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Genetic variability studies in low land elite rice genotypes for yield and cellulose content

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Abstract

In the present study wide genetic variability among the selected genotypes was recorded which was supported by mean performance, variance and range. The phenotypic coefficient of variation was found to be higher than that of genotypic coefficient of variation for all the characters studied among the set of materials. The estimates of PCV and GCV were lowest in case of days to 50% flowering (4.84 and 4.61) and cellulose (43.28 and 42.62) was found to be highest. Characters like panicle length (69.76%) exhibited moderate heritability (40%-70%) and all other characters exhibit high heritability suggesting effectiveness of selection on the basis of phenotypic expression of the traits. High heritability accompanied with high genetic advance observed in number of fertile grains per panicle, panicle weight, cellulose and single plant yield indicate that additive gene effect has played a major role in the expression of these characters and simple selection will improve these characters. The high estimates of correlation at phenotypic and genotypic level was between yield and number of fertile grains per panicle. The predicted genetic advance from different indices ranged from 4.53 q/ha in one-character index to 4.79 q/ha in eleven character index and it varied from 100.00 % in index 1 to 105.7 % in index 11 in terms of relative efficiency. Thus, in terms of predicted genetic advance, the results of the present study brought out superiority of eleven character index over direct selection on yield per se.

Keywords: Rice, genetic variability, correlation, path analysis, cellulose

Introduction

Rice occupies an important position as the second most widely cultivated cereal after wheat but it is the primary source of staple food for more than half of global population. It occupies 11% of the world's total cultivated area which is estimated to have 161.54 million hectares during 2017-18 with a production and productivity of 487.46 million metric tons and 4.5 metric tons per hectare during 2017-18 (Rice Outlook, 2018 USDA). Rice occupies a pivotal role in Indian agriculture as it is the staple food for two thirds of the population of India. The area, production and productivity of rice in India is 433.88 Lakh ha, 104.32 million tons and 2404 kg/ha respectively (Annual report 2016-17). About 60 million hectares of rainfed lowlands supply about 20% of the world's rice production. Rainfed rice environments experience many abiotic stresses, such as salinity, high uncertainty in timing, duration, and intensity of rainfall. Because of such environments the yields are so unreliable, farmers rarely apply fertilizer and take no interest to sow improved varieties. Productivity in rainfed lowland areas is typically very low, with yields of 1 to 2.5 t/ha. Rice farming is practiced in several agroecological zones in India. No other country in the world has such diverse rice ecosystems. In India, lowland rice area is about 14.4 million hectares, which accounts 32.4% of the total area under rice crop in the country. There is an urgent need to identify high yielding genotypes suitable for lowland condition.

Information on nature and magnitude of variability present in the existing material and association among the various characters is a prerequisite for any breeding program for high yield and quality. To make selection effective, it is necessary to separate genetic variability from total variability which enable breeder to adopt strategies for involvement of suitable breeding program. Since yield is associated with its component characters, it is essential to know the degree of mutual association prevailing between yield and its component characters, which forms a basis for selecting the desirable genotypes. When the population being handled is large, it is difficult to select genotype based on the yield figure alone. Further, because of the complexity of yield and its close association with component characters, direct selection for yield is often ineffective in bringing out expected results. In such situation the success of selection could be enhanced with the use of selection indices formulated based on discriminant function technique involving important character.

Ethanol from biomass has become an increasingly popular alternative to gasoline. Rice straw has several characteristics that make it a potential feedstock for fuel ethanol production. It has

high cellulose and hemicelluloses content that can be readily hydrolyzed into fermentable sugars. In terms of chemical composition, the rice straw predominantly contains cellulose (32–47%), hemicellulose (19–27%) and lignin (5–24%) (Garrote *et al.*, 2002; Maiorella, 1983; Saha, 2003; Zamora and Crispin, 1995) ^[1–4]. Sustainable biofuel production from cellulose feed stock is a major challenge and will require significant breeding efforts to maximize plant biomass production. So, the present investigation is carried out to estimate cellulose content from rice straw which is the major component that can be converted to bioethanol.

Under this context the present investigation was carried out to evaluate variability and to determine the association of yield and its contributing traits in some lowland elite rice genotypes. The information thus, gathered from the study would throw light on the prospects and potentialities for genetic improvement of productivity and aid selection through identification of character(s) for accelerating the pace of improvement in lowland rice.

Materials and methods

The experimental material for the present investigation comprised of thirty-four rice genotypes screened for yield and its attributing characters as well as cellulose content at Rice Research Station, College of Agriculture, Orissa University of Agriculture and Technology, Bhubaneswar, India during kharif season of the agricultural year 2017-18. The field lay out was done in randomized block design with two replications. Each of the entries was transplanted in 4 rows with 24 plants in each row. A spacing of 20 cm between rows and 15 cm between plants within a row was maintained. Recommended agronomic practices were followed.

Five competitive plants were selected at random for each entry per replication for recording the observation on plant height, productive tillers per plant, flag leaf area, panicle length, panicle exertion, spikelet fertility, number of fertile grains per panicle, panicle weight, 100 grain weight, single plant yield and cellulose content. Days to fifty percent flowering was recorded on plot basis. For cellulose content the plant samples were sundried for 2 weeks prior to analysis. After removing the panicles, the above ground parts are sun dried and then oven dried at $45 \pm 3^{\circ}\text{C}$ for 3 hours. Following this, the sample was weighed and dried at 45°C for 1 hour. The process was repeated until the change in mass of the sample is <1% in 1 hour. The cellulose estimation was done by colorimetric method following the modified procedure of Updegraff (Sadasiyam and Manickam, 2004) ^[5].

The data was subjected to statistical analysis of variance technique as proposed by Panse and Sukhatme (1961) ^[6]. The phenotypic and genotypic coefficient of variability was computed as per Burton and Devane (1952) ^[7] and were classified as per Sivasubramanian and Menon (1973) ^[8]. Heritability (broad sense) was estimated for all the characters as suggested by Lush (1949) ^[9]. Genetic advance for each character was estimated as per the formula given by Johnson *et al.* (1955) ^[10]. Correlation coefficients for yield and yield components were evaluated utilizing the formula suggested by Al-jibouri *et al.* (1958) ^[11]. The path coefficients were worked out as per Dewey and Lu (1959) ^[12]. Selection indices were constructed using the methods developed by Smith (1936) ^[13] based on discriminative function of Fisher (1936) ^[14].

Results and discussion

The analysis of variance revealed that there exists a highly significant difference among the test genotypes for all the

characters under study. These indicate the presence of wide genetic variability among the selected genotypes. Hence, correlation and path coefficient analysis was computed to estimate the association existing between yield and yield contributing components and direct and indirect effects of yield related traits, respectively. Selection based on the detailed knowledge of magnitude and direction of association between yield and its attributes is very important in identifying the key characters, for crop improvement through suitable breeding program.

Coefficient of variation

From the investigation it was found that phenotypic coefficient of variation was found to be higher than that of genotypic coefficient of variation for all the characters studied among the set of materials (Table 1). The coefficient of variability encompasses the genetic variation that responds to selection. The magnitude of phenotypic coefficient of variation (PCV) estimates in the present study was found to be slightly higher than their respective genotypic coefficient of variations (GCV) for all the studied characters which might be the result of influence of environment on the development of characters.

Many researchers like Ogunbayo (2014) ^[15], Idris (2012) ^[16] and Abebe (2017) ^[17] have noticed similar findings in rice earlier. The difference between PCV and GCV estimates were relatively low for all the traits except for number of productive tillers, fertile grains per panicle and single plant yield, indicating less environmental influence on these traits. Thus, selection based on phenotypic performance of these characters would be effective to bring about considerable genetic improvement. High estimates of both PCV and GCV were recorded for panicle exertion, filled grains per panicle, panicle weight, cellulose content and single plant yield, which suggests the possibility of improving these traits through selection. No of effective tillers has high PCV and moderate GCV. This is in accordance with the findings of Khatun *et al.* (2015) ^[18], Mazid *et al.* (2013) ^[19], Pandey and Anurag (2010) ^[20], Sabu *et al.* (2009) ^[21] and Kiani (2013) ^[22] for filled grains per panicle and single plant yield; Sabu *et al.* (2009) ^[21] and Kiani (2013) ^[22] for panicle weight. On the other hand, the estimates of GCV and PCV were low in the present study for days to fifty per cent flowering, panicle length and plant height. This is in accordance with the findings of Shrivastava (2015) ^[23], Sangaré (2017) ^[24] for days to fifty per cent flowering and plant height; Sabu *et al.* (2009) ^[21] and Kiani (2013) ^[22] for panicle length.

Heritability and genetic advance

The heritability estimates obtained were high for all the characters studied (Table 1). The estimates of heritability ranged from 69.76% for panicle length to 96.97% for cellulose. The expected genetic advance over mean for different characters ranged from 7.74 (days to 50% flowering) to 73.86 (cellulose content). Expected genetic advance was low in case of days to 50 per cent flowering (7.74), panicle length (11.01) plant height (14.80). Moderate genetic advance was recorded for number of productive tillers (29.36), flag leaf area (29.12), spikelet fertility % (27.85) and 100-seed weight (27.55). For characters like panicle exertion (56.65), number of fertile grains per panicle (33.17), panicle weight (53.02), cellulose (73.86) and single plant yield (61.12), genetic advance was high (> 30%). High heritability accompanied with moderate to high genetic gain for number of fertile grains per panicle, panicle weight, number of

productive tillers, flag leaf area, spikelet fertility percent, 100-seed weight, cellulose and single plant yield indicated presence of additive gene action and hence selection based on phenotypic performance would be effective. The results are at par with Shrivastava (2015) [23], Gour (2017) [25], Khare (2014) [26], Karande *et al.* (2017) [27], Kishore *et al.* (2018) [28], Bhinda *et al.* (2017) [29], Lingaiah *et al.* (2014) [30] and Limbani (2017) [31]. Characters like days to 50 per cent flowering and plant height recorded high heritability accompanied with low genetic advance which indicates the predominance of epistasis and dominant gene action. Selection for such traits may not be rewarding, in that case heterosis breeding may be useful. This is in accordance with the findings of Karande *et al.* (2017) [27], Panigrahi (2017) [32], Sangaré (2017) [24] for days to 50% flowering; Sangaré (2017) [24], Konate *et al.* (2016) [33] for plant height.

Association analysis

Yield is a complex polygenic trait for which direct selection may not be effective always. So component traits would be helpful in the improvement of yield. The results on correlations revealed that genotypic correlation coefficient was higher than the corresponding phenotypic correlation coefficient, indicating strong inherent association between the traits under study (Table 2). Positive and significant correlation of grain yield with the component traits *viz.*, no. of fertile grains per panicle, panicle weight, spikelet fertility percent, number of productive tillers, panicle exertion, 100-grain weight were observed. The rest of the characters had non-significant correlation with yield. The findings indicated that plants with heavy panicles tend to have high number of fertile grains thereby increasing rice yield. The positive correlation that was obtained between number of grains and weight of panicles implies that increasing the weight of panicle would also effectively increase the number of grains per plant and thus increase grain yield. This indicated that all these characters were important for yield improvement.

Similar results were observed by Baloch *et al.* (2016) [34], Sravan *et al.* (2016) [35], Harsha *et al.* (2017) [36], Patel *et al.* (2014) [37], Rao *et al.* (2014) [38], Rathod (2017) [39], Das (2015) [40] for test weight and number of productive tillers; Patel *et al.* (2014) [37], Rahman *et al.* (2014) [41], Rathod (2017) [39], Das (2015) [40], Karande (2017) [27], for number of filled grains per panicle and spikelet fertility; Ketan and Sarkar (2014) [42], Gour (2017) [25] and Shrivastava *et al.* (2014) [23] for panicle weight.

Cellulose: an important biofuel trait

The cellulose content in the thirty four rice genotypes studied ranged from 1.79% to 12.97% with an overall mean of 6.71%. Thirteen genotypes recorded high cellulose content above 6.94% ($> \text{mean} \pm \text{SE}$). Flag leaf area had positive significant correlation with cellulose at both phenotypic and genotypic level. The trait was positively correlated, though not significant, with plant height, panicle length, and 100 seed weight. The result indicates that flag leaf area can be utilized for indirect selection of cellulose content in rice genotypes.

Path analysis of yield components

The correlation coefficient of component traits with grain yield were partitioned in to direct and indirect effects following path coefficient analysis, to ascertain further conclusive evidence on choice of characters required for selection of high yielding genotypes. During the present investigation, path analysis was carried out both at phenotypic and genotypic level (Table 3). It was observed that, at phenotypic level, number of fertile grains per panicle exerted highest direct effect on yield followed number of productive tillers, 100-grain weight, spikelet fertility percent, panicle weight, flag leaf area, panicle length and days to 50% flowering, thus, indicating the importance of such traits as criteria for selection in that order for realization of higher productivity. The other traits like plant height and panicle exertion exhibited negative direct effect on yield. At genotypic level number of productive tillers exhibited maximum direct effect on yield followed by spikelet fertility percent, panicle weight, flag leaf area, 100-grain weight and panicle exertion. The characters like plant height, panicle length and number of fertile grains exhibited negative direct effect on single plant yield. Spikelet fertility percent had positive indirect effect via 100-grain weight. Thus, it can be concluded that traits like number of fertile grains per panicle, number of productive tillers, 100-grain weight, spikelet fertility percent, panicle weight and panicle exertion should be considered as important selection criteria for increasing yield. These findings in relation to different component traits were in agreement with published report on path analysis by Rathod *et al.* (2017) [39], Lingaiah *et al.* (2014) [30], Rahman *et al.* (2014) [41], Islam *et al.* (2015) [43], Shankar *et al.* (2016) [44], Harsha (2017) [36], Sarker *et al.* (2014) [45], Das (2015) [40], Gour (2017) [25] and Pradhan *et al.* (2015) [46].

Selection indices

Plant breeding program are mostly aimed at selection of high yielding genotypes with better quality. But selection on the basis of yield *per se* in the initial stage of evaluation is often, not effective owing to low heritability. Therefore, several workers in different crop plants have emphasized the importance of indirect selection for yield of component traits governed by genes with additive effect and strong correlation with yield. The predicted genetic advance from different indices at 10% selection intensity ranged from 4.53 q/ha in one character index to 4.79 q/ha in eleven character index. It varied from 100% in index 1 to 105.7 % in index 11 in terms of relative efficiency. Thus, in terms of predicted genetic advance, the results of the present study brought out superiority of eleven character index over direct selection on yield *per se* (Table 4). As per the mean index score (12.18), sixteen genotypes out of 34 test genotypes were above the mean index. It indicates that the eleven character index is far superior to the yield *per se* alone. The results obtained were similar to Biswaranjan *et al.* (2017) [47], Choudary *et al.* (2017) [48] and Aslam *et al.* (2014) [49]. The genotypes which are better performing with eleven character index can be selected for further breeding program.

Table 1: Descriptive statistics along with genotypic and phenotypic coefficient of variation, genetic advance and genetic advance percentage over mean for 12 characters in rice

Characters	Range	Mean	CV%	GCV	PCV	Heritability	GA% over Mean
DF	96-118	107.26	2.07	4.61	4.84	90.83	7.74
PH (cm)	89.60-141.50	109.59	6.17	9.29	10.27	81.91	14.80
EF	6.5-15.0	9.75	13.86	18.81	21.21	78.65	29.36
FA (cm ²)	16.90-39.11	27.85	11.66	18.17	19.95	82.92	29.12
PL (cm)	16.85-28.20	23.87	6.98	7.49	8.97	69.76	11.01
PE (cm)	0.85-3.42	2.10	14.35	33.62	35.12	91.65	56.65
SF (%)	41.5-87.74	64.73	8.17	16.74	17.71	89.36	27.85
FG	52.5-160	99.17	15.78	21.28	24.03	78.44	33.17
PW (g)	0.80-3.96	2.07	12.46	31.30	32.51	92.66	53.02
HSW (g)	1.41-2.64	1.97	4.04	15.90	16.16	96.88	27.55
C (%)	1.79-12.97	6.71	10.66	42.62	43.28	96.97	73.86
SPY(g)	1.94-12.93	7.42	19.00	36.97	39.35	88.26	61.12

DF- Days to 50% flowering, PH- Plant height (cm), EF- Number of effective tillers, FA- Flag leaf area (cm²), PL- Panicle length (cm), PE- Panicle exertion (cm), SF- Spikelet fertility %, FG- Number of fertile grains / panicle, PW- Panicle weight(g), HSW- 100- grain weight (g), C- cellulose content (%), SPY- Single plant yield (g)

Table 2: Phenotypic (above the diagonal) and genotypic (below the diagonal) correlation coefficients among yield and capsule shattering characters in sesame

Character	DF	PH	EF	FA	PL	PE	SF %	FG	PW	HSW	C(%)	SY/P
DF		-0.118	0.071	-0.201	0.011	-0.018	-0.238	-0.011	0.012	-0.088	-0.133	-0.037
PH (cm)	-0.127		-0.071	0.291	0.496**	-0.018	0.132	0.003	0.023	0.355*	0.247	-0.026
EF	0.053	-0.089		-0.283	0.089	0.365*	0.298	0.486**	0.309	0.114	-0.289	0.634**
FA	-0.19	0.372*	-0.354*		0.175	-0.029	-0.022	0.096	0.084	-0.047	0.355*	-0.032
PL (cm)	0.069	0.657**	0.049	0.091		0.09	0.122	0.079	0.18	0.316	0.069	0.156
PE (cm)	-0.011	-0.069	0.404*	-0.007	0.077		0.448**	0.740**	0.446**	0.073	-0.151	0.547**
SF %	-0.273	0.156	0.354*	-0.004	0.204	0.502**		0.651**	0.594**	0.488**	-0.131	0.709**
FG	-0.026	-0.031	0.611**	0.072	0.108	0.859**	0.769**		0.732**	0.12	-0.178	0.775**
PW (g)	0.017	0.027	0.32	0.09	0.248	0.480**	0.642**	0.907**		0.447**	-0.216	0.721**
HSW (g)	-0.088	0.377*	0.131	-0.065	0.394*	0.056	0.528**	0.122	0.473**		0.053	0.439**
C (%)	-0.13	0.261	-0.333	0.391*	0.087	-0.162	-0.158	-0.202	-0.222	0.058		-0.095
SY/P	-0.034	-0.063	0.723**	-0.059	0.115	0.607**	0.806**	0.964**	0.790**	0.474**	-0.12	

*, ** significant by the t-test at 1% and 5% of probability, respectively. Values of 0.436 and 0.339 at 1% and 5% of probability respective

Table 3: Direct (diagonal) and indirect effects of component traits on yield at phenotypic (P_p) and genotypic (P_g) level for 34 low land rice genotypes

Characters		DF	PH	ET	FA	PL (cm)	PE (cm)	SF %	FG	PW	HSW	Correl. with SPY
DF	P _p	0.010	0.020	0.025	-0.017	0.000	0.000	-0.049	-0.004	0.001	-0.023	-0.037
	P _g	0.078	0.023	0.028	-0.039	-0.002	-0.001	-0.120	0.004	0.006	-0.010	-0.034
PH (cm)	P _p	-0.001	-0.168	-0.025	0.024	0.020	0.000	0.027	0.001	0.002	0.093	-0.026
	P _g	-0.010	-0.178	-0.048	0.076	-0.022	-0.007	0.069	0.004	0.009	0.045	-0.063
EF	P _p	0.001	0.012	0.346	-0.024	0.004	-0.003	0.062	0.175	0.032	0.030	0.634
	P _g	0.004	0.016	0.536	-0.072	-0.002	0.044	0.156	-0.085	0.111	0.016	0.723
FA	P _p	-0.002	-0.049	-0.098	0.083	0.007	0.000	-0.005	0.035	0.009	-0.012	-0.032
	P _g	-0.015	-0.066	-0.190	0.204	-0.003	-0.001	-0.002	-0.10	0.031	-0.008	-0.059
PL (cm)	P _p	0.000	-0.083	0.031	0.015	0.040	-0.001	0.025	0.028	0.019	0.082	0.156
	P _g	0.005	-0.117	0.026	0.019	-0.034	0.008	0.090	-0.015	0.086	0.047	0.115
PE (cm)	P _p	0.000	0.003	0.126	-0.002	0.004	-0.008	0.093	0.266	0.046	0.019	0.547
	P _g	-0.001	0.012	0.216	-0.001	-0.003	0.108	0.221	-0.120	0.167	0.007	0.607
SF %	P _p	-0.002	-0.022	0.103	-0.002	0.005	-0.003	0.208	0.234	0.062	0.127	0.709
	P _g	-0.021	-0.028	0.190	-0.001	-0.007	0.054	0.440	-0.107	0.223	0.63	0.806
FG	P _p	0.000	-0.001	0.168	0.008	0.003	-0.006	0.135	0.359	0.076	0.031	0.775
	P _g	-0.002	0.006	0.327	0.015	-0.004	0.093	0.339	-0.140	0.316	0.014	0.964
PW (g)	P _p	0.000	-0.004	0.107	0.007	0.007	-0.003	0.123	0.263	0.104	0.117	0.721
	P _g	0.001	-0.005	0.171	0.018	-0.008	0.052	0.283	-0.127	0.348	0.056	0.790
HSW (g)	P _p	-0.001	-0.060	0.039	-0.004	0.012	-0.001	0.101	0.043	0.047	0.261	0.439
	P _g	-0.007	-0.067	0.070	-0.013	-0.013	0.006	0.232	-0.017	0.165	0.119	0.474

Phenotypic path: P (R)=0.403, R² (%) = 83.79 Genotypic path: P(R)= 0.054, R² (%) = 99.71

Table 4: Expected genetic advance and relative efficiency of selection index over direct selection on grain yield

Index No./ Number of characters	Characters	Expected genetic advance	Relative efficiency in per cent
1	Y	4.53	100.00
2	Y+DF	4.53	100.00
3	Y+DF+PH	4.53	100.00
4	Y+DF+PH+PT	4.54	100.22
5	Y+DF+PH+PT+FA	4.54	100.22
6	Y+DF+PH+PT+FA+PL	4.55	100.44
7	Y+DF+PH+PT+FA+PL+PE	4.56	100.66
8	Y+DF+PH+PT+FA+PL+PE+SF%	4.63	102.21
9	Y+DF+PH+PT+FA+PL+PE+SF%+FG	4.69	103.53
10	Y+DF+PH+PT+FA+PL+PE+SF%+FG+PW	4.70	103.75
11	Y+DF+PH+PT+FA+PL+PE+SF%+FG+PW+HSW	4.79	105.70

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