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Parent Progeny Regression Analysis for Yield and Yield Contributing Traits in F_3 and F_4 Generations in Rice (*Oryza sativa* L.)

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ABSTRACT

The present study was carried out during *kharif* (June–September, 2019) and from January to mid of May 2020 at AC&RI, Madurai, Tamilnadu state, India. From the segregating populations of F_3 and F_4 generations of the cross ASD16×Improved Pusa Basmati 1 to estimate the effectiveness of selection for yield and its contributing traits. F_3 generation was raised in single seed decent method in the non-replicated manner and line sowing was taken in F_4 generation. Positively skewed and platykurtic curve was observed for the trait hundred seed weight in the both generations this result revealed that the trait was controlled by the complementary type of gene action hence showing that intense selection is needed to obtain more genetic gain from these traits. The parent progeny regression and intergenerational correlation showed positive and highly significance for the quantitative traits i.e., days to 50% flowering, number of productive tillers, number of filled grains panicle^{-1}, and single plant yield, plant height and hundred grain weight. Narrow sense heritability was observed for the traits *viz.*, days to 50% flowering, single plant yield, number of productive tillers, panicle length, number of filled grains panicle^{-1} infer that these traits carried their additive×additive component and helped in the fixation of the characters in the early generation itself.

KEYWORDS: Correlation, heritability, kurtosis, parent-progeny regression, rice, skewness

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Data Availability Statement: Legal restrictions are imposed on the public sharing of raw data. However, authors have full right to transfer or share the data in raw form upon request subject to either meeting the conditions of the original consents and the original research study. Further, access of data needs to meet whether the user complies with the ethical and legal obligations as data controllers to allow for secondary use of the data outside of the original study.

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1. INTRODUCTION

Rice is the major consumed staple food crop Mathure et al. (2011), Kahani, Hittalmani (2015), Abhilash et al., 2018). 90% of the world's rice production and consumption occurs in Asia Sala et al. (2015). Rice is cultivated in 45.76 mha with a total production of 124.36 million tonnes on an average yield of 2.171 tonnes per hectare (Anonymous, 2020-2021). Hence India is considered as the second worlds producing country Kumar et al. (2013). More than 80% of the country's population depends fully or partially on rice. Due to the adoption of rice as a part of the lifestyle, development of high yielding rice varieties should come into the scenario to break the yield barrier and boost yield by roughly 15–20% (Ramya et al., 2012, Islam et al., 2015, Ma and Yuan, 2015). So, for the yield improvement, direct selection will not be much effective (Bartley and Weber, 1952, Johnson et al., 1955, Whan et al., 1981, Rahman and Bahl, 1986). Grain yield is polygenetically controlled character with complex in inheritance Zeng et al. (2004) and Sharma et al. (2020). Hence hybridization followed by the selection will provide superior genotypes for improvement in different trait because this complex trait grain yield is the product of interactions between different genetic and environmental fluctuations (Nandeshwar et al., 2010). It is crucial for a breeder to comprehend the relationship between grain production and the component characters in order to meet this criterion because the majority of the characters to select involve the interaction of multiple characters. Rice quality in India differs from state to state (Prom-u-thai et al., 2020). In North India aromatic long, slender rice is preferrable like Basmati where as in the south India the short slender fine grain types are mostly preferred (BPT5204, Akshaya).

Segregating populations had wide range of variability which allows the gene expression of different traits Govinthraj et al., 2017. As per the diversity group of Basmati is categorized under group V which is cultivated in these geographics of Gangetic plains of India and Pakistan where the expression of the aroma is best due to the favourable environmental conditions Singh et al., 2000. In the present study the parents are ASD16 and Improved Pusa Basmati 1(IPB1) which is a long slender grain with good cooking quality, scentedness equipped with BLB resistance gene has been taken to take the advantage of obtaining desirable segregants for fine grain types combined with high yield, good cooking quality and aroma in the tropical conditions. Skewness and kurtosis give the information about the type of gene interaction and number of genes taking the control for the expression of the specific trait Nadarajan et al., 2016. The failure of parental yield to predict progeny yield may be caused by significant environmental changes hence Parent off-spring regression reveals the lesser influence of environment thus surfacing the true genetic potentiality of the genotypes and thereby helps in the selection in segregating population Barman and Borah, 2012 and Kumar et al., 2020 and is calculated according to Lush (1940).

Intergenerational correlation was figured out to see how far the genetic potential can be carried to the next generations like yield and yield attributing traits Sarwar et al., 2016, Rukmini Devi et al., 2017 Narrow sense heritability was carried out to access the true heritability of the trait which is due to the additive gene action Falconer, 1964, Nadarajan et al., 2016. These analysis assists the plant breeder to select the desirable segregants from the segregating populations and hence the present study was undertaken to exploit the advantages offered by using them and thus helps to fix the traits in the early generations itself in the cross of ASD16× Improved Pusa Basmati 1.

2. MATERIALS AND METHODS

The present study was taken to explore the genetic potential of the cross ASD16×Improved Pusa Basmati 1 in the F_3 and F_4 generation in the season of *kharif* (June–September, 2019) and from January to mid of May 2020 with the latitude and longitude of 9.9699° N, 78.2040° E respectively at AC&RI, Madurai, Tamilnadu, India. ASD 16 is a short bold grain type and Improved Pusa Basmati 1 is an aromatic long slender grain type. Hence the cross may exhibit wide variability for plant type, grain appearance and quality traits. Segregants showed variability with various grain sizes, shapes with wide range of yield. In the present study quantitative traits were given importance viz., days to 50% flowering, plant height, number of productive tillers, number of filled grains panicle^{-1}, panicle length and single plant yield. A total of 238 Recombinant Inbred Lines (RIL's) were obtained in the F_3 generation. Observations were taken from each individual plant in the F_3 generation and mean data was recorded from the five random plants in the F_4 generation for all the 238 RIL's. Data were compiled from F_3 and F_4 generations to study the parent progeny regression analysis, correlation coefficient and narrow sense heritability. Data from each generation (F_3 and F_4) was used to study the skewness and kurtosis also. All the 238 F_3 and F_4 RIL's were raised in non- replicated pattern. Based on the data obtained in F_3 and F_4 generations intergenerational correlation, parent progeny analysis was done using TNAUSTAT software. Mean values were used for calculating skewness and kurtosis using Microsoft excel and graphs were plotted to understand the gene interactions using SPSS software.

Narrow sense heritability was estimated by using the formula given by Smith and Kinman (1965)

h^2=(byx/2rxy)×100 ....……………(1)

byx is the regression coefficient of F_4 upon the parent values of F_3 generation calculated for the respective trait. rxy is the intergeneration correlation coefficient between the parent F_3 and F_4 generation respectively.

The skewness and kurtosis were divided by the respective standard errors to calculate 't' value. The calculated 't' value was compared with 't' table value with (n-1) degrees of freedom to assess significance. Non significance indicates that the traits were in normal distribution rather showing asymmetric distribution.

3. RESULTS AND DISCUSSION

The F_3 and F_4 are the segregating generations exhibited maximum variations for most of the traits. In the F_3 generation the range for days to 50% flowering was 72–123.8 days. The height of the plant ranged from 69–150 cm. The number of productive tillers from 6-28, panicle length from 15–36 cm. Number of filled grains panicle^{-1} from 100–250. Regarding to hundred grain weight it falls within the range of 1.95–4.04 g. The single plant yield ranged from 10–42.5 g. Where as in the F_4 generation, the range for days to 50% flowering was 70–127 days, plant height 62.9–134 cm, number of productive tillers with 5.6–32.8. The range for length of the panicle was17.9-36.1 cm. Number of filled grains panicle^{-1} was 75.4-233. The range for hundred grain weight was 1.4–3.9 g and single plant yield was 11.4–41.38 g (Table 1) (Table 2). The RIL No: 185 had a greater number of productive tillers and number of filled grains considered as best with 28 (F_3 and F_4) and 250 and 226 grains panicle^{-1} in the F_3 and F_4 generations respectively. Regarding the panicle length RIL 180 was considered as best with the length of 36.16 cm in F_4 (Table 3).

Table 1: Range in F_3 generation (ASD 16×Improved Pusa Basmati 1) for quantitative traits

	Days to 50% flowering	Plant height (cm)	No. of productive tillers	Panicle length (cm)	No. of filled grains panicle^{-1}	Hundred grain weight (g)	Single plant yield (g)
Range	72.6-123.86	69-150	6-28	15-36	100-250	1.95-4.04	10-42.5
ASD16	87	89	18	22.5	230	2.3	40.8
IPB1	115.0	99	18	25.6	194	2.10	34

Table 2: Range in F_4 generation (ASD 16×Improved Pusa Basmati 1) for quantitative traits

	Days to 50% flowering	Plant height (cm)	No. of productive tillers	Panicle length (cm)	No. of filled grains panicle^{-1}	Hundred grain weight (g)	Single plant yield (g)
Range	70-127.8	62.9-134	5-32	17.9-36.1	75-233	1.4-3.9	11.4-41.38
ASD16	88	89	18	22.5	232	2.32	40
IPB1	116	97	18	26	195	2.12	36

Table 3: Per se performance of superior RIL's in F_3 and F_4 generations for quantitative traits

	RIL NO	DFF	PH	NPT	PL	NFG	HgW	Spy
F_3	185	82	96	28	19	250	1.95	42.5
F_4	185	75.5	105.58	28.4	19.28	226	1.89	41.38
F_4	180	81.6	118.74	17.8	36.16	123.6	2.41	23.12

3.1. Skewness

Skewness and kurtosis are used for fixing frequency curves, surfaces and flatness. Skewness is the third degree of statistics which provides the information to understand the nature of gene action and appears in the asymmetric distribution. The value of $\beta1>0$ it represents the positive skewness (skewed to the right) representing the presence of complimentary gene action where scores move towards the high end of the curve. $\beta1<0$ it indicates the skewness is falling under negativeness (skewed to the left) thus showing the presence of duplicate gene action when score move towards the low end of the curves. $\beta1=0$ it indicates symmetric distribution (Choo and Reinbergs, 1982). The genes controlling the trait with skewed distribution are to be predominantly governed by dominant gene action whether they are having increasing or decreasing effect on the specific traits Savitha and Kumari (2015). The complementary gene action contributes for the increase in the selection intensity and also improves the population performance thus yielding the best performance of the population. In the F_3 generation, normal distribution has been observed plant height (0.629), single plant yield (0.43), number of productive tillers (-0.29), panicle length (0.13), days to 50% flowering (0.11) and number of filled grains panicle^{-1} (0.02). Positive skewness was observed for hundred seed weight (0.55). In F$_4$ generation, normal distribution has been recorded for number of filled grains panicle^{-1} (0.31),days to 50% flowering (0.49), plant height (0.282), single plant yield (0.205), number of productive tillers (0.03) and panicle length (0.13) Positive skewness has been observed for hundred seed weight (1.017*) (Table 4, Figure 1 and 2). Positively skewed and platykurtic curve was observed for the trait hundred grain weight in both generations which revealed that they are controlled by the complementary type of gene action. Hence intense selection is needed to obtain more genetic gain for this trait. Similar results for hundred grain weight was obtained by Savitha and Kumari (2015).

Table 4: Skewness and Kurtosis for the quantitative traits (ASD 16×Improved Pusa Basmati 1) for quantitative traits

Characters	Skewness	kurtosis	Skewness	kurtosis
	F$_3$		F$_4$	
Days to 50% flowering	0.011	-0.39	0.49	-0.24
Plant height	0.69	-0.42	0.28	-0.14
No. of productive tillers	-0.29	-0.67**	0.03	-0.87**
Panicle length	0.13	-0.37	0.13	-0.07
No. of filled grains panicle^{-1}	0.02	-0.54	0.31	0.27
Hundred grain weight	0.55**	0.132**	1.01**	0.35**
Single plant yield	0.43	-0.24	0.20	-1.04**

3.2. Kurtosis

Kurtosis is the third degree of statistics which tells about the number of genes controlling the trait and is a measure of "peakedness ". if β2>1 it indicates leptokurtic curve with few numbers of genes controlling the concerned traits. If β2<1 it includes platykurtic curve with large number of genes controlling the trait. β2=0 then it is mesokurtic curve. In the F$_3$ generation the Mesokurtic curve was observed for plant height (0.42), number of filled grains panicle^{-1} (-0.54), days to 50% flowering (-0.39), panicle length (-0.37) and single plant yield (-0.24). It indicates the normal distribution for these traits. Platykurtic curve was observed for number of productive tillers (-0.67) and hundred seed weight (0.132). In F$_4$ generation the mesokurtic curve was plotted for number of filled grains panicle^{-1} (0.27), days to 50% flowering (-0.24), panicle length (-0.07), and plant height (-0.14). Platykurtic curve was observed for the number of productive tillers (-0.87) and hundred seed weight (0.350). leptokurtic curve was obtained for single plant yield (-1.04) (Table 4, Figure 1 and 2). Platykurtic curve was observed

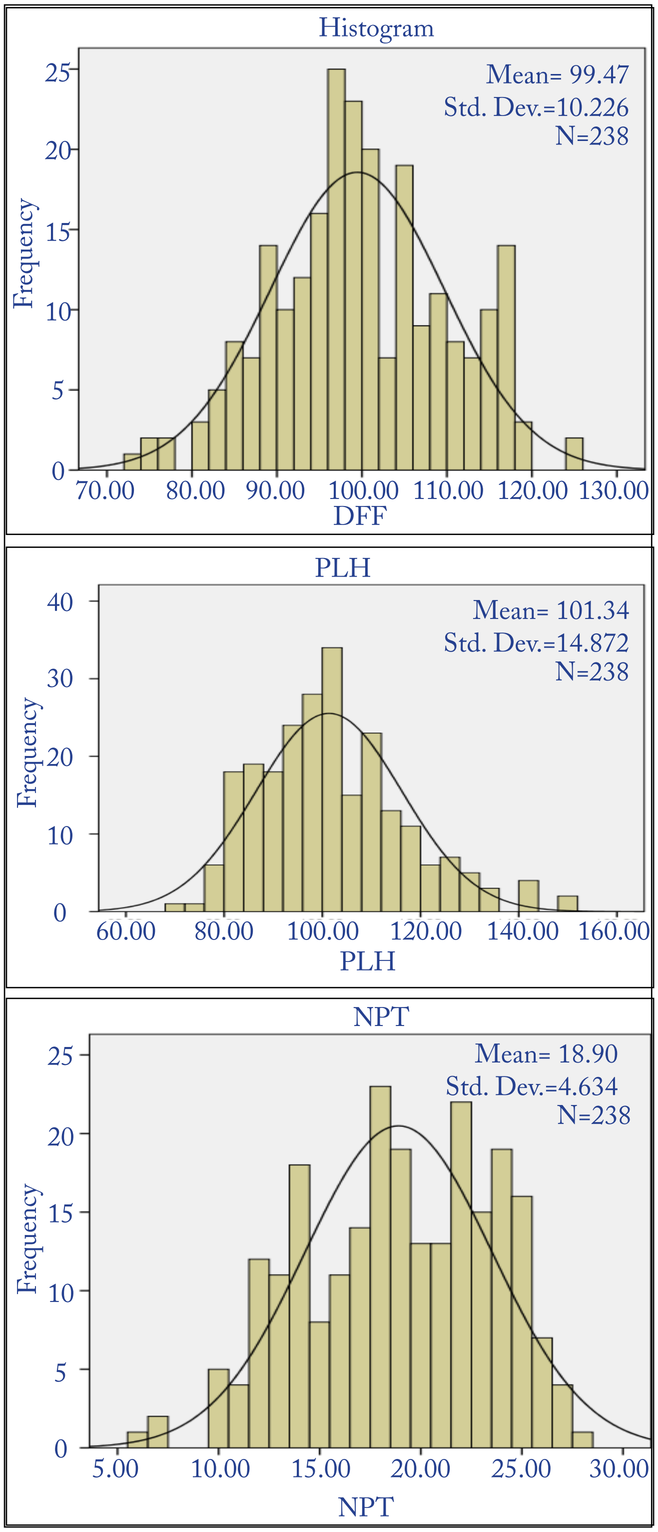

Figure 1: Continue...

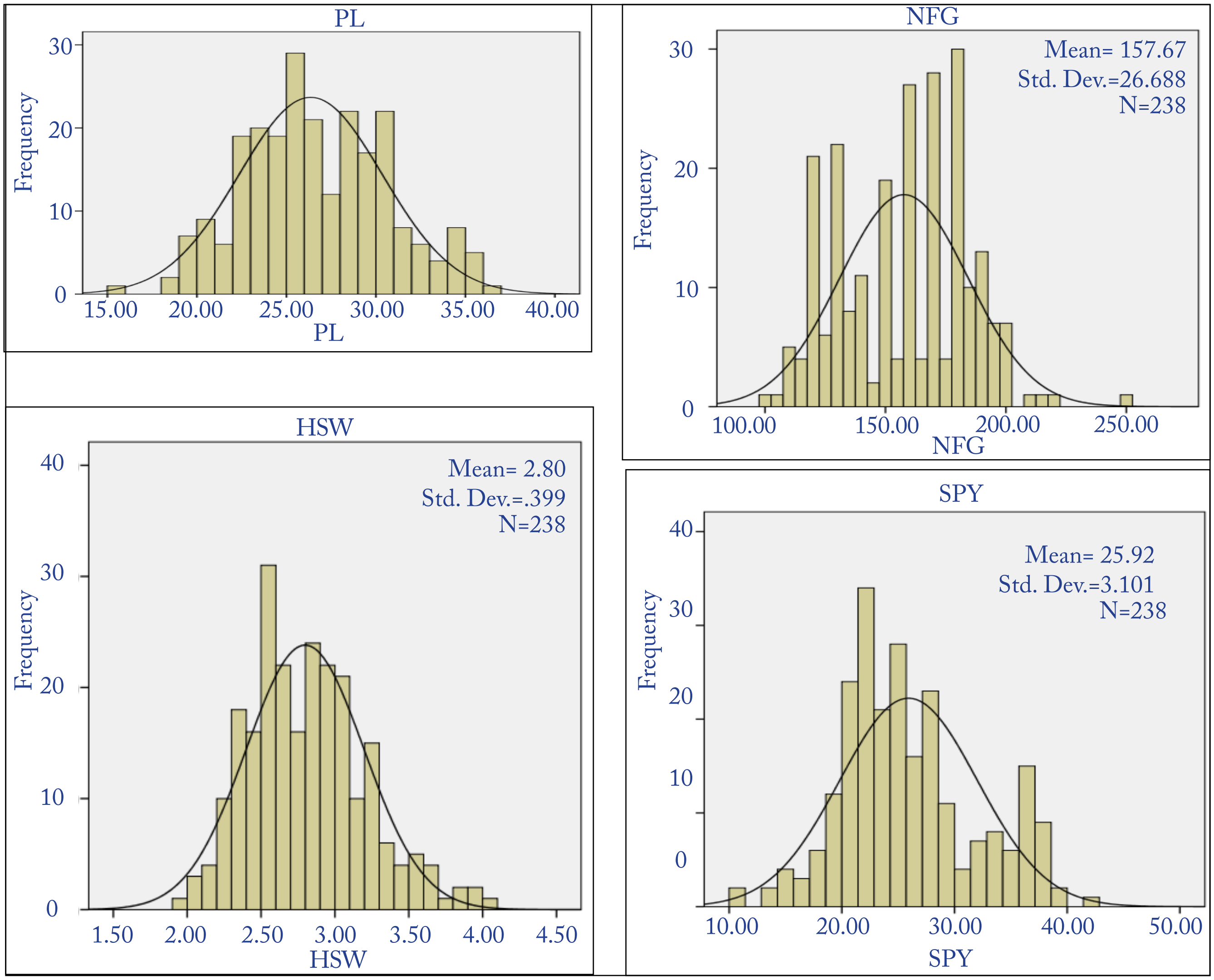

Figure 1: Skewness and kurtosis for quantitative traits in F_3 generation

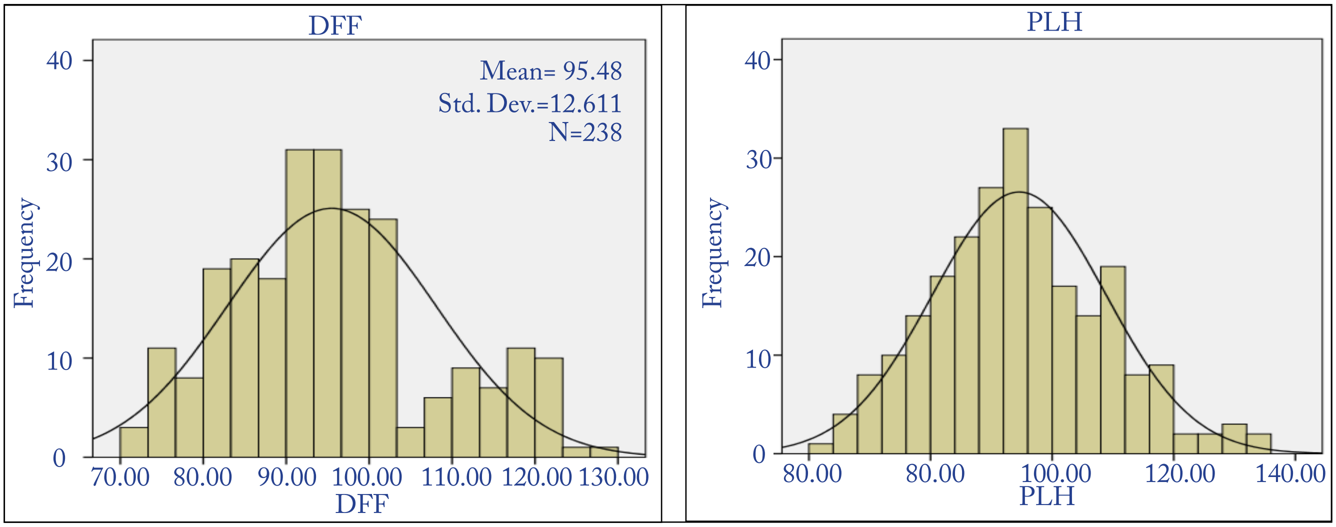

Figure 2: Continue...

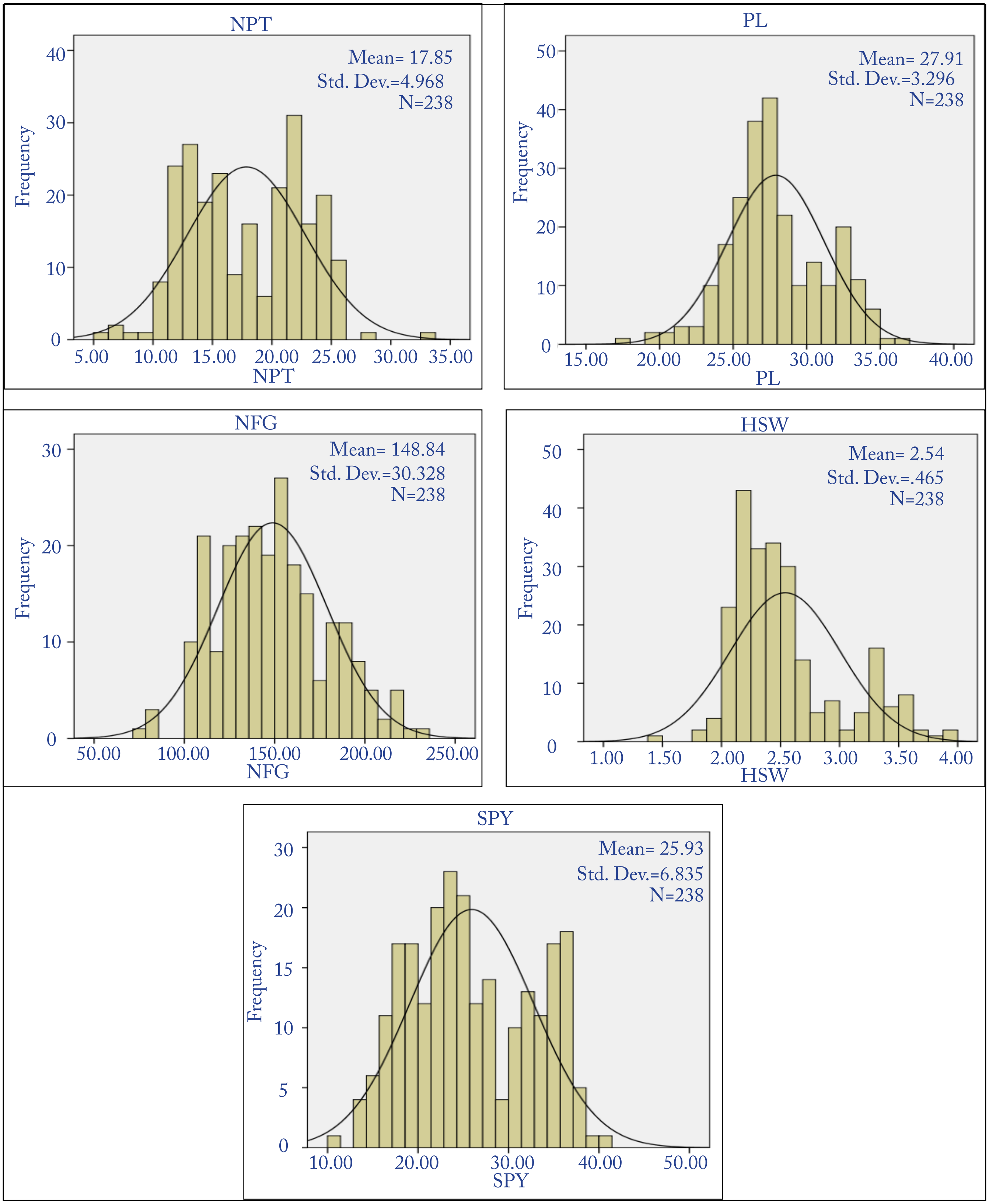

Figure 2: Skewness and kurtosis for quantitative traits in F_4 generation

for number of productive tillers in both generations. Leptokurtic curve for single plant yield was obtained in F_4 generation alone which signifies that mild selection is needed for selection of the trait. Similar findings for number of productive tillers was reported by Seeli et al. (2021).

Parent off spring regression is a useful tool to sort out the best performing genotypes with less environmental influences. It is a useful measure of the resemblance degree because it is simply related to the casual component of the variance Nadarajan et al., 2016. It was estimated by using the mean values of F_4 generation up on the F_3 generation which are used as parental values. The regression coefficient showed significance ($p<0.01$)and ($p<0.05$) for all of the quantitative traits *viz.*, days to 50% flowering (0.79),single plant yield (0.64),number of productive tillers (0.56), number of filled grains panicle^{-1} (0.35), plant height (0.20) hundred seed weight (0.11) and panicle length (0.039) (Table 5). Similar findings for single plant yield was reported by Anilkumar et al. (2011) and for days to 50% flowering, number of productive tillers by Kavithamani et al. (2013) and for the number of productive tillers by Govintharaj et al. (2017) and Kumar et al. (2020).

Correlation coefficient expressed high significance for all of the quantitative traits. Intergenerational correlations were estimated to know how far the genetic potential of the trait will be transferred to the next generation. In the present study, correlation coefficient showed high significance for the traits viz., hundred seed weight (0.616), days to 50% flowering (0.61), number of filled grains panicle^{-1} (0.56), single plant yield (0.55) number of productive tillers (0.53), and plant height (0.48) and panicle length (0.04) (Table 5). Similar results for days to 50% flowering, number of productive tillers and single plant yield were recorded by Seeli et al. (2021).

Table 5: Intergenerational correlation and regression values for the quantitative traits (ASD 16×Improved Pusa Basmati 1) for quantitative traits

Characters	Regression	Corelation	Narrow sense heritability
Days to 50% flowering	0.79^{**}	0.61^{**}	64
Plant height	0.20^{**}	0.48^{**}	21.2
No. of productive tillers	0.56^{**}	0.53^{**}	52.6
Panicle length	0.03^{**}	0.04^{**}	48.7
No. of filled grains panicle^{-1}	0.35^{**}	0.56^{**}	31.48
Hundred grain weight	0.11^{**}	0.61^{**}	9
Single plant yield	0.64^{**}	0.55^{**}	57.6

Narrow sense heritability was estimated based on the parent progeny regression analysis. Real heritability was high for days to 50% flowering (64.6), single plant yield with (57.6), number of productive tillers (52.6), number of filled grains panicle^{-1} (48.8), and panicle length (48.7), plant height (21.2), hundred grain weight (9) (Table 5). Real heritability is high for days to 50% flowering, number of productive tillers, number of filled grains panicle^{-1} Similar findings were obtained by the Kavithamani et al. (2013) and Seeli et al. (2021).

4. CONCLUSION

Based on the skewness and kurtosis, the traits number of productive tillers, hundred grain weight and single plant yield were needed to emphasis stringent selection pressure for the improvements of those traits. Regarding Parent off-spring regression analysis and intergeneration coefficient and narrow sense heritability, days to 50% flowering, number of productive tillers plant^{-1}, number of filled grains panicle^{-1} and single plant yield may be given importance to select the superior genotypes in ASD16×Improved Pusa Basmati 1cross in further generations.

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