

GENETIC VARIABILITY, CHARACTER ASSOCIATION AND PATH ANALYSIS OF RICE GENOTYPES

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ABSTRACT

The twenty-five rice germplasm accessions were evaluated to assess their genetic variability, heritability, genetic advance, character association and path coefficient analysis for grain yield and yield traits. The high estimate of genotypic and phenotypic coefficient of variation, heritability and genetic advance were observed for effective tillers per plant, filled grains per panicle, total grains per panicle and grain yield per plant. High heritability accompanied with high genetic advance were observed for days to maturity, plant height, filled grain per plant, test weight positive and significant correlation were observed between grain yield per plant with days to 50 % flowering, plant height, number effective tiller per plant, panicle length and test weight. Path coefficient analysis showed that panicle length, plant height, days to flowering and effective tiller per plant had high direct positive effect on grain yield per plant.

Keywords: Variability, heritability, genetic advance, correlation, path analysis, rice

INTRODUCTION

Rice is a cereal crop belongs to genus *Oryza* of family Poaceae. The genus *Oryza* has twenty two wild and two cultivated species namely; *Oryza sativa* and *Oryza glaberrima*. All these represents to 10 different genomic types viz., AA, BB, CC, BBCC, CCDD, EE, FF, GG, HHJJ and HHKK (Brar and Khus 1986). *Oryza sativa* is a cultivated diploid species having 24 chromosomes of AA genome. The *sativa* rice germplasm of the world are commonly divided into three sub-species i.e. Indica, Japonica and Javanica grown in tropical, temperate and in intermediate climate respectively. The Association of different characters was essential to determine their contribution towards yield. The knowledge about genetic variability of yield contributing characters, inter relationship among them and their relation with yield are necessary for a effective breeding programme. Moreover knowledge of heritability was used for selection, as it indicates the extent of transmissibility of trait in to future generations (Sabesan *et al.* 2009). The correlation coefficient also help to identify characters that have little or no importance in the selection programme where as path coefficient analysis helps in determining the direct and indirect cause of association and permit to examine the specific forces acting to produce the given correlation. Correlation and path coefficient analysis together have been

successfully used for plant selection for increasing yield and provide information about cause and effect relationship between direct pair of variables. Therefore, the present investigation was undertaken to estimate the variability, heritability, genetic advance as percentage of mean, correlation among the traits and their path coefficient analysis for grain yield and yield attributing traits among the genotypes.

MATERIALS AND METHODS

Plant Material and Experimental Design: The seeds of Twenty five diverse rice germplasm accessions viz., TSAO WANCHING, JC-1, LUMBINI, MADHUKAR, N-22, BINULAVAN, KALA-RATA 1-24, TATAN, BAPKARIBUNA, COTA, KHAIJAN, KAMNAM, LEMOHT, LATSIKA, AKITAKOMACHI, M-202, Mr. AMROO, NIPPONBARE, ASAMI DHAN, CHANGHAT, BAD KODI, DUB CELONG, SABVITRI, ASHU BHAJNA, TUNDAHIYA were received from DBT Networking Project, Institute of Agricultural Sciences, Banaras Hindu University, Varanasi and their seed were multiplied during kharif season 2013 and further accessions were evaluated in randomized block design with three replications during kharif season 2014. The twenty one days old seedlings were transplanted in small separate plot 20 cm apart between row and 15 cm within row. The standard cultural practices were followed to raise a healthy crop.

Data Collection: Observations were recorded on ten randomly selected plants from each entry and replication on days to 50% flowering (DF), days to maturity (DM), plant height (cm) (PH), panicle length (cm) (PL), number of effective tillers per plant (ET), panicle weight (PW), total number of grains per panicle (TGP), filled grains per panicle (FGP), spikelet fertility percentage (SF), test weight (g) (TW), and grain yield per plant (GYP).

Statistical Analysis: The experimental data were compiled by their mean value over randomly selected plants from all the three replication and subjected to statistical analysis for genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) as per procedure given by Burton and De Vane (1953) and heritability and genetic advance by Johanson *et al.* (1955). Correlation coefficient was worked as per Al- Jibour *et al.* (1958) and path analysis given by Dewey and Lu (1959).

RESULTS AND DISCUSSION

The improvement of rice crop is highly dependent on the level and magnitude of phenotypic and genotypic coefficient of variation,

heritability and genetic gain on which the breeding methods are formulated for improvement of yield and yield traits. Analysis of variance revealed the highly significant differences among the genotypes for all the characters studied. The genotypes exhibited wide range of variability for most of the traits indicating good scope for selection of promising genotypes for yield improvement. The extent of variability as measured by phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) provides information regarding the relative amount of variation for various traits. In present investigation, we observed that estimates of phenotypic coefficient of variation were slightly higher than genotypic coefficient of variation for the traits under study. Similar observations were also made by Satyanarayana *et al.* (2005), Patra *et al.* (2006) and Singh *et al.* (2014). Both phenotypic coefficient of variation and genotypic coefficient of variation were higher for grain yield per plant (34.12, 29.70), number of grains per panicle (29.09, 27.49), filled grains per panicle (28.05, 26.46), number of effective tillers per plant (26.53, 22.75) and panicle weight (25.28, 23.34) respectively (Table 1).

Table 1: variability parameter for eleven quantitative traits in twenty five rice varieties

Character	GCV	PCV	h^2 (bs)	GA	GA as % of mean
Days to 50% flowering	33.368	33.398	99.8	68.578	88.011
Days to maturity	21.063	21.161	99.1	68.117	55.35
Plant height	29.53	29.771	98.4	99.081	77.32
Panicle length	20.41	20.81	96.2	12.33	52.87
Panicle weight	32.59	34.97	86.9	2.136	80.19
Effective tillers per plant	54.502	55.522	96.4	25.649	141.24
Filled grains per panicle	35.397	36.403	94.5	97.189	90.86
Total grains per panicle	30.95	32.09	93	108.37	78.89
Spikelet fertility (%)	16.716	17.367	92.6	33.077	42.47
Test weight	21.09	23.67	79.4	10.36	49.61
Grain yield per plant	35.097	36.21	93.9	19.606	89.80

Result suggested that these traits were under the major influence of genetic control and less variable due to environmental factor. Therefore, such traits could be relied upon and selection can be practiced for further improvement. The present findings were in consonance with earlier reports made by Anjaneyulu *et al.* (2010), Chouhan, *et al.* (2014), Singh *et al.* (2013) and Singh *et al.* (2015). The genetic coefficient of variation does not provide clear picture of the extent of genetic gain to be expected from selection of phenotypic traits, unless heritable function of variation (heritability)

is known (Burton 1952). In present investigation the high value of heritability was observed for days to 50% flowering, plant height, panicle length, number of grains per panicle, filled grains per panicle, test weight, days to maturity, panicle weight, grain yield per plant and effective tillers per plant. High heritability does not always indicate high genetic gain. Genetic advance as percent of mean was high for number of grains per panicle (108.37) followed by plant height (99.081), number of filled grain (97.189), while medium for days to 50 % flowering (68.578), days to maturity (68.117) .While lowest for test

weight (10.36) and panicle weight (2.136) (Table 1). The high heritability coupled with high genetic advance as per cent of mean were recorded for the number of grains per panicle, filled grains per panicle, grain yield per plant, panicle weight,

number of effective tillers per plant, flag leaf width and plant height indicating the less influence of environmental variance in the inheritance of trait.

Table 2: Estimation of phenotypic matrix of direct and indirect effects on grain yield per plant in twenty five rice varieties

Traits	DF	DM	PH	ET	PL	PW	FGP	TGP	SF	TW	GYP
DF	0.0167	0.0114	0.0113	0.0071	0.0029	-0.0042	-0.0048	-0.0006	-0.0087	-0.0010	0.3461**
DM	0.0123	0.0179	0.0114	0.0034	0.0012	-0.0035	-0.0012	0.0024	-0.0056	-0.0019	0.2023
PH	0.2960	0.2791	0.4385	0.1503	0.2131	-0.0712	-0.0004	0.1011	-0.1778	0.0880	0.4916**
ET	0.0818	0.0363	0.0658	0.1918	0.0124	-0.0528	-0.0628	-0.0444	-0.0426	0.0061	0.3022**
PL	0.0403	0.0159	0.1122	0.0149	0.2309	0.0509	0.0851	0.1038	-0.0244	0.0324	0.4454**
PW	-0.1172	-0.0931	-0.0762	-0.1293	0.1034	0.4695	0.3755	0.3024	0.2108	0.1076	0.1900
PG	-0.2624	-0.0607	-0.0009	-0.2991	0.3370	0.7313	0.9142	0.7895	0.4295	0.1720	0.1190
TG	0.0389	-0.1491	-0.2592	0.2601	-0.5053	-0.7240	-0.9708	-0.124	0.0305	-0.0780	0.1429
SF	0.2403	0.1452	0.1874	0.1027	0.0488	-0.2075	-0.2171	0.0126	-0.4621	-0.0803	-0.0493
TW	-0.0004	-0.0007	0.0013	0.0002	0.0009	0.0015	0.0012	0.0004	0.0011	0.0065	0.2515*

RESIDUAL EFFECT= 0.7432

Similar results were observed by Karad *et al* (2008), Gyanendrapal (2011) and Singh *et al* (2015) in rice. Thus, these characters were under the influence of additive gene action and selection breeding is possible for improvement of yield and other traits. Character association provides information about the estimates of interrelationship of various yield components in the manifestation of yield. Correlation among different traits is generally due to the presence of linkage and pleiotropic effect of different genes. Selection of parents based on yield alone is often misleading. Therefore, it is important to have the knowledge about the correlation between the different component characters of yield, among themselves and with the yield to ease the selection strategy for improvement in yield. The present findings revealed that the grain yield per plant was significant and positively correlated with the days to 50 per cent flowering, plant height, effective tillers per plant, panicle length and test weight (Table 2). Similar

results were reported by), Sravan *et al.*, (2012) and Singh *et al.*, (2015). Path coefficient analysis to provide an effective means of finding the direct and indirect causes of association which provides means to indicate whether the influence of different yield contributing components are directly reflected in the yield or take some other pathways for ultimate effects and to understand the relative importance of traits with each other. The result of path coefficient analysis exhibited that the days to 50 % flowering, days to maturity, plant height, number of effective tiller per plant, panicle length, panicle weight, filled grain per panicle and test weight had the maximum direct effect on grain yield (Table 3). The panicle weight also contributed to grain yield via filled grain per panicle and total grain per panicle. Result of present study support by earlier findings of Ullah *et al.* (2011) and Singh *et al.* (2015). Therefore, selection based on these traits will be effective in improving grain yield and other related traits.

Table 3: Estimation of phenotypic correlation coefficient between yield and yield traits

Traits	DM	PH	ET	PL	PW	FGP	TGP	SF	TW	GYP
DF	0.6857**	0.6750**	0.4263**	0.1744	-0.2497*	-0.2870*	-0.0346	-0.5201**	-0.0586	0.3461**
DM		0.6365**	0.1892	0.0688	-0.1984	-0.0664	0.1326	-0.3143**	-0.1040	0.2023
PH			0.3428**	0.4860**	-0.1623	-0.0009	0.2305*	-0.4054**	0.2007	0.4916**
ET				0.0646	-0.2753*	-0.3272*	-0.2313*	-0.2223	0.0318	0.3022**
PL					0.2203	0.3687**	0.4495**	-0.1507	0.1404	0.4454**
PW						0.7999**	0.6440**	0.4490**	0.2291*	0.1900
FG							0.8635**	0.4698**	0.1882	0.1190
TG								-0.0272	0.0694	0.1429
SF									0.1737	-0.0493
TW										0.2515*

*, ** & ***: Significant at 5 %, 1 % and 0.1 % level, respectively

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