

## Studies on genetic variability, heritability and genetic advance of elite salt tolerant lines of rice under dry direct seeded conditions

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### ABSTRACT

In the present study 24 elite salt tolerant lines including two checks were evaluated in a randomized complete block design (RBD) for yield, yield components and lodging related traits of dry direct seeded conditions at Agricultural College Farm, Bapatla, Andhra Pradesh during *kharif*, 2023 to estimate the extent of genetic variability, heritability (broad sense) and genetic advance as per cent of mean. The analysis of variance revealed significant variability for all the characters. Among the traits, high phenotypic and genotypic coefficients of variation were recorded for root length at 15 DAS, number of productive tillers per plant, number of filled grains per panicle, culm strength, lodging (%), biological yield and grain yield indicating large amount of variation among the genotypes. High heritability coupled with high genetic advance as per cent of mean was recorded for root length at 15 DAS, root length at 30 DAS, shoot length at 15 DAS, shoot length at 30 DAS, field emergence % (15 DAS), number of productive tillers per plant, number of filled grains per panicle, culm strength, lodging (%), basal internodal length (cm), culm diameter (mm), culm thickness (mm), biological yield, grain yield and harvest index (%) indicating that these traits were governed by additive gene action and direct phenotypic selection may be rewarding for improvement of these traits in rice.

**Keywords:** Genetic advance, GCV, Heritability, PCV and Variability.

Rice (*Oryza sativa* L.) is one of the most significant cereal food crops of the world which fulfills the nutritional requirements of half of the world's population. Most of the world's population carbohydrate needs are met by rice and is one of the principal cereal crops. Indian rice systems are undergoing tremendous changes in response to climate change, economic factors and technological opportunities in farming. One such change is to adopt direct seeding in rice to overcome rising cost of labour and need of intensification of double and triple cropping systems. The availability of high yielding short duration rice varieties and chemical weed control methods has made this shift economically profitable. Besides, direct seeding may also helpful to achieve higher water use efficiency (Gupta *et al.*, 2006). Direct seeded rice under no/reduced tillage is an efficient resource conserving technology (RCT) holding good promise in coming days. Early vigour is an important trait in DSR systems (Cairns *et al.*, 2009).

Rice varieties suitable for direct seeding in irrigated areas must possess early seedling vigour,

enhanced foliar growth to combat weeds at the vegetative stage, sustained high foliar nitrogen concentration at the reproductive stage, strong culm to withstand lodging and to store assimilates and improved reproductive sink capacity with a prolonged ripening period (Dingkuhn *et al.*, 1991). Lodging resistance is another desirable trait for direct seeding.

All breeding efforts take into account the genetic variability of yield contributing traits as well as how yield interacts with these variables to generate new lines. Thus, the present study was conducted to know the genetic traits of variability in the present material.

### MATERIAL AND METHODS

The present investigation was carried out using 24 elite salt tolerant lines including two checks and were evaluated in randomized complete block design (RBD) for yield and component traits related to dry direct seeded condition at Agricultural College Farm, Bapatla, Andhra Pradesh during *kharif*, 2023. Each genotype was grown in five rows of 3.0 m length

with a spacing of 20 cm between rows and 15 cm between plants, within the row. The data was recorded on five competitive plants taken from each replication on root length at 15 DAS & 30 DAS (cm), shoot length at 15 DAS & 30 DAS (cm), field emergence (%), root volume at 15 DAS & 30 DAS (cm<sup>3</sup>), days to 50 per cent flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, spikelet fertility (%), culm strength, per cent lodging (%), basal internodal length (cm), culm diameter (mm), culm thickness (mm), biological yield (Kg/ha), grain yield (Kg/ha) and harvest index (%). Analysis of variance was worked out by the method suggested by Panse and Sukhatme (1961) and the genotypic and phenotypic coefficient of variations were estimated by the method suggested by Burton and Devane (1953). The data analysed by using INDOSTAT software. The GCV and PCV are classified as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Sivasubramanian and Madhavamenon (1973). Heritability was estimated by using the formula given by Johnson *et al.* (1955) and are classified as low (<30%), moderate (30- 60%) and high (> 60%). The range of genetic advance as per cent of mean was classified as low (< 10%), moderate (10-20%) and high (> 20%) as suggested by Johnson *et al.* (1955).

## RESULTS AND DISCUSSION

Analysis of variance for 21 characters revealed significant differences among the genotypes for all the characters under study indicating the presence of greater variability among the genotypes (Table 1). Low GCV and PCV (<10%) values were recorded for the traits, root volume at 15 DAS & 30 DAS (cm<sup>3</sup>), days to 50 per cent flowering, plant height (cm), panicle length (cm) and spikelet fertility (%) indicating that the variability for these characters among the genotypes was meagre. Contrasting results were reported for these characters by Manivelan *et al.* (2022), Zayed *et al.* (2023), Harisha *et al.* (2024) and Umamaheswar *et al.* (2024).

Moderate GCV and PCV (10-20%) values were recorded for the traits root length at 30 DAS (cm), shoot length at 15 DAS & 30 DAS (cm), field emergence (%), basal internodal length (cm), culm diameter (mm), culm thickness (mm) and harvest index (%). These results are in agreement with the earlier reports of Barik *et al.* (2019), Keerthiraj and Biju

(2020), Chacko *et al.* (2023), Singh *et al.* (2023) and Kumar *et al.* (2024). The characters, root length at 15 DAS, number of productive tillers per plant, number of filled grains per panicle, culm strength, lodging (%), biological yield and grain yield registered higher GCV and PCV (>20%) values indicating that large amount of variation is present among the genotypes for these characters. Similar results were obtained by Barik *et al.* (2019), Keerthiraj and Biju (2020), Arun (2022), Silva *et al.* (2022) and Singh *et al.* (2023).

High heritability coupled with high genetic advance as per cent of mean (Table 2 and Figure 1) was reported for root length at 15 DAS, root length at 30 DAS, shoot length at 15 DAS, shoot length at 30 DAS, field emergence % (15 DAS), number of productive tillers per plant, number of filled grains per panicle, culm strength, lodging (%), basal internodal length (cm), culm diameter (mm), culm thickness (mm), biological yield (Kg/ha), grain yield (kg/ha) and harvest index (%) indicating that these traits mostly under the control of additive gene action and direct phenotypic selection of these traits would be effective for improvement. Similar findings were earlier reported for these characters by Barik *et al.* (2019) for root volume for 15 DAS & 30 DAS (cm); Garg *et al.* (2023) for shoot volume for 15 DAS & 30 DAS (cm); Kumar *et al.* (2024) for field emergence (% 15 DAS); Arun (2022) for number of productive tillers per plant and number of filled grains per panicle; Silva *et al.* (2022) for culm strength; Keerthiraj and Biju (2020) for lodging (%), basal internodal length, culm diameter (cm) and culm thickness (cm); Singh *et al.* (2023) for biological yield (kg/ha), grain yield (kg/ha) and harvest index (%). High heritability coupled with moderate genetic advance as per cent of mean was observed for the traits, days to 50 per cent flowering and plant height (cm) indicating the presence of both additive and non-additive genetic effects and genetic improvement of these characters can be utilized through heterosis breeding. Similar findings were earlier reported by Manivelan *et al.* (2022) for days to 50 per cent flowering; Patra *et al.* (2020) and Zayed *et al.* (2023) for plant height.

## CONCLUSION

High PCV and GCV were recorded for the traits, root length at 15 DAS, number of productive

Table 1. Analysis of variance for yield, yield components and lodging related traits in rice (*Oryza sativa* L.)

Source	Degrees of freedom		Root length at 15 DAS		Shoot length at 15 DAS		Shoot length at 30 DAS		Root length at 30 DAS		Field emergence % 15 DAS		Root volume cm <sup>3</sup> at 15 DAS		Root volume cm <sup>3</sup> at 30 DAS		Days to 50 % flowering		Plant height (cm)		Panicle length (cm)		No. of Productive tillers per plant	
Replication	1		0.427	1.021	3.152	9.1	40.333	0.067	0.036	37.953	6.825	0.302	4.045											
Treatments	23		6.976**	5.663**	8.809**	46.625**	432.594**	0.092*	0.073*	76.996**	191.496**	4.137**	24.818**											
Error	23		0.118	0.553	0.886	3.443	23.887	0.034	0.018	12.824	40.328	0.98	1.309											
Mean sum of squares																								

Source	No. of filled grains per panicle		Spikelet fertility (%)		Culm strength		Lodging (%)		Basal internodal length (cm)		Culm diameter (mm)		Culm thickness (mm)		Biological yield (Kg/ha)		Grain yield (Kg/ha)		Harvest index (%)				
Replication	553.937	12.738	0.083	2.114	0.114	0.005	0.007	6358350.426	1470349.712	8.325													
Treatments	3968.478**	23.561**	8.518**	2029.651**	6.073**	0.020*	0.024*	30752823.344**	4812858.209**	79.774**													
Error	247.118	7.216	0.142	5.872	0.477	0.002	0.002	1907304.857	346991.242	8.66													
Mean sum of squares																							

\*\* Significant at 1 per cent level of probability

\* Significant at 5 per cent level of probability

Table 2. Estimation of genetic parameters for grain yield, yield components and lodging related traits in rice (*Oryza sativa* L.)

S. No.	Characters	GCV (%)	PCV (%)	Heritability (Broad Sense) (%)		Genetic Advance	Genetic Advance as % of Mean
1	Root length at 15 DAS	29.68	30.18	96.68		3.75	60.11
2	Root length at 30 DAS	12.47	13.76	82.219		2.99	23.3
3	Shoot length at 15 DAS	11.25	12.45	81.729		3.71	20.96
4	Shoot length at 30 DAS	13.57	14.62	86.246		8.89	25.97
5	Field emergence % (15DAS)	18.49	19.54	89.534		27.87	36.03
6	Root volume (cm <sup>3</sup> ) at 15 DAS	6.43	9.45	46.225		0.24	9
7	Root volume (cm <sup>3</sup> ) at 30DAS	2.99	3.85	60.042		0.27	4.77
8	Days to 50 % flowering	5.83	6.89	71.445		9.86	10.15
9	Plant height (cm)	7.95	9.85	65.208		14.46	13.23
10	Panicle length (cm)	5.33	6.79	61.712		2.03	8.63
11	No. of Productive tillers per plant	23.34	24.61	89.979		6.7	45.61
12	No. of filled grains per panicle	21.95	23.36	88.276		83.49	42.49
13	Spikelet fertility (%)	3.19	4.38	53.109		4.29	4.79
14	Culm strength	36.93	37.55	96.721		4.15	74.82
15	Lodging (%)	80.09	80.32	99.423		65.34	164.51
16	Basal internodal length (cm)	16.44	17.78	85.422		3.19	31.29
17	Culm diameter (mm)	14.12	15.34	84.742		0.18	26.77
18	Culm thickness (mm)	14.63	16.04	83.129		0.2	27.48
19	Biological yield (kg/ha)	21.67	23.06	88.32		7352.27	41.95
20	Grain yield (kg/ha)	24.86	26.72	86.55		2863.78	47.64
21	Harvest index (%)	17.28	19.27	80.414		11.02	31.93

PCV-Phenotypic Coefficient of Variation; GCV-Genotypic Coefficient of Variation

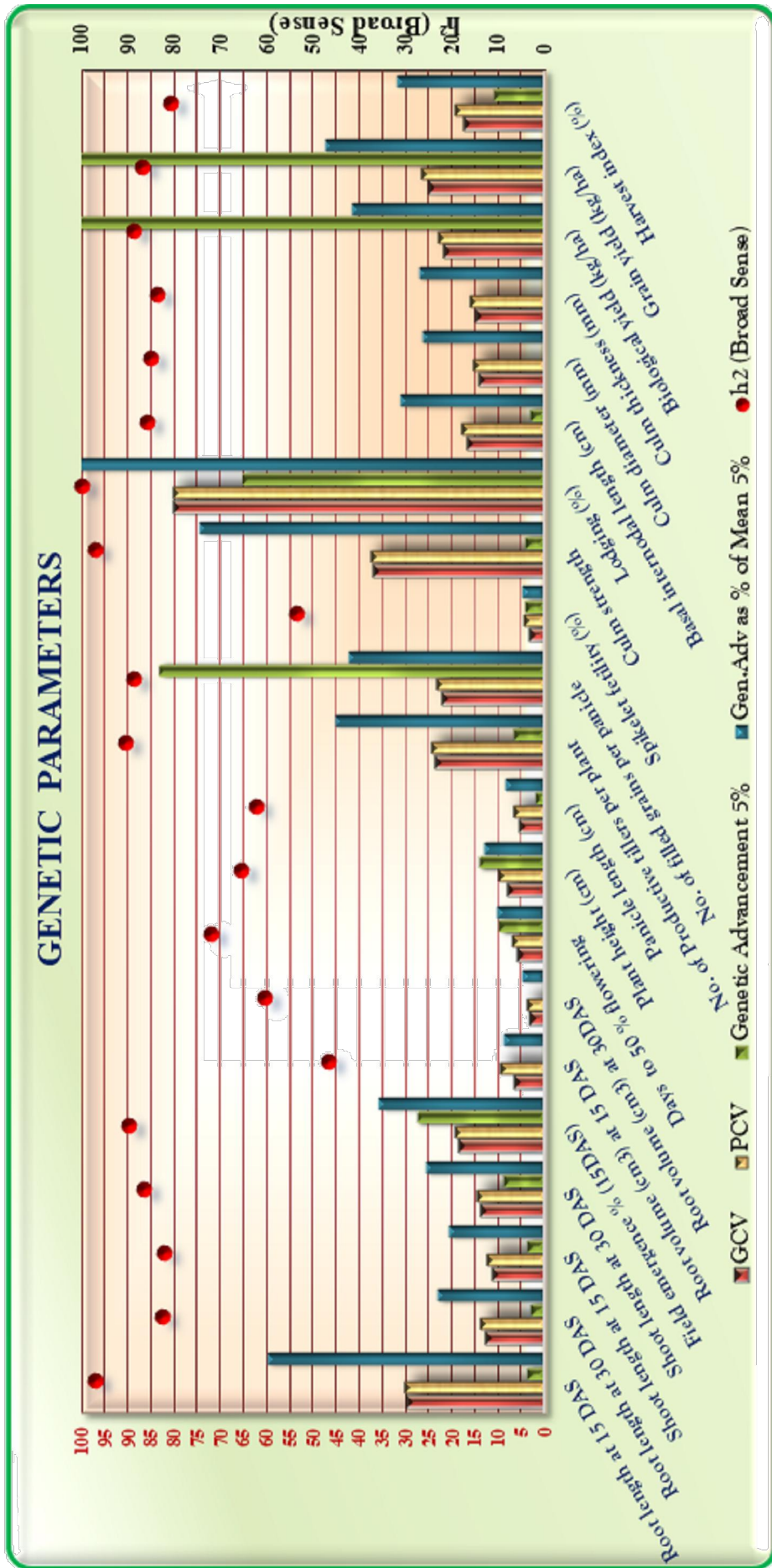


Figure 1. Pattern of GCV, PCV, heritability and genetic advance as per cent of mean for 21 traits in 24 genotypes of rice (*Oryza sativa* L.)

tillers per plant, number of filled grains per panicle, culm strength, lodging (%), biological yield and grain yield indicating that the large amount of variation among the genotypes. High heritability coupled with high genetic advance as per cent of mean was recorded for some traits, root length at 15 DAS, root length at 30 DAS, shoot length at 15 DAS, shoot length at 30 DAS, field emergence % (15 DAS), number of productive tillers per plant, number of filled grains per panicle, culm strength, lodging (%), basal internodal length (cm), culm diameter (mm), culm thickness (mm), biological yield (kg/ha), grain yield (kg/ha) and harvest index (%) indicating that these traits under the control of additive gene action and direct phenotypic selection of these traits would be effective in improvement of these traits in rice.

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