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Research Article

Genetic variability and frequency distribution studies in F_2 segregating generation of rice

A. R. Priyanka[1], R. P.Gnanamalar[1*], S. Banumathy[1], N. Senthil[2] and G. Hemalatha[3]
[1]Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai – 625 104, Tamil Nadu.
[2]Department of Plant Molecular Biology and Bioinformatics, CPMB&B, TNAU, Coimbatore, 641 003
[3]Department of food science and Nutrition, Community Science College and Research Institute, 625 104
***E-Mail**: malarjustin@gmail.com

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Abstract

The present investigation was conducted to assess the variability, frequency distribution and association between grain yield and yield component traits to identify a superior segregant in F_2 generation of ASD 16 × Improved Pusa Basmati 1. High GCV and high PCV coupled with high heritability and high genetic advance as per cent of mean were recorded for number of filled grains per panicle, flag leaf length and grain yield per plant suggesting an additive type of gene action. Early generation selection may be effective to improve these traits due to presence of additive gene action. 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. Number of productive tillers per plant and number of filled grains per panicle had positive significant correlation and high positive direct effect on grain yield per plant and these characters should be given importance during selection.

Keywords

Grain yield, variability, skewness, selection, rice.

Introduction

Rice is a food grain crop of global importance with special preference in Asian countries. India was the largest exporter of rice in 2017-18 followed by Thailand, Vietnam and Pakistan. The country has exported 4.05 million tonnes of basmati rice and 8.63 million tonnes of non-basmati rice during the year 2017 – 2018 (www.agricoop.nic.in). As 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).

Segregating generation is a perfect generation which have high segregation and recombination for imposing selection (Thirugnanakumar *et al*., 2011). Genetic variability is a prerequisite for successful selection of superior progenies from segregating generations for further selection. The genetics of the traits can be better understood using third and fourth degree statistics *i.e.* skewness and kurtosis in segregating generations (Savitha and Ushakumari, 2015). The degree of correlation between the traits is a key factor especially in complex and economic trait such as yield. Correlation coefficient is a statistical measure, which is used to find out the degree of relationship between two or more variables. Path coefficient analysis helps in designing appropriate breeding procedure for evolving high yielding genotypes. Hence, the present study was conducted to assess the variability, frequency distribution and association between yield and yield component traits to identify a superior segregants in F_2 generation of ASD 16 × Improved Pusa Basmati 1.

Materials and Methods

The present investigation was carried out at Department of Plant Breeding and Genetics, Agricultural College and Research Institute, Madurai. Hybridization was done between ASD 16 and Improved Pusa Basmati 1 during *kharif* 2017. ASD 16 is a short bold grain type with the duration of 110 to 115 days and also high yielding variety with 5.6 tonnes/ha. The variety, Improved Pusa Basmati 1 is an extra-long slender grain type with aroma and known for its high linear elongation ratio. It was developed through marker assisted selection for Bacterial Leaf Blight resistance with *xa*13 and *Xa*21 genes. Totally 196 F_2 segregants of ASD 16 × Improved Pusa Basmati 1 were raised during *kharif* 2018. Recommended agronomic practices were followed throughout the crop growth period. Data were recorded in all the segregants for days to first flowering, plant height (cm), number of productive tillers per plant, panicle length (cm), number of filled grains per panicle, flag leaf length (cm), hundred grain weight (g) and grain yield per plant (g). Genotypic and phenotypic coefficient of variation was calculated by the formula suggested by Burton (1952) and GENERES software was used for path analysis.

Results and Discussion

Variability, correlation and path analysis were carried out for eight biometrical traits and results were presented in Table 1 to table 3. In this study number of filled grains per panicle, flag leaf length and grain yield per plant showed high genotypic and phenotypic coefficient of variation. These results are in agreement with Revathi *et al*. (2016) and Rukmini *et al*. (2017) for number of filled grains per panicle, Sala and Shanthi (2016) for number of productive tillers per plant and single plant yield, Lakshmi *et al*. (2017) for number of productive tillers per plant and Abhilash *et al*. (2018) for number of filled grains per panicle and grain yield per plant. The difference between phenotypic and genotypic coefficient of variation for number of productive tillers per plant was high. It indicated that environmental influence was high on this character. Due to high environment influence on number of productive tillers per plant, low heritability was observed for this trait. High heritability and high genetic advance as per cent of mean was observed for plant height, panicle length, flag leaf length, number of filled grains per panicle and 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 filled grains per panicle, flag leaf length and grain yield per plant suggesting an additive type of gene action. 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. This result was in accordance with Pavan Shankar *et al*. (2016).

In F_2 population of ASD 16 × Improved Pusa Basmati 1, significant positive skewness was observed for days to first flowering, number of productive tillers per plant, flag leaf length, number of filled grains per panicle, hundred 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 days to first flowering which implies that more early flowering segregants were obtained from this cross and selection can be done for earliness. Significant negative skewness was observed for plant height, panicle length and hundred grain weight. Though negative skewness was observed for plant height, for improvement of this trait, selection may be done from lower end of distribution to obtain dwarf plant type segregants. More proportion of plants with high panicle length and hundred grain weight 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. Frequency distribution of biometrical traits were represented in Figure 1. Regarding kurtosis, even though significant leptokurtic nature of distribution was observed for hundred grain weight and grain yield per plant, wide range of distribution was 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*. 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.Correlation studies provide an effective basis of phenotypic selection in plant populations, whereas Path Coefficient analysis evaluates the participation of each component to the resultant variable directly as well as indirectly (Chamundeswari *et al*., 2014). Except days to first flowering, all other traits *viz*., plant height, number of productive tillers per plant, panicle length, flag leaf length, number of filled grains per panicle and hundred grain weight showed significant positive correlation with grain yield per plant. The same results were reported by Kishore *et al.,* 2015 for number of productive tillers per plant and number of filled grains per panicle. Days to first flowering had negative and significant inter correlation with all other traits. Plant height showed positive significant inter correlation with all other traits. Panicle length exhibited positive significant inter correlation with flag leaf length, number of filled grains per panicle and hundred grain weight. Number of filler grains per panicle showed positive inter correlation with hundred grain weight. The same result was observed by Pavan shankar *et al*. (2016), Gopikannan and Ganesh (2013) and Lakshmi *et al*. (2017).

Number of productive tillers per plant and number of filled grains per panicle had high positive direct effect with grain yield per plant. This was in accordance with Kishore *et al*. (2015) and Lakshmi *et al*. (2017). Hence importance should be given to number of productive tillers per plant and number of filled grains per panicle during selection for improvement of grain yield per plant. Plant height, Number of productive tillers per plant and panicle length had low positive indirect effect with number of filled grains per panicle. Flag leaf length had low positive indirect effect with number of productive tillers per plant and number of filled grains per panicle. Number of filled grains per panicle showed low positive indirect effect with number of productive tillers per plant. Although panicle length exhibited negative direct effect, its positive correlation and indirect causal factors are to be considered simultaneously for selection to improve yield (Fig. 2).

Hence selection based on productive tillers per plant and number of filled grains per panicle would be most effective for grain yield improvement in this population as these two traits exerted the highest positive direct effect on grain yield.

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Table 1. Genetic Variability analysis for biometrical traits in F_2 generation

Character	P_1	P_2	Mean	Min	Max	PCV	GCV	Heritability	GAM	Skewness	Kurtosis
DFF	82.8	114	96.0	82	117	8.24	7.83	90.30	15.33	0.73**	0.11
PH	85.9	98.1	92.4	59	119.4	14.05	13.60	93.63	27.11	-0.59**	-0.00
NPT/P	17.0	17.6	13.2	6	28	33.66	15.02	19.91	13.80	0.73**	0.39
PL	23.2	27.4	25.4	14	36	13.36	12.68	90.05	24.80	-0.42*	0.50
FLL	22.9	24.9	27.3	14	52	25.61	24.94	94.78	50.02	0.59**	0.15
NFG/P	240.0	197	133.8	60	224	26.50	26.10	97.00	52.97	0.44*	-0.02
HGW	2.1	2.2	2.1	1.3	2.9	12.26	10.26	70.02	17.69	-0.41*	1.12**
GY/P	40.2	37.4	17.8	7.0	45.6	45.30	43.97	94.18	87.90	1.18**	1.40**

DFF: Days to first flowering, PH: Plant height, NPT/P: Number of productive tillers per plant, PL: Panicle length,
FLL: Flag leaf length, NFG/P: Number of filled grains per plant, HGW: Hundred grain weight, GY/P: Grain yield per plant.
PCV: Phenotypic coefficient of variation, GCV: Genotypic coefficient of variation, GAM: Genetic advance as per cent of mean.

Table 2. Genotypic correlation coefficient among the grain yield and yield characters in F_2 generation

Traits	DFF	PH	NPT/P	PL	FLL	NFG/P	HGW	GY/P
DFF	**1.0000**	-0.5124**	-0.2354**	-0.2804**	-0.2284**	-0.1650**	-0.1184	-0.0840
PH		**1.0000**	0.2441**	0.4861**	0.4800**	0.3918**	0.4111**	0.3467**
NPT/P			**1.0000**	0.1948**	0.2969**	0.4236**	0.2029**	0.5867**
PL				**1.0000**	0.3381**	0.3365**	0.2493**	0.2064**
FLL					**1.0000**	0.4030**	0.2405**	0.3424**
NFG/P						**1.0000**	0.1500**	0.6012**
HGW							**1.0000**	0.2581**
GY/P								**1.0000**

**** significant at 1 % level, * significant at 5 % level**

Table 3. Path coefficient of the yield and yield contributing traits on single plant yield in F_2 generation

Traits	DFF	PH	NPT/P	PL	FLL	NFG/P	HGW	GY/P
DFF	**0.1555**	-0.0831	-0.0960	0.0190	-0.0058	-0.0646	-0.0090	-0.0840
PH	-0.0797	**0.1622**	0.0995	-0.0330	0.0122	0.1535	0.0321	0.3467
NPT/P	-0.0366	0.0396	**0.4077**	-0.0132	0.0075	0.1659	0.0158	0.5867
PL	-0.0436	0.0789	0.0794	**-0.0679**	0.0086	0.1318	0.0194	0.2065
FLL	-0.0355	0.0779	0.1211	-0.0230	**0.0253**	0.1578	0.0189	0.3425
NFG/P	-0.0257	0.0635	0.1727	-0.0229	0.0102	**0.3917**	0.0117	0.6013
HGW	-0.0178	0.0660	0.0818	-0.0167	0.0060	0.0579	**0.0790**	0.2563

Residual effect: 0.683

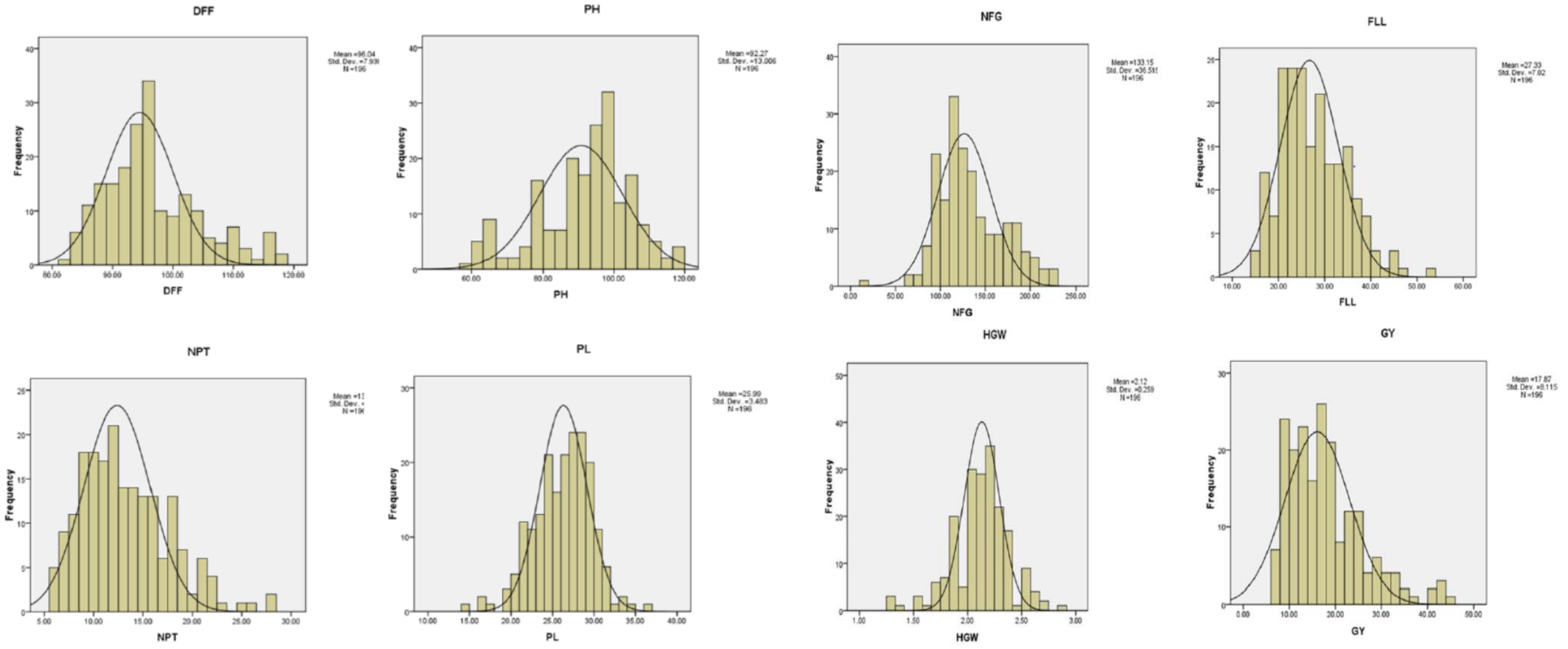

Fig. 1. Frequency distribution of biometrical traits in F_2 generation

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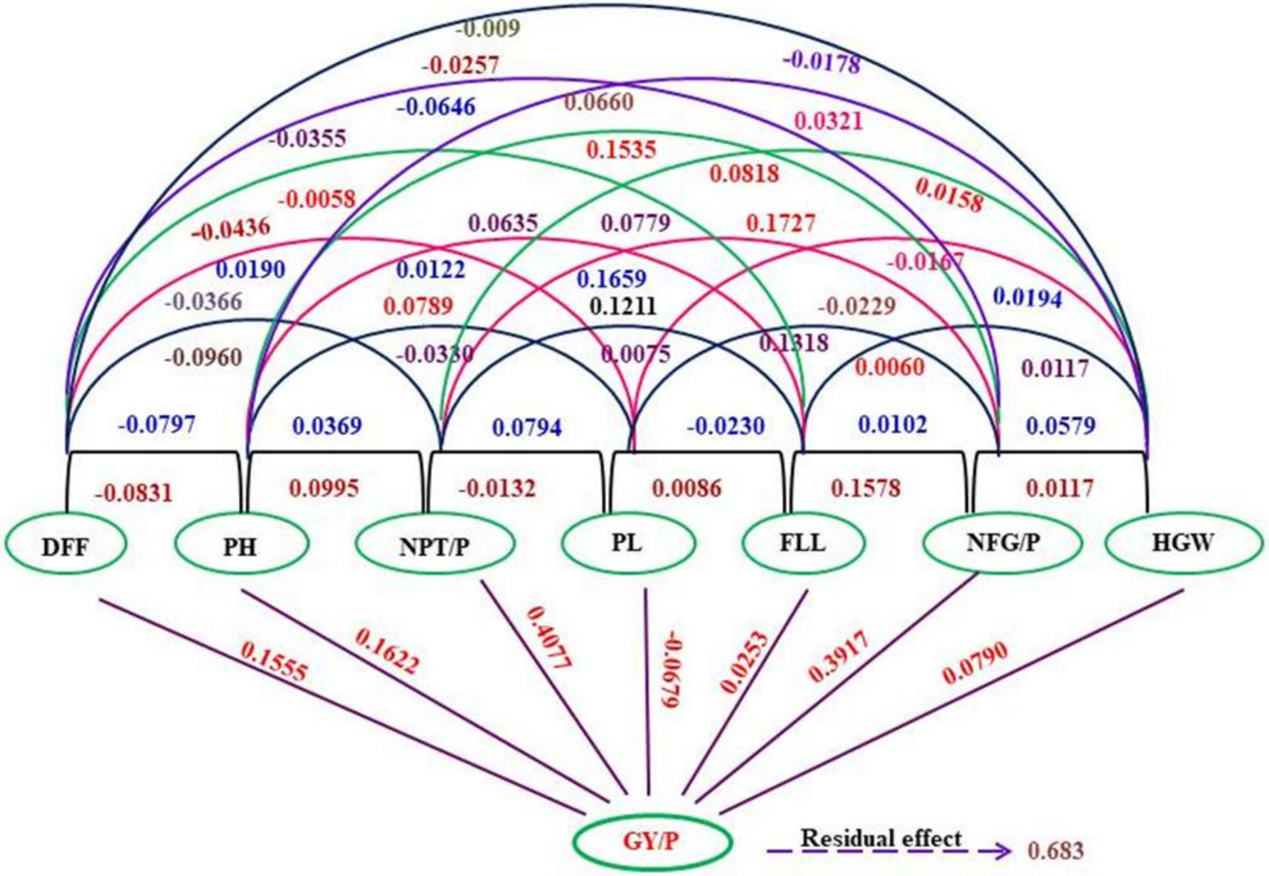

Fig. 2. Path diagram for yield and yield contributing traits