest Season of 2016. The rice cultivars were randomly collected from the Local Government Areas in the three senatorial zones of the state namely; Ebonyi North senatorial zone (Abakaliki Area), Ebonyi Central senatorial zone (Ikwo Area) and Ebonyi South Senatorial zone (Afikpo Area). The different rice cultivars (which were all O.sativa types) were all planted on the field under similar cultural practices.

Field experimental layout

The nursery bed was prepared by clearing, tilling and leveling. The various rice cultivars were sprayed in each allocated positions and tagged for easy identification. Grasses were used to cover the rice seeds to avoid birds feeding on them till the germination time.

The rice field went through the same process of preparation as the nursery; clearing, tilling and leveling. After which ropes were used to demarcate the prepared land into different plots. The experimental layout was a complete radomised complete block design and the seedlings were randomly transplanted with tags in three replicates on each experimental plot measuring 1.0 x 1.0m after twenty one days in the nursery bed. A basal dose of N-P-K fertilizer (15:15:15) at the rate of 200 kg/ha was applied at 15 days after transplanting. Subsequently, urea was top-dressed at the rate of 100 kg/ha at 30 days before weeding. Weeding was carried out manually at 21 days after transplanting. Second weeding was also done during panicle initiation (42 days after transplanting).

Data collection for agronomic characters

Data collection was done after 60 days of transplanting. Number of Primary Tillers (NPT), Number of Secondary Tillers (NST), Plant Height (PH), Flag Leaf Length (FLL), Number of Primary Panicles (NPP), Number of Secondary Panicles (NSP), Panicle Length (PanL), Panicle Exsertion (PanEx), Grain Length (Grain L), Grain Width (Grain W), Panicle Thresh-ability (Pthresh), and 1000grain/weight (1000G/W) were all measured in four replicates using standard method of rice evaluation in four replicates. The rice grains were sun-dried to about 14 % moisture content and preserved for the analysis.

Statistical Analysis

All data were analyzed using Analysis of Variance (ANOVA) procedure of SPSS software version 2.0. Mean differences were declared statistically significant when $P < 0.05$. Interrelationships among traits were estimated using Pearson correlation method of SPSS and significance value were declared at $P < 0.05$ and $P < 0.01$.

Table 1. Rice Genetic Resources used in the Study

S/No	Local name/cultivar	Species	Location collected
1	Faro 44	O. sativa	Ohaukwu
2	306	O. sativa	Ezza North
3	Government	O. sativa	Ikwo
4	Miri-miri	O. sativa	Ikwo
5	Iron 2	O. sativa	Ezza North
6	Faro 14	O. sativa	Ikwo
7	Mars	O. sativa	Ikwo
8	306	O. sativa	Ikwo
9	Iron	O. sativa	Ezza south
10	Atom 2	O. sativa	Ohaukwu
11	CP	O. sativa	Ikwo
12	Mars	O. sativa	Ezza South
13	Offia	O. sativa	Ezza North
14	306	O. sativa	Ohaukwu
15	Akuje	O. sativa	Ezza North
16	Atom 1	O. sativa	Ezza North
17	Chinyere	O. sativa	Ikwo
18	306	O. sativa	Izzi
19	Mars/cp	O. sativa	Izzi
20	Atom 3	O. sativa	Ikwo
21	306	O. sativa	Ezzillo
22	Iron	O. sativa	Ezzillo
23	China	O. sativa	Ikwo
24	Faro 44	O. sativa	Izzi
25	Iron	O. sativa	Ikwo
26	Faro 15	O. sativa	Ohaukwu
27	Chinyere	O. sativa	Ezza North
28	Miri-miri	O. sativa	Ezza South
28	R8	O. sativa	Abakaliki
30	Nwadaugo	O. sativa	Ikwo
31	Adaigbo	O. sativa	Ikwo
32	Kpuru kpuru	O. sativa	Ikwo
33	Nwangbasianya	O. sativa	Abakaliki
34	Faro 55	O. sativa	Ohaukwu
35	Omejiaji	O. sativa	Ezza South
36	Faro 18	O. sativa	Ezzangbo

37	Kpuru kpuru	O. sativa	Ezza North
38	R8	O. sativa	Ikwo
39	Mass	O. sativa	Izzi
40	Ogologo mbada	O. sativa	Izzi

RESULTS

The results of the correlation analysis showed positively significant correlation amonge most of the variables. Positive and significant correlations were observed between pairs of traits such as number of secondary panicles and number of primary panicles (r = 0.198, p = 0.003), number of secondary panicles and flag leaf length (r = 0.199, p = 0.008), plant height and flag leaf length (r = 0.782, p = 0.00), length of grain and panicle length (r =342, p= 0.000), length of grain and number of secondary panicles (r = 0.280, p = 0.002), panicle exsertion and plant height (r = 0.245, p = 0.007); panicle exsertion and number of primary panicles (r = 0.265, p = 0.003), Generally negative and non-significant correlations were observed between most of the traits including the correlation between number of primary panicles and Flag Leaf Length (r = 0.074, p= 0.421), panicle exsertion and number of primary panicles (r-= 0.47, p = 0.612) and host of others (Table 1). The Abakaliki rice genotypes studied showed high variability amongst the characters measured. The minimum values for genotypes ranged from 0.0 to 1.0; while maximum values ranged from 1.2 to 196.0 (Table 2). The genotypic values ranged from 1.2 to 103190.7 while the variance ratio ranged from 0.8 to 85.6 (Table 2). The genotypic variance ranged from 0.4 to 33514.9 for grain width (GrainW) and plant height (PH) respectively, while phenotypic variance ranged from 0.6 to 51595.3 for grainW and plant height respectively (Table 2). Generally the phenotypic coefficient of variation (PCV) were all higher than the genotypic coefficient of variation (GCV) with values that ranged from 123 to 827.3 for PanL and Pthresh respectively while GCV ranged from 99.1 to 666.8 for grain length and panicle thresh-ability respectively (Table 3). The difference between PCV-GCV ranged from 23.7 to 160.5 for the same characters. Broad sense heritability (h2B) had values ranged from 55 to 67.0 for NPT and PanL respectively. Genetic variance (GA) ranged from 6.036 to 40.589 for 1000g/w and PH while GA as percent of mean ranged from 8.006 to 45.892 for 1000g/w and PH, respectively.

Table 3: Interrelatedness Amongst Traits

Attributes	Mean	Minimum value	Maximum value	Genotypic	Error	Variance ratio	VG	VP	VE
NPT	4.700	0.000	16.000	211.000	5.400	1.400	68.500	105.500	2.700
NST	2.100	0.000	8.000	80.100	2.100	1.000	26.000	40.100	1.000
PH	110.500	0.000	196.000	103190.700	2645.900	1.400	33514.900	######	######
FLL	37.000	0.000	81.100	13798.800	353.800	1.200	4481.700	6899.40	176.90
NPP	11.100	0.000	113.000	3737.700	95.800	0.900	1214.000	1868.90	47.900
NSP	27.200	0.000	47.000	3878.500	99.500	1.200	1259.700	1939.30	49.700
PanL	24.400	0.000	36.000	1805.800	46.300	1.000	586.500	902.900	23.200
PanEx	2.900	0.000	5.000	114.900	2.900	1.300	37.300	57.500	1.500
Grain L	0.900	0.000	1.200	1.700	0.000	0.800	0.600	0.900	0.000
Grain W	0.300	0.000	2.000	1.200	0.000	1.000	0.400	0.600	0.000
Pthresh	0.500	0.000	10.100	35.900	0.900	1.100	11.700	17.900	0.500
1000g/w	3.100	0.000	4.200	28.500	0.700	8.773**	9.300	14.200	0.400

Table 3: Interrelatedness amongst Traits

Attributes	PCV	GCV	PCV-GCV	h2B	GA	GAM
NPT	220.400	177.600	42.800	55.000	19.678	25.762
NST	301.400	242.900	58.500	65.000	16.584	18.761
PH	205.600	165.700	39.900	65.000	40.589	45.892
FLL	224.600	181.100	43.600	58.000	16.219	23.194
NPP	388.800	313.300	75.400	56.000	14.608	19.081
NSP	161.900	130.500	31.400	65.000	10.197	16.871
PanL	123.000	99.100	23.900	67.000	13.212	17.125
PanEx	262.300	211.400	50.900	65.000	11.728	14.981
Grain L	106.600	85.900	20.700	66.000	8.570	11.432
Grain W	271.300	218.700	52.700	66.000	9.862	12.652
Pthresh	827.300	666.800	160.500	65.000	7.046	10.327
(1000g/w	123.000	99.200	23.900	61.000	6.036	8.006

Table 3: Interrelatedness Amongst Traits

	NPT	NST	PH	FL	NPP	NSP	PanL	Panex	LG	WGrain	Pthresh	FlagL	SpikF	(1000g/w
NPT	1.00													
NST	0.06	1.00												
	0.52													
PH	0.01	0.07	1.00											
	0.89	0.44												
FL	0.04	0.12	.782**	1.00										
	0.69	0.20	0.00											
NPP	-0.07	0.03	-0.14	-0.13	1.00									
	0.42	0.72	0.14	0.16										
NSP	0.17	-0.04	0.06	.199*	.198*	1.00								
	0.07	0.66	0.55	0.03	0.03									
PanL	0.09	-0.05	0.08	0.08	0.14	.331**	1.00							
	0.34	0.56	0.37	0.39	0.14	0.00								
Panex	-0.05	0.13	.245**	.265**	0.05	.203*	.229*	1.00						
	0.61	0.17	0.01	0.00	0.58	0.03	0.01							
LG	-0.11	-0.07	-0.01	0.02	0.09	.280**	.342**	0.15	1.00					
	0.22	0.44	0.89	0.82	0.33	0.00	0.00	0.10						
WGrain	-0.11	0.07	0.02	-0.02	0.09	0.05	.228*	-0.03	.333**	1.00				
	0.22	0.45	0.87	0.80	0.34	0.59	0.01	0.74	0.00					
Pthresh	-0.16	0.03	0.07	0.03	-0.02	-0.15	0.09	0.10	0.13	0.15	1.00			
	0.08	0.76	0.42	0.77	0.85	0.11	0.36	0.26	0.17	0.10				
FlagLL	-0.02	.182*	.205*	0.13	-0.03	0.12	.200*	.229*	0.15	0.12	0.05	1.00		
	0.85	0.05	0.03	0.15	0.75	0.19	0.03	0.01	0.11	0.18	0.57			
(1000g/w	0.09	.195*	.217*	.198*	-0.04	0.11	0.12	-0.03	.187*	-0.01	-0.01	.238**	0.07	1.00
	0.34	0.03	0.02	0.03	0.69	0.24	0.20	0.78	0.04	0.94	0.89	0.01	0.42	

***. Correlation is significant at the 0.05 level (2-tailed).**

****. Correlation is significant at the 0.01 level (2-tailed).**

DISCUSSION

A critical estimate of nature and magnitude of phenotypic variability is a prerequisite for any crop improvement programme. The variability observed in any population could be due to the genetic and environment factors or probably an interaction between these factors. Hence, the high gentoptic varabilities amongst the characters measured suggested minimal effect of environment. The studies of [10] attributed the variation in a segregating population to heritable and non-heritable factors, while the variation within pure lines was attributed to environmental factors. The significant variation observed in agronomic traits evaluated among the 40 rice cultivars, were in agreement with [11]. The estimated variance ratios among the 40 genotypes indicats high significant differences among the genotypes with respect to all the characters studied. All the genotypes displayed considerable amount of differences in their mean performance and considerable low error variance point to greater genotypic influence on the characters. The coefficients of variations (PCV and GCV) which were calculated by considering the respective means indicated wider variability. High PCV to GCV recorded for almost all the characters and more significant in panicle thresh-ability, Grain weight, number of primary panicle, and number of secondary tillers were similar to the results of [12], [13], [14], [15], [16]. This observed higher phenotypic coefficient of variation (PCV) to genotypic co-efficient of variation (GCV) amongst all the studied characters implies less influence of environmental factors on the traits, thus ordinary filed selection may be more appropriated in its improvement. The moderate phenotypic co-efficient of variation and genotypic co-efficient of variation observed for characters like, 1000g/wight, panicle Length and number of secondary panicles indicates the existence of comparatively moderate variability for these traits, which could be exploited for improvement of these traits through selection in advanced generations. This result is in consonance with earlier reports wherein, moderate PCV and GCV for characters like plant height, grain weight and flag leaf length were reported by [17], [18], [19], [20]. Again, the moderate GCV and PCV for grain length were reported by [21], [22], [23], [24]. Overall, co-efficient of variations indicated high to moderate variability for most of the traits..

The heritability and genetic advance gives an idea about portion of observed variability attributable to genetic differences. The higher the broad sense heritability for a character, the higher the genotypic influence. While average or low broad sense heritability indicates phenotypic influence or both. The difference between PCV and GCV estimates indicates the relative variability of the characters, which in turn decides the extent of their heritability. If the PVC value is significantly higher than the GCV value for a character, then the influence of environment is less or nil coupled with high heritability. According to [25], heritability estimates along with genetic advance would be more useful than the former alone in predicting the effectiveness of selecting the best individual. Therefore, it is essential to consider the predicted genetic advance along with heritability estimate as a tool in selection programme for better efficiency. In the current study, all the characters recorded high broad sense heritability with varying genetic advance, indicating greater genotypic influence to phenotypic influence. High heritability coupled with high genetic advance as percent of mean were recorded for plant height, flag leaf length and number of primary panicles. This indicates low environmental influence on the expression of these characters and hence one can practice selection. [26], [27]; [28], [29], [30], earlier reported high heritability and genetic advance as percent of mean for plant height and panicle numbers. High heritability coupled with moderate genetic advance was observed for panicle length, panicle thresh-ability, number of tillers and panicle exsertion while high heritability coupled with low genetic advance was recorded for grain length, grain width and 1000g/w. The studies of [31]; [32] reported same for grain length/width and 1000g/w. In overall, the present study revealed high heritability coupled with high to moderate genetic advance as percent of mean for most of the characters indicating the presence of considerable genetic variation and additive gene effects. Hence, improvement of these characters could be effective through phenotypic selection

The correlation analysis helps in examining the possibility of improving yield through indirect selection of its component traits, when charaters are highly correlated. Hence, the highly significant and positive correlation observed between plant heights in this study, suggests that improving one of these characters will have resultant effect on the other, thereby reducing the timing and resources needed to improve one trait at a time. Reports of [33], [34], [35] are in conformity with the above results. Non-significant correlation observed between panicle length and panicle exsertion, panicle length and grain length, panicle length and grain width, panicle length and 1000g/w, number of tillers/plant and 1000g/w suggests little or no relationship. Hence, breeder may likely spend much time and resources by improving each of the traits separately. The former was in conformity with the reports of [36], [37], [38], while the later corresponds with the findings of [12]. There was also non-significant and negative correlation observed between traits in the study, which explicitly implies unrelatedness.

CONCLUSION

Significant variation existed considerably in all the characters of the different rice genotypes studied. The study equally showed that low influence of environment on the genotypes considering the values of PCV and GCV in our study.

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