Electronic Journal of Plant Breeding,
ISSN 0975-928X
DOI : 10.5958/0975-928X.2016.00023.5

Analysis of Variability and Character Association in Indigenous Aromatic Rice (*Oryza sativa* L.)

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(Received: May 2015; Accepted: July 2015)

Abstract

Sixty rice genotypes were evaluated during kharif 2013 for sixteen quantitative and quality traits to examine the nature and magnitude of variability, heritability, genetic advance and correlation. Analysis of variance revealed that the differences among sixty genotypes were significant for all the characters. The characters *viz.*, number of effective tillers per plant, seeds per panicle and brown rice length exhibited high Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV). Small differences between GCV and PCV were recorded for all the characters studied which indicated less influence of environment on these characters. The characters *viz.*, plant height, days to 50 per cent flowering, days to maturity and seeds per panicle exhibited high heritability coupled with high genetic advance indicating that simple selection could be effective for improving these characters. Grain yield per plant had significant and positive correlation with days to 50% flowering, days to maturity, plant height, effective tillers per plant, panicle length, seeds per panicle and kernel breadth after cooking.

Keywords: Variability, heritability, genetic advance, correlation, Rice.

Introduction

Rice (*Oryza sativa* L.) is a staple food crop for more than 40% of the world population. Millions of people depend on it, as a source of food and income. Thus, it requires a continuous improvement in productivity, besides profitability in rice farming system on sustainable basis. Apart from yield, food consumption pattern in the recent years has encouraged the attention towards grain quality. Aromatic rice has a special place in world rice market. There is an increasing demand for the production of high grain quality aromatic rice in India due to its export earnings and rising standard of living. India has an immense wealth of aromatic short grain rices. But a lot has been already lost as an aftermath of the green revolution where major emphasis was on yield rather than quality (Singh and Singh, 1998). This is despite the fact that some of the non basmati scented rices are much superior to basmati types with respect to traits like aroma, kernel elongation after cooking, fluffiness, taste, etc. Nevertheless, due to the special attachment of the farmers with Basmati rices, a large number of them are still in existence.

The cultivation of small and medium grain non basmati scented rices have adapted to specific localities and conditions, but are widely distributed in different parts of the country. All the traditional varieties are tall, photosensitive, with average to very strong aroma, and up to 100 to 200 per cent of kernel elongation after cooking, but have long duration and low yields. Therefore, there is urgentneed to improve the yield potential of such rice. The present investigation was carried out with the objectives of estimating the genetic variability in aromatic short grain rice for yield, yield attributing characters and quality traits.

Materials and Methods

The present experiment was conducted with 60 genotypes collected from different regions (table-3) during *kharif* 2013 at Agriculture Research Farm, Banaras Hindu University in randomized complete block design. Each entry was sown in five row plots of 5m length with 20 cm inter row space with three replications. Five plants from each replication were selected at random and observations were recorded on 16 characters viz., days to 50% flowering, days to maturity, plant height (cm), effective tillers per plant, panicle length (cm), seeds per panicle, seed weight (g), brown rice length (mm), brown rice width(mm), kernel length(mm), kernel breadth(mm), kernel length after cooking(mm), kernel breadth after cooking(mm), alkali spread value, AC- amylose content, yield per plant(g). Days to 50 percent flowering and Days to maturity was computed on plot basis. The mean over replication of each character was subjected to statistical analysis. The phenotypic, genotypic coefficient of variability (PCV, GCV), heritability in broad sense and expected genetic advance at 5 percent selection intensity were computed by using formulae suggested by Johnson *et al* (1955)**.** The phenotypic and genotypic correlations were calculated following the method of Singh and Choudhary (1985).

Results and discussion

Greater variability in the initial breeding material ensures better chances of producing desired forms of a crop plant. Thus, the primary objective of germplasm conservation is to collect and preserve the genetic variability in indigenous collection of crop species to make it available to present and future generations. The analysis of variance indicated the existence of significant differences among all the genotypes for all the traits studied. Analysis of variance revealed significant differences within the genotypes for all the traits studied. The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values. Among the yield characters, highest PCV and GCV values were recorded for effective tillers per plant, followed by seeds per panicle and the lowest PCV and GCV values were recorded for panicle length. Among the grain quality characters highest PCV and GCV values were recorded for brown rice length, followed by kernel length and the lowest values were recorded for amylose content (Table-1). Similar findings were also reported by Rita *et al.,* (2009) and Gangashetty *et al.,* (2013).Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the traits studied indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. The characters studied in the present investigation expressed low to high heritability estimates ranging from 53 to 99 percent. Among the yield characters, highest heritability was recorded for days to maturity followed by days to flowering, plant height and 100 seed weight, whereas, all grain quality characters exhibited high heritability. Similar findings were also reported by Karthikeyan *et al.,* (2010) and Anandrao *et al.,* (2011). High heritability values indicate that the characters under study are less influenced by environment in their expression. High heritability indicates the scope of genetic improvement of these characters through selection.

The genetic advance is a useful indicator of the progress that can be expected as a result of exercising selection on the pertinent population. Heritability in conjunction with genetic advance gives a more reliable index of selection value (Johnson *et al.* 1955). Genetic advance was highest for plant height followed by days to 50% flowering and days to maturity and lowest for 100 seed weight among yield characters where as all grain quality characters exhibited low genetic advance. The characters *viz.,* plant height, days to 50 per cent flowering, days to maturity and seeds per panicle exhibited high heritability coupled with high genetic advance indicating that simple selection could be effective for improving these characters. The genetic advance as per cent of mean was highest for seeds per panicle followed by 100 seed weight and effective tillers per plant while moderate value recorded by panicle length among yield characters, whereas, for grain quality characters, brown rice length showed highest genetic advance as per cent of mean, while moderate value was recorded for amylose content (Table-1). Similar findings were also reported by Patil *et al.,* (2003) and Gangashetty *et al.,* (2013). The information on genetic variation, heritability and genetic advance helps to predict the genetic gain that could be obtained in later generations, if selection is made for improving the particular trait under study.

The genotypic correlations in general were higher than the corresponding phenotypic correlations. This is due to the redesign effect of environment on character association at the tillers per plant, seeds per panicle, days to maturity, days to 50 per cent flowering, kernel breadth after cooking, panicle length and kernel breadth at both genotypic and phenotypic levels indicating the importance of these characters for yield improvement.

The correlation analysis revealed that there is significant and positive association of grain yield with days to 50% flowering, days to maturity, plant height, effective tillers per plant, panicle length, seeds per panicle and kernel breadth after cooking at both phenotypic and genotypic level. When characters having direct bearing on yield are selected, their associations with other characters are to be considered simultaneously as this will indirectly affect yield. Significant positive correlations at both the levels were recorded for days to 50 percent flowering with days to maturity, plant height, effective tillers per plant, seeds per panicle, brown rice width, kernel breadth, kernel breadth after cooking and alkali spread value (Table-2). The observed positive correlation of grain yield with various traits was supported by earlier workers *viz.,* Rao and Srivastava (1999), Rajeshwari and Nandarajan (2004) and Ekka *et al.* (2011) for days to 50% flowering; Chaturvedi *et al.,* (2008), Reddy *et al.,* (2008), Ekka *et al.* (2011) and Rangare *et al.,* (2012) for plant height; Ekka *et al.* (2011) for panicle length; Hari *et al.,* (2006), Nandan *et al.*, (2010) and Rangare *et al.*, (2012) for spikelets per panicle.

Significant negative correlations were noted for 100 seed weight with days to 50 percent flowering, days to maturity, plant height, effective tillers per plant and seeds per panicle (Table-2). Pleiotropy or linkage may also be the genetic reasons for this type of negative association. 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.

The results of correlation coefficients implied that effective tillers per plant, seeds per panicle days to maturity and days to 50 percent flowering may be considered for selection for yield improvement.

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Table- 1. Estimation of Genetic parameters for different quantitative & qualitative characters in indigenous short grain rice**.**

S.No	CHARACTER	PCV	GCV	h^2 (bs)%	GA	GA as % of mean
1	DTF	14.35	14.33	98	36.03	29.47
2	DTM	11.27	11.24	99	34.95	23.09
3	PH	17.52	17.30	98	53.68	35.21
4	ETP	33.16	24.17	53	3.21	36.30
5	PL	12.10	10.16	71	4.69	17.58
6	SP	32.15	30.65	91	26.88	60.18
7	100SW	27.95	27.66	98	0.95	56.36
8	BRL	23.73	23.62	94	2.61	48.43
9	BRW	12.55	12.28	96	0.49	24.77
10	KL	23.40	23.30	99	2.54	47.79
11	KB	13.52	13.02	93	0.49	25.85
12	KLAC	20.63	20.53	96	3.85	42.07
13	KBAC	17.29	16.72	94	0.90	33.31
14	ASV	20.53	18.42	81	1.54	34.05
15	AC	7.52	7.46	98	3.51	15.25
16	Y/P	38.60	28.17	53	8.67	42.36

DTF-days to 50% flowering, DTM-days to maturity, PH- plant height, ETP-effective tillers per plant, PL-panicle length, SP- seeds per panicle, 100SW- seed weight, BRL-brown rice length, BRW- brown rice width, KL-kernel length, KB-kernel breadth, KLAC-kernel length after cooking, KBAC-kernel breadth after cooking, ASV- alkali spread value, AC- amylose content, Y/P-yield per plant.

Table -2. Estimation of genotypic and phenotypic correlation coefficient for different quantitative & qualitative characters in indigenous short grain rice.

Character		DTM	PH	ETP	PL	SP	100SW	BRL	BRW	KL	KB	KLAC	KBAC	ASV	AC	Y/P
DTF	Rg	0.9880**	0.7764**	0.2700**	0.0999	0.6044**	-0.6291**	-0.7559**	0.4040**	-0.7508**	0.5010**	-0.4152**	0.3460**	0.1885*	-0.0514	0.4218**
	Rp	0.9863**	0.7663**	0.1913*	0.0835	0.5770**	-0.6205**	-0.7511**	0.3956**	-0.7462**	0.4832**	-0.4124**	0.3336**	0.1669*	-0.0513	0.3093**
DTM	Rg	**1.0000**	0.8077**	0.2702**	0.1730*	0.6056**	-0.5661**	-0.7069**	0.4526**	-0.7003**	0.5433**	-0.3295**	0.4073**	0.1705*	-0.0803	0.4332**
	Rp		0.7963**	0.1942**	0.1507*	0.5767**	-0.5567**	-0.7011**	0.4430**	-0.6958**	0.5226**	-0.3273**	0.3921**	0.1497*	-0.0807	0.3188**
PH	Rg		**1.0000**	0.0833	0.3734**	0.5104**	-0.3197**	-0.5080**	0.4752**	-0.5149**	0.5853**	-0.0351	0.4443**	0.0091	-0.2100**	0.3721**
	Rp		**1.0000**	0.0556	0.3164**	0.4726**	-0.3111**	-0.5015**	0.4613**	-0.5070**	0.5548**	-0.0347	0.4240**	0.0061	-0.2046**	0.2661**
ETP	Rg			**1.0000**	-0.0941	-0.0670	-0.3365**	-0.2146**	-0.1286	-0.1764*	-0.1342	-0.2277**	0.1700*	0.0392	-0.1057	0.6463**
	Rp			**1.0000**	0.0031	0.0058	-0.2463**	-0.1435	-0.0904	-0.1181	-0.0915	-0.1651*	0.1096	0.0195	-0.0724	0.4742**
PL	Rg				**1.0000**	0.3171**	0.0721	-0.0458	0.3440**	-0.0185	0.3876**	0.3157**	0.2672**	0.1104	-0.3303**	0.3075**
	Rp				**1.0000**	0.2588**	0.0715	-0.0320	0.2638**	-0.0231	0.3087**	0.2555**	0.2183**	0.0917	-0.2716**	0.2046**
SP	Rg					**1.0000**	-0.4961**	-0.5171**	0.2444**	-0.5162**	0.3441**	-0.2721**	0.2549**	0.0243	0.0772	0.5548**
	Rp					**1.0000**	-0.4615**	-0.4936**	0.2358**	-0.4863**	0.3162**	-0.2525**	0.2338**	0.0457	0.0739	0.3892**
100 SW	Rg						**1.0000**	0.8340**	-0.0253	0.8381**	-0.1054	0.7148**	-0.0923	-0.0968	-0.1253	-0.2723**
	Rp						**1.0000**	0.8229**	-0.0234	0.8256**	-0.0964	0.7033**	-0.0929	-0.0835	-0.1230	-0.1932**
BRL	Rg							**1.0000**	-0.3968**	0.9811**	-0.5319**	0.7072**	-0.2982**	-0.1396	-0.1172	-0.2339**
	Rp							**1.0000**	-0.3869**	0.9738**	-0.5107**	0.6987**	-0.2892**	-0.1265	-0.1155	-0.1612*
BRW	Rg								**1.0000**	-0.4320**	0.8522**	-0.0563	0.5704**	0.0198	-0.1318	0.1248
	Rp								**1.0000**	-0.4209**	0.8168**	-0.0505	0.5374**	0.0398	-0.1274	0.0624
KL	Rg									**1.0000**	-0.5279**	0.7210**	-0.3284**	-0.1144	-0.1151	-0.2236**
	Rp									**1.0000**	-0.5004**	0.7170**	-0.3159**	-0.0956	-0.1144	-0.1686*
KB	Rg										**1.0000**	-0.0900	0.5718**	-0.0074	-0.0836	0.2194**
	Rp										**1.0000**	-0.0839	0.5404**	0.0058	-0.0825	0.1394
KLAC	Rg											**1.0000**	0.0165	0.0500	-0.1720*	-0.0591
	Rp											**1.0000**	0.0250	0.0596	-0.1718*	-0.0644
KBAC	Rg												**1.0000**	0.0234	-0.2348**	0.4080**
	Rp												**1.0000**	0.0515	-0.2275**	0.2320**
ASV	Rg													**1.0000**	0.0543	-0.0323
	Rp													**1.0000**	0.0493	-0.0987
AC	Rg														**1.0000**	-0.1276
	Rp														**1.0000**	-0.0881

* &** represents significant levels at 5% and 1% respectively. DTF-days to 50% flowering, DTM-days to maturity, PH- plant height, ETP-effective tillers per plant, PL-panicle length, SP- seeds per panicle, 100SW- seed weight, BRL-brown rice length, BRW- brown rice width, KL-kernel length, KB-kernel breadth, KLAC-kernel length after cooking, KBAC-kernel breadth after cooking, ASV- alkali spread value, AC- amylose content, Y/P-yield /plan

Table- 3. Origin of rice genotypes.

Genotypes	No. of Accessions	Origin
Adam chini	7	Uttar Pradesh
Jeera battis	1	Uttar Pradesh
Thurun bhog	1	Orissa
Dhana prasad	1	Orissa
Chinnor	1	Madhya Pradesh
Jaiphula	1	Orissa
Dubraj	1	Chhattisgarh
Shakkar chini	1	Uttar Pradesh
Ketki joha	1	Assam
Lal chandan	1	Madhya Pradesh
Jeeriga sambha	1	Tamil Nadu
Jawa phool	1	Madhya Pradesh
Indra bhog	1	Uttar Pradesh
Lanjhi	1	Madhya Pradesh
Tulsi manjari	1	Bihar
Lalmati	1	Uttar Pradesh
Basmati local	6	Uttar Pradesh
Kala namak	11	Uttar Pradesh
Juhi bengal	3	West Bengal
Kanak jeera	7	Uttar Pradesh
Ram bhog	1	Uttar Pradesh
Dhania	1	Uttar Pradesh
Hariram	1	Uttar Pradesh
Shyam jeera	1	Uttar Pradesh
Govind bhog	1	Orissa
Krishna hamsa	1	Andhra Pradesh
Badshahbhog	5	Assam