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Study of Genetic Variability in F_2 Population for Yield Enhancing Traits under Direct Seed Condition in Rice (*Oryza sativa* L.)

Prashanth M [a*], Gireesh C [b], Sree Lakshmi [a], G.S. Laha [c], P Lavanya Kumari [a], Anantha M S [c], R M Sundaram [c] and Senguttuvel P [c]

[a] Acharya N.G. Ranga Agricultural University, Lam, Guntur-522034, India.
[b] ICAR- Indian Institute of Seed Science, Bengaluru-560065, India.
[c] ICAR-Indian Institute of Rice Research, Hyderabad-500030, India.

Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

The present investigation was conducted to assess the variability, frequency distribution of grain yield and yield attributing traits in F_2 generation of DRR Dhan 60 × Pusa 44 (NIL). In order to better understand the genetics of DSR and develop rice genotypes that are aerobic conditions-suited, genetic diversity is crucial. The experimental material consists of 236 F_2 plants along with parents

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**Corresponding author: E-mail: prabha489official@gmail.com;*

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which were planted in DSR plot at ICAR-IIRR, Hyderabad. Data recorded for the traits viz., Days to 50% flowering, Plant height, Number of tillers per plant, Flag leaf length, Flag leaf width, Number of panicles per plant, Panicle length, Number of spikelets per panicle, Number of filled grains per panicle, Number of chaffy grains per panicle, Spikelet fertility, Spikelet sterility, 1000-grain weight and Grain yield per plant. The traits, number of productive tillers per plant, number of tillers per plant, flag leaf length and grain yield per plant have high genotypic and phenotypic coefficient of variation. For productive tillers per plant, number of tillers per plant, flag leaf length, and grain yield per plant, high GCV and PCV along with high heritability and high genetic advance as a percentage of mean were noted. This suggests an additive type of gene action and that selection for these traits is effective. These findings indicate that, in aerobic conditions, there was adequate genetic diversity for most of the characters under investigation.

Keywords: Grain yield; variability; skewness; selection; rice.

1. INTRODUCTION

Rice is the world's most significant crop, with half of the population eating it every day. Rice provides 20% of the world's dietary energy, whereas wheat and maize provide 19 and 5%, respectively. In certain Asian nations, rice accounts for more than 70% of calorie intake. Furthermore, rice is the primary staple meal for the world's poorest and undernourished people residing in Asia and Africa, who cannot afford or have access to nutritional items [1]. As a result, rice is regarded as one of the world's most strategic commodities, tied not just to global food security but also to economic development, employment, social stability, and regional peace, developing countries achieved rice self-sufficiency and the ability to export surplus rice, consumers became selective in preferring high-quality rice in the succeeding decades. Since consumer preferences in Asia and all over the world are diverse due to varied demographics and culture, defining uniform attributes to capture regional grain quality preferences becomes more challenging [2]. In view of depleting water resources and shortage of labour for agriculture, alternate method of rice cultivation is imperative. This necessitates a shift in cultivation practice from transplanted to direct-seeded rice (DSR).

DSR is a potential alternative technology for sustainable rice farming, as it can save water up to 35-54%, labour up to 11-66%, reduces methane emission and increases net profit to farmers [3]. Direct-seeding refers to the process of establishing a rice crop from seeds sown in the field rather than by transplanting. Once germination and seedling establishment are complete, the crop can then be sequentially flooded and water regimes maintained as for transplanted rice. Alternatively, the crop can remain rainfed, the upper surface soil layers fluctuating from aerobic to nonaerobic conditions. Direct-seeding is the oldest method of rice establishment and, prior to the late 1950s, direct-seeding was the major method used in developing countries [4].

The ideal generation for imposing selection is one that exhibits significant levels of segregation and recombination [5]. For the effective selection of better progenies from segregating generations for further selection, there must be existence of genetic variability in the population. By employing third- and fourth-degree statistics, such as skewness and kurtosis in segregating generations, the genetics of the characteristics may be better understood [6]. A crucial component is the degree of connection between the qualities, particularly for complicated and economically significant variables like yield.

The success of any crop improvement programme relies upon the nature and magnitude of genetic variability. The level of genetic variety within the plant population determines how effective selection is. Due to the polygenic nature of traits like yield and its constituents, breeders must separate desirable genotypes from knowledge of variation's constituent parts. The fundamental component involves dividing all variation into genotypic and phenotypic components. The degree to which these components apply to different characteristics indicates the kind of gene activity, which aids in selecting a breeding strategy for the genetic development of a trait. High heritability values alone provide no indication of the amount of genetic progress that would result from selection of the better individuals. Heritability values coupled with genetic advance are more reliable and useful genetic parameters in predicting the genetic gain under selection than heritability estimates alone [7]. Hence, the present study was conducted to assess the variability, frequency distribution of yield and yield component traits to identify a superior segregants in F_2 generation of DRR Dhan 60 × Pusa 44 (NIL) under DSR conditions.

2. MATERIALS AND METHODS

The present investigation was carried out at Indian Institute of Rice Research (ICAR-IIRR), Rajendranagar, Hyderabad. The crossing was performed between DRR Dhan 60 (Recipient parent) and Pusa 44(NIL) (Donor parent) which is having herbicide tolerance to imazythapyr during *Rabi*, 2021-22 at crossing block in IIRR. A total of 236 F_2 segregants of DRR Dhan 60 × Pusa 44 (NIL) were raised during *Kharif*, 2023. Recommended agronomic practices were followed throughout the crop growth period. The details of the parents are explained in the Table 1. For confirmation F_1's molecular markers are used, the details of the markers used are presented in the Table 2.

Data was recorded in all the segregants for Days to 50% flowering, Plant height (cm), Number of tillers per plant, Flag leaf length (cm), Flag leaf width (cm), Number of panicles per plant, Panicle length (cm), Number of spikelets per panicle, Number of filled grains per panicle, Number of chaffy grains per panicle, Spikelet fertility (%), Spikelet sterility (%), 1000-grain weight(gm) and Grain yield per plant(gm). The detailed information about parameters studies are explained as follows.

Traits studied:

1. Days to 50 per cent flowering

The number of days taken by each entry, from sowing to complete exertion of the panicle tip above the sheath of the flag leaf in fifty per cent of total plants in the net plot for parents was recorded, whereas for F_2s, individual plant observation was recorded.

2. Plant height (cm)

It was measured at maturity stage by using meter scale from base of the plant to tip of the main panicle, excluding awn if present.

3. Number of tillers per plant

The total numbers of tillers in each plant was counted manually at the time of maturity.

4. Flag leaf length (cm)

The flag leaf is the leaf that emerges just below the panicle or reproductive structure of the rice plant. It is usually the last fully developed leaf. Using a ruler, the length was measured from the ligule to the tip of the leaf blade. In order to get accurate length, it should be measured along the centre of the leaf.

5. Flag leaf width (cm)

Using a ruler, the width was measured from middle of the leaf from one margin to other margin.

6. Number of panicles per plant

The number of ear bearing tillers, which produced healthy panicles were counted on each plant at the time of maturity

7. Panicle length (cm)

The panicle length was measured in centimetres from the basal node of the panicle to the tip of upper most grains. It was recorded as average value of three panicles per plant.

8. Number of spikelets per panicle

It is recorded by counting all the spikelets (both filled and unfilled) of particular panicle produced. These values represent average of three panicles per plant.

9. Number of filled grains per panicle

It was measured by counting the filled grains that are present on one panicle. These values represent average of three panicles per plant.

10. Number of chaffy grains per panicle

It was measured by counting number of chaffy grains that are present on one panicle. These values represent average of three panicles per genotype.

11. Spikelet fertility (%)

The observation was recorded by counting the number of filled spikelets and total number of spikelets in each panicle.

$$\text{Spikelet fertility (\%)} = \frac{Number\ of\ filled\ spikelets\ per\ panicle}{\text{Total number of spikelets per panicle}} \times 100$$

12. Spikelet sterility (%)

The observation was recorded by counting number of unfilled spikelets and total number of spikelets.

$$\text{Spikelet sterility (\%)} = \frac{Number\ of\ unfilled\ spikelets\ per\ panicle}{\text{Total number of spikelets per panicle}} \times 100$$

13. Thousand grain weight (gm)

One thousand well filled grains were counted from each genotype and weighed with the help of electronic top pan balance in grams.

14. Grain yield per plant (gm)

All the panicles from a single plant were harvested at maturity, threshed, cleaned and sun dried to 12 percent moisture content and the weight was recorded with the help of electronic top pan balance in grams in grams.

Statistical analysis:

Phenotypic and genotypic coefficient of variation: The co-efficient of variability both at phenotypic and genotypic levels for all the characters were computed by applying the formula as suggested by Burton and De-Vane [8].

$$\text{Coefficient of variation (GCV)} = \frac{\text{Genotypic standard deviation Genotypic}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

GCV and PCV were classified into Low (0-10 per cent), Moderate (10-20 per cent) and High (> 20 per cent) as suggested by Sivasubramanian and Madhavamenon [9].

Heritability (h^2): Heritability in broad sense for all the characters was computed by the formula as suggested by Allard [10].

$$h^2\ (b) = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where, h^2=Heritability (Broad sense), $\sigma^2 g$ = Genotypic variance, $\sigma^2 p$ = Phenotypic variance

Heritability was classified as suggested by Johnson *et al.* [11] and described as Low (0-30 per cent), Moderate (30-60 per cent) and High (> 60 per cent).

Genetic advance: Genetic advance for each character was predicted by the formula given by Johnson *et al.* [11].

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

Where,
GA = Expected genetic advance
K=Selection differential, the value of which is 2.06 at 5 per cent selection intensity
s_P= Phenotypic standard deviation h^2 (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. The expected GA as per cent of mean (GAM) was estimated as

$$\text{Genetic advance as per cent of mean} = \frac{\text{GA}}{\text{Grand Mean}} \times 100$$

The range of genetic advance as per cent of mean was classified as suggested by Johnson *et al.* (11) and described as Low (0-10 per cent), Moderate (10-20 per cent) and High (> 20 per cent).

The R software version 4.4.1 was used for all statistical analysis. IBM SPSS software version 20 was used to generate frequency distribution curves for all the traits among F_2 population.

Table 1. Details of the parents used in the present investigation

S. No.	Parent	Details
1.	DRR Dhan 60 (Improved sambha mahsuri × Kasalath)	DRR Dhan 60 is released from Indian Institute of Rice Research (ICAR-IIRR). It is having medium slender grain type with the duration of 120-125 days yielding 4.8 – 5.19 tonnes/ha and it is having BLB resistance genes (*xa5, xa13* and *Xa21*) and low P tolerance due to presence of *Pup 1* QTL developed through marker assisted selection.
2.	Pusa 44 (NIL)	It is a Near isogenic line of PUSA44 (a high yielding short duration variety and possess resistance to blast (*Pi 54*) and bacterial leaf blight having long bold grains) developed with a gene *AHAS* (Aceto hydroxy acid synthase) leading to herbicide (imazethapyr) tolerance

Table 2. Details of gene specific markers used for F_1 confirmation in the present study

Molecular Markers	Linked gene	Primer sequence	Chromosome Location	Reference
RM 6844	*AHAS*	F: AGTCCAAGAAAGGCACGAGAGG R: CTGCATCGAAGAAGAAGAAGAAGC	2	Shoba *et al*. [12]
Pi 54 MAS	*Pi 54*	F: CAATCTCCAAAGTTTTCAGG R: GCTTCAATCACTGCTAGACC	11	Ramkumar *et al.* [13]

3. RESULTS AND DISCUSSION

Mean Performances of F_2 generation: The results on genetic variability and other genetic parameters are shown and represented in Table 3 and Figs. 1 and 2. Frequency distribution of all the traits were presented in Fig. 3a,3b & 3c. A perusal of the results on mean performance and range of the yield contributing traits were studied in the present investigation (Table 3 and Figs. 1 and 2) revealed maximum range for spikelets per panicle followed by filled grains per panicle while minimum range was observed for Flag leaf width. Grain yield per plant ranges from 6.4 gm to 25.3 gm with a mean of 14.86 gm. Similar results were reported by Priyanka *et al.* [14]. The phenotypic variation for days to 50% flowering (DFF) ranged from 88 to 130 days. The average value for DFF trait was 108.94 days as it is represented in Table 3. Similarly, the average value for number of productive tillers per plant was 9.48 and the maximum and minimum value for the trait was 17 and 3 respectively. Thousand grain weight ranged from 13 gm to 24.4 gm with a mean of 18.26 gm. These results are in agreement with Priyanka *et al.* [14]. Flag leaf length and width, in the present study, were also noticed to range from 13 cm to 32 cm with an average of 22.33 cm and 1.2 cm to 2.0 cm with a mean of 1.63. Similar results were reported earlier by Bakya *et al.* [15]. Panicle length in the F_2 population ranged from 16.1 cm to 28.9 cm with a mean value of 22.64 cm. The results are in conformity with the reports of Priyanka *et al.* [14]. Spikelet fertility had a maximum value of 98.18% while minimum value was 37.82% with the average performance of 85.62%. Spikelet sterility had a maximum value of 90.86% while minimum value was 3.74% with the average performance of 14.34%. The present study uncovered the presence of sufficient genetic variation for all the traits under study in the F_2 population studied and the materials could be used for association mapping and as donors in Direct Seeded Rice (DSR) conditions.

The results on genotypic (GCV) and phenotypic (PCV) coefficients of variation are presented in Table 3 and Figs 1 and 2. The analysis of these results revealed higher PCV value, compared to GCV value for all traits studied, indicating the effect of environment. Among the traits, chaffy grains per panicle recorded greater difference between phenotypic (46.90%) and genotypic coefficients of variation (33.52%), compared to other traits, indicating higher influence of environment on the trait, resulting in medium heritability values for the trait. However, number of tillers per plant (37.11% & 34.52%), number of productive tillers per plant (38.34% & 35.32%), panicle length (14.5% &11.56%), grain yield per plant (30.19% & 26.60%) recorded minimum variation between GCV and PCV values respectively, indicating lesser influence of environment resulting in high heritability values. The observations are in agreement with the inferences of Harisha *et al.* [16]. The traits, number of productive tillers per plant, number of tillers per plant, flag leaf length and grain yield per plant have high genotypic and phenotypic coefficient of variation. These results are in agreement with Sala and Shanthi [17] for number tillers per plant and grain yield per plant, Lakshmi *et al.* [18] for number of productive tillers per plant, Harijan *et al.* [19] for flag leaf length (26.34% & 23.59%). The results also revealed low genotypic and phenotypic coefficient of variation for days to 50% flowering (9.51% & 8.35%) and spikelet fertility (8.49% & 6.86%). The findings are in conformity with the reports of Sudeepthi *et al.* [20] for spikelet fertility.

High heritability (>60%) and high genetic advance as % of mean (>20) was observed for number of tillers per plant (86.57% & 66.17%), number of productive tillers per plant (84.87% & 67.04%), flag leaf length (80.21% & 43.52%), flag leaf width (19.17% & 5.73%), number of spikelets per panicle (50.11% &24.10%), number of filled grains per panicle (43.53% &24.69%) and grain yield per plant (77.65% & 48.29%). These results are in agreement with the observations of Fathima *et al.* [21] for productive tillers per plant; Bakya *et al.* [15] for flag leaf length and width; Lakshmi *et al.* [22] for number of filled grains per panicle and total grains per panicle; Shankar *et al.* [23] for grain yield per plant. High GCV and high PCV coupled with high heritability and high genetic advance as per cent of mean were recorded for number of tillers per plant, number of productive tillers per plant, flag leaf length and grain yield per plant suggesting an additive type of gene action. Both GCV and PCV were presented in the bar graph and also Heritability and Genetic Advance as per cent of Mean are presented in the Figs. 1 and 2. Hence, good response to selection can be attained for improvement of these traits and early generation selection may be effective to improve these traits due to presence of additive gene action.

Positive skewness was observed for thousand grain weight and grain yield per plant. Traits observed with positive skewness indicate that

Table 3. Genetic Variability analysis for yield and yield contributing traits in F_2 generation

Character	P1	P2	F_2 Population								
			Mean	Range		PCV	GCV	Heritability	GAM	Skewness	Kurtosis
				Min	Max						
DFF	103	96	108.94	88	130	9.51	8.35	77.16	15.11	-0.04	-1.02
PH	76	86	82.21	63	102	13.81	10.81	61.21	17.41	0.04	-1.11
NTPP	10	8	10.40	3	18	37.11	34.52	86.57	66.17	-0.14	-1.05
NPTPP	7	5	9.48	3	17	38.34	35.32	84.87	67.04	-0.03	-1.07
FLL	25.4	29.1	22.33	13	32	26.34	23.59	80.21	43.52	-0.01	-1.24
FLW	1.3	1.6	1.63	1.2	2	14.52	6.36	19.17	5.73	-0.22	-1.17
PL	21.4	24.2	22.64	16.1	28.9	14.50	11.56	63.60	18.99	-0.21	-0.84
SPP	250	194	241.02	110	345	23.26	16.47	50.11	24.01	-0.39	-0.70
CGPP	30	45	32.34	10	87	46.90	33.52	51.10	49.36	6.75	77.64
FGPP	220	159	208.43	79	319	27.54	18.17	43.53	24.69	-0.37	-0.71
SF	88	81.95	85.62	37.82	98.18	8.49	6.86	65.36	11.43	-2.06	8.31
SS	12	18.04	14.34	3.74	90.86	55.11	46.38	70.81	80.39	4.33	36.75
TGW	19.56	22.3	18.26	13	24.4	16.77	12.98	59.95	20.71	0.11	-0.92
GYPP	18.6	15.6	14.86	6.4	25.3	30.19	26.60	77.65	48.29	0.09	-1.10

DFF- *Days to 50% flowering,* ***PH***-*Plant height,* ***NTPP***-*No of tillers per plant,* ***NPTPP***-*No of productive tillers per plant,* ***FLL***-*Flag leaf length,* ***FLW***-*Flag leaf width,* ***PL***- *Panicle length,* ***SPP***-*Spikelet's per panicle,* ***CGPP***-*Chaffy grains per panicle,* ***FGPP***-*Filled grains per panicle,* ***SF***-*Spikelet fertility,* ***SS***-*Spikelet sterility,* ***TGW***-*Thousand grain weight,* ***GYPP***-*Grain yield per plant.*

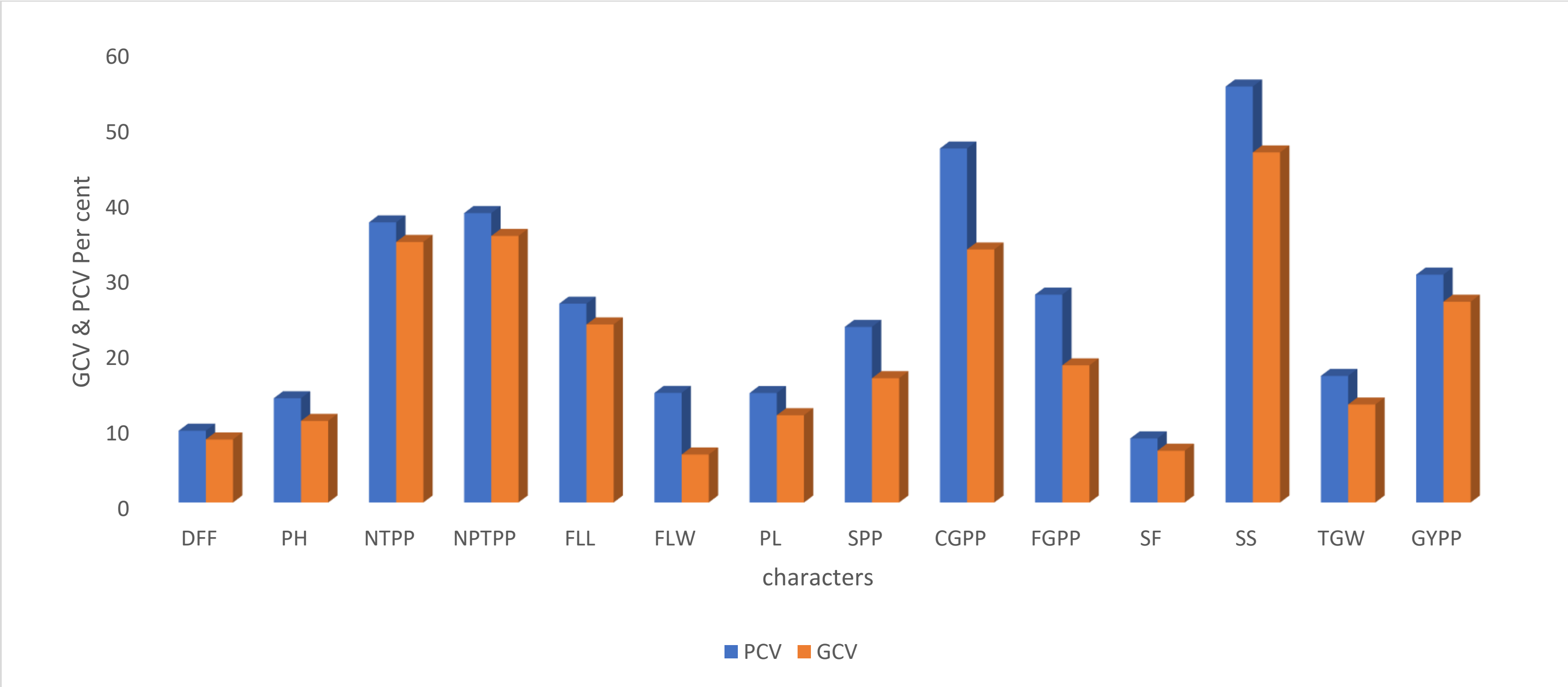

Fig. 1. Genotypic and Phenotypic coefficient of variation (GCV&PCV) for various traits in F_2 population

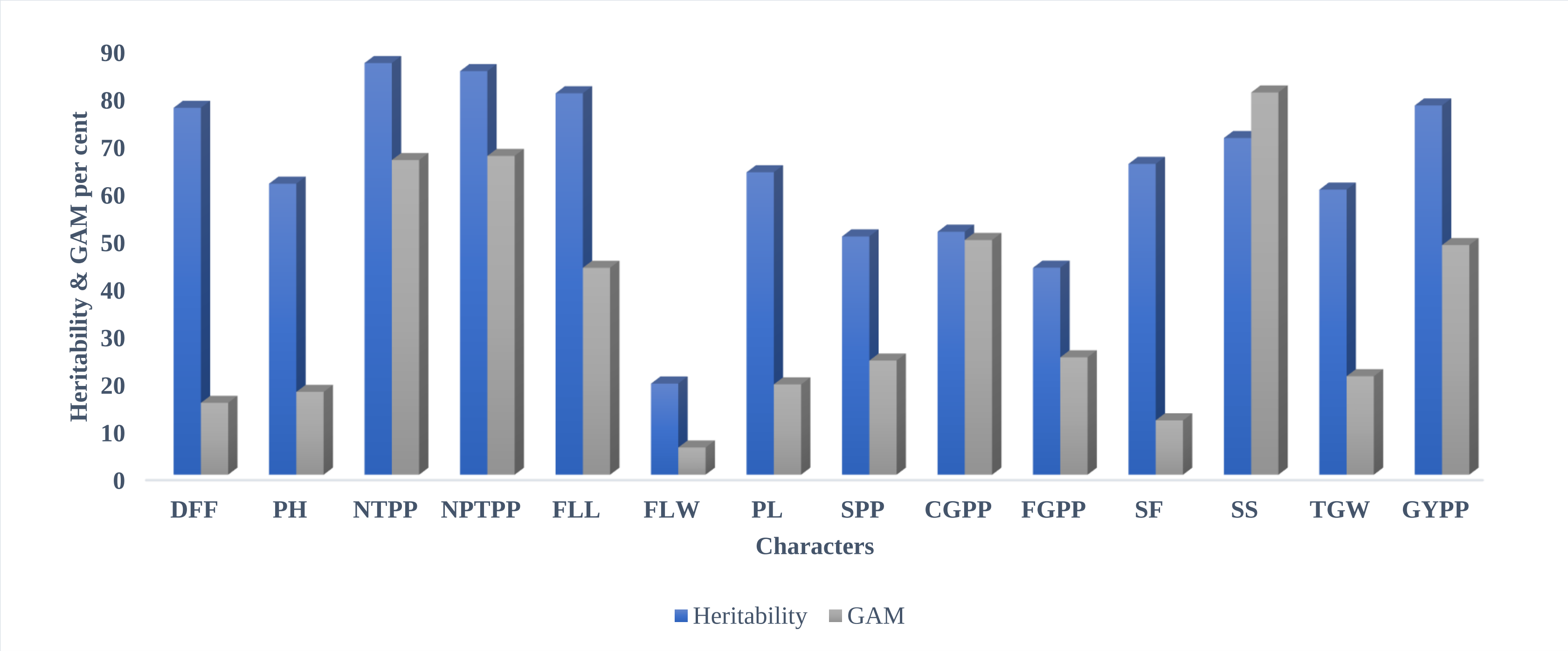

Fig. 2. Heritability and Genetic Advance as per cent of Mean (GAM) for various traits in F_2 population

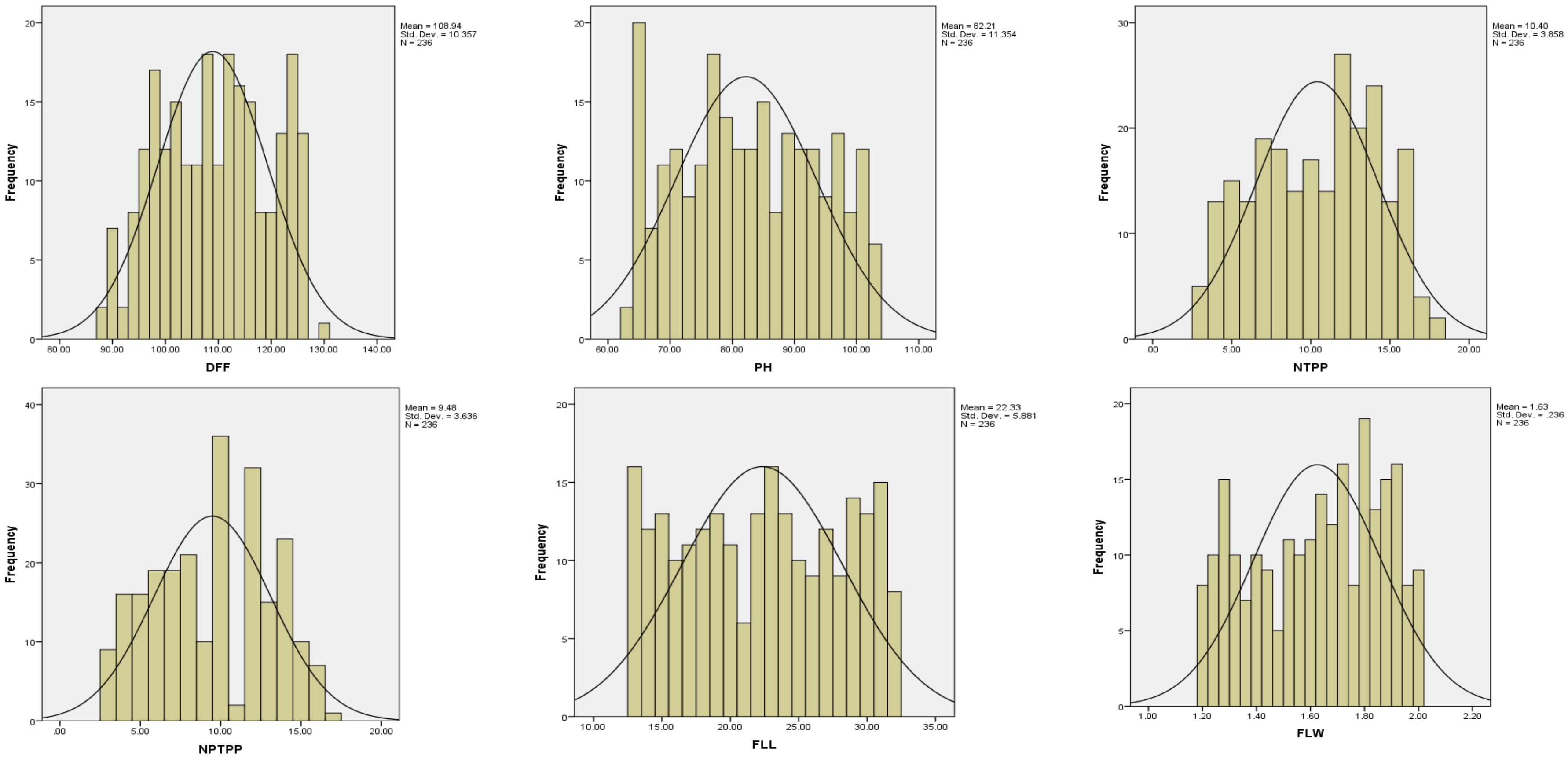

Fig. 3a. Frequency distribution of biometrical traits in F_2 generation

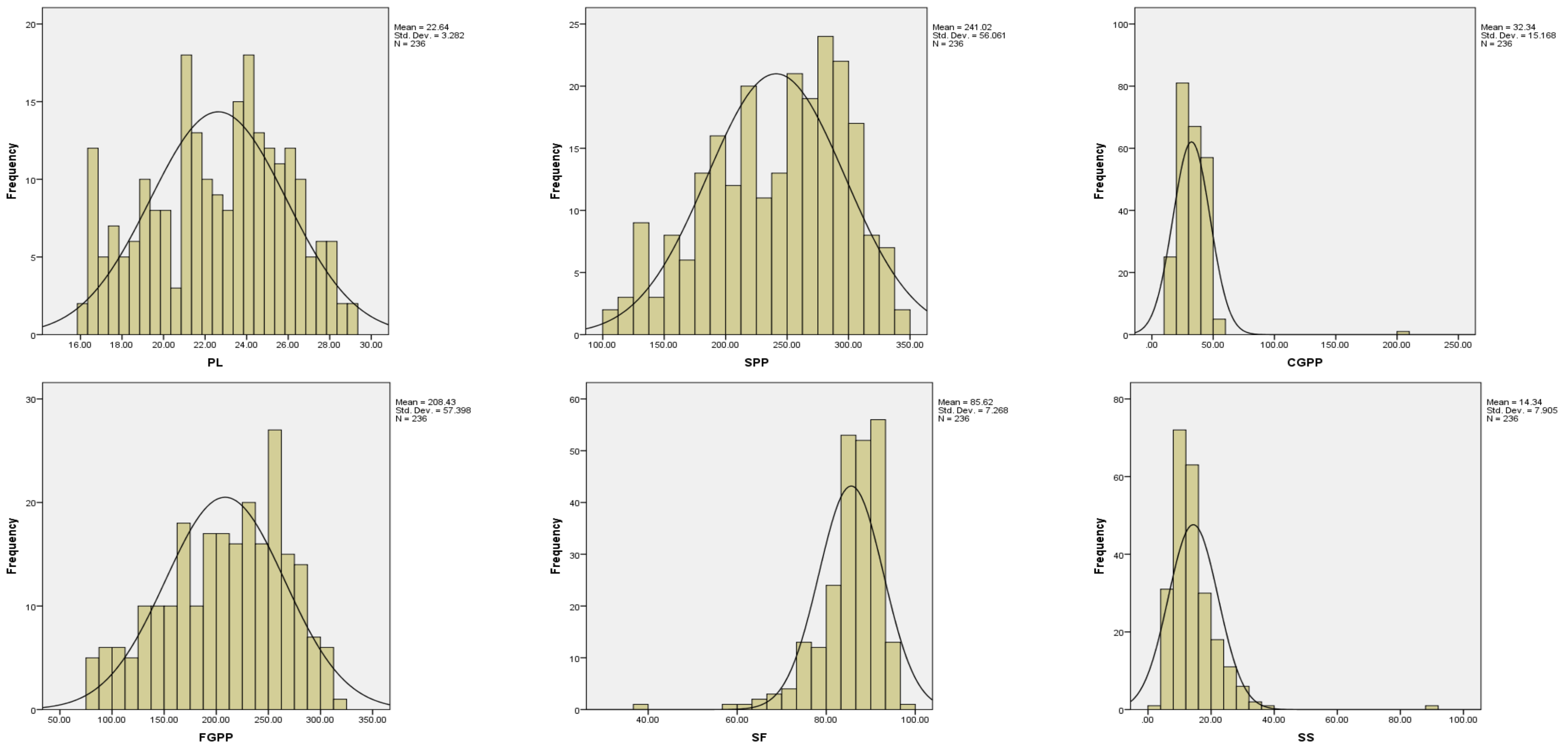

Fig. 3b. Frequency distribution of biometrical traits in F_2 generation (continue)

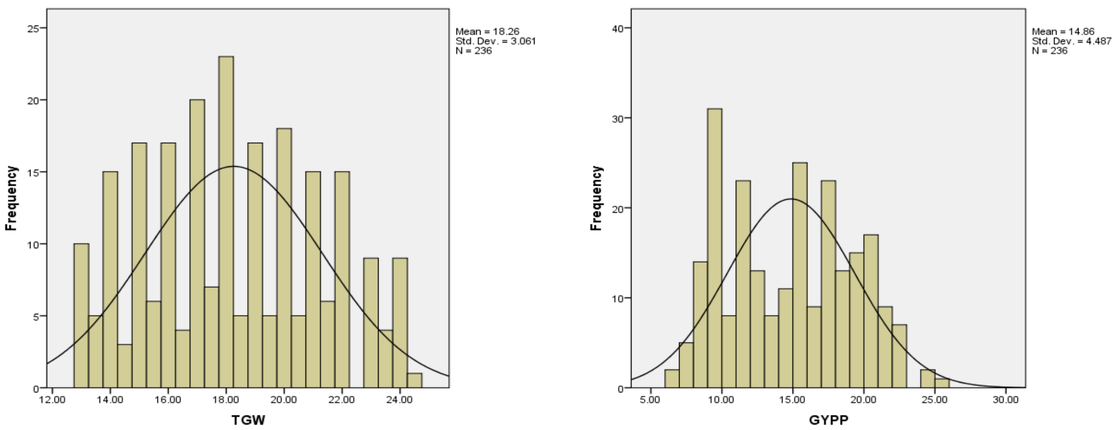

Fig. 3c. Frequency distribution of biometrical traits in F_2 generation

more proportion of individuals present in low end of distribution but transgressive segregants were also obtained for these traits. Hence, selection of single plants from the transgressive segregants will improve the positively skewed traits. Positive skewness was also observed for plant height. Segregants can be obtained from this cross and selection can be done for genotypes with semi dwarf plant height. Negative skewness was observed for days to 50% flowering, panicle length, number of productive tillers per plant, flag leaf length and number of filled grains per panicle. All these traits are mostly observed in majority of F_2 plants with high values. More proportion of plants with high panicle length, number of filled grains per panicle were obtained. Sufficient variability was available for most of the traits in this population, superior segregants with high yield could be isolated for developing a high yielding variety. Regarding kurtosis, even though platycurtic distribution was observed for most of the traits, wide range of variations among F_2's were recorded for these traits. Transgressive segregants occurred most frequently in intraspecific crosses involving inbred and least frequently in interspecific crosses between outbred. Transgression occurred due to part by heterosis, which is mostly prominent in first generation hybrids, complementary gene, overdominance and epistasis also contribute Rieseberg *et al*. [24] In this study transgressive segregants were observed for all the traits which might be due to the complementary gene action of positive alleles present in both the parents.

4. CONCLUSION

The outcome of the current study indicated high GCV, PCV, heritability and genetic advance as per cent of mean for number of tillers per plant, number of productive tillers per plant, flag leaf length, filled grains per panicle grain yield per plant indicating the effectiveness of direct selection for improvement of these traits.

FUTURE PROSPECTS

It highlights the presence of substantial genetic variability among the rice genotypes under study for yield and its attributing traits related aerobic rice breeding programmes. It opens the way for breeders to study further and utilizing these resources for mapping experiments for determination of major QTLs and genes related to seed vigour in direct seeded rice.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declares that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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