Study of Genetic Variability for Yield and Yield Attributes and Bran Oil Content in Maintainer Lines of Rice (*Oryza sativa* L.)

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ABSTRACT

The present investigation was carried out during *kharif,* 2016 (June to October) at Regional Agricultural Research Station, Jagtial, Telangana, India to study the phenotypic coefficient of variation and genotypic coefficient of variation, heritability (bs), and genetic advance (GA) for yield contributing characters of 40 maintainer lines of rice. The experiment was designed in RBD replicated twice. Analysis of variance revealed significant differences among rice lines for 15 quantitative traits. The phenotypic coefficient of variation (PCV) value was higher than the genotypic coefficient of variation (GCV), indicating a negligible environmental influence in the phenotypic expression of traits. The PCV and GCV values were highest for the grains panicle^{-1} and moderate for bran oil percentage, indicating that these two characteristics have a higher variability within and between populations than other characteristics. All of the characters had high heritability. The range of bran oil content in the 40 maintainer lines used to assess the range of bran oil content was from 11.87% in line B11 to 19.35% in line JMS17B. The genetic advancewas greatest for number of grains panicle^{-1} (87.86%) and modest for bran oil %. The high and moderate estimations of genetic advance show that traits such as the number of tillers plant^{-1}, test weight, L/B ratio, plant height, bran oil percentage, kernal breadth, grain yield plant^{-1} and kernal length were selected. The genetic advance obtained from the high and moderate estimates indicate that the selection for these characters can be used to improve the yield of the crop.

KEYWORDS: Coefficient of variation, genetic advance, heritability, maintainer lines

1. INTRODUCTION

The development and widespread use of hybrid rice varieties using male sterility and fertility restoration systems has been one of the turning moments in the history of rice improvement. The hybrid rice technology now in use seeks to increase yield through greater levels of exploitable heterosis (Islam et al., 2010). All of the hybrids that have been released in the nation are based on the Wild Abortive (WA) system, a single source of cytoplasmic male sterility (CMS). Hybrids with a narrow genetic base and genetic vulnerability may be more vulnerable to sudden outbreaks of disease and insect pests as a result of long-term reliance on a single CMS source. The incorporation of the alloplasmic cytoplasm of suitable species can potentially enhance the genetic basis of the sterile cytoplasm and decrease genetic vulnerability. (Hyde et al., 2012). Hence, it is essential to generate maintenance lines with a wide genetic basis for major biotic stresses in order to include them into CMS lines, which will aid in the generation of hybrids with resistance to major biotic stresses.

Genetic variability plays an important role in crop breeding for selecting the elite genotypes for making rapid improvement in yield and other desirable characters as well as is selecting the potential parent for hybridization programmes (Mishra et al., 2015). Greater the variability in a population, there will be the greater chance for effective selection for desirable types (Vavilov, 1951). The genotypic and phenotypic coefficient of variation helps in estimating the magnitude of genetic variation present in a population (Mallor et al., 2011b). Heritability (broad sense) is defined as the proportion of phenotypic variance comprising the sum of additive, dominance, and epistatic effects (Nyquist, 1991, Falconer and Mackay, 1996). Heritability is important parameter in quantitative genetics to determine the response to selection (Piepho and Mohring, 2007). Heritability estimates give a measure of transmission of characters from one generation to another (Sabri et al., 2020, Saidaiah et al., 2021a, Saidaiah et al., 2021b, Saidaiah et al., 2021c). knowledge of heritability of a trait assists in development of efficient breeding strategies by assessing the degree of transmissibility of a character (Porta et al., 2014, Netrapal and Chowdhary, 1988, Singh et al., 2010) and enables selection for enhancing the genetic progress (Ghodke et al., 2020, Gedam et al., 2021). There is a strong relationship between heritability and genetic advance. Genetic advance describes the degree of gain acquired in a trait under a particular selection pressure (Ogunniyan and Olakojo, 2014). High genetic advance along with high heritability offers the most effective condition for selection of a specific trait (Islam et al., 2016).

Rice bran is a by product of the rice milling process. In several nations, including Japan, India, Korea, China, and Indonesia, rice bran oil (RBO) is widely used as a cooking oil. The benefits of rice bran oil for health and nutrition are also well-established. Gamma oryzanol, phytosterols, polyphenols, and squalene are just a few of the micronutrients found in RBO's unsaponifiable fraction, which is abundant in RBO. It contains a lot of omega-3 fatty acids and is high in the antioxidants oryzanol, tocotrienol, tocopherol, and squalene (Pali, 2013). The present study was aimed to investigate the phenotypic coefficient of variation and genotypic coefficient of variation, heritability (bs), and genetic advance (GA) for yield contributing characters of 40 maintainer lines of rice.

2. MATERIALS AND METHODS

The experimental investigation was conducted during *kharif,* 2016 (June to October) at Regional Agricultural Research Station, Polasa, Jagtial, Telangana State, India where all the 40 maintainer lines were sown in the nursery on raised beds in a Randomized Block Design replicated twice (Table 1). Twenty-five days old seedlings of each genotype were transplanted plot by adopting a spacing of 20 cm between rows and 15 cm between plants. Five plants of each genotype in each replication were selected are used to record data on days to 50% flowering (DFF), days to maturity (DM), plant height (PH), number of tillers per plant (NTPP), panicle length (PL), number of grains per panicle(NGPP), kernal length (KL), kernal breadth (KB) L/B ratio (L/B), 1000 grain weight (TW), hulling percentage (HL), milling percentage (ML), head rice recovery percentage (HRR), grain yield per plant (GYP), bran oil percentage (BO).

Table 1: List of rice genotypes (maintainer lines) utilized for the study

Sl. No.	Genotype	Source
1.	B1	RARS, Jagtial
2.	B2	RARS, Jagtial
3.	B3	RARS, Jagtial
4.	B4	RARS, Jagtial
5.	B5	RARS, Jagtial
6.	B6	RARS, Jagtial
7.	B7	RARS, Jagtial
8.	B8	RARS, Jagtial
9.	B9	RARS, Jagtial
10.	B11	RARS, Jagtial
11.	B12	RARS, Jagtial
12.	B13	RARS, Jagtial
13.	B15	RARS, Jagtial

Table 1: Continue...

Sl. No.	Genotype	Source
14.	B16	RARS, Jagtial
15.	B17	RARS, Jagtial
16.	B18	RARS, Jagtial
17.	B19	RARS, Jagtial
18.	B20	RARS, Jagtial
19.	B22	RARS, Jagtial
20.	B23	RARS, Jagtial
21.	B24	RARS, Jagtial
22.	B35	RARS, Jagtial
23.	B42	RARS, Jagtial
24.	B86	RARS, Jagtial
25.	B88	RARS, Jagtial
26.	JMS11B	RARS, Jagtial
27.	JMS13B	RARS, Jagtial
28.	JMS14B	RARS, Jagtial
29.	JMS17B	RARS, Jagtial
30.	JMS18B	RARS, Jagtial
31.	JMS19B	RARS, Jagtial
32.	JMS20B	RARS, Jagtial
33.	JMS21B	RARS, Jagtial
34.	CMS11B	IRRI, Philippines
35.	CMS14B	IRRI, Philippines
36.	CMS23B	IRRI, Philippines
37.	CMS46B	IRRI, Philippines
38.	CMS52B	IRRI, Philippines
39.	CMS59B	IRRI, Philippines
40.	CMS64B	IRRI, Philippines

2.2. Statistical analysis

2.2.1. Variance

The genotypic and phenotypic variance was calculated as per the formulae (Burton and Devane, 1953)

Genotypic variance (σ^2_g)=(Mean sum of squares due to treatments-Mean sum of squares due to error)/Number of replications

Phenotypic variance (σ^2_p)=(σ^2_g)+(σ^2_e)

Where, (σ^2_e)=Error variance

2.2. Genotypic and phenotypic coefficients of variance

The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer, (1981).

Genotypic coefficient of variation=(Genotypic standard deviation/Mean)×100

Phenotypic coefficient of variation=(Phenotypic standard deviation/Mean)×100

Categorization of the range of variation was effected as proposed by Sivasubramanian and Madhavamenon (1973).

<10%: low

10–20%: Moderate

>20%: high

2.3. Heritability and genetic advance

2.3.1. Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h²) in the broad sense was calculated according to the formula given by Allard (1960).

$h^2 = \sigma^2_g / \sigma^2_p$

Where,

h²=Heritability in broad sense

σ^2_g=Genotypic variance

σ^2_p=Phenotypic variance (σ^2_g)+(σ^2_e)

σ^2_e=Environmental variance

As suggested by Johnson et al. (1955) (h²) estimates were categorized as:

Low: 0–30%

Medium: 30–60%

High: Above 60%

2.4. Genetic advance (Expected)

Genetic advance refers to the expected gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$GA = K.h^2(b).\sigma_p$

Where,

GA=Expected genetic advance

K=Selection differential, the value of which is 2.06 at 5% selection intensity

σ_p=Phenotypic standard deviation

h² (b)=Heritability in broad sense

In order to visualize the relative utility of genetic advance among the characters, genetic advance as per cent for mean was computed.

Genetic advance as per cent of mean=(GA/Grand mean)×100

The range of genetic advance as per cent of mean was classified as suggested by Johnson et al. (1955).

Low: less than 10%

Moderate: 10–20%

High: more than 20%

3. RESULTS AND DISCUSSION

The 40 maintainer lines for all 15 characters showed highly significant variance analysis differences (Table 2).

Table 2: Analysis of variance for yield and yield attributes in 40 maintainer lines of rice

Sl. No.	Character	Mean sum of squares		
		Replications (d.f.=1)	Treatments (d.f.=39)	Error (d.f.=39)
1.	Days to flowering	0.05	148.04**	0.53
2.	Days to maturity	3.20	113.59**	1.40
3.	Plant height (cm)	0.02	300.81**	1.69
4.	No. of tillers plant^{-1}	7.32**	9.70**	0.22
5.	Panicle length (cm)	0.68	7.21**	0.48
6.	No. of grains panicle^{-1}	101.29	7828.56**	123.48
7.	Kernel length (mm)	0.04*	1.08**	0.04
8.	Kernel breadth (mm)	0.08	0.09**	0.05
9.	L/B ratio	0.17	0.46**	0.01
10.	Grain yield plant^{-1} (g)	1.18	15.36**	0.38
11.	1000-grain weight (g)	0.90	20.37**	0.51
12.	Hulling percentage	11.08**	19.95**	0.41
13.	Milling percentage	0.06	24.82**	0.50
14.	Head rice recovery	14.93*	47.72**	1.45
15.	Bran oil percentage	0.93*	6.40**	0.20

**: Significant at (*p*=0.01) level; *: Significant at (*p*=0.05) level

The lowest yield plant^{-1} among the 40 maintenance lines was found by B88 with 19.00 g, the highest by B16 with 29.80 g, and the overall value was 24.91 g. The number of grains panicle^{-1}, a yield-related trait, wasrecorded as being lowest for B42 with 76.50 and highest for JMS 18B with 333.80, with a mean performance of 143.26 grains plant^{-1} across all genotypes. With a mean performance of 12.57, the number of tillers plant^{-1} varied from 7.70 in B88 to 16.70 in B18. With a mean value of 19.68 g, test weight ranged from 12.77 g for JMS17B to 25.75 g for B3. The mean performance was 14.96%, while B11 reported the lowest bran oil content 11.88%. JMS17B recorded the greatest bran oil content was 19.35% (Table 3).

It is calculated by dividing the standard deviation by the mean. A higher coefficient of variation indicates a higher degree of variability among the observations. A lower coefficient of variation indicates a lower degree of variability among the observations. The PCV is an estimate of how much variation there is in a given trait among individuals within a population. It is the ratio of the standard deviation of the observed phenotypic values to the mean. This measure is used to detect the differences in performance between individuals in a population. The GCV is an estimate of the degree of variability among individuals due to genetic factors. It is the ratio of the variance of the genotypic values to the mean. This measure is used to detect the differences in performance between individuals due to genetic factors. In general; the PCV will be much higher than the GCV because the environment can have a much larger effect on the expression of a trait than the genes can. However, it is important to note that the environment can also interact with the genetic factors to influence the expression of a trait, so the PCV and GCV may be similar in such cases (Table 3). Days to 50% blooming and kernal length (0.04%) were the lowest differences between PCV and GCV, followed by plant height (0.06%), days to maturity (0.08%), hulling percentage (0.08%), and milling percentage (0.09%). The change was less than 1%, showing that the environment had a relatively small impact on how each character expressed them. For hulling percentage and the number of grains panicle^{-1}, respectively, PCV ranged from 3.82% to 44.02% while GCV ranged from 3.74% to 43.33%. Number of tillers plant^{-1}, test weight, L/B ratio, plant height, bran oil percentage, kernal breadth, grain yield plant^{-1}, and kernal length all had moderate PCV and GCV estimations (10–20%). Early reports by (Padmaja et al., 2008, Mishu et al., 2016). The High PCV and GCV estimates for number of grains panicle^{-1} of ample variability among the rice genotypes and the possibility of improvement through selection. Early reports by (Gangashetty et al., 2013).

Heritability ranged from 87% in panicle length to 99% in

Table 3: Genetic parameters for 15 characters estimated from 40 maintainer lines

Characters	Range		mean	CV	CD (*p*=0.05)	SEm±	Coefficient of variation %			h²	GA (%)
	lowest	highest					ECV	PCV	GCV		
DFF	74.50	118.50	86.20	0.8503	1.48	0.52	0.85	10.00	9.96	0.99	20.45
DM	109.50	149.50	120.65	0.9825	2.40	0.84	0.98	6.29	6.21	0.98	12.63
PH	77.60	151.00	101.03	1.2877	2.63	0.92	1.29	12.17	12.11	0.99	24.8
NTP	7.70	16.70	12.57	3.7825	0.96	0.34	3.78	17.73	17.33	0.96	34.87
PL	17.50	27.90	24.31	2.8752	1.41	0.49	2.88	8.07	7.54	0.87	14.52
NGP	76.50	333.80	143.26	7.7571	22.48	7.86	7.76	44.02	43.33	0.97	87.86
KL	5.15	8.25	6.76	0.9756	0.13	0.05	0.98	10.90	10.86	0.99	22.27
KB	1.65	2.70	1.92	3.7484	0.15	0.05	3.75	11.82	11.21	0.9	21.91
LB	2.06	4.40	3.56	3.58	0.26	0.09	3.58	13.79	13.31	0.93	26.48
GYP	19.00	29.80	24.91	2.47	1.25	0.44	2.47	11.27	10.99	0.95	22.09
STW	12.77	25.75	19.68	3.66	1.46	0.51	3.66	16.42	16.01	0.95	32.15
HL	75.11	89.76	83.62	0.77	1.30	0.46	0.77	3.82	3.74	0.96	7.54
ML	68.91	80.90	75.81	0.93	1.43	0.50	0.93	4.69	4.60	0.96	9.29
HRR	51.73	71.89	64.04	1.88	2.44	0.85	1.88	7.74	7.51	0.94	15.01
BO	11.88	19.35	14.96	3.03	0.92	0.32	3.03	12.15	11.77	0.94	23.48

Days to 50% flowering followed by (99%), plant height (99%) and kernel length (99%). Among 40 maintainer lines, heritability for all the characters was high also reported by Padmaja et al. (2008), Manjunatha and Kumara (2019), Jayasudha and Sharma (2010), Fiyaz et al. (2011) and Anyaoha et al. (2018). Genetic gain is the improvement in the average value of a trait within a given population over time. This is typically achieved through selective breeding, in which the most desirable traits are allowed to reproduce, thus increasing the frequency of those traits in the population. A high heritability value for character does not always turn into a high genetic gain according to Panse and Sukatme (1954), because heritability only measures the amount of variation in a trait that can be explained by genetic factors. It does not measure the amount of genetic gain that can be achieved through selective breeding or other genetic manipulation. Genetic gain is the increase in the value of a trait resulting from selection or other genetic manipulation. The anticipated genetic gain would be low if the heritability was primarily caused by non-additive genetic effects (dominance and epistasis), and large if the heritability was primarily caused by additive effects. Therefore, estimating genetic advancement as a percentage of the mean can be used as a direction in this regard.

Genetic advance is the gradual change in the genetic composition of a population over time, usually due to natural selection. This process is also known as evolutionary change. It can also be caused by artificial selection, which is when

breeders select for certain traits in an organism. Genetic advance can lead to new species or changes in existing species over time.

Estimates of genetic advance for head rice recovery, panicle length, and days to maturity were moderate. High genetic advancement in terms of grain panicle⁻¹, tillers plant⁻¹, test weight, L/B ratio, plant height, bran oil percentage, kernal length, and days to 50% flowering. All of these traits displayed estimates of moderate to high genetic advancement, suggesting that selection for these traits will be successful for further improvement, as earlier reported by Manjunatha and Kumara (2019) and Padmaja et al. (2008).

The range of variation observed for bran oil content ranged from 11.87 to 19.35% with a mean value of 14.95%. The genotype B11 (11.87%) had low bran oil content while the genotype JMS17B (19.35%) had maximum bran oil content. Highest bran oil content was recorded four genotypes JMS19B (19.35%), B23 (18.70%), B35 (18.55%) and B42 (18.00) presented in (Table 4). In almost a similar findings, rice bran contained 18–23% oil. It is oil that is abundant in both vital fatty acids and nutritional components (Roberts et al., 2019). According to Awad-Allah et al. (2022) stabilised rice bran NRL 66 had the highest crude protein content, which was 17.85% and 17.75%, followed by NRL63, which had a value of 17.38% and 17.30%, and NRL64 had the lowest value, which was 16.36% and 16.30% for stabilised rice bran over the two years, respectively.

Table 4: Mean of 15 characters in 40 maintainer lines of rice

Lines	DFF	DM	PH	NTPP	PL	NGPP	KL	KB	L/B	GYP	TW	HL	ML	HRR	BO
B1	85.50	119.50	96.00	12.50	25.80	78.50	6.45	1.85	3.49	25.00	19.65	86.76	74.18	65.64	13.10
B2	88.50	122.50	93.55	9.55	26.10	125.50	6.85	1.95	3.52	21.15	18.50	81.87	73.03	69.88	12.85
B3	84.50	119.50	99.95	10.10	26.80	81.50	6.65	2.35	2.83	22.15	25.75	85.78	69.99	61.63	13.10
B4	88.00	122.00	90.85	14.70	21.85	82.76	6.45	1.75	3.69	27.00	17.96	88.22	74.65	57.95	12.65
B5	75.50	111.00	95.65	16.20	24.00	152.80	6.85	1.95	3.52	29.45	21.00	81.58	77.93	67.89	13.80
B6	76.50	112.00	102.30	12.70	23.80	146.50	6.65	1.95	3.41	24.00	20.09	83.12	78.30	69.61	16.25
B7	87.50	121.50	100.20	13.50	24.40	141.50	6.45	1.85	3.49	26.10	19.00	84.82	77.23	68.10	13.75
B8	76.50	111.00	103.50	14.30	24.40	97.63	6.45	1.80	3.59	27.75	18.60	84.17	78.65	71.89	13.90
B9	84.00	117.50	106.20	11.50	25.50	86.78	8.05	1.85	4.35	25.05	18.99	76.83	76.89	67.80	13.90
B11	85.50	119.50	98.65	14.35	24.90	184.50	7.30	1.95	3.74	27.90	21.75	79.46	75.05	62.83	11.88
B12	85.00	119.50	99.50	11.50	23.70	86.50	6.45	1.95	3.31	25.10	20.58	79.75	75.06	60.73	14.03
B13	75.50	111.00	92.10	9.70	25.50	94.50	6.95	2.05	3.39	22.20	22.00	81.56	78.10	65.90	14.93
B15	76.00	114.50	101.70	13.10	24.60	102.50	7.85	2.05	3.83	26.10	21.50	83.19	72.74	69.00	16.77
B16	84.50	119.00	96.90	16.10	25.00	139.50	7.15	1.95	3.67	29.80	24.47	84.96	77.29	59.78	14.25
B17	84.50	117.50	114.40	12.70	25.70	125.60	7.45	1.95	3.82	24.00	23.23	80.94	80.00	63.83	14.02
B18	87.50	122.50	117.50	16.70	27.90	85.50	7.45	1.85	4.03	29.60	20.85	85.92	78.40	51.73	14.29
B19	85.50	119.50	106.10	14.50	24.70	129.50	7.05	2.05	3.44	26.05	23.05	87.07	75.65	54.66	14.24
B20	84.50	118.50	103.10	14.50	26.10	162.70	8.25	2.05	4.03	25.00	23.17	84.06	78.86	63.57	14.20
B22	94.50	128.50	112.00	13.70	23.00	143.70	8.05	1.95	4.13	25.15	18.45	85.72	68.91	61.74	15.00
B23	77.50	113.50	99.30	11.10	20.90	115.90	7.25	1.65	4.40	22.75	15.08	84.20	72.87	68.52	18.70
B24	86.50	120.50	106.70	9.90	24.90	199.50	5.85	1.65	3.55	21.00	16.78	80.52	69.72	66.10	16.45
B35	93.50	126.50	113.90	15.00	25.90	195.50	6.05	1.85	3.27	28.65	17.16	86.11	80.18	68.57	18.55
B42	98.50	131.50	151.00	14.10	25.80	76.50	6.65	2.55	2.61	26.75	24.07	83.80	71.75	69.87	18.00
B86	99.00	109.50	115.60	11.70	25.20	135.50	7.15	2.05	3.49	23.70	19.96	85.18	69.80	63.03	15.40
B88	74.50	118.50	93.30	7.70	17.50	84.73	5.55	2.70	2.06	19.00	19.87	75.11	69.75	68.69	18.95
JMS11B	83.50	118.50	98.90	9.80	25.00	121.50	6.85	1.85	3.71	20.00	19.55	83.10	71.20	56.58	16.25
JMS13B	93.50	128.50	97.10	11.00	23.40	177.50	6.15	1.75	3.51	25.49	18.22	77.76	75.71	63.66	14.00
JMS14B	96.50	131.50	101.70	14.10	22.30	205.50	5.55	1.65	3.37	25.80	13.61	81.07	78.94	67.95	14.25
JMS17B	90.50	124.50	111.95	12.60	24.40	270.80	7.45	1.85	4.03	25.00	12.77	84.94	79.73	67.84	19.35
JMS18B	89.50	125.00	101.20	12.10	23.60	333.80	7.25	1.65	4.40	24.90	13.00	85.48	80.86	65.73	16.00
JMS19B	91.50	126.50	80.60	13.40	23.20	267.50	5.25	1.85	2.84	26.25	15.97	88.10	76.67	57.11	14.50
JMS20B	83.50	119.00	103.10	14.80	24.40	277.50	5.15	1.65	3.13	27.26	13.22	84.08	78.07	67.88	14.25
JMS21B	77.50	112.50	97.10	8.30	23.20	220.50	6.00	1.75	3.43	19.35	20.80	80.95	80.22	64.08	16.25
CMS11B	74.50	110.50	82.50	14.90	23.30	90.50	6.65	1.85	3.60	28.05	21.66	86.18	78.94	62.21	14.07
CMS14B	86.50	121.50	92.30	10.10	23.70	84.50	6.75	1.95	3.46	22.15	18.91	83.67	78.20	57.87	15.63
CMS23B	77.50	121.50	84.10	10.10	22.30	96.70	6.05	2.05	2.95	22.35	23.34	87.62	80.90	58.24	14.00
CMS46B	118.50	149.50	96.60	13.30	25.20	121.80	7.15	2.05	3.49	26.10	21.75	84.89	71.14	64.81	14.00
CMS52B	80.50	115.50	96.90	12.90	26.30	110.50	6.45	1.85	3.49	24.10	21.99	89.76	75.03	59.18	14.45
CMS59B	91.50	125.50	109.50	13.00	26.80	151.50	7.05	1.85	3.81	27.15	21.88	81.96	76.98	70.19	14.20
CMS64B	94.00	129.50	77.60	10.80	21.15	144.50	7.25	1.65	4.40	22.00	18.98	84.68	74.94	59.62	14.15

4. CONCLUSION

High heritability coupled with high genetic advance was observed for the characters grain panicle[-1], tillers plant[-1], test weight, L/B ratio, plant height, bran oil percentage, kernal length, and days to 50% flowering indicated importance of characters and selection for these traits may be effective.

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