Biological Forum – An International Journal 14(2): 1338-1343(2022)

ISSN No. (Print): 0975-1130
ISSN No. (Online): 2249-3239

Variability Analysis for Yield and Yield Attributing Traits in Direct Sown Upland Rice

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(Received 04 May 2022, Accepted 09 June, 2022)
(Published by Research Trend, Website: www.researchtrend.net)

ABSTRACT: A study was conducted to measure the genetic variability, heritability, and association between yield and yield component traits of upland rice. In Kharif season, 38 different upland genotypes were tested in the field. An experiment in rainfed conditions was designed with complete block randomization and three replications. In order to investigate the effect of years on the traits studied, 14 yield related traits across 38 genotypes of rice were examined by analysis of variance (ANOVA). Most of the traits showed significant differences between years, except for number of effective tillers, kernel length-breadth ratio, and kernel length and kernel breadth. In most traits, the year x variety interaction was significant except for the kernel length-breadth ratio and kernel length. In kharif among all the genotype, HUR-3022 followed by PHY-220, PHY-223 and PHY-227 showed highest per se performance for most of the yield attributing traits. HUR-3022, PHR- 220 and PHY- 219 are the genotypes which showed highest per se performance for most the traits studied. During kharif, phenotypic co-efficient of variation ranged from 5.915 (D50F) to 28.527 (GW/Pt) and in next year it ranged from 6.948 (D50F) to 37.244 (GW/Pt). In first year broad sense heritability estimate was highest for days to panicle initiation (95.60%), days to 50% flowering (93.8%) and plants height (91.6%), whereas, lowest heritability estimate was recorded for number of effective tillers (39.9) followed by number of tiller (46.1%), kernel breadth (48.5%) kernel length (54.6%) and kernel length - breadth ratio (57.9%). The number of days to panicle initiation was positively correlated with number of days to first flowering and days to 50% flowering in both seasons. Based on this study, total number of tillers, number of effective tillers, grain per panicle, and seed index generally correlated positively and significantly with grain weight per plant.

Keywords: Rice, genetic variability, heritability and yield.

INTRODUCTION

In terms of annual production, rice (*Oryza sativa* L.) is the second most important staple crop worldwide, only behind wheat. Rice is a member of the genus *Oryza* of the family Poaceae. Twenty-two wild species as well as two cultivated species are found in the genus Oryza, namely *Oryza sativa* and *Oryza glaberrima*. There are 24 chromosomes in the AA genome of *Oryza sativa, which is a diploid species.* In India, rice crops account for approximately 22 percent of the total cropped area under cereals, and about 31 percent of the total area under food grains (Singhal, 2003). Rice production in Asia is more than any other cereal, and Asia is considered the "Rice Bowl" of the world (Lu and Chang 1980). The area under rice cultivation in India is 42.56 million hectares (ha), which is equivalent to 95.33 million tonnes of rice produced at a productivity of 2240 kilograms per hectare. Rice is cultivated throughout India. Breeding programs' primary objective is to develop rice cultivars with the maximum yield potential (Jing and Jianchang 2011). It is crucial to determine how different traits contribute to yield. The knowledge of genetic variability of yield contributing characters, their inter relationships, and how those relationships influence yield is essential for an effective breeding program. Heritability has been used in selection as it indicates how transmissible a trait is in future generations (Sabesan *et al.*, 2009). Breeding programs that aim to develop high yielding cultivars must consider genetic variation for traits under selection and high heritability and genetic advancement (Ulloa, 2006). Genetic progress is not reflected by estimating heritability alone (Chaghakaboodi *et al.*, 2012). In addition, genetic advance is of considerable significance since it indicates the degree of improvement expected from one selection (Hamdi *et al.*, 2003). An integrated function of many component traits, grain yield is a complex characteristic. As a result, selecting for yield may not be as satisfactory as considering other traits that contribute to yield (Akinwale *et al*., 2011). There has been very little work done on rice grown on upland areas, which led to this study being undertaken to examine the variability of the genetic makeup of upland rice and the traits that affect yield. Therefore, the objective of this study was to estimate genetic variability, heritability, and genetic advance and to determine the correlations among yield characteristics and yield attributing characteristics through use of phenotypic correlation coefficients. The results of this study could serve as a basis for developing desirable rice genotypes for upland environments in future breeding programs.

MATERIALS AND METHODS

Thirty-eight diverse genotypes *viz*. PHY-201, PHY-202, PHY-203, PHY-204, PHY-205, PHY-206, PHY-207, PHY-208, PHY-209, PHY-210, PHY-211, PHY-212, PHY-213, PHY-214, PHY-215, PHY-216, PHY-217, PHY-218, PHY-219, PHY-220, PHY-221, PHY-222, PHY-223, PHY-224, PHY-225, PHY-226, PHY-227, PHY-228, HUR-3022, PHY-230, PHY-231, PHY-232, PHY-233, PHY-234, PHY-235, PHY-236, PHY-237, PHY-238, PHY-239, PHY-240 were collected from All India Coordinated Research Project on Rice and were used as experimental materials. At the Agricultural Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, the experiment was conducted in randomized block design (RBD) with three replications. Varanasi is located at 25.18° N latitude and 83.03° East longitude, at an altitude of 123.3 meters above mean sea level. During the experiment, the soil was classified as an Indo-Gangetic plain type soil and was characterized as fertile, alluvial loam. A total of 1100 mm of rain falls annually at this place, 88 percent of which is received between July and September. Twenty one days old seedlings were transplanted into small plots 20 cm apart between rows and 15 cm apart within rows. A healthy crop was raised by following standard cultural practices. Per hectare, 120 kg of N, 80 kg of P_2O_5, and 80 kg of K_2O were applied as fertilizers. IRRI standard evaluation system was followed for the collection of morphological data at appropriate growth stages. Other intercultural operations were carried out whenever required.

Data Collection: Observations were recorded on ten randomly selected plants from each entry and replication on days to 50% flowering (D50F), days to maturity, plant height (cm), days to panicle initiation (DPI), Days to first flowering (DFF), panicle length (cm) (PL), total number of tillers (TNT), number of effective tillers plant^{-1} (NET), number of filled grains panicle^{-1} (Gr/P), Seed index (SI), Kernel length (KL), Kernel breadth (KB), Kernel L:B ratio, Grain weight per plant (GW/Pt).

Statistical Analysis: Based on randomly selected plants from all three replications, the experimental data were calculated by their mean value. According to the procedures outlined by Johnson *et al*. (1955); Burton, (1952); Allard (1975), the genotypic and phenotypic coefficients of variation were determined statistically. Based on Johanson *et al.* (1955); Hanson (1961), heritability and genetic advance were estimated. Correlation coefficient was calculated according to Al-Jibour *et al.* (1958).

RESULTS AND DISCUSSION

According to the analysis of variance, there were significant differences between genotypes for all the thirty eight genotypes of characters investigated. As a result, there are many potential genotypes from the current germplasm set that can be selected for yield improvement.

Table 1: Analysis of variance (ANOVA).

Source of variation	d.f	DPI	DFF	D50F	CHc	PH	TNT	NET
Replication	2	1.289	1.684	1.684	26.153	501.521.**	1.289	0.947
Year	1	827.477**	2122.526**	2122.526**	128043.800**	2857.979**	5.457**	0.825
Variety	37	63.889**	75.548**	76.615**	2188.308**	894.537**	4.387**	3.194**
Year x Variety	37	7.853**	13.972**	14.499**	1250.&62**	70.625**	3.510**	3.556**
Error	75	2.209	2.231	2.378	153.638	33.172	0.517	0.583
Total	151	24.145	37.111	37.575	1767.142	275.221	2.237	1.955

Source of variation	d.f	PL	Gr/P	L:B	SI	KL	KB	GW/Pt
Replication	2	3.390	288.476	0.039	0.038	0.139	0.001	0.925
Year	1	108.295**	11169.800	0.217	0.824**	0.221	0.013	409.738**
Variety	37	7.449**	1456.737	0.393**	0.323**	0.619**	0.114	51.968**
Year x Variety	37	2.298**	740.296	0.102	0.091**	0.213	0.025	43.403**
Error	75	1.003	115.852	0.055	0.027	0.136	0.014	5.024
Total	151	3.626	671.771	0.150	0.121	0.274	0.041	28.585

*p ≤0.5, ** p≤0.1

Per se performance: PHY-223 and PHY-227 were the genotypes that achieved the greatest mean grain yield per plant of all genotypes analyzed. These genotypes may be utilized in a hybridization programme to achieve higher grain yield. It is possible to develop an early maturity or short duration rice genotype using PHY-227 as a donor parent in breeding programs by using this as an early-flowering and mature genotype. The PHY-227 genotype showed the greatest mean performance for panicle length, followed by the PHY-226 genotype. The shortest and the tallest were PHY-228 and PHY-225, respectively. Grain yields per panicle were highest for genotype 238. Results similar to these are reported by Bekele *et al.* (2013).

Genetic Variability: All the traits studied in this study had a PCV that was higher than their respective GCVs (Table 2). The PCV and GCV values differ very little for almost all the traits considered, indicating that environment is less of a factor affecting expression. Estimates of genetic parameters suggest that phenotypic differences may be taken into account as genotypic differences when selecting genotypes. The results were similar to those seen by Lingaiah *et al*. (2015); Mishu *et al.* (2016). PCV and GCV were highest for grain weight per plant, confirming that additive gene action is involved in determining these traits. Lal and Chauhan (2011); Singh *et al.* (2011); Singh *et al*. (2013) and Lingaiah (2015) also reported similar findings. A low PCV and GCV estimate showed that selection for traits such as the days to 50% flowering, the days to first flowering, the days to panicle initiation and kernel length and kernel breadth would be ineffective. It can be used to compare variability and sometimes provide clues on the validity of a trait for selection.

For grain weight per plant, the PCV ranged from 5.915 % days to 50% panicle initiation, whereas for panicle length, the GCV ranged from 5.452 % to 24.252 %. The PCV and GCV values over 20% are considered high according to Sivasubramanian and Menon (1973), while values less than 10% are considered to be low and values between 10 and 20% are considered moderate. According to the delineated values, PCVs were high for panicles per plant, grain weight per plant, medium for chlorophyll, plant height, total number of tillers, effective number of tillers, kernel length to breadth ratio, and low for days to first panicle, days to first flowering, days to 50% flowering, panicle length, kernel length, kernel breadth. The highest genotype and phenotypic co-efficient of variation was obtained for grain weight per plant, followed by grain per panicle, number of effective tillers, and chlorophyll content. The lowest genotype and phenotypic co-efficient of variation was obtained for grains per panicle, and the highest were obtained for the number of effective tillers in both years. The highest number of grains per panicle as well as the highest number of tillers per plant was reported by Singh *et al.* (2006); Akhtar *el al.* (2011). According to Adhikari *et al.* (2018), grain yield per plant, number of panicles per plant, and number of fillers per plant were all associated with high genotypic and phenotypic coefficients of variation.

The variance analysis found that all characters had significant differences between genotypes. Most of the traits under study displayed a wide range of variability. Estimates of phenotypic (δ^2p) and genotypic variances (δ^2g), phenotypic coefficient variance (PCV) and genotypic coefficient of variance (GCV), heritability (%), and genetic advance (GA) are shown in Table 2. With chlorophyll contents of 1044.61 and 258,772, respectively, there was a high degree of phenotypic and genotypic variance. High phenotypic and genotypic variances were equally observed for grains per panicle (693.356 and 103.223), plant height (271.062 and 112.492), grain weight per plant (24.796 and 17.455), days to first flowering 19.925 and 66.302), days to first panicle initiation (17.871 and 58.197), days to 50% flowering (17.787 and 71.302), panicle length (2.930 and 24.815), total number of tillers (0.828 and 8,502), seed index (0.127 and 2.610), kernel length (0.285 and 6.489) kernel breadth (0.038 and 2.093), kernel length-breadth ratio (0.130 and 3.122) grain weight per plant (37.244 and 24.252), respectively. Across all characters, phenotypic variance was higher than genotypic variance.

Correlation: In order for grain yield to be expressed, a variety of factors need to be taken into account. Grain yield is controlled by minor genes. Selection for yield in and of itself isn't always effective. The inclusion of yield-attributing traits which show positive and significant associations with grain yield is therefore highly desirable for improving grain yield. An analysis of correlations revealed a significant positive correlation between days to panicle initiation and days to 50% blooming over both years. The days from panicle initiation to plant height correlated negatively and significantly. On the other hand, plant height did not show a significant correlation with days to first flower. Chrorophyll content and seed index correlated positively with days to first flowering. Kernel length and seed index showed a strong positive relationship over time. As well, kernel length and kernel length-breadth ratios were positively correlated over years, whereas kernel breadth was negatively correlated with kernel length-breadth ratio. Similarly, Satyanarayana *et al.* (2005); Ramakrishnan *et al*. (2006) reported similar findings. Thus, it is necessary to understand the nature of the relationship between yield and its components during crop improvement programmes so that the character of the crop can be simultaneously enhanced.

Table 2.

Traits	**Year**	**Mean ±S.E.**	**Range**	**Phenotypic**	**PCV**	**GCV**	**H^2 (broad sense)**	**GA (K=2.06)**	**GA (percent of mean)**
DPI	Y 1	58.197± 0.625	50.5-69.0	17.871	7.264	7.103	95.6	8.328	14.309
	Y2	62.855 ±							
DFF	Y 1	66.302±0.734	56.0-75.0	19.925	6.732	6.548	94.6	8.698	13.118
	Y2	73.776±1.262	64.5-85.5	26.968	7.039	6.610	88.2	9.434	12.787
D50F	Y 1	71.302±0.741	60.5-79.5	17.787	5.915	5.729	93.8	8.151	11.431
	Y2	78.776±1.279	68.5-89.0	29.958	6.948	6.557	89.1	10.043	12.748
CHC	Y 1	258.772±8.735	200.5-329.2	1044.641	12.490	11.542	85.4	56.855	21.971
	Y2	200.724 ±7.988	146.9-268.2	815.018	14.223	13.062	84.3	49.600	24.710
PH	Y 1	112.492 ± 3.369	78.3-138.6	271.062	14.636	14.009	91.6	31.075	27.624
	Y2	103.819 ± 4.416	69.5- 141.5	142.376	14.996	13.736	83.9	26.909	25.919

TNT	Y 1 Y2	8.502 ± 0.472 8.881± 0.547	7.3-10.6 6.0-14.0	0.828 3.643	10.704 21.491	7.269 19.644	46.1 83.6	0.865 3.285	10.168 36.990
NET	Y 1 Y2	6.931 ±0.512 7.078 ± 0.571	5.5-9.0 4.5-11.5	0.873 3.090	13.483 24.833	8.514 22.054	39.9 78.9	0.768 2.856	11.076 40.348
PL	Y 1 Y2	24.815 ±0.741 23.127 ± 0.676	21.9-28-6 19.8-26.3	2.930 2.950	6.898 7.427	5.452 6.169	62.5 69.0	2.203 2.441	8.876 10.556
GR/P	Y 1 Y2	103.223 ± 7.998 86.079±6.343	61.0-178.5 43.5-133.0	693.356 509.373	25.509 26.219	23.036 24.059	81.5 84.2	44.234 39.146	42.853 45.477
SI	Y 1 Y2	2.610 ± 0.0835 2.463 ± 0.132	1.6-3.1 1.5-3.0	0.127 0.104	13.666 13.111	12.895 10.700	89.0 66.6	0.654 0.443	25.065 17.990
KL	Y 1 Y2	6.489 ± 0.254 6.565 ± 0.269	5.5-7.0 5.7-7.4	0.285 0.268	8.227 7.886	6.077 5.338	54.6 46.0	0.600 0.490	9.249 7.471
KB	Y 1 Y2	2.093 ± 0.098 2.075 ± 0.067	2.0-2.5 1.6-2.8	0.038 0.046	9.252 10.329	6.446 9.266	48.5 80.5	0.194 0.355	9.251 17.125
LB	Y 1 Y2	3.122 ± 0.165 3.198 ± 0.168	2.4-3.5 2.0-3.8	0.130 0.173	11.535 13.024	8.781 10.669	57.9 67.1	0.430 0.576	13.769 18.003
GW/PT	Y 1 Y2	17.455 ± 1.854 14.171 ± 1.236	10.3-27.5 5.4-25.4	24.796 27.859	28.527 37.244	24.252 35.141	72.3 89.0	7.414 9.680	42.471 68.302

PCV= Phenotypic coefficient of variation; GCV= Genotypic coefficient of variation; h^2= Heritability in broad sense; GA= Genetic advance (at 5% selection intensity *i.e.*, k= 2.06), DPI- days to panicle initiation; DFF= days to first flowering ; Chc- Chlorophyll content; TNT= total number of tillers; NET= number of effective tillers; PL= panicle length; Gr/P= grain per panicle; SL= seed index; KL= kernel length; KB= Kernel breadth; L:B= kernel-breadth ratio; GW/Pt- grain weight per plant

Table 3.

Traits	Year	DFF	D50F	Cho	PH	TNT	NET	PL	Gr/P	SI	KL	KB	L:B	GW/Pt
DPI	Y1	0.888**	0.865**	0.126	-0.302*	0.095	-0.038	-0.035	0.192	-0.157	-0.038	-0.193	0.111	0.093
	Y2	0.868**	0.794**	0.188	-0.240	-0.135	-0.119	-0.176	0.063	-0.262	0.121	-0.080	0.137	-0.119
DFF	Y1		0.949**	0.156	-0.269	0.156	0.028	-0.033	0.166	-0.063	0.062	-0.061	0.088	0.155
	Y2		0.950**	0.345*	-0.276*	-0.062	-0.018	-0.198	0.031	-0.316*	0.003	-0.175	0.143	-0.100
D50F	Y1			0.153	-0.273*	0.199	0.093	-0.008	0.217	-0.078	0.050	-0.079	0.088	0.221
	Y2			0.390**	-0.301	-0.037	0.015	-0.183	0.004	-0.344*	-0.023	-0.246	0.188	-0.111
Chc	Y1				-0.462**	0.018	0.003	-0.233	0.083	-0.007	-0.004	-0.089	0.071	0.134
	Y2				-0.124	0.358*	0.361*	-0.045	0.182	-0.127	-0.043	-0.147	0.094	0.311*
PH	Y1					-0,045	-0.019	0.426**	0.192	-0.054	-0.045	0.039	-0.070	0.100
	Y2					0.084	0.087	0.669**	0.110	0.154	0.021	0.157	-0.145	0.164
TNT	Y1						0.804**	0.052	0.114	0.031	-0.050	-0.020	-0.038	0.497**
	Y2						0.903**	0.258	-0.072	0.179	0.094	0.061	0.055	0.614**
NET	Y1							0.024	0.018	0.161	-0.115	0.032	-0.122	0.555**
	Y2							0.255	-0.032	0.101	0.151	0.011	0.099	0.676**
PL	Y1								0.163	-0.002	0.263	-0.150	0.287*	0.122
	Y2								0.026	0.242	0.017	-0.009	0.009	0.251
Gr/P	Y1									-0.337*	-0.242	-0.205	-0.039	0.649
	Y2									0.080	-0.244	0.322*	-0.399**	0.623**
SI	Y1										0.320	0.118	0.144	0.297*
	Y2										0.313*	0.160	0.021	0.425**
KL	Y1											0.016	0.710**	-0.115
	Y2											-0.175	0.707**	0.047
KB	Y1												-0.691**	-0.080
	Y2												-0.802**	0.258
L:B	Y1													-0.039
	Y2													-0.177

Y1= Kharif-2012 Y2= kharif-2013, DFF-days to first flowering, D50F- days to 50% flowering, Chc- Chlorophyll content; TNT= total number of tillers; NET= number of effective tillers; PL= panicle length; Gr/P= grain per panicle; SL= seed index; KL= kernel length; KB= Kernel breadth; L:B= kernel-breadth ratio; GW/Pt- grain weight per plant

Heritability. Heritability estimates were high for days to panicle initiation (95.6%), days to flowering at 50% (94.6%), and plant height (91.6%). On the other hand, the lowest heritability estimate was recorded for number of effective tillers (39.9), total number of tillers (46.1%), kernel breadth (48.5%), kernel length (54.6%), and kernel length-breadth ratio (57.9%). Similar studies have also been published by Singh *et al.* (2007), Fiyaz *et al.* (2011), Singh *et al.* (2013), and Islam *et al.* (2016). These results indicate that these traits can be effectively selected compared to others. Gene action can occur both additively and non-additivley, based on heritability estimates. High heritability is not necessarily indicative of high genetic gain. It is more efficient to use both heritability and genetic advance as selection parameters rather than the heritability alone, since both indicate that the heritability is most likely the result of additive gene effects.

CONCLUSION

According to the study, the traits like total number of tillers, grain weight per plant, grain weight/panicle exhibited the highest PCV, GCV, heritability, and genetic advance values. The selection of these traits is highly recommended for rice improvement. HUR-3022 recorded highest mean performance for grain yield per plant followed by PHY-223 and PHY-227.

Acknowledgements. The authors are thankful to the Plant Breeding and Genetics, Institute of Institute of Agricultural Science. Banaras Hindu University, Varanasi, Dept. of GPB is also acknowledged.
Conflict of Interest. None.

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How to cite this article: Sangita Kumari, Satish Kumar, Aditya Pratap Singh and R.P. Singh (2022). Variability Analysis for Yield and Yield Attributing Traits in Direct Sown Upland Rice. *Biological Forum – An International Journal*, *14*(2): 1338-1343.