

GENETIC VARIABILITY, INTERRELATIONSHIP AND PATH ANALYSIS FOR YIELD IMPROVEMENT OF RICE GENOTYPES

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ABSTRACT

An investigation was carried out to study the genetic variability, association among the yield component traits, their direct and indirect effects on the yield. All the genotypes showed considerable amount of variation in their mean performances with respect to the characters studied, indicates presence of sufficient variability and scope for further selection and breeding superior and desirable genotypes. Genotypic coefficient of variation played a major role for the expression of the traits and ranged from 4.15 (days to maturity) to 27.58 (grain yield per plant). Heritability is ranged from 18.00 (flag leaf length) to 92.17 (number of spikelets per panicle). High genetic advance was observed for the trait, number of spikelets per panicle (99.83) coupled with high heritability (92.17), indicating the preponderance of the non-additive gene action; suggesting that hybridization breeding will be effective. Biological yield per plant (0.78, 0.72), harvest index (0.57, 0.58) and number of spikelets per panicle (0.18, 0.18) were positively associated with grain yield at both genotypic and phenotypic levels respectively, indicating improvement in these traits will increase the grain yield. Number of panicle per plant (4.33, 0.08), biological index per plant (1.04, 0.80), harvest index (0.90, 0.67), panicle length (0.23, 0.03) and test weight (0.02, 0.03) had positive direct effect on yield at both genotypic and phenotypic levels respectively, indicating importance of these characters and which can be strategically used to improve the yield of rice grains. The present study concluded that the genotypes CB 08-534 and CRK-27 were identified as best genotypes for grain yield.

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important world food crops, serving as the staple food for over one-third of the world's population (Davla *et al.*, 2013 and Reddy *et al.*, 2013). India being the second largest producer of rice still lacks behind. The other continents in which rice is grown are Africa (7.78% of the global area), South America (6.4%) and North America (1.4%). (Viraktamath, 2007). The rising demand, saturation of cultivable field and low gross domestic production of rice are likely to cause a supply shortage of a crop in the near future (Dhanwani *et al.*, 2013). By the year 2025, about 785 million tonnes of paddy which is 70 per cent more than the current production will be needed to meet the growing demand (Manomani and Khan, 2003). Therefore being the staple food of the population in India, improving its productivity has become a crucial importance (Subbaiah *et al.*, 2011). The basic objective of the crop improvement programme is to realize a marked improvement in crop yield. But yield is a complex character which is controlled by association of various characters. The success of any breeding programme depends on the nature and magnitude of genetic variability present in the genotypes. The presence of sufficient variability, the knowledge of nature of association among different characters and relative contribution of different characters to yield is a prerequisite to any breeding programme (Sharma *et al.*, 2012). Genetic variability, character association and path coefficients are pre-requisites for improvement of

any crop including rice for selection of superior genotypes and improvement of any trait (Krishnaveni *et al.*, 2006). Knowledge of correlation between yield and its contributing characters are basic to find out guidelines for plant selection. Partitioning of total correlation into direct and indirect effect by path coefficient analysis helps in making the selection more effective. Keeping in view the above facts, the present investigation was undertaken to know variability and correlation among yield and its contributing characters.

MATERIALS AND METHODS

The present experiment was carried out at experimentation center of the Department of Genetics and Plant Breeding, Allahabad school of Agriculture, Sam Higginbottom Institute of Agriculture, Technology and Sciences, Allahabad, Uttar Pradesh, India, situated at 25.87°N Latitude, 81.5°E Longitude and altitude of 78 meters above mean sea level. The experiment was laid out in a Randomized Block Design (RBD) with three replications in *Kharif* 2013. The experimental material was planted in three blocks. Each block consisted of thirty two genotypes randomized and replicated within each block. Twenty seven days old seedlings were transplanted 20cm apart between rows and 15cm within the row. All necessary precautions were taken to maintain uniform plant population in each treatment per replication. All the recommended package of practices was followed along with necessary prophylactic plant protection measures to raise a

good crop. Observations were recorded and the data was subjected to statistical analysis. The mean performance of individual genotype employed for statistical analysis. Analysis of variance to test the significance for each character was carried out as per methodology advocated by Panse and Sukhatme (1967). PCV and GCV were calculated by the formula given by Burton (1952), heritability in broad sense (h^2) by Burton and De Vane (1953), and genetic advance *i.e.* the expected genetic gain were calculated by using the procedure given by Johnson *et al.* (1955). Statistical analyses for the above characters were done following Al Jibouri *et al.* (1958) for correlation coefficient and Dewey and Lu (1959) for path analysis. The estimated values were compared with table values of correlation coefficient to test the significance of correlation coefficient prescribed by Fisher and Yates (1967).

RESULTS AND DISCUSSION

The analysis of variances indicated the existence of significant differences among the genotypes studied revealing that sufficient variability is present for the different characters and selection would be effective to develop the varieties with desired forms of crop plants. The result of analysis of variance is present in the Table 1.

The development of an effective plant breeding programme depends on the existence of genetic variability. Genotypic coefficients of variation ranged from 4.15 to 27.57 whereas phenotypic coefficient of variation ranged from 4.91 to 29.59 among various parameters studied. The difference between genotypic and phenotypic coefficient of variation was less for all characters studied except grain yield (27.58 and 29.59), spikelets per panicle (25.67 and 26.74), biological yield per plant (23.80 and 25.40), harvest index (18.19 and 21.38), test weight (17.35 and 19.73) and number of tillers per plant (15.80 and 19.66) (Zahid *et al.*, 2006), indication of the more influence of the environment over these characters. The slight difference between GCV and PCV was also reported by Mustafa and Isheikh (2007), Kole *et al.* (2008) and Seyoum *et al.* (2012). The high magnitude of phenotypic variation were composed of high genotypic coefficient of variations and less of the environment variations, which indicated high genetic variability for different traits and less influence of environment. Therefore selection on the basis of phenotype alone can be effective for the improvement of these traits. Similar results were also found by Prajapati *et al.* (2011), Singh *et al.* (2013) and Sawarkar *et al.* (2014).

The reliability of the phenotypic value depends on the estimates of heritability for a particular character. Therefore high heritability helps in the effective selection for a particular character. In the present investigation heritability in broad sense was calculated for all characters under study and is presented in Table 1. Heritability is classified as high (above 60%), medium (30%-60%) and low (below 30%). High estimate of heritability were exhibited for spikelets per panicle (92.17%), biological yield per plant (87.79%), grain yield per plant (86.84%), days to 50% flowering (78.77%), test weight (77.34%), harvest index (72.38%), days to maturity (71.25%), panicle length (70.47%), flag leaf length (70.21%), panicles per plant (68.42%) and tillers per

Table 3: Estimates of direct and indirect effects between yield and its related traits in 32 rice genotypes at genotypic level

S.No	Character	Days to 50% flowering	Plant height	Flag leaf length	Flag leaf width	cm	tillers/ plant	Panicles/ plant	Panicle length	Spikelets/ panicle	Days to maturity	Biological yield/ plant	Test weight	Harvest index	Grain yield per plant
1	Days to 50% flowering	0.4504	-0.2425	-0.2211	0.0260	0.1159	0.1362	-0.0465	-0.0173	0.4690	-0.0230	-0.0111	-0.0919	-0.1803	
2	Plant height	0.1990	-0.3696	-0.1541	-0.0353	0.0629	0.0299	0.1355	0.0123	0.1821	-0.0460	-0.0370	0.1350	-0.1255	
3	Flag leaf length	0.0221	-0.0188	-0.0451	0.0192	-0.0105	-0.0102	-0.0104	0.0098	0.0191	-0.0047	-0.0135	-0.0048	0.1713	
4	Flag leaf width	0.0228	0.0378	-0.1687	0.3966	-0.2717	-0.2640	-0.1790	0.2760	0.0156	0.1460	-0.0096	-0.0810	0.1338	
5	tillers/ plant	-0.9947	0.6577	-0.8995	2.6485	-3.8651	-3.8159	0.4320	0.3853	-0.9249	0.3808	-1.2787	0.3067	-0.0849	
6	Panicles/ plant	1.3095	-0.3504	0.9834	-2.8840	4.2768	4.3319	-0.6763	-0.4683	1.2451	-0.5355	1.1624	-0.8484	-0.1715	
7	Panicle length	-0.0244	-0.0866	0.0543	-0.1066	-0.0264	-0.0369	0.2363	-0.0376	-0.0376	-0.0596	0.0898	0.0306	-0.0808	
8	Spikelets/ panicle	0.0053	0.0046	0.0299	-0.0954	0.0137	0.0148	0.0218	-0.1370	-0.0055	-0.0393	0.0585	0.0133	0.1890	
9	Days to maturity	-0.9308	0.4406	0.3788	-0.0352	-0.2139	-0.2570	0.1424	-0.0361	-0.8941	-0.0431	0.1501	0.2510	-0.1400	
10	Biological yield/ plant	-0.0536	0.1306	0.1087	0.3861	-0.1033	-0.1296	-0.2643	0.3011	0.0505	1.0487	-0.3843	-0.0389	-0.1400	
11	Test weight	-0.0007	0.0027	0.0080	-0.0007	0.0089	0.0072	0.0102	-0.0115	-0.0045	-0.0098	0.0268	-0.0019	-0.3123	
12	Harvest index	-0.1852	-0.3315	0.0967	-0.1854	-0.0720	-0.1778	0.1174	-0.0879	-0.2548	-0.0336	-0.0657	0.9077	0.5774	

plant(64.60%). This suggests that selection can be practiced by using these traits to improve grain yield in rice. Similar findings were reported by Yadav *et al.* (2011), Dhanwani *et al.* (2013), Panchta *et al.* (2013) and Sawarkar *et al.* (2014) for high heritability of these characters.

High heritability coupled with genetic advance can be more useful in selection types with such yield contributing characters. Genetic advance denotes the improvement in the genotypic value of the new population over the original population. The estimates of genetic advance as per cent of mean provide more reliable information regarding the effectiveness of selection in improving the traits. A relative comparison of heritable estimates and expected genetic advance expressed as percentage of mean will give an idea about the nature of gene action governing a particular character. A comparison of heritability and genetic advance as percentage of mean revealed that number of tillers per plant (92.17% and 50.78%), biological yield per plant (87.79% and 45.93%) grain yield per plant (86.84% and 52.94%), and harvest index (72.38% and 31.89%) suggesting preponderance of additive gene action in the expression of these character (Kumar *et al.*, 2007 and Karthikeyan *et al.*, 2010). This type of character could be improved by mass selection and breeding methods based on progeny testing (Table 1).

Phenotypic and genotypic correlations between yield and yield components viz., days to 50 per cent flowering, plant height, flag leaf length, flag leaf width, panicle length, number of panicles per plant, number of tillers per plant, number of spikelets per panicle, days to maturity, biological yield per plant harvest index and test weight were computed separately for rice genotypes. The results are presented in Table 2. They provide basic information extremely useful to the breeder for proper understanding of the nature of the traits. The genotypic correlations in general were higher than the corresponding phenotypic correlations (Table 2). Days to 50 per cent flowering registered strong and positive significant correlation with number of panicles per plant(0.33** and 0.22*) and days to maturity (1.00*** and 0.83***) at both genotypic and phenotypic levels. This is due to the modified effect of environment on character association at the genetic level. This corroborates with the findings of Reddy *et al.*, (2008), Saravanan and Sabesan (2009) and Reddy *et al.*, (2013) for days to maturity. Grain yield per plant exhibited significant positive correlations with biological yield per plant (0.78*** and 0.72) and harvest index (0.57*** and 58***) at both genotypic and phenotypic levels. This indicates the relative utility of both traits for selection with respect to grain yield. The observed positive correlation of grain yield with various traits was supported by (Rajeshwari and Nandrajana, 2004). The association expressed by grain yield with flag leaf length, flag leaf width and number of spikelets per panicle positive at both levels (Table 3). It suggests that, priority should be given to these traits while making selection for yield improvement. The correlation of number of spikelets per panicle exhibited positive and significant association with panicle length and biological yield per plant. Similar results were reported by Seyoum *et al.* (2012) and Reddy *et al.* (2013). The correlation coefficient showed biological yield per hill serves as important selection

indices of grain yield. Kole *et al.* (2008) emphasized the importance of biological yield per plant in determining grain yield in rice. Negative significant correlation was observed between harvest index with plant height at both genotypic and phenotypic levels. The genetic reasons for this type of negative association may be linkage or pleiotropy. According to NeWall and Eberhart (1961) when two characters show negative phenotypic and genotypic correlation it would be difficult to exercise simultaneous selection for these characters in the development of a variety. Hence, under such situations, judicious selection programme might be formulated for simultaneous improvement of such important developmental and component characters.

As simple correlation does not provide the true contribution of the characters towards the yield, these genotypic correlations were partitioned into direct and indirect effects through path coefficient analysis. It allows separating the direct effect and their indirect effects through other attributes by apportioning the correlations (Wright, 1921) for better interpretation of cause and effect relationship. The estimates of path coefficient analysis are furnished for yield and yield component characters in Table 3. In the present study path coefficient analysis has been conducted for grain yield per plant. Path coefficient analysis revealed that number of panicles per plant (4.33) had highest positive direct effect on grain yield per plant, followed by biological yield per plant (1.04), harvest index (0.90), days to 50% flowering (0.45), flag leaf width (0.39), panicle length (0.23) and test weight (0.02), Chakraborty *et al.* (2010), Pandey *et al.* (2012), Panchta *et al.* (2013), Singh *et al.* (2013) and Seesang *et al.* (2013) days to 50% flowering, flag leaf width, number of panicle per plant, biological yield and test weight and harvest index at genotypic level. This may indicate that the direct selection for number of panicles per plant, biological yield per plant, harvest index, days to 50% flowering, flag leaf width, panicle length and test weight would likely be effective in increasing grain yield. The path analysis indicated that there is no common causal factor that directly influences grain yield per plant.

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