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Genetic analysis for grain yield and yield contributing traits in rice (*Oryza sativa* L.) Genotypes

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Abstract

The experiment was conducted during *Kharif-2014* with 30 rice genotypes in Randomized Block Design having three replications at the field experimentation center of Department of Genetics and Plant Breeding, SHIATS, Allahabad, Uttar Pradesh. Pooled data of 13 quantitative and 9 qualitative characters to study genetic variability and its components. Analysis of variance among 30 genotypes showed highly significant differences for all the characters indicated the presence of substantial amount of genetic variability. On the basis of mean performance highest grain yield per hill was exhibited by the genotype HKR 08-62 followed by UPR 3425-11-1-1. Highest genotypic coefficient of variance (GCV) phenotypic coefficient variance (PCV) was observed for grain yield per hill followed by harvest index indicating that these characters could be used as selection for crop improvement. High estimates of heritability coupled with high genetic advance were observed for spikelets per panicle and biological yield per hill.

Keywords: Rice, genetic variability, GCV, PCV, heritability and genetic advance

Introduction

Rice (*Oryza sativa* L.), a member of poaceae family is one of the world's most important food crops, feeding more than half of the world's population. It is the most diversified crop due to its adoption to wide range of geographical and climatic regims. Globally, rice is cultivated now on 163.1 million hectares with annual production of around, 744.4 million tones and average productivity of 6.5 tons/ha (Food and Agriculture Organization, 2014). Rice plays a pivotal role in Indian economy being the staple food for two third of the population. In India during 2014-15 the production of rice was 106.54 Million tons from 43.95 million ha (Department of Economic and Statistics, Department of Agriculture and Cooperation, 2014-2015).

Genetic variability for quantitative traits is the key component of breeding programme for broadening the gene pool of rice and other crops. High magnitude of variability in a population provides the opportunity for selection to evolve a variety having desirable characters.

The genetic coefficient of variation together with heritability estimate would give the best picture of the amount of advance to be expected from the selection. The amount of genetic advance under selection mainly depends on the amount of genetic variability (Jayasudha S. and Sharma, 2010) [10].

Materials and methods

The experimental material consisted of 30 rice genotypes and present investigation was carried out at the field experimentation center, Department of Genetics and Plant Breeding, Allahabad school of Agriculture, Sam Higginbottom Institute of Agriculture Technology and Sciences, (deemed-to-be-university), Allahabad (U.P.) during *kharif* 2014-15. Genotypes were tested in a randomized block design with three replications each in transplanted condition. Distance between plant to plant and row to row were 20 cm and 15 cm respectively. Standard agronomic practices were followed throughout the crop growth period to obtain good harvest. Observations were recorded on five randomly selected plants from each progeny row for 13 biometrical characters viz, days to 50% flowering, plant height, flag leaf length, flag leaf width, tillers per hill, panicles per hill, panicle length, spikelets per panicle, days to maturity, biological yield, harvest index, test weight and grain yield per hill. The Analysis of variance was estimated as per procedure suggested by Panse and Sukhatme (1961) [13], coefficient of variation (GCV and PCV), Heritability for the grain yield and yield components in rice were

worked out in broad sense by adopting formula suggested by Burton and De Vane (1953) [4].

Results and discussion

The success of any breeding programme depends upon the genetic variability present in the base population and relationship of various characters towards yield. The analysis of variation revealed highly significant differences among the genotypes for all the traits studied indicating the presence of considerable genetic variation among the study materials (Table 1). High genetic variability for different quantitative traits in rice was also reported earlier by Singh *et al.* (2005) [17], Khan *et al.* (2009) [11], Akinwale *et al.* (2010), Jayasudha and Sharma (2010) [10], Babu *et al.* (2011) [3] and Kumar *et al.* (2015) [12].

Highest significant variation was observed in number of spikelet's per panicle followed by biological yield per hill and harvest index. For the trait days to 50% flowering was ranged from 92-112.67 days with mean performance of 99.82. CR 2706 9IR 84895-B-CRA-171-32-1-2-1 (92.00) found as the earliest flowering genotype which is also found superior over the check NDR 359 (96.00) which is in support of Vivek *et al.* (2005). Plant height was ranged from 67.81-112.06 cm with mean value of 88.56 cm among the 30 genotypes the R 1528-1058-1-110-1 (67.81) found as the dwarf genotype. Flag leaf

length is measured between 19.58-39.23 with mean value of 26.99 cm similarly, flag leaf width was observed between 1.20-1.65 and mean was 1.40 cm. Number of tillers per hill is found highest in the genotype TM 07275 (18.20) while the trait is ranged from 8.26-18.20 with the mean performance of 13.23 also supported by Chaudhary and Motiramant (2003) [5]. Number of panicles per hill was ranged between 7.00-16.33 with the mean value of 11.51 among the genotypes TM 07275 (16.33) recorded as the superior variety. Panicle length was varied from 16.04- 27.31 with mean value of 22.13 cm. LALAT (RC) 27.31 cm is found as the best genotype for the panicle length among the 30 genotypes under study. Check variety NDR-359 (256.12) recorded as the superior among the 30 different genotypes for number of spikelet's per plant, for the trait genotypes were ranged from 145.56-256.12 with mean performance of 202.16. Days to maturity was ranged between 122.29-145.14 with mean value of 130.41, genotype CR 2706 9IR 84895-B-CRA-171-32-1-2-1 (122.84) took least days for maturity, which is also found as the early flowering genotype. Biological yield per hill was ranged from 37.55 to 110.41 g with mean value of 70.17 g. Among the 30 studied genotype NDR- 359 (110.41) followed by KAGR 426 (95.38) and IR 78091-6-2-3-1-1 (91.44) exhibited superiority for this trait.

Table 1: Analysis of Variance for thirteen traits of rice genotypes

S. No.	Character	Mean	Range	Mean Sum of Square			Cv
				Treatment (df= 29)	Replication (df= 2)	Error (\pm) (df= 58)	
1.	Days to 50% flowering	99.82	92.00-112.67	93.35	13.61	4.97	2.23
2.	Plant height (cm)	88.56	67.81-122.06	366.76	0.70	5.11	2.55
3.	Flag leaf length (cm)	26.99	19.58-39.23	53.11	1.90	1.93	5.15
4.	Flag leaf width (cm)	1.40	1.20-1.65	0.03	0.002	0.002	3.51
5.	No. of tillers/ hill	13.23	8.26-18.20	14.70	0.87	0.90	5.89
6.	No. of Panicles/ hill	11.51	7.00-16.33	12.90	0.63	0.84	7.17
7.	Panicle length (cm)	22.13	16.04-27.31	20.29	1.31	1.70	7.98
8.	No. of spikelets/ panicle	202.16	145.56-256.12	1325.93	36.05	8.90	1.47
9.	Days to maturity	130.41	122.29-145.17	99.09	0.20	1.38	0.90
10.	Biological yield/ hill (g)	70.17	37.55-110.41	910.70	3.57	3.97	2.83
11.	Harvest index (%)	57.42	30.05-83.15	669.19	13.52	3.95	3.46
12.	Test weight (g)	24.15	22.59-25.87	1.97	0.39	0.48	2.87
13.	Grain yield/ hill (g)	40.81	16.59-63.13	389.07	1.42	5.15	5.56

Harvest index for studied genotypes were ranged from 30.05% to 83.15%, while its mean was 57.42%. CN 1446-5-8-17-1-MLD-4 (83.15) recorded as the superior genotype for harvest index. Test weight's mean was 24.15 g and it ranged between 22.59-25.87 g. UPR 3425-11-1-1 (25.87) found superior over the rest 29 genotypes for test weight. Grain yield is the most important trait in all the breeding programme, for this study it was varied between 16.59-63.13 g with mean value of 40.81 g. HKR 08-62 (63.13) followed by UPR 3425-11-1-1 (56.26) and NDR 370133 (55.94) recorded as superior genotypes.

Coefficient of variation truly measure of variance among the

different traits (Table 2). The estimates of phenotypic coefficient of variation (PCV) were slightly higher than those of genotypic coefficient of variation (GCV) for all the traits studied. In this study slight differences indicated minimum environmental influence and consequently greater role of factors on the expression of the traits. Genotypic coefficient of variation and phenotypic coefficient of variation was highest for grain yield per plant (27.71; 28.27) followed by harvest index (25.93; 26.16) and biological yield per hill (24.77; 24.93). Similar results were obtained by Akinwale *et al.* (2011) [2], Dhurai *et al.* (2014) [7], Sandhya *et al.* (2014) [16] & Kumar *et al.* (2015) [12].

Table 2: Estimates of components of variance and genetic parameters for 13 characters in rice germplasm

Characters	V _g	V _p	Coefficient of variation		h ² (bs) (%)	GA	GA (% of mean)
			PCV (%)	GCV (%)			
Days to 50% flowering	29.45	34.43	5.87	5.43	85.50	10.34	10.35
Plant height	120.54	125.66	12.65	12.39	95.90	22.15	25.01
Flag leaf length	17.06	18.99	16.14	15.30	89.80	8.06	29.87
Flag leaf width	0.01	0.01	8.61	7.86	83.30	0.20	14.79
Tillers/ hill	4.60	5.50	17.72	16.20	83.60	4.04	30.53
Panicles/ hill	4.02	4.86	19.14	17.40	82.60	3.75	32.59

Panicle length	6.19	7.89	12.69	11.24	78.40	4.54	20.51
Spikelets/ panicle	439.01	447.91	10.46	10.36	98.00	42.73	21.13
Days to maturity	32.57	33.95	4.46	4.37	95.90	11.51	8.82
Biological yield/ hill	302.24	306.21	24.93	24.77	98.70	35.58	50.69
Harvest index	221.74	225.70	26.16	25.93	98.20	30.40	52.95
Test weight	0.49	0.98	4.09	2.91	50.70	1.03	4.28
Grain yield/ hill	127.97	133.13	28.27	27.71	96.10	22.84	55.98

V_g = Genotypic variance, V_p = Phenotypic variance, GCV=Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, h^2 (bs)= Heritability broad sense, GA= Genetic advance.

Heritability plays an important role in deciding the suitability and strategy for selection of a character. In this study high heritability was observed for traits viz. biological yield per hill (98.70) followed by harvest index (98.20) and spikelet's per panicle (98.00). All the traits except for test weight (50.70) showed high heritability. It suggests high component of heritable portion of variation that can be exploited by breeders in the selection of superior genotypes on the basis of phenotypic performance. Similar results were reported by Dhurai *et al.* (2014)^[7] Ramanjaneyulu *et al.* (2014)^[15].

The characters exhibiting high heritability may not necessarily give high genetic advance. Johnson *et al.* (1955)^[9] reported that high heritability should be accompanied by high genetic advance to arrive at more reliable conclusion. The breeder should be cautious in making selection based on heritability as it includes both additive genes actions.

High heritability coupled with high genetic advance was also found in spikelet's per panicle (98.00; 42.73) followed by biological yield per hill (98.70; 35.58) and harvest index (98.20; 30.40). These characters shows additive gene action indicates ample scope of selection. Similar result reported earlier in rice by Prasad *et al.* (2005). High heritability coupled with moderate genetic advance was found in days to maturity (95.90; 11.51) and days to 50% flowering (85.50; 10.34). While high heritability coupled with low genetic advance is observed in flag leaf length (89.80; 8.06) and panicle length (78.40; 4.54). Moderate heritability coupled with low genetic advance is recorded in test weight (50.70; 1.03). Heritability with genetic advance as % of mean was found high on grain yield per hill (96.10; 55.98) followed by harvest index (98.20; 52.95) and biological yield per hill (98.70; 50.69). Similar results were also reported by Sandhya *et al.* (2014)^[16] and Kumar *et al.* (2015)^[12].

Authors contribution: Conceptualization of research work and designing of experiments (TNA, BGS, GRL); Execution of field/lab experiments and data collection (TNA, TDN, Abhinav, KA); Analysis of data and interpretation (TNA, BGS); Preparation of manuscript (TNA, BGS, GRL).

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