Original Research Article

Genetic Analysis of F_2 Population for Yield Enhancing Traits Under Direct Seed Condition in Rice (*Oryza Sativa* L.)

Abstract

The present investigation was conducted to assess the variability, frequency distribution grain yield and yield component traits to identify a superior segregant in F_2 generation of DRR Dhan 60 × Pusa 44 (NIL). 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). Genetic variability for DSR is of utmost importance to understand the genetics and improvement of rice genotypes suitable for aerobic conditions. The experimental material consists of 236 F_2 population along with parents which were planted in DSR plot at ICAR-IIRR, Hyderabad. Data recorded for the traits viz., Daysto 50% flowering, Plantheight, Numberoftillers perplant, Flag leaf length, Flag leaf width, Number ofpanicles per plant, Paniclelength,Numberofspikelets perpanicle, Numberoffilledgrains per panicle, Numberofchaffygrains perpanicle, Spikeletfertility,Spikeletsterility,1000-grainweight andGrain yield perplant.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.High GCV and high PCV coupled with high heritability and high genetic advance as per cent of mean were recorded for productive tillers per plant, number of tillers per plant, flag leaf length and grain yield per plant suggesting an additive type of gene action and selection for these traits is effective. These results signify that there was sufficient amount of genetic variability for all the studied traits under aerobic conditions.

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

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. 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 (Butardo *et al*., 2019). 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).

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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 (Chakraborty *et al*., 2017). 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 (Grigg, 1974).

The ideal generation for imposing selection is one that exhibits significant levels of segregation and recombination (Thirugnanakumar *et al*., 2011). 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 (Savitha and Ushakumari, 2015). A crucial component is the degree of connection between the qualities, particularly for complicated and economically significant variables like yield.A statistical tool for determining the strength of the association between two or more variables is the correlation coefficient. The examination of path coefficients aids in the creation of suitable breeding protocols for the evolution of genotypes with high yields.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.

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 (Recurrent 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.

Data was recorded in all the segregants for Daysto 50% flowering, Plantheight (cm), Numberoftillers perplant, Flag leaf length (cm), Flag leaf width (cm), Number ofpanicles per plant, Paniclelength (cm),Numberofspikelets perpanicle, Numberoffilledgrainsper panicle, Numberofchaffygrains perpanicle, Spikeletfertility(%),Spikeletsterility(%),1000-grainweight(gm) andGrain yield perplant(gm).The genetic variability parameters, namely, Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated using the formula given by Mirza *et al.*(2011). Heritability was calculated using the formula given by Allard *(*1960) and genetic advance as percentage of mean was calculated by adopting the formula given by Johnson *et al*. (1955). The R software version 4.4.1 was used for all statistical analysis and for illustrating the association plot. 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 of the intra-specific cross studied 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 (*xa5*, *xa13* and *Xa21*) and low P tolerance due to presence of *Pup 1* QTLdeveloped 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 hybridity confirmation in the present study

Molecular Markers	Linked gene	Primer sequence	Chromosome Location	Reference
RM 6844	*AHAS*	F: AGTCCAAGAAAGGCACGAGAGG R:CTGCATCGAAGAAGAAGAAGAAGC	2	Shoba *etal*. (2017)
Pi 54 MAS	*Pi 54*	F: CAATCTCCAAAGTTTTCAGG R: GCTTCAATCACTGCTAGACC	11	Ramkumar *et al.* (2011)

Results and Discussion:

Mean Performances of Rice Genotypes

The results on genetic variability and other genetic parameters are shown and represented in Table3 and figures1-2.Frequency distribution of all the traits were presented in figure 3. A perusal of the results on mean performance and range of the yield contributing traits were studied in the present investigation (Table 3 and figures1-2) revealed maximum range for spikelets per panicle followed by filled grains per panicle while minimum range 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 per plant. Similar results were reported by Priyanka *et al.* (2019).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.* (2019). 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.*(2020). 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.*(2019).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 rice genotypes used and the materials could be used for association mapping and donors Direct Seeded Rice(DSR) conditions.

The results on genotypic (GCV) and phenotypic (PCV) coefficients of variation are presented in Table 3 and Fig1-2. 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.*(2024). 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 (2016) for number tillers per plant and grain yield per plant, Lakshmi *et al.*(2017) for number of productive tillers per plant, Harijan *et al.* (2021) 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.*(2020) 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.*(2021) for productive tillers per plant ;Bakya *et al.*(2020) for flag leaf length and width; Lakshmi *et al.*(2021) for number of filled grains per panicle and total grains per panicle; Shankar *et al.* (2016) 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 figures (1-2). 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 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 were 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 platy curtic 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 contributeRieseberg *et al.* (1999). 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.

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. It highlights the presence of substantial genetic variability among the rice genotypes under study for yield and its attributing traits related to low soil P tolerance. It opens the way for breeders to study further and utilizing these resources for mapping experiments.

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

Character	P1	P2	F_2Population								
			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.

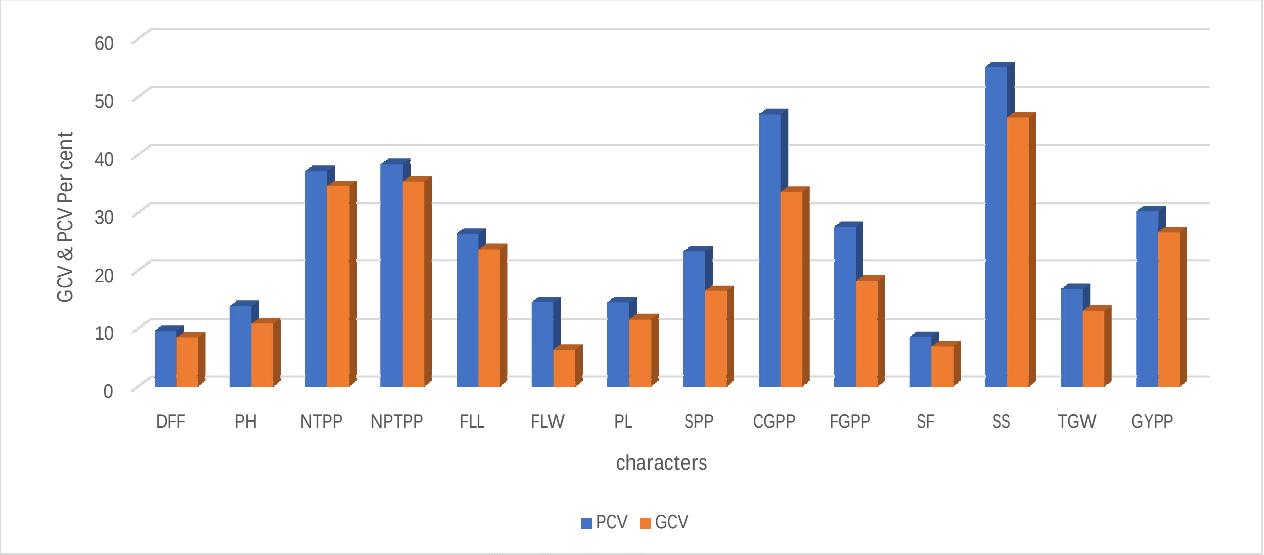

Fig. 1. Genotypic and Phenotypic coefficient of variation (GCV&PCV)for various traits in F_2 population

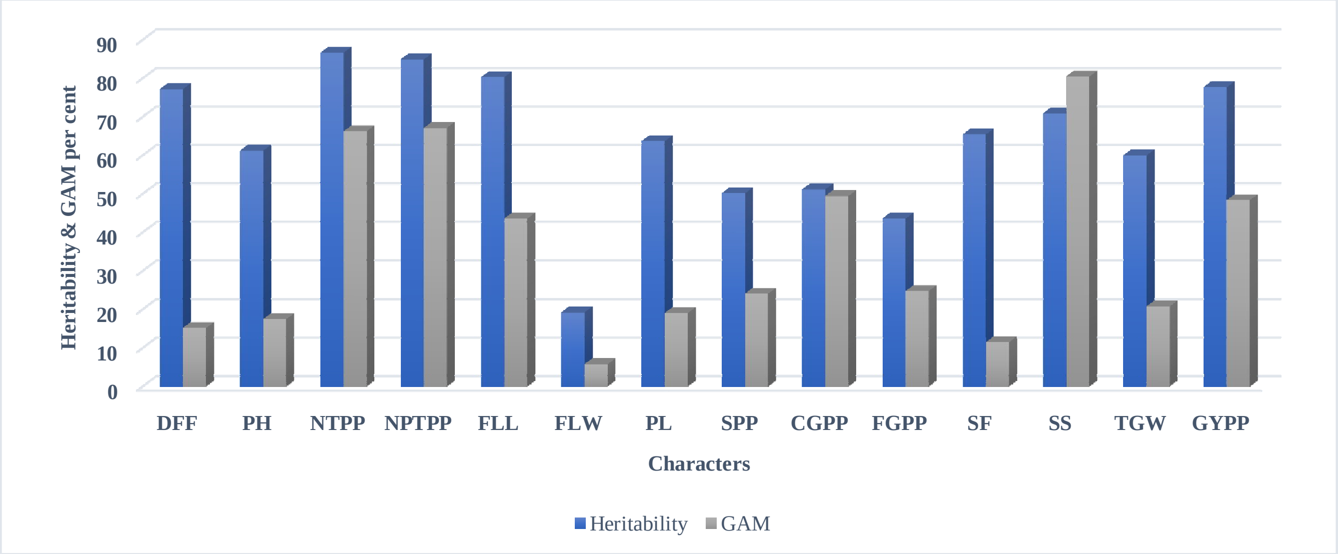

Fig. 2. Heritability and Genetic Advance as per cent of Mean(GAM) for various traits in F_2 population

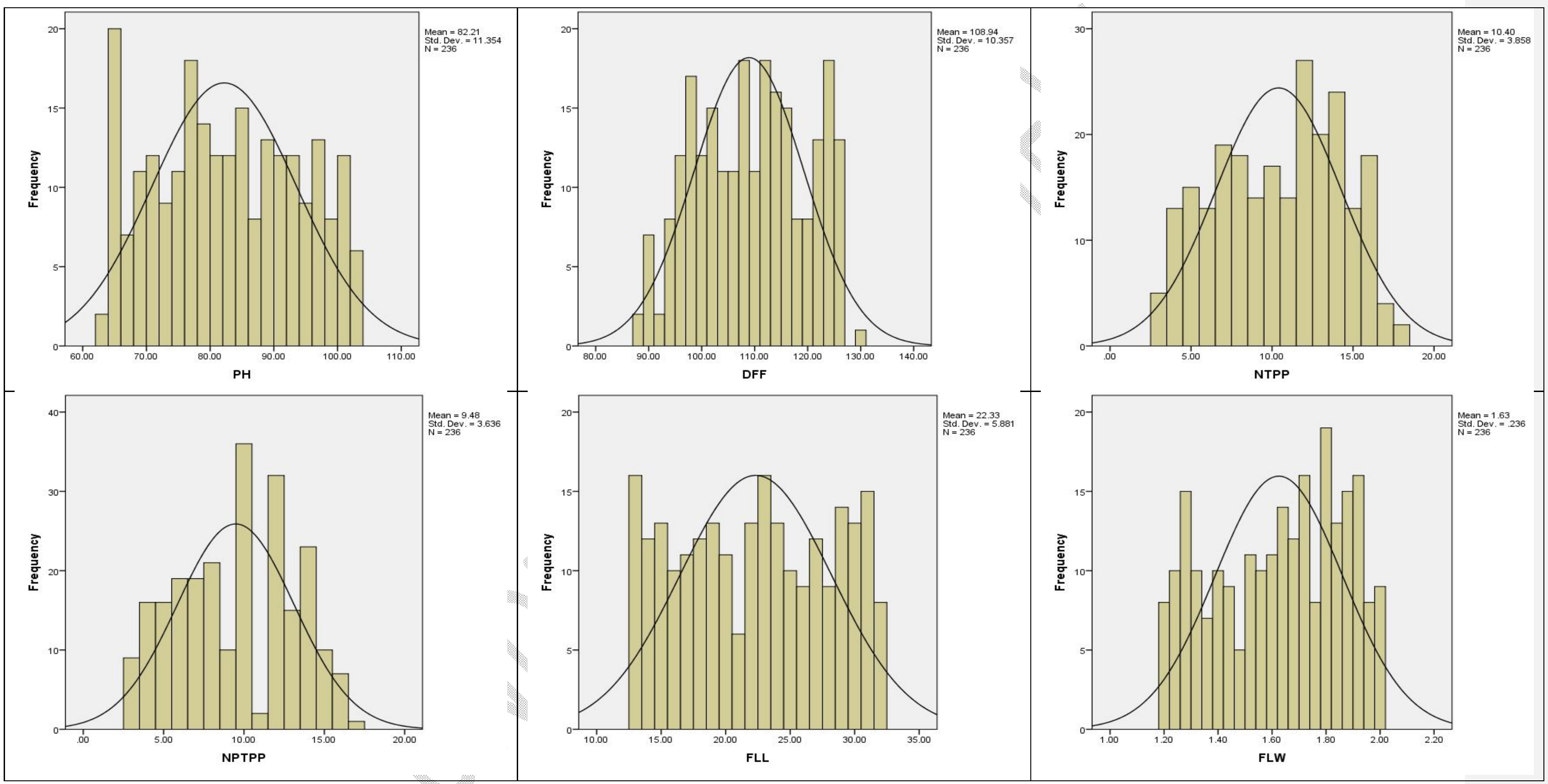

Fig. 3. Frequency distribution of biometrical traits in F_2 generation

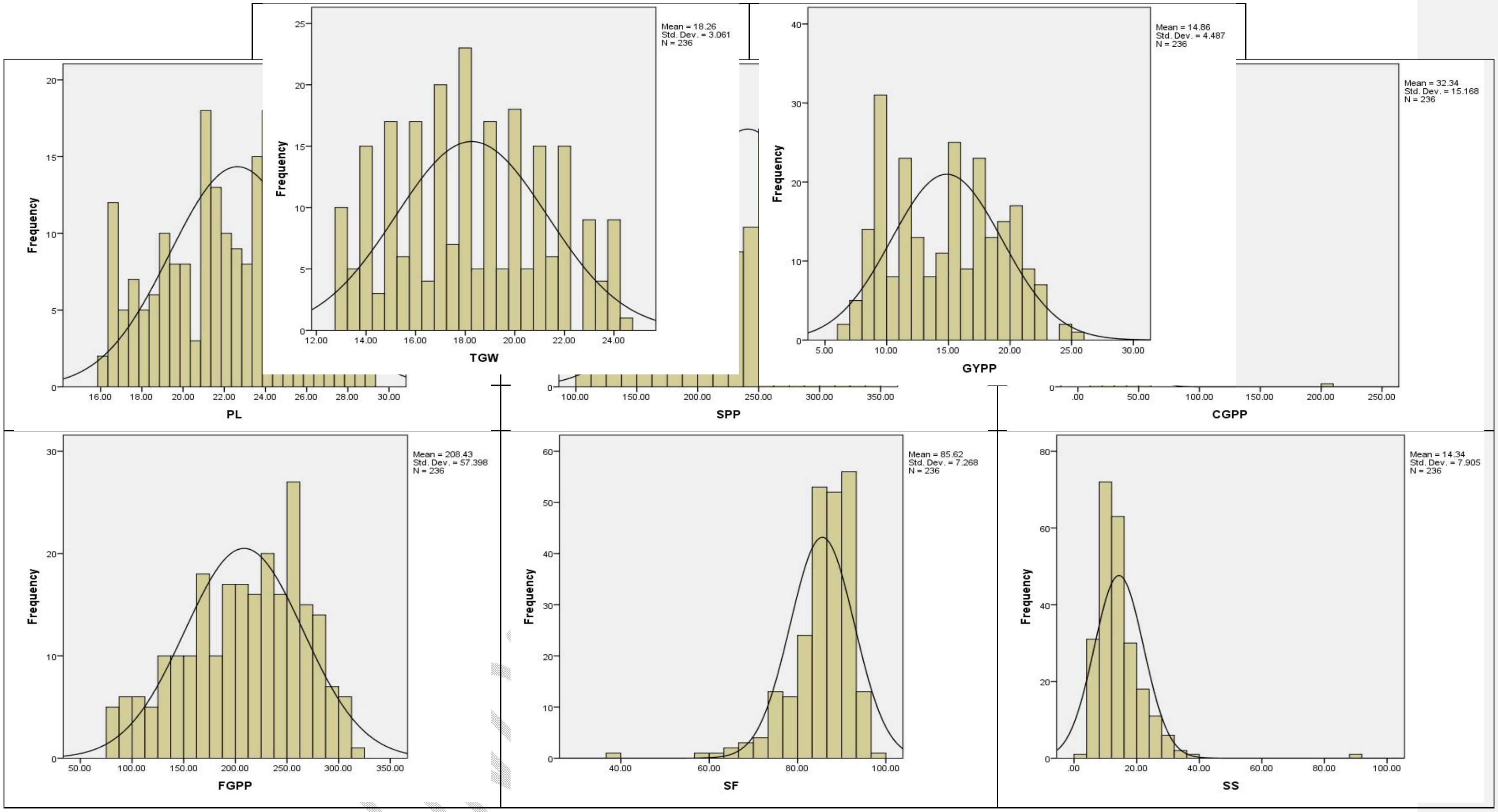

Fig. 3. Frequency distribution of biometrical traits in F_2 generation (continue)

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

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