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RESEARCH PAPER

Genetic variability and correlation studies of different rice (*Oryza sativa* L.) genotypes under aerobic condition

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Abstract: Nineteen rice (*Oryza sativa* L.) genotypes along with two checks were evaluated for yield and its attributing traits under aerobic condition to study genetic variability parameters and correlation among its component traits during *kharif* 2021 by taking mean values of characters across six environments under aerobic condition. For all of the yield and yield contributing traits, variance tests revealed incredibly substantial significant differences between all of the rice (*Oryza sativa* L.) genotypes for all the characters studied, indicating the presence of a variable amount of genetic variability. High values of GCV and PCV were observed for the characters *viz.,* number of panicles sqm^{-1}, grain yield plant^{-1}, number of productive tillers panicle^{-1}, grain breadth (mm) indicating huge amount of variation within these characters. Moderate GCV and PCV values were observed for the characters *viz.,* plant height, number of tillers bearing panicle, L/B ratio, biomass and grain length indicating moderate genetic variability within these characters. High GCV and PCV values coupled with high heritability and high genetic advance over mean were observed for the characters *viz.*, number of panicles sqm^{-1}, grain yield plant^{-1}, number of productive tillers panicle^{-1}indicating the lesser influence of environment on the expression of these characters and are also governed by additive genes which provides perfect criteria for selection of these characters for further improvement. Correlation studies suggests the characters *viz*., panicle length, number of panicles sqm^{-1}, grain yield plant^{-1}, number of productive tillers panicle^{-1}, grain breadth (mm), grain breadth, L/B ratio, test weight, biomass and spikelet fertility had significant and positive correlation with grain yield indicating indirect selection of these characters could be perfect criteria for the genetic improvement of particular genotype during breeding programme.

Key words: Additive gene action, Genotypic coefficient of variation (GCV), Genetic advance, Heritability, Phenotypic coefficient of variation (PCV)

Introduction

Rice (*Oryza sativa* L.) is one of the major cereal crops which feeds half of the world's population. Ninety percent of the world's production and consumption of rice is produced and consumed in Asia. Globally, around 167.2 million ha of area is under rice cultivation, producing 769.6 million tons of rice per year at a productivity of 4600 kg/ha. In India, rice is grown on 43.77 m hectares, with an annual production of 117.47 mt and a productivity of 2,570 kg/ha. In Karnataka, it is grown on 1.24 m ha, with an annual production of 3.54 mt and a productivity of 2,670 kg/ha (INDIA STAT, 2020-21). It is the most varied crop since it can grow in a variety of geographical and climatic conditions. In India, out of 43.77 m ha of harvested area, about 30.8% of the country's land is lowland, 44.9% is irrigated, 17.4% is upland and 6.9% is flood-prone, all of which have a significant impact on the nation's overall rice yield. Due to green revolution, there was drastically rise in production and productivity, which is mostly credited to the irrigated ecosystem because most high yielding varieties were produced to meet this ideal habitat. When compared to other main cereal crops, including wheat and maize, rice is the only crop that uses two to three times as much water (from irrigation or rain) to produce per unit of grain.

Due to inadequate precipitation and overuse of groundwater, water is currently the scarcest natural resource. The conventional method of producing irrigated rice is threatened by the decreasing water supply. Numerous field methods for conserving irrigation water have been investigated. Aerobic rice is one such strategy to decrease water requirements in rice production. Direct sowing of high yielding varieties in non-puddled conditions without standing water and maintenance of aerobic soils throughout the growing season describe this novel technique for cultivating rice, whenever necessary, supplemental irrigation is required. Hence, for this condition there should be special bred aerobic genotypes which combines the feature of both upland (drought tolerance) and lowland (high yielding) which is pre-requisite for successful cultivation of rice with limited water resource (Manjappa *et al.,* 2022 and Grace *et al.,* 2013)

For a better understanding of the type and extent of the genetic variability present in the base material, assessments of several genetic parameters are crucial. With adequate selection criteria and a wide range of genetic variability among genotypes, there are more options for choosing the right genotypes throughout the seasons. Breeding for high yielding crops necessitates knowledge of the extent of several genetic characteristics such as PCV, GCV, broad sense heritability and genetic gain, on which breeding procedures are formulated for further improvement. The primary variable to take into account when making a selection is genetic variability. A character's heritability is a sign of heritability in subsequent generations (Satheesh Kumar and Saravanan, 2012). It is more accurate to predict genetic gain when high heritability is combined with high genetic advance.

Yield being very complex character and greatly influenced by environment and having lower heritability, hence direct selection is not rewarding for genetic improvement.Further, there are numerous yield attributing traits which is indirectly related to yield and has high heritability governed by additive gene action. So, correlation studies help to identify the yield attributing characters which are positively correlated with yield.Selection of those characters indirectly could be fruitful for genetic improvement during breeding programme. With this background, present investigation was undertaken to estimate genetic variability and correlation studies of different rice genotypes under aerobic condition.

Material and methods

The present research was conducted at selected six locations in paddy ecosystems of Northern Karnataka *viz.,* ARS, Arabhavi, ARS, Sankeshwar, ARS, Bailahongal, ARS, Mugadh, ARS, Malagi and a farmer's field at Mukkunda, Sindhanoor during *kharif* 2021. So, for this we have collected nineteen different aerobic genotypes from different institutions *viz*., National Rice Research Institute, Cuttack, ICAR-Indian Rice Research Institute, Hyderabad and University of Agricultural Sciences, Bangalore (Table 1) and also, we have included two local check cultivars Belgaum basmati and Indrani. These genotypes were sown at all these locations using random block design with three replications of spacing of 30 × 20 cms under non-puddled and non-flooded aerobic soil. Irrigation was given frequently once in week during vegetative stages but when crop is at reproductive stage supplementary irrigation was provided once in two days to avoid stress. In order to estimate the components of genetic variance fourteen different morphological and quality traits were considered for the study. So, we have taken mean values of all these characters from all locations and we have worked out components of genetic variability and phenotypic correlation coefficient as suggested by Sunderaraj *et al.* (1972).

We have recorded different morphological parameters *viz*., days to 50% flowering, days to grain maturity, plant height (cm), panicle length (cm), number of tillers per hill, number of panicles per m^2,number of productive tillers bearing panicle, grain yield per plant (g), test weight (g), biomass (g) and spikelet fertility (%) and quality parameters *viz.,* grain length (mm), grain breadth (mm) and L/B ratio and mean values of all these characters were subjected for statical analysis to estimate components of genetic variance and phenotypic correlation coefficient which is prime objective of our research (Uday G, 2013).

Results and discussion

The improvement of character basically depends on variability present within the population. The environmental components of variation, as measured by range, include the influence of environment and genotype. The true breeding value of the genotype can be precisely assessed by separating genetic variance from environmental variance because all of these variations are not heritable. By dividing phenotypic variation into heritable (genetic) and non-heritable (environmental) components. The components of variation in this direction, such as PCV and GCV, heritability and anticipated genetic advance as percent were estimated for all the characters and are presented in Table 2.

In the present investigation, analysis of variance found to be highly significant for all the characters studied which indicated there is huge amount of variation within genotypes selected and also the values of phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all traits studied and these differences in

Table 1. List of genotypes used in the current investigation

Genotypes	Pedigree	Developed/ Released from
CR DHAN – 200	UPLRI5 × IR-12979-24-1	National Rice Research Institute, Cuttack
CR DHAN – 201	IRRI 105 × IR-72022-46-2-3-2	
CR DHAN – 202	IRRI 148 × IR-78877-208-B-1-1	
CR DHAN - 203	IR 78877 × IRRI 132	
CR DHAN – 204	IRR 76569-259-1-2-1 × CT6510-24-1-2	
CR DHAN – 205	N22 × SWARNA	
CR DHAN – 206	BRAHMANAYAKI × NDR 9930077	
CR DHAN – 207	IR 71700-247-1-1-1-2 × IR 57514-5-B-1-2	
CR DHAN – 209	IR 72022-46-2-3-2 × IRRI 105	
CR DHAN – 210	IRB717002-247-1-1-2 × IR 77080B-34-1-1	
DRR DHAN- 41	RP 5311 -PR 26703-3B-PJ7	Directorate of Rice Research, Hyderabad
DRR DHAN – 54	RP 5124-11-4-3-2-1 ×IR 78877-208-B-1-1.	
DRR DHAN – 55	MTU 1010/ × IR79915-B-83-4-3	
PAUSTIC – 1	BPT 5204 × HPR 14	University of Agricultural Sciences, Bangalore
PAUSTIC – 7	BPT 5204 × HPR 14	
PAUSTIC – 9	BPT 5204 × HPR 14	
MAS – 26	IR 64 × AZUCENA	
MAS- 946-1	IR 64 × AZUCENA	
BPT- 5204	GEB 24 × TN1 × Mahsuri	
BELGAUM BASMATI ©	Check cultivar	Check cultivars in Belgaum region
INDRANI ©	Check cultivar	

Table 2. Estimates of variability and genetic parameters for fourteen yield and yield contributing characters in rice (*Oryza sativa* L)genotypes for aerobic cultivation across six locations

Characters	Mean	Range		Coefficient of variation		Heritability	Genetic advance
		Min.	Max.	PCV (%)	GCV (%)	(%)	mean (%)
Days to 50% flowering	89.03	79.22	100.17	5.52	5.50	93.32	11.29
Days to maturity	138.54	132.28	141.50	2.00	1.96	91.92	3.96
Plant height (g)	78.40	57.89	93.24	12.23	12.14	89.54	24.83
Panicle length (g)	20.01	18.14	21.52	5.69	5.28	86.06	10.09
No.of Tillers per panicle	14.79	9.15	20.90	18.77	18.57	87.84	37.84
No.of panicles per m^2	298.60	249.61	555.17	33.39	33.33	95.20	68.52
No.of productive tillers per panicle	13.16	7.72	20.04	23.33	23.03	91.37	46.81
Grain yield per plant (g)	20.02	11.17	36.86	25.16	24.78	90.03	50.29
Grain length (mm)	8.05	6.46	9.38	10.24	10.13	91.30	20.66
Grain Breadth (mm)	3.07	2.66	3.88	15.61	13.77	77.77	25.01
L/B ratio	2.66	2.17	3.79	13.96	11.98	73.57	21.16
Test weight (g)	23.82	22.27	24.67	3.04	2.91	91.64	5.73
Biomass (g)	35.94	29.56	48.44	11.61	11.09	91.26	21.83
Spikelet fertility (%)	88.19	82.21	93.36	3.73	3.60	93.46	7.17

the values of GCV and PCV inferred that the variation is not only due to genotype but also environment which drastically create variation in expression of set of genes of character (Mahadeviah *et al.,* 2016 and Uday *et al.,*2014).

High PCV and GCV values were observed for the characters like number of panicles per m^2, number of productive tillers per panicle, grain yield per plant indicating huge amount of variability for these characters in genotypes selected. Moderate GCV and PCV values were observed for the characters plant height, number of tillers per panicle, grain length, grain breadth, L/B ratio and biomass indicating moderate level of variability and low amount of variation were observed for the days to 50% flowering, days to maturity, panicle length, test weight, spikelet fertility as they have low values of GCV and PCV and also it reflects the high influence of environment on expression of the characters. Similar results were in true with findings of Iqbal *et al.* (2018), Uday *et al.* (2014), Shashidhara *et al.* (2019) and Farhad *et al.* (2015).

High GCV and PCV values coupled with high heritability and high genetic advance were observed for the characters *viz.,* number of panicles per m^2, number of productive tillers per panicle and grain yield per plant indicating less influence of environment on the expression of these characters and are governed by additive gene action indicating the perfect criteria for selection during breeding programme. Similar results were confirmed with findings of Ratnakar *et al.* (2012). Hence, the characters which are having high GCV and PCV values along with high heritability with high genetic advance over mean are more reliable characters for effective selection for further improvement during breeding programme.

Correlation studies revealed that grain yield was known to be positively correlated with panicle length, number of tillers bearing panicles, number of productive tillers per panicle, number of panicles per m^2, grain yield per plant, grain length, grain breadth, L/B ratio, biomass and Spikelet fertility indicating indirect selection of these characters could be helpful to improve the grain yield. Hence selection for this specific character was known to have correlated response in other yield attributing characters. Some characters *viz.,* days to maturity, days to 50%

Table 3. Phenotypic correlation coefficients among grain yield and its thirteen component traits in rice genotypes (*Oryza sativa* L) over six locations

	DF	DM	PH	PL	NTP	NPM	NPTP	GL	GB	L/B	TW	BM	SFR	GY/P
DF	1	0.514*	-0.133	-0.356	-0.695**	-0.547*	-0.686**	-0.334	-0.128	-0.113	-0.101	-0.055	-0.17	-0.532*
DM		1	0.019	-0.147	-0.128	-0.243	-0.11	-0.072	0.281	-0.386	-0.155	-0.068	0.115	-0.149
PH			1	0.544*	0.034	-0.286	0.01	0.575**	0.323	0.101	-0.005	-0.052	0.075	-0.232
PL				1	0.358	0.298	0.342	0.449*	0.169	0.205	0.377	0.222	0.167	0.262
NTP					1	0.826**	0.992**	0.526*	0.476*	-0.106	0.335	0.424	0.641**	0.906**
NPM						1	0.838**	0.363	0.292	-0.044	0.449*	0.407	0.576**	0.893**
NPTP							1	0.511*	0.476*	-0.119	0.308	0.379	0.674**	0.916**
GL								1	0.594**	0.157	0.496*	0.461*	0.604**	0.446*
GB									1	0.693**	0.452*	0.015	0.653**	0.411
L/B										1	-0.091	0.456*	-0.242	0.089
TW											1	0.519*	0.273	0.487*
BM												1	0.307	0.465*
SFR													1	0.639**
GY/P														1

DF= days to 50% flowering, DM= days to maturity, PH= plant height, NTP= number of tillers bearing panicle,
NPM= number of panicles per m^2, NPTP= number of productive tillers bearing panicles, GL= grain length, GB= grain breadth, L/B ratio, TW=test weight, BM= biomass, SFR= seed fertility ratio, GY/P =grain yield per plant

flowering and plant height was found to be negatively correlated with grain yield indicated early flowering, early maturity and semidwarf genotypes are known to be high yielding and better adaptable to various climatic conditions without much affecting the grain yield (Table 3) and also grain improvement becomes very difficult while practising selection if the characters are negatively correlated with yield. Similar results are confirmed with findings of Ratnakar *et al*. (2012) and Manjappa *et al.* (2014).

Conclusion

The present study concludes that, the grain yield can be improved through the selection of the characters *viz*., number of productive tillers per panicles, number of panicles per m^2, number of tillers bearing panicles since they have high GCV values and there is no much difference in GCV and PCV values and also are positively associated with grain yield. Hence, for effective breeding programme selection is most reliable for these characters as they are governed by additive gene action.

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