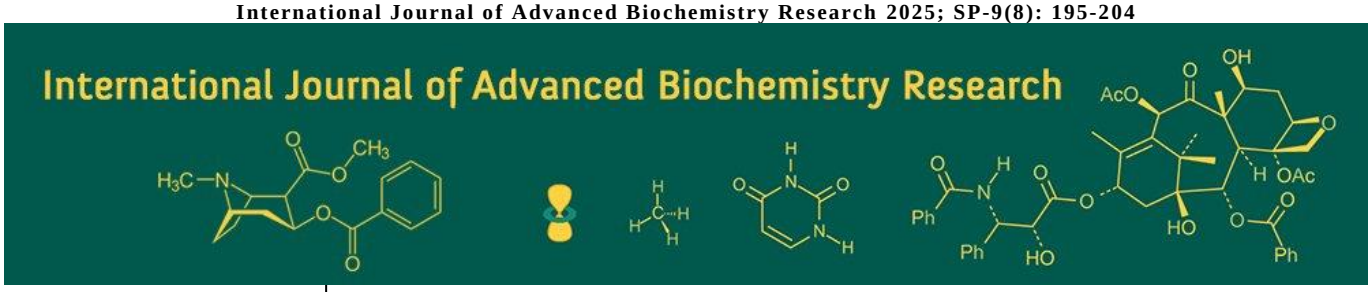

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Investigations on variability, heritability and genetic advance in short and medium slender grain rice (*Oryza sativa* L.) genotypes

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Abstract
Medium and short slender rice lines have lower yields compared to other grain type varieties owing to low genetic diversity and absence of improved cultivars. The present investigation aimed to evaluate genetic variability, heritability and genetic advance in short and medium slender rice grain genotypes to identify the traits for further yield improvement. A total of 56 rice genotypes, along with four checks were evaluated in Alpha Lattice Design at Agricultural Research Station, Kunaram, Telangana, during season *Kharif*, 2024. Analysis of variance revealed that wide range of variability was observed among 60 genotypes for all traits studied. Genotypic coefficient of variation (GCV) was slightly lower than phenotypic coefficient of variation (PCV) for days to 50 percent flowering, plant height, panicle length, panicle weight, 1000-grain weight, kernel length, kernel breadth, length to breadth ratio, head rice recovery, water uptake, volume expansion ratio, and amylose content (%), indicating low environmental influence. Whereas for the traits like, number of productive tillers, number of filled grains per panicle, and grain yield (kg/ha) demonstrating the high environmental influence. Moderate values of the genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) were recorded for days to 50 percent flowering, plant height, panicle weight, number of filled grains per panicle, 1000-grain weight, grain yield and volume expansion ratio, which indicated that the selection for these traits would be fruitful. High heritability coupled with high genetic advance as percent of the mean was observed for days to 50 percent flowering, plant height, panicle weight, number of filled grains per panicle,1000-grain weight, grain yield, water uptake and volume expansion ratio as depicted by box plots suggesting the variability among the trait's. For the traits, number of productive tillers, panicle length, kernel length, kernel breadth, length to breadth ratio and amylose content (%), high heritability along with moderate genetic advance was reported. High heritability was noticed for head rice recovery; however, low genetic advance was recorded for this trait. These findings emphasize the potential of select traits for genetic enhancement of yield and quality in slender grain rice genotypes.

Keywords: Box plot, genetic advance, heritability, rice, variability

Introduction
Rice (*Oryza sativa* L.) is one of the important staple foods in the world as it feeds more than half of the world's population and accounts for over 21% of total calorie intake. Asia dominates rice production and consumption, shouldering more than 90% of the total. In India, rice is cultivated in 47828.29 hectares with production of 137824.58 tones and productivity of 2882 kg ha^{-1} (INDIASTAT., 2023-24) [17]. As rice serves as staple food across the world, mounting of human population caused a simultaneous upsurge in its demand. Rice breeding programs face the daunting task of meeting the escalating demand while ensuring quality. Sometimes breeders have forgotten the quality in the race of development of high yielding varieties to feed the world population.
Phenotypic variability reflects the differences seen among individuals in a population, arising from both their genetic makeup and the influence of their growing environment. Sumanth *et al*., (2017) [30]. The planning and execution of breeding programs, especially those targeting quantitative traits, depend on the magnitude of genetic variability present. Phenotypic variability refers to the observed differences among individuals for a trait, arising from both genetic variation and environmental factors.

In breeding programs, the genotypic coefficient of variation and phenotypic coefficient of variation quantify this variability: GCV reflects the genetic portion, while PCV captures the total observed variation, including environmental influences. Box plot (also known as a box-and-whisker plot) is a standardized way of displaying the distribution of a dataset variability. Box plots are particularly useful for visualizing the spread of data, comparing distributions across groups, and identifying outliers

Heritability and genetic advance are important parameters for improving yield. Yield is a complex trait; enhancing this trait is beneficial when achieved by increasing related traits with high heritability. Singh *et al*., (2021) [28]. High heritability suggests that genetic factors strongly influence the trait, making selection more reliable; conversely, low heritability indicates that environmental effects have a greater impact. Chacko *et al*., (2023) [8].

By combining genetic variability with heritability estimates, breeders can more accurately forecast the expected genetic gain from selection. Heritability alone does not fully predict the effectiveness of selection, but when paired with genetic advance, it becomes a powerful tool for anticipating the response to selection. Therefore, evaluating both genetic variability and heritability is indispensable for designing effective selection strategies tailored to improve seed yield and associated traits. Traits that exhibit high heritability coupled with substantial genetic advance are most likely governed by additive gene action and are strong candidates for effective selection. Anusha *et al*., (2024) [4].

Materials and Methods

The experimental material for the present investigation comprised of 56 genotypes along with 4 check varieties were evaluated at Agricultural Research Station Kunaram (Table 1). The seed was raised on nursery beds and 25 days old seedlings of each entry was transplanted under irrigated system with three replications in Alpha Lattice Design during the *kharif*, 2024 season by adopting spacing of 20 x 15 cm2 between the rows and within the row. The data was collected from five random plants of each genotype for each replication. All the genotypes were phenotyped for fifteen yield, and yield attributing traits and quality traits *viz*., days to 50 percent flowering, plant height (cm), number of productive tillers, Panicle length(cm), panicle weight (g), number of filled grains per panicle,1000-grain weight (g),grain yield (kg/ha), kernel length (mm),kernel breadth (mm), length to breadth ratio (L/B ratio), head rice recovery, water uptake, volume expansion ratio and amylose content (%). Statistical analysis of variance was conducted using R studio software for the analysis related to yield and yield component traits and grain quality traits. Statistical Analysis of variance using descriptive statistics such as mean, standard deviation and coefficient of variation for each one of the fifteen studied traits were computed by using Microsoft excel (2007). The phenotypic and genotypic coefficients of variation (Falconer 1981) [13], heritability (h^2) in the broad sense (Allard 1960) [2], genetic advance (Burton 1952) [7] were calculated, and Box plots using PB tools software.

Table 1: List of short and medium slender grain rice genotypes studied in the present investigation.

S. No.	Designation	S. No.	Designation
1	JGL 17004	31	KNM 15268
2	JGL 11727	32	KNM 15849
3	JGL 28545	33	KNM 15939
4	JGL 27356	34	KNM 16878
5	JGL 33124	35	KNM 16887
6	RNR 15048	36	KNM 17800
7	RNR 31479	37	KNM 17816
8	WGL 962	38	KNM 17835
9	WGL 44	39	KNM 18403
10	WGL 1119	40	KNM 18414
11	KPS 2874	41	KNM 18438
12	KPS 14734	42	KNM 18468
13	KPS 10642	43	KNM 18583
14	DRR DHAN 48	44	KNM 18645
15	CG ZR 2	45	KNM 18666
16	SURABI	46	JAI SRIRAM
17	HPR 2720	47	KAVERI CHINTU
18	KNM 733	48	PUJA GOLD
19	KNM 1638	49	HMT SONA
20	KNM 7715	50	SHREE-101
21	KNM 12368	51	CHITTI POTTI
22	KNM 12449	52	N.R.I.P 0013
23	KNM 12472	53	NLR 4001
24	KNM 12510	54	M.C.M 103
25	KNM 14282	55	BPT 5204
26	KNM 14316	56	BPT 2841
27	KNM 14319	57	CO 51
28	KNM 15148	58	CO 55
29	KNM 15236	59	CO 56
30	KNM 15239	60	T.K.M 13

3. Results and Discussion

3.1. Analysis of variance (ANOVA)

Analysis of variance of 60 short and medium slender genotypes (Table 2). including checks exhibited highly significant differences for the traits i.e. days to 50 percent flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), panicle weight (g), number of filled grains per panicle,1000-grain weight (g),grain yield (kg/ha), kernel length (mm), kernel breadth (mm), length to breadth ratio (L/B ratio), head rice recovery, water uptake, volume expansion ratio and amylose content (%) highlighting considerable variability in the evaluated population. Such pronounced variability could be ascribed to the fact that they originated from different areas, in turn, they present valuable potential for their applications in various selection procedures and hybridization efforts. While mean sum of squares due to replications were found to be non-significant for all the characters except plant height indicating the presence of soil heterogeneity and fertility gradient.

Table 2: Analysis of Variance (ANOVA) for yield, yield components and grain quality characters in rice.

S. No.	Traits	Replications (df =2)	Treatment (df =59)	Block (df =6)	Error (df =112)	CV (%)
1	DFF	21.62	338.9***	9.02	11.01	3.4
2	PH	1110.23***	441.26***	37.25	19.77	4.3
3	NPT	1.03491	2.70337***	0.81282	0.6498	8.9
4	PL	1.1461	15.5812***	2.3133	1.762	5.4
5	PW	0.10208	1.60305***	0.08441	0.06286	6.8
6	NFGPP	1188.6	4547.8***	542.8	545.6	9.3
7	TGW	2.0637	8.1173***	0.1611	0.7747	6.8
8	GY	1469667	5795279***	1241072	651666	11.1
9	KL	0.04425	0.40707***	0.03349	0.3374	3.5
10	KB	0.003085	0.043118***	0.010718	0.00671	5.5
11	LBR	0.027303	0.293707***	0.076087	0.047992	6.2
12	HRR	3.541	32.271***	7.482	4.33	3.4
13	WU	769.4	10877.1***	432.6	493.8	9.7
14	VER	0.35103	1.3629***	0.12499	0.12067	7
15	AC	1.9126	7.129***	0.8976	0.7518	3.7

*= Significant at 5%, **= Significant at 1% and ***Significant at 0.1%

S.No.-Serial number, d.f: degrees of freedom.

DFF: Days to 50% flowering, PH: Plant height, NPT: Number of productive tillers, PL: Panicle length, PW: Panicles weight, NFGPP: Number of filled grains per panicle, TGW: 1000 grain weight, GY: Grain yield, KL: Kernel length, KB: Kernel breadth, LBR: Kernel length to kernel breadth ratio, HRR: Head rice recovery percent, WU: Water uptake, VER: Volume expansion ratio, AC: Amylose content.

3.2. Mean performance

Mean performance and range of genotypes studied are given in (Table 3). Mean for days to 50% flowering was found 98.37 days, while range for this trait was 72.67 (JGL 17004) and 126.33 (KNM 18438). These results indicated that there is a considerable variation for this trait, and earliness, medium and lateness can be created by selecting best genotypes that will ultimately lead to development of early, medium and late duration short and medium slender rice varieties suitable for the various ecosystems. Plant height is an important selection criterion for the development of modern rice varieties. The mean value for plant height was 102.67 cm, with a range of 76.97 cm for (KNM 14397) and 123.73 cm for (RNR 15048). Among all the genotypes, the highest number of productive tiilers recorded for JGL 27356 (11.33), while lowest for RNR31479 (8.76). On the other hand, for the panicle length, longest and shortest panicle length was observed in JGL11727 (30.95 cm) and CHITTI POTTI (20.48), respectively. Plants having greater panicle length, thus producing an increased number of primary and secondary rachis, resulting in an increased number of grains in the panicle, which ultimately improves the yield.

Panicle weight and number of filled grain per panicle are major contributors to high grain yield. The genotype JGL33124 recorded highest panicle weight of 5.58 g, while KNM15236 (363.0) had a greater number of filled grains per panicle. Test weight varied from 9.47 g (CHITTI POTTI) to 18.13 g (CO-51) and grain yield per plant from 4411.11 kg/ha (SURABI) to 10167 kg/ha (KNM1638). This shows as there is great variation among the studied genotypes for this trait, so higher yield variety can be developed through selection.

Grain quality parameters like JGL11727 produced longest kernel (6.29mm), while RNR 31479 reported shortest kernel (4.44 mm) with mean value of 5.23 mm. The accession categorized by narrowest kernel breadth was RNR 31479 (1.18 mm) while SURABI (1.72 mm) produced widest grain width with mean value of 1.50 mm. The result indicated that there is great variation (0.54 mm) for this trait and slender varieties can be developed by selecting best genotypes. Mean for LBR was observed 3.52 with a range of 2.90-4.23 for (KNM15268 and HMT SONA. This data indicated that there was significant differences between cultivars on this trait. The short and medium slender grain cultivars ranged between 50.05 (NLR 4001) to 65.88 (RNR15048) in head rice recovery with a mean range 61.12. The HRR value depends on the grain type, chalkiness, cultivation or management practices and post-harvest technology. The HRR measured the milling quality that greatly influences the rice market price. It is often determined influenced by the environment. From this investigation, line RNR 15048 can be used as donor parent for the development of rice varieties with high grain HRR. On other hand, cultures ranged between 110.51 (NLR 4001) and 354.71 (CO-55)% in water uptake, and from 3.80 (RNR 31479) to 6.42 (KNM 14319) in VER. Regarding amylose content, an intermediate value (20 to 25%) is preferred among the Indian consumers. The highest amylose% (27.09) was recognized with (HPR 2720) while, the lowest values (19.44%) was found with (KPS 10642) rice line. Hence, the selection of varieties with considerable amylose content that can ensure desirable texture of the cooked rice. Sarif *et al*., (2020).

Table 3: Mean performance of 15 characters for 60 rice genotypes.

S. No	Treatment	DFF	PH	NPT	PL	PW	NFGPP	TGW	GY	KL	KB	LBR	HRR	WU	VER	AC
1	JGL 17004	72.67	90.94	7.60	21.45	3.22	156.33	14.76	4935.56	5.47	1.54	3.57	60.88	150.09	6.17	23.58
2	JGL 11727	103.00	120.09	9.53	30.95	4.78	228.20	17.07	9815.56	6.29	1.57	4.02	63.53	321.44	6.22	25.08
3	JGL 28545	105.33	120.60	10.07	27.46	3.50	286.73	14.13	7335.56	5.69	1.39	4.11	63.89	249.44	5.97	24.27
4	JGL 27356	100.00	113.41	11.33	22.72	4.80	263.73	11.13	7077.78	5.24	1.30	4.05	62.83	180.74	4.40	22.64
5	JGL 33124	100.00	112.59	7.57	27.11	5.58	330.00	13.40	7996.67	5.25	1.56	3.37	61.73	330.76	4.68	24.75
6	RNR 15048	97.00	123.73	7.80	25.86	3.26	267.53	12.49	6430.00	5.42	1.39	3.89	65.88	242.76	5.80	24.43
7	RNR 31479	97.33	104.92	6.80	22.01	2.91	220.20	9.60	6013.33	4.44	1.18	3.78	64.03	217.04	3.80	21.83
8	WGL 962	99.33	95.75	8.10	22.19	3.54	255.93	13.27	7013.33	5.19	1.57	3.31	59.91	179.83	5.45	22.10
9	WGL 44	108.00	100.09	9.57	26.10	3.46	277.53	13.89	9172.22	5.32	1.59	3.35	63.69	229.27	5.97	24.00
10	WGL 1119	84.33	86.61	9.40	23.89	4.35	240.27	14.66	7507.78	5.33	1.53	3.50	61.18	227.25	5.27	24.79
11	KPS 2874	92.67	96.57	8.53	22.28	3.60	212.00	13.91	7160.00	4.47	1.39	3.24	58.19	311.68	4.86	23.08
12	KPS 14734	99.33	123.57	9.33	24.99	3.76	271.53	11.54	7281.11	4.69	1.50	3.14	62.05	158.49	6.08	23.40
13	KPS 10642	102.00	116.70	9.10	25.36	4.36	303.00	11.42	6707.78	5.03	1.56	3.22	61.13	185.73	5.52	19.44
14	DRR DHAN 48	100.33	94.11	7.70	22.41	3.24	208.13	12.59	5260.00	5.11	1.63	3.14	61.16	273.08	5.52	20.06
15	CG ZR 2	103.67	99.80	9.17	24.77	4.58	239.93	14.21	5860.00	5.68	1.66	3.41	56.01	144.28	4.40	23.56
16	SURABI	105.33	78.01	8.17	23.12	2.51	232.87	11.92	4411.11	5.15	1.72	3.02	56.75	165.98	5.90	21.69
17	HPR 2720	91.67	123.71	7.93	28.56	3.71	215.53	14.13	5003.33	6.00	1.60	3.75	57.64	243.79	5.34	27.09
18	KNM 733	86.00	101.67	10.67	27.10	3.68	230.20	14.54	8636.67	5.60	1.51	3.72	62.98	278.20	5.85	25.60
19	KNM 1638	90.33	103.44	8.93	26.03	3.48	311.80	14.47	10167.78	5.48	1.49	3.67	63.70	199.63	4.84	23.71
20	KNM 7715	103.00	96.32	9.93	25.44	3.68	292.93	12.86	9868.89	5.39	1.43	3.77	64.08	220.29	4.86	23.69
21	KNM 12368	92.67	93.91	9.07	26.57	4.53	300.13	12.63	8431.11	4.91	1.41	3.49	61.45	225.42	4.61	23.87

DFF: Days to 50% flowering, PH: Plant height, NPT: Number of productive tillers, PL: Panicle length, PW: Panicles weight, NFGPP: Number of filled grains per panicle, TGW: 1000 grain weight, GY: Grain yield, KL: Kernel length, KB: Kernel breadth, LBR: Kernel length to kernel breadth ratio, HRR: Head rice recovery percent, WU: Water uptake, VER: Volume expansion ratio, AC: Amylose content.

S. No	Treatment	DFF	PH	NPT	PL	PW	NFGPP	TGW	GY	KL	KB	LBR	HRR	WU	VER	AC
22	KNM 12449	91.00	102.97	9.67	26.65	3.32	276.07	13.40	7998.89	5.21	1.56	3.34	62.91	145.12	4.35	24.45
23	KNM 12472	123.00	120.73	8.40	26.98	3.67	237.47	14.20	8405.56	5.10	1.53	3.36	65.11	220.39	5.79	26.53
24	KNM 12510	98.00	112.74	8.80	26.71	3.62	290.20	12.30	9535.56	5.37	1.38	3.91	61.78	261.85	4.16	24.32
25	KNM 14282	102.00	92.62	8.80	24.47	3.55	245.00	13.06	7708.89	5.11	1.54	3.31	61.12	216.62	4.30	23.62
26	KNM 14316	86.67	94.11	9.00	22.02	2.44	211.20	11.89	6478.89	5.31	1.54	3.46	63.33	258.13	4.17	23.84
27	KNM 14319	78.00	76.97	9.13	23.85	3.73	240.07	13.91	7691.11	5.19	1.72	3.03	59.64	262.22	6.42	20.99
28	KNM 15148	88.67	88.94	7.90	24.65	4.81	312.00	12.47	7107.78	5.01	1.58	3.19	58.72	313.83	4.62	23.79
29	KNM 15236	95.33	95.47	8.93	25.43	5.47	363.00	11.92	8608.89	4.95	1.45	3.42	63.95	218.76	4.83	23.27
30	KNM 15239	97.00	100.95	9.53	26.68	4.37	266.53	13.60	9174.44	5.27	1.59	3.33	62.41	255.48	3.93	23.52
31	KNM 15268	100.67	100.85	7.80	23.06	3.66	220.73	11.30	6153.33	4.58	1.58	2.90	60.44	315.59	4.27	22.20
32	KNM 15849	90.00	105.91	8.60	23.85	4.83	233.93	12.30	8386.67	5.43	1.59	3.41	60.16	195.64	4.64	24.28
33	KNM 15939	91.33	110.08	8.47	23.67	4.10	243.93	13.45	8443.33	5.63	1.68	3.36	60.10	211.54	5.26	23.65
34	KNM 16878	100.00	88.59	8.07	22.33	3.96	192.73	11.97	8895.56	5.21	1.62	3.22	53.55	282.82	5.35	22.28
35	KNM 16887	98.00	83.19	8.20	23.31	2.91	193.73	11.63	5646.67	5.18	1.50	3.44	60.51	320.24	4.18	23.44
36	KNM 17800	125.00	103.23	7.93	25.95	3.57	205.33	12.66	8456.67	5.06	1.37	3.71	64.18	157.27	5.13	24.01
37	KNM 17816	88.00	118.82	8.73	26.17	3.40	244.13	12.55	8477.78	4.87	1.51	3.24	62.20	189.12	4.68	25.60
38	KNM 17835	102.00	98.38	7.93	25.27	3.46	254.53	12.26	7034.44	5.54	1.53	3.62	63.71	313.52	4.52	23.56
39	KNM 18403	92.67	108.89	8.12	26.82	4.69	249.93	15.83	9667.78	5.64	1.38	4.08	62.01	233.52	3.85	25.08
40	KNM 18414	83.00	108.47	10.20	27.13	3.79	258.20	12.36	7814.44	5.06	1.50	3.38	63.18	325.91	4.43	25.12
41	KNM 18438	126.33	121.45	7.73	26.31	3.33	257.20	11.86	6761.11	5.01	1.46	3.43	64.02	209.67	4.23	23.70
42	KNM 18468	123.33	104.73	9.07	21.19	3.17	262.00	11.25	7704.44	5.04	1.60	3.17	64.78	179.32	5.23	22.94
43	KNM 18583	92.33	102.53	10.13	24.10	3.52	330.27	12.23	7236.67	5.08	1.35	3.76	63.49	179.15	4.47	21.04

DFF: Days to 50% flowering, PH: Plant height, NPT: Number of productive tillers, PL: Panicle length, PW: Panicles weight, NFGPP: Number of filled grains per panicle, TGW: 1000 grain weight, GY: Grain yield, KL: Kernel length, KB: Kernel breadth, LBR: Kernel length to kernel breadth ratio, HRR: Head rice recovery percent, WU: Water uptake, VER: Volume expansion ratio, AC: Amylose content.

S. No	Treatment	DFF	PH	NPT	PL	PW	NFGPP	TGW	GY	KL	KB	LBR	HRR	WU	VER	AC
44	KNM 18645	111.67	122.12	7.93	24.82	4.22	274.80	9.94	6977.78	4.88	1.46	3.35	65.14	314.46	4.85	21.19
45	KNM 18666	98.33	111.71	7.67	27.97	3.78	249.80	11.71	8286.67	4.70	1.50	3.13	63.10	320.09	5.46	23.98
46	JAI SRIRAM	95.33	99.69	9.73	22.11	2.94	279.67	10.60	6565.56	4.84	1.29	3.75	61.70	247.05	4.66	23.03
47	KAVERI CHINTU	103.33	110.38	8.93	24.04	2.69	263.67	11.12	6950.00	5.19	1.34	3.88	63.11	217.53	3.83	25.21
48	PUJA GOLD	96.67	87.97	7.93	20.93	3.36	215.87	12.86	6172.22	5.30	1.28	4.14	62.52	183.87	4.31	21.74
49	HMT SONA	102.00	90.89	8.07	20.87	2.70	231.33	12.65	6207.78	5.48	1.29	4.23	60.25	133.57	5.16	22.83
50	SHREE-101	106.67	88.75	7.47	21.87	1.82	233.40	10.75	5586.67	4.90	1.30	3.79	61.06	304.49	5.21	20.23
51	CHITTI POTTI	102.33	94.83	7.40	20.48	2.42	211.87	9.47	5293.33	4.89	1.29	3.78	59.87	234.37	4.53	23.45
52	N.R.I.P 0013	92.67	98.35	9.07	24.07	3.78	243.07	12.30	5545.56	5.17	1.42	3.65	60.82	144.81	4.34	24.60
53	NLR 4001	106.00	99.65	9.00	21.85	3.30	236.80	14.26	6182.22	5.05	1.51	3.36	50.05	110.51	4.23	21.63
54	M.C.M 103	105.33	91.88	10.60	22.26	3.52	212.67	12.69	6190.00	4.78	1.49	3.20	60.17	191.52	4.54	23.29
55	BPT 5204	107.00	85.09	9.87	22.34	3.59	209.20	14.22	5433.33	5.13	1.51	3.39	61.39	213.26	5.34	25.33
56	BPT 2841	88.00	123.46	10.00	26.42	4.74	268.73	14.47	7111.11	5.28	1.66	3.19	53.69	248.62	4.70	24.49
57	CO 51	81.00	98.55	8.00	24.70	3.53	214.00	18.13	5393.33	5.88	1.63	3.61	58.90	246.30	5.69	23.29
58	CO 55	91.67	109.71	9.40	26.97	4.23	326.87	14.29	8662.22	6.17	1.58	3.94	50.51	354.71	5.58	25.03
59	CO 56	112.67	110.27	7.73	27.77	3.49	229.80	15.56	6608.89	5.49	1.63	3.36	57.60	141.12	5.14	25.66
60	T.K.M 13	95.33	99.61	9.13	26.77	4.26	237.90	12.06	7477.78	5.45	1.54	3.54	63.02	151.77	4.84	24.82
	Mean	98.37	102.67	8.76	24.65	3.70	251.20	12.90	7268.65	5.23	1.50	3.52	61.12	229.32	4.95	23.56
	CV%	3.4	4.3	8.9	5.4	6.8	9.3	6.8	11.1	3.5	5.5	6.2	3.4	9.7	7	3.7
	SEM	1.91	2.62	0.45	0.77	0.15	13.48	0.50	476.67	0.11	0.05	0.13	1.22	12.79	0.20	0.50
	CD@ 0.05	5.34	7.35	1.27	2.16	0.41	37.76	1.39	1334.92	0.30	0.13	0.36	3.43	35.82	0.56	1.41

DFF: Days to 50% flowering, PH: Plant height, NPT: Number of productive tillers, PL: Panicle length, PW: Panicles weight, NFGPP: Number of filled grains per panicle, TGW: 1000 grain weight, GY: Grain yield, KL: Kernel length, KB: Kernel breadth, LBR: Kernel length to kernel breadth ratio, HRR: Head rice recovery percent, WU: Water uptake, VER: Volume expansion ratio, AC: Amylose content.

3.3. Variability using box plots

Box plots are the visual representation of the provided quantitative variables which depict the distantness of extreme values from most of the data points. In the study, box plots (Fig. 3) were used for depicting the frequency distribution of eight traits for yield and attributing traits and seven traits for grain quality. The traits are represented visually by box plots, which show how far away extreme values are from the majority of the data points. Box plots were employed in this study to illustrate the frequency distribution of fifteen yield and contributing variables, and quality traits. The traits, plant height, panicle weight, number of filled grains per panicle, grain yield and water uptake exhibited higher variability. Box plot for plant hight indicated that wider variation which will be useful for selection in breeding programmes targeting plant architecture. The trait, panicle weight also showed high variability in box plot besides having tendency of for a fewer lower outlier. High variability along with several outliers were observed for the trait, number of filled grains per panicle. While wide range of IQR and whiskers indicate larger variation in case of grain yield over the genotypes demonstrating the larger variation. Water uptake exhibits the high variabity across most of the samples without outliers, indicating the uniform spread of the variability over the genotypes.

Box plot analysis depicted the moderate variability for the traits, days to 50% flowering, panicle length, 1000-grain weight, length breadth ratio, head rice recovery and amylose content. Moderate variability was found in case of days to 50% flowering, and several outliers were present especially on the higher end. Panicle length showed the moderate variability having single high-end outlier with a most consistent variability distribution. The trait, 1000-grain weight recorded medium heritability with few upper outliers. Moderate to high variability alongside having several high outliers were observed for length breadth ratio. Moderate variability was observed for the trait, head rice recovery in which majority of values were in between 59 and 65, however, several genotypes demonstrated lower side of recovery led to reduction in the uniformity. Amylose content expressed the moderate variability where in values are mostly concentrated in between 22 and 26 besides having few low outliers.

Box plot showed that number of productive tillers per m^2, kernel length, kernel breadth and volume expansion ratio having low variability. Number of productive tillers per m^2 showed stable tillering across the genotypes. While kernel length is consistent trait with low variability and few deviations. Others both traits, kernel breadth and volume expansion ratio were found to be a very consistent traits across the genotypes, making them a stable selection trait's.

3.4. Variability Parameters

The results of coefficient of variation, heritability and genetic advance of each trait in the present study are given in (Table 4). Graphs Depicting the (Fig. 1) and (Fig. 2) as Estimates of Heritability and Genetic advance as% of mean and Genotypic and Phenotypic coefficient of variation, respectively.

Phenotypic and genotypic coefficient of variations showed that PCV values were higher than GCV values for all the traits indicating that environmental factors play a role in how these traits are expressed. The results of this study provided confirmation with Chacko *et al*., (2023) [8].

It was reported that genotypic coefficient of variation (GCV) was slightly lower than phenotypic coefficient of variation (PCV) for days to 50 percent flowering, plant height, panicle length, panicle weight, 1000-grain weight, kernel length, kernel breadth, length to breadth ratio, head rice recovery, water uptake, volume expansion ratio, and amylose content (%), indicating a significant genetic influence. The observation that PCV values for the traits like, number of productive tillers, number of filled grains per panicle, and grain yield were significantly greater than GCV indicates that there is a significant environmental influence and predominance of non-additive gene effects.

The trait, water uptake showed higher phenotypic and genotypic coefficients of variation indicating the presence of a high degree of variation for these traits among the

genotypes which could be improved through selection in a desirable direction. These results are in agreement with the findings obtained by Devi *et al.* (2019) [9].

Moderate levels of PCV and GCV for days to 50% fowering, plant height, panicle weight, number of grains per panicle, 1000 grain weight, grain yield, and volume expansion ratio indicated the considerable level of variability in these traits and suggested the possibility of improving these traits through selection. These results are in confirmation with Bhusan *et al*., (2019) for days to 50% flowering, Nithya *et al*., (2020) [22] reported for plant height, panicle weight by Sandeep *et al*., (2018) [25], number of filled grains per panicle and 1000 grain weight by Amegan *et al*., (2020), grain yield by Girma *et al*., (2018) [14], and also for volume expansion ratio by Bandi., *et al.l*., (2018) [15] has recorded with moderate GCV and PCV values.

However, low levels of PCV and GCV were observed for the traits, panicle length, kernel length, kernel breadth, length breadth ratio, head rice recovery, and amylose content suggesting less variability among the genotypes for these traits. In contrary to these results are correlate with Panicle length by Saha *et al*., (2019) [24], Kernel length with Dhurai *et al*., (2014) [51], Kernel breadth with Devi *et al*., (2022) [11], Length breadth ratio with Manivelan *et al*., (2022) [20], Head rice recovery with Hari *et al*., (2018) and also amylose content with Parvathi *et al*., (2011) [23] for low level of GCV and PCV. While low GCV and moderate PCV was observed for number of productive tillers per plant. It is correlate with Devi *et al*., (2022) [11].

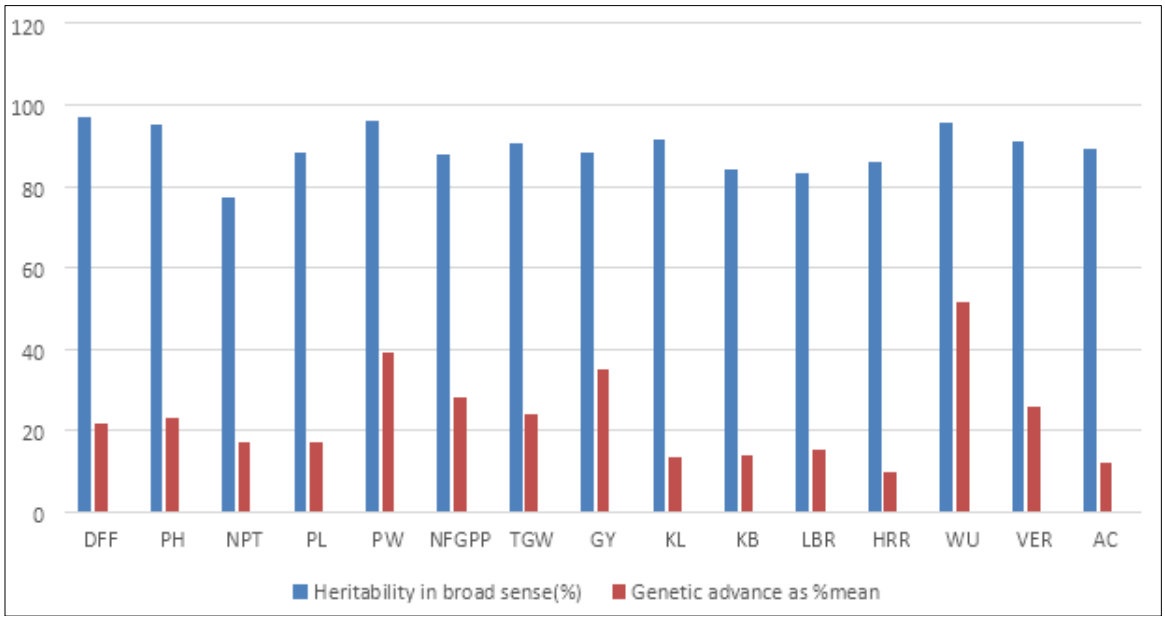


Fig 1: Estimates of heritability and genetic advance as% of mean for yield and its component traits.

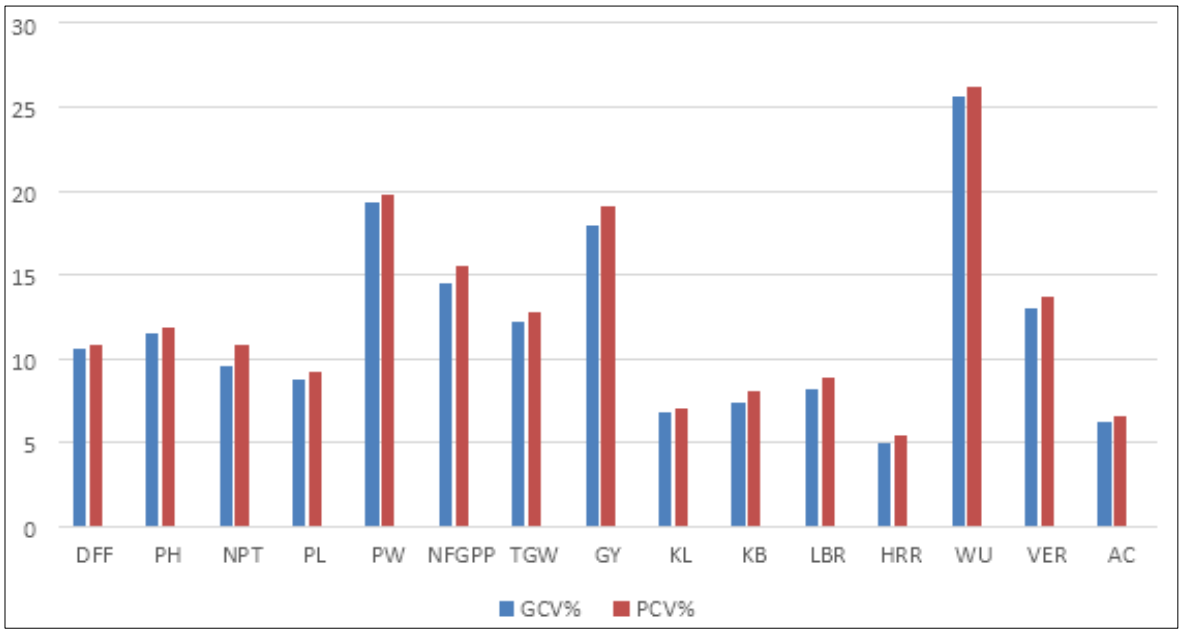
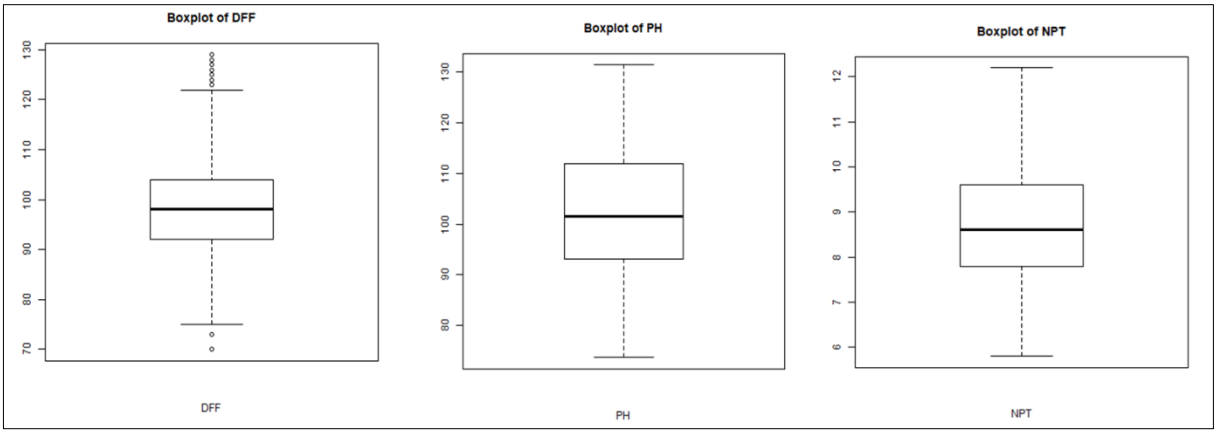
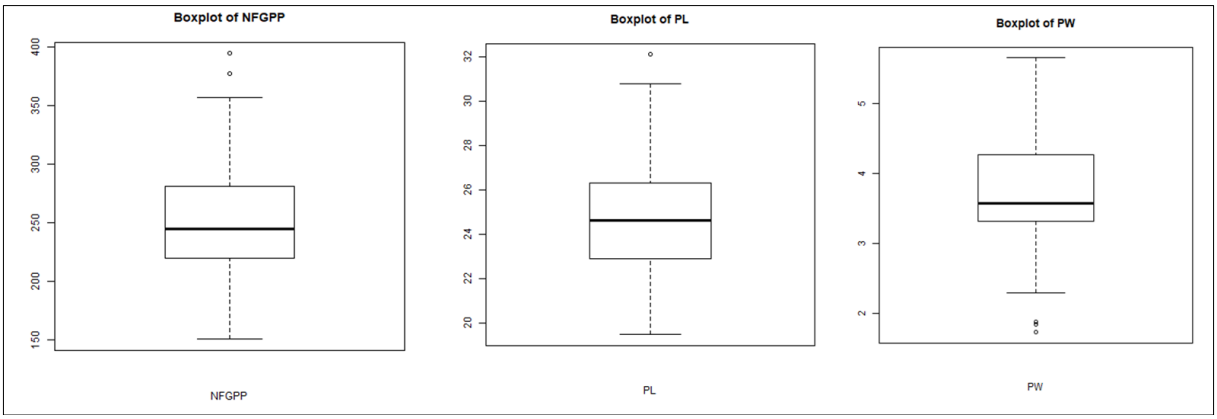
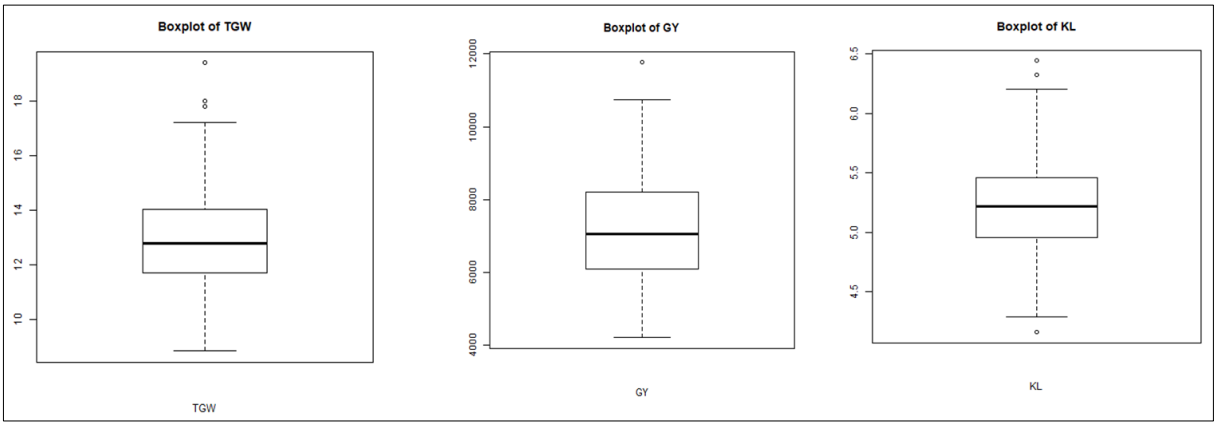
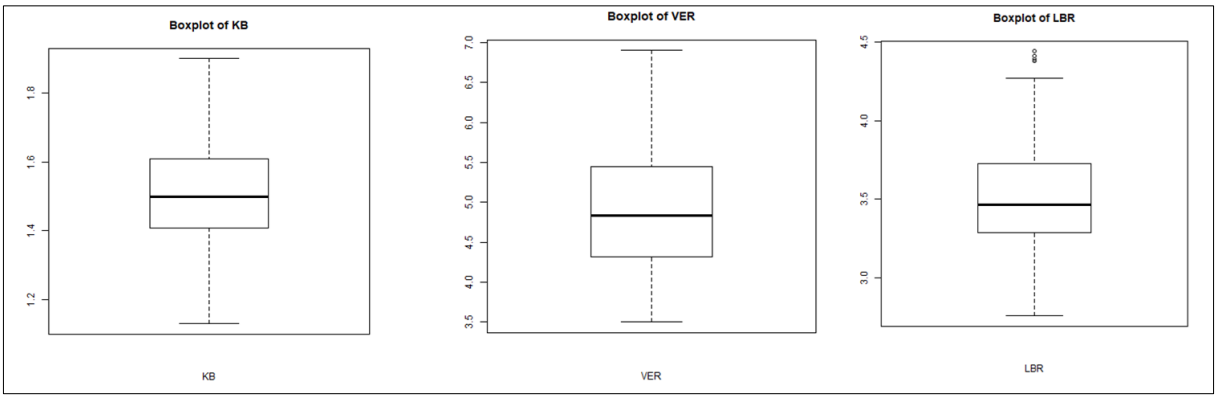


Fig 2: Phenotypic and genotypic coefficient of variation for yield and yield contributing characters


Boxplot of DFF
DFF
Boxplot of PH
PH
Boxplot of NPT
NPT


Boxplot of NFGPP
NFGPP
Boxplot of PL
PL
Boxplot of PW
PW


Boxplot of TGW
TGW
Boxplot of GY
GY
Boxplot of KL
KL


Boxplot of KB
KB
Boxplot of VER
VER
Boxplot of LBR
LBR

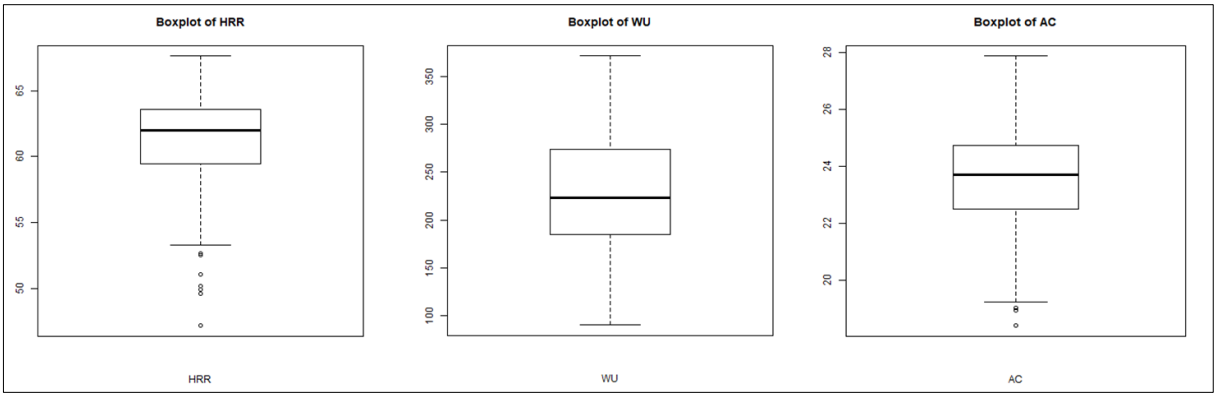


Fig 3: Box plots showing variation in the yield, yield attributing traits and quality traits.

Table 4: Genetic parameters for yield, yield components and grain quality characters in rice with column graphs

TRAIT	Range		Mean	GCV	PCV	h^2	GAM
	Max	Min					
DFF	126.33	72.67	98.37	10.63	10.80	96.80	21.50
PH	123.73	76.97	102.67	11.53	11.81	95.30	23.20
NPT	11.33	6.80	8.76	9.53	10.84	77.20	17.20
PL	30.95	20.48	24.65	8.70	9.24	88.50	16.90
PW	5.58	1.82	3.70	19.33	19.73	96.00	39.00
NFGPP	363.00	156.33	251.20	14.54	15.50	88.00	28.10
TGW	18.13	9.47	12.90	12.15	12.75	90.80	23.90
GY	10167.78	4411.11	7268.65	17.96	19.12	88.20	34.80
KL	6.29	4.44	5.23	6.75	7.05	91.70	13.30
KB	1.72	1.18	1.50	7.34	8.01	84.00	13.90
LBR	4.23	2.90	3.52	8.12	8.90	83.20	15.30
HRR	65.88	50.05	61.12	4.98	5.37	86.10	9.50
WU	354.71	110.51	229.32	25.66	26.26	95.50	51.70
VER	6.42	3.80	4.95	13.01	13.63	91.10	25.60
AC	27.09	19.44	23.56	6.18	6.54	89.30	12.00

Genetic Parameters Graphs Depicting the Fig 1: and Fig 2 as Estimates of Heritability and Genetic advance as% of mean and Genotypic and Phenotypic coefficient of variation, respectively.

3.5 Heritability and genetic advance

All the characters recorded high estimates of heritability indicating that they were least influenced by the environmental effects. High broad-sense heritability estimates were observed for all the traits, 50% flowering, plant height, number of productive tillers, panicle length, panicle weight, number of filled grains per panicle, thousand grain weight, grain yield, kernel length, kernel breadth, length to breadth ratio, head rice recovery, water uptake, volume expansion ratio and amylose content.

The genetic advance as a percentage of the mean revealed high estimates for days to 50% flowering, plant height, panicle weight, number of filled grains per panicle, thousand grain weight, grain yield, water uptake and volume expansion ratio. It was observed moderate for number of productive tillers per plant, panicle length, kernel length, kernel breadth, length to breadth ratio and amylose content, while low genetic advance percent mean estimates observed for head rice recovery.

Heritability values along with estimates of genetic advance would be more useful on correlating selection criteria than heritability alone. High heritability coupled with high genetic advance as percent mean observed for the trait's days to 50% flowering, plant height, panicle weight, number of filled grains per panicle, 1000 grain weight, grain yield, water uptake and volume expansion ratio. These results are correlate with Edukondalu *et al*., (2017) [12] for High heritability coupled with high genetic advance as percent mean. High heritability coupled with moderate genetic advance as percent mean observed for number of productive tillers, panicle length, kernel length, kernel breadth, length to breadth ratio and amylose content. Similar kind of high heritability with moderate genetic advance as percent mean was correlated with Shivani *et al*., (2018) [27].

However, high heritability with low genetic advance as percent mean observed for head rice recovery. These results are significant with Kurmanchali *et al*., (2019) [19].

Conclusion

Based on the above-mentioned research findings, analysis of variance reveals significant differences among short and medium slender rice genotypes for all traits, suggesting the considerable diversity within the genotypes. GCV was lower than PCV for all the yield traits and grain quality traits suggesting significant role of environment in the trait's expression. Water uptake recorded high PCV and GCV values. The box plots reveal that these key yield-contributing traits are highly variable, making them promising targets for selection in genetic improvement and varietal development efforts. High heritability coupled with high genetic advance as percent mean observed for the traits days to 50% percent flowering, plant height, panicle weight, number of filled grains per panicle, thousand grain weight, grain yield, water uptake and volume expansion ratio indicates the role of additive gene action in controlling the traits and less influenced by the environment, hence pedigree method of breeding will be a rewarding one to

improve the traits under investigation. These traits are useful for the breeder for further selection improvement. Plant features like days to 50% percent flowering, plant height, panicle weight, number of filled grains per panicle, thousand grain weight, grain yield, water uptake and volume expansion ratio should indeed receive more focus in future breeding programmes.

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