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Heritability and genetic advance for yield and quality traits in aromatic rice (*Oryza sativa* L.) genotypes

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Abstract

The present investigation was undertaken to study heritability and genetic advance (GA) for grain yield and quality traits in aromatic rice (*Oryza sativa* L.). Four rice hybrids were evaluated to their genetic heritability and genetic advance for quality traits. The analysis of variance illustrated that all the traits differed significantly indicating that enough variation is presenting the studied materials. High heritability coupled with high genetic advance were observed in cross-III (IET-26214 × GAR-1) for grain yield per plant and kernel breadth for cross-II (IET-24617 × NWGR-9081) and cross-IV (IET-26215 × GNR-2); straw yield per plant for all crosses except cross-III (IET-26214 × GAR-1); protein content for cross-IV (IET-26215 × GNR-2); milling for cross-II (IET-24617 × NWGR-9081) and cross-III (IET-26214 × GAR-1) and hulling (%) for cross-I (GR-104 × IET-26215),which indicated that heritability of these traits were under the control of additive gene action and a good scope of selection using their phenotypic performance. Considering, all of these yield and yield related characters could be used for selection in rice breeding programs.

Keywords: aromatic rice, heritability, genetic advance, generation mean analysis

Introduction

Rice is one of the most important food crops in the world. The crop is cultivated in large area but is characterized by very low productivity due to lack of high yielding varieties adapted to different seasons and agronomic conditions at different parts of country. As we know, yield is a complex end product of a number of components most of which are under polygenic control. So, all changes in yield must be accompanied by changes in one or more of the components as have been pointed out by Grafius (1959) [2]. The ultimate goal of any plant breeding programme is to develop improved genotypes which are better than their existing ones in one or more traits which producing the economic yield. Sufficient understanding of the inheritance of quantitative traits and information about heritability of grain yield, its components and quality traits are essential to develop an efficient breeding strategy.

Estimate of heritability serves as a useful guide to the plant breeder. The breeder is able to appreciate the proportion of variation that is due to genotypic (broad sense heritability) or additive (narrow sense heritability) effects, that is, the heritable portion of variation in the first case, and the portion of genetic variation that is fixable in pure lines in the later case. If heritability of a character is very high, selection for the character should be fairly easy because there would be a close correspondence between the genotype and phenotype due to relatively smaller contribution of the environment to phenotype. But for a character with low heritability, selection may be considerably difficult or virtually impractical due to the masking effect of the environment on genotypic effects. Thus, estimates of heritability are useful in predicting the transmission of characters from the parents to their offspring. Heritability and genetic advance are important selection parameters while selection is made based on yield contributing traits. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Therefore, the objective of this study was to assess the heritability and genetic advance (GA) of yield and quality traits in rice genotypes to assist the future breeding programs for yield and quality improvement.

Materials and Methods

The material comprising of seven diversified aromatic and non-aromatic elite lines of rice (GR-104, IET-26215, IET-24617, NWGR-9081, IET-26214, GAR-1 and GNR-2). The four crosses (GR-104 x IET-26215, IET-24617 x NWGR-9081, IET-26214 x GAR-1 and IET-26215 x GNR-2) obtained by crossing of seven diverse parents during summer 2017 at Main

Rice Research Centre, Navsari Agricultural University, Navsari. Backcrossing was done in kharif-2017 with its respective parents. Selfing of F_1s was done in the same season (kharif-2017) to get F_2s. The evaluation trial was conducted in kharif-2018 at Main Rice Research Centre, Navsari Agricultural University, Navsari. The experimental material consisting of six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of each of the four crosses were sown during kharif-2018 in compact family block design with three replications. Each replication was divided in four compact blocks. Each four crosses consisting of six generations were randomly allotted to each plot within a block. Each plot consisted of one row (10 plants) of parents and F_1s, two rows of the backcrosses and four rows of the F_2 generations of each cross. The recommended package of practices was followed to raise a good crop. Observations were recorded on yield and quality traits *viz*., Kernel length (mm), Kernel breadth (mm) Kernel L/B ratio, grain yield per plant(g), Protein content (%), amylose content (%), hulling (%), milling (%) and head rice recovery (%).

Generation mean analysis was conducted using six generations *viz*. parental (P_1 and P_2), F_1, F_2, and backcrosses (BC_1 and BC_2) of four selected crosses involving seven diverse parents. Heritability in broad sense (h^2bs) was estimated according to the formula suggested by (Warner 1952) and estimation of genetic advance was done by following formula given by (Johnson *et al*., 1955) and (Allard, 1960) [7, 4, 1].

The narrow sense heritability, as suggested by Warner (1952) [7] was calculated as follows

$$h^2_{(ns)} = \frac{[2V_{F2}-(V_{BC1}+V_{BC2})]}{V_{F2}} \times 100$$

The expected genetic advance at 5 percent level of selection intensity was estimated by using the following formula.

$$\text{Expected genetic advance} = K \cdot h^2_{(ns)}\, \hat{\sigma}P$$

Where,

h^2 (ns) = Heritability in narrow sense

$\hat{\sigma}P$ = Phenotypic standard Deviation

K = Selection differential

(K = 2.06 at 5% selection pressure)

Expected genetic advance as percent of mean was estimated by the following formula.

$$\text{Expected genetic advance as \% of mean} = \frac{\text{Genetic advance}}{\bar{X}} \text{ x } 100$$

Results and Discussion

The analysis of variance revealed significant differences among the generations of all the four cross for all the traits indicating sufficient diversity present among all the generations under study (Table 1). Thus, there is ample scope for the selection of various quantitative traits for rice improvement.

Heritability is a measure of the efficiency of a selection system in separating genotypes. High, moderate and low heritability are not rigidly defined as it varies with character to character, but the following values are widely accepted (Robinson *et al*. 1949) [5].

1. Low heritability: 0-30%
2. Moderate heritability: 30-60%
3. High heritability:> 60%

The value of expected genetic advance for various characters is demarcated into three categories *viz*., low, moderate and high, as follows (Johnson *et al*. 1955) [4].

1. Low genetic advance: 0-10%
2. Moderate genetic advance: 10-20%
3. High genetic advance: > 20%

Narrow sense may be more helpful in the selection of segregating populations and that is why the genetic advance was calculated on the basis of narrow sense heritability to ascertain more reliable results. The results obtained on these aspects for different characters studied in all the crosses are presented (Table 2).

Table 1: Analysis of variance for six generations for yield and quality traits in aromatic rice genotypes

Source	d.f.	Mean sum of square								
		Kernel length (mm)	**Kernel breadth (mm)**	**Kernel L/B ratio**	**Grain yield per plant (g)**	**Protein Content (%)**	**Amylose Content (%)**	**Milling (%)**	**Hulling (%)**	**Head rice recovery (%)**
Cross-I (GR-104 × IET-26215)										
Replication	2	0.02	0.01	0.06	1.14	0.01	0.05	32.61	18.58	10.00
Generation	5	0.24**	0.33**	0.57**	32.34*	0.60**	5.08**	99.54*	66.74*	276.31**
Error	10	0.03	0.01	0.02	6.14	0.03	0.62	21.54	17.98	11.84
Cross-II (IET-24617 × NWGR-9081)										
Replication	2	0.01	0.01	0.01	0.05	0.11	0.79	30.26	21.43	24.07
Generation	5	0.20*	0.33**	0.24**	45.78*	0.53**	2.40*	119.57**	91.53*	302.56**
Error	10	0.05	0.003	0.03	10.32	0.04	0.56	20.16	24.99	13.89
Cross-III (IET-26214 × GAR-1)										
Replication	2	0.01	0.002	0.01	2.39	0.02	0.39	6.65	27.75	28.77
Generation	5	0.10*	0.34**	0.35**	38.90**	4.43**	1.58*	51.14*	66.97*	115.61**
Error	10	0.02	0.01	0.02	5.07	0.02	0.47	14.17	19.45	15.79
Cross-IV (IET-26215 × GNR-2)										
Replication	2	0.02	0.003	0.01	10.49	0.02	0.31	11.13	16.13	33.52
Generation	5	0.07*	0.40**	0.50**	56.86**	5.28**	3.40**	250.51**	87.00*	172.93**
Error	10	0.01	0.002	0.01	4.51	0.02	0.35	16.72	22.98	12.10

* and **, significant at 5% and 1%, respectively

Table 2: Estimates of heritability and genetic advance for yield and quality traits in aromatic rice genotypes

Estimates (%)	Kernel length (mm)	Kernel breadth (mm)	Kernel L/B ratio	Grain yield per plant (g)	Protein content (%)	Amylose content (%)	Milling (%)	Hulling (%)	Head rice recovery (%)
Cross-I (GR-104 × IET-26215)									
Heritability (BS) %	42.80	89.00	75.40	57.90	15.30	36.90	-17.00	-13.70	-11.80
Heritability (NS) %	97.20	49.60	34.40	94.90	20.40	87.50	16.40	76.30	26.20
Genetic Advance %	17.02	40.26	19.11	60.48	5.81	18.62	6.68	22.32	11.47
Cross-II (IET-24617 × NWGR-9081)									
Heritability (BS) %	48.30	94.80	85.00	58.60	0.60	50.50	43.00	0.80	-111.20
Heritability (NS) %	77.30	63.10	32.40	76.80	-0.80	13.30	94.40	4.50	14.10
Genetic Advance %	12.08	54.78	17.95	46.87	-0.24	2.10	41.80	1.48	6.17
Cross-III (IET-26214 × GAR-1)									
Heritability (BS) %	57.30	86.20	73.90	62.40	50.90	58.00	11.70	62.48	16.60
Heritability (NS) %	25.70	53.50	38.10	99.20	5.70	95.40	69.40	19.96	14.90
Genetic Advance %	5.16	44.82	19.96	77.10	1.61	18.82	24.77	5.03	7.92
Cross-IV (IET-26215 × GNR-2)									
Heritability (BS) %	61.40	96.60	87.20	55.48	26.60	5.40	12.80	66.44	-8.40
Heritability (NS) %	19.00	63.00	56.80	43.57	94.20	58.80	12.30	9.41	29.60
Genetic Advance %	3.41	53.03	29.70	26.82	27.40	11.12	5.58	2.97	12.11

Genetic advance was calculated from narrow sense heritability

In cross-I (GR-104 × IET-26215), high narrow sense heritability was recorded for grain yield per plant,kernel length, amylose content and hulling %, whereas in cross-II (IET-24617 × NWGR-9081), for kernel length, kernel breadth, grain yield per plant, amd milling % showed high narrow sense heritability. For cross-III (IET-26214 × GAR-1), grain yield per plant, amylose content and milling % had recorded high narrow sense heritability. In cross-IV (IET-26215 × GNR-2), high narrow sense heritability was recorded for kernel breadth and protein content.

In cross-I (GR-104 × IET-26215), moderate narrow sense heritability was recorded for kernel breadth, kernel L/B ratio, while rest of the traits had low narrow sense heritability for this cross. In case of cross-II (IET-24617 × NWGR-9081), kernel L/B ratio exhibited moderate narrow sense heritability, while rest of the traits had low narrow sense heritability in this cross. Moderate narrow sense heritability recorded for traits *viz*., kernel breadth, kernel L/B ratio in cross-III (IET-26214 × GAR-1), while rest of the traits had low narrow sense heritability in this cross. In case of cross-IV (IET-26215 × GNR-2), kernel L/B ratio grain yield per plant amylose content exhibited moderate narrow sense heritability, while rest of the traits had low narrow sense heritability in this cross.

The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotypes are good reflection of genotypes and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these quality traits but in case of lower heritability, pedigree, sib or progeny test can be employed for genetic improvement. The moderate to low estimates of heritability for most of the traits including yield components indicated the preponderance of non-additive variance for yield and quality attributes in the material under study.

Genetic advance

Since heritability estimates vary with change in environment, experimental material etc. their scope is restricted. Hence, heritability values used in conjunction with the genetic advance would be more reliable than heritability alone (Johnson *et al*., 1955) [4] which will be helpful in forming selection procedures.

High expected genetic advance was recorded for kernel breadth, grain yield per plant and hulling % in cross-I (GR-104 × IET-26215); kernel breadth, grain yield per plant and milling % for cross-II (IET-24617 × NWGR-9081); kernel breadth, grain yield per plant and milling % for cross-III (IET-26214 × GAR-1); kernel breadth, kernel L/B ratio, grain yield per plant and protein content, in cross-IV (IET-26215 × GNR-2).

Moderate expected genetic advance was recorded for kernel length, kernel L/B ratio, amylose content and head rice recovery in cross-I (GR-104 × IET-26215); kernel length and kernel L/B ratio, in II (IET-24617 × NWGR-9081); kernel L/B ratio and amylose content in cross-III (IET-26214 × GAR-1); amylose content and head rice recovery, in cross-IV (IET-26215 × GNR-2).

Heritability coupled with genetic advance:

High heritability coupled with high genetic advance were estimated in cross-I (GR-104 × IET-26215) for grain yield per plant and hulling %, in II (IET-24617 × NWGR-9081) for kernel breadth, grain yield per plant and milling %, in cross-III (IET-26214 × GAR-1) for grain yield per plant and milling %, in cross-IV (IET-26215 × GNR-2) for kernel breadth, kernel L/B ratio and protein content, which indicated that heritability of these traits were under the control of additive gene action. For improvement of such traits, selection will be rewarding.

Moderate to high heritability coupled with high to moderate genetic advance was for kernel length, kernel breadth, grain yield per plant and amylose content in cross-I (GR-104 × IET-26215); kernel length and kernel L/B ratio in cross-II (IET-24617 × NWGR-9081); kernel L/B ratio and amylose content in cross-III (IET-26214 × GAR-1); kernel L/B ratio, grain yield per plant, amylose content and head rice recovery in cross-IV (IET-26215 × GNR-2); which indicate that heritability of these traits were due to additive gene action, suggesting that these characters can be further improved by adopting selections in succeeding generations.

Low heritability coupled with low genetic advance was recorded for protein content and milling % in cross-I (GR-104 × IET-26215); amylose content, hulling % and head rice recovery in cross-II (IET-24617 × NWGR-9081); kernel length, protein content, hulling % and head rice recovery in cross-III (IET-26214 × GAR-1); kernel length, milling % and hulling % in cross-IV (IET-26215 × GNR-2); which indicated that heritability was under the control of non-additive gene action for this cross and selection would be ineffective for this trait.

Conclusion

The higher estimates of heritability indicates that these traits were comparatively less affected by environment and their phenotypes are good reflection of genotypes and thus possessed paramount importance in making selection of superior genotype on the basis of phenotypic performance of these quality traits but in case of lower heritability, pedigree, sib or progeny test can be employed for genetic improvement. The moderate to low estimates of heritability for most of the traits indicated the preponderance of non-additive variance for yield and quality attributes in the material under study.

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