The Pharma Innovation Journal 2023; 12(10): 681-688

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(10): 681-688

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www.thepharmajournal.com
Received: 01-07-2023
Accepted: 06-08-2023

Sowmiya CA
Research Scholar, Department of Genetics and Plant Breeding, Agricultural College, and Research Institute, Killikulam, Thoothukudi, Tamil Nadu, India

Ramalingam J
Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Pushpam R
Centre for Plant Breeding and Genetics Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Shoba D
Department of Genetics and Plant Breeding, Agricultural College and Research Institute, Killikulam, Thoothukudi, Tamil Nadu, India

Kumar KK
Centre for Plant Molecular Biology and Biotechnology, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, India

Arumugam Pillai M
Department of Genetics and Plant Breeding, Agricultural College and Research Institute, Killikulam, Thoothukudi, Tamil Nadu, India

Corresponding Author:
Arumugam Pillai M
Department of Genetics and Plant Breeding, Agricultural College and Research Institute, Killikulam, Thoothukudi, Tamil Nadu, India

Studies on genetic variability, heritability and genetic advance in BC$_2$F$_2$ population of rice

Sowmiya CA, Ramalingam J, Pushpam R, Shoba D, Kumar KK and Arumugam Pillai M

Abstract

The BC$_2$F$_2$ population of ADT43 X RP-Bio-Patho-2 was used for the current experiment. The present study examined sixteen quantitative variables for genetic variability, heritability, genetic advance, skewness, and kurtosis. For the trait's number of productive tillers, number of filled grains per panicle, and number of grains per panicle, a high level of variability was observed. This variability was expressed as a high phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV), along with high heritability and genetic advance as percent of the mean. Plant height, number of productive tillers per plant, number of filled grains per panicle, grain L/B ratio, kernel L/B ratio before cooking, and grain yield per plant showed higher to moderate estimates of PCV and GCV. Higher estimates of heritability and genetic advance for the same traits also suggest the presence of additive genes in the traits. Therefore, crop advancement programs will be benefitted from selection based on these traits.

Keywords: Genotypic coefficient of variance, phenotypic coefficient of variance, heritability, genetic advance, skewness, kurtosis

1. Introduction

Rice is the utmost central source of carbohydrate-cultivated cereal crops in 114 countries across the planet [1]. About one-half of the world's population depends on rice as the staple food preferably as the food refuge and dietary source in Asian countries [2]. China is the top producer (142.30 Mt) trailed by India (110.4 Mt), Thailand, Vietnam, and Pakistan [3] in rice. The world population is expected to reach 9.6 billion in 2050 [4], thus an anticipated increase in consumption to about 650 Mt. The importance of rice extends far beyond its role as a basic food item. It's intertwined with human nutrition, culture, livelihoods, economies, and environmental sustainability on a global scale. Efforts to ensure the continued availability and improvement of rice varieties are crucial for addressing the challenges of food security and supporting the well-being of communities worldwide. Though India produces 22% of the world's rice production, food security is being challenged by various biotic and abiotic factors. Major biotic stresses such as insects, pests, and diseases affect the cultivation of rice in foremost rice-growing areas. Diseases like blast and bacterial blight cause heavy yield losses, hence development of durable resistant varieties is the dependable solution for the above. Development of varieties with disease and insect resistance, agro-morphological, and grain quality traits must be measured in tropical environments [5]. The availability of molecular markers made the world of resistance breeding a reliable source for the betterment of present and future food security.

High segregation and recombination are found in segregating populations which can be imposed for selection of superior progenies [6, 7]. The crop improvement program is based on the genetic variability for yield and related traits, and the implementation of proper selection techniques [8]. Added, the heritability of the variation from the parent to the progenies [9]. Wide variability, high heritability, and high genetic advance will lead to the successful selection of genotypes. Understanding the association between yield and its components paves the way for the selection of suitable breeding programs.

Grain yield is a complex trait structured by numerous plant traits, genes, and quantitative trait loci yet prejudiced by management practices and environmental factors [10, 11]. To appraise the agronomic performances of backcross-derived lines, it is important to use quantitative genetics for the traits taken under study [12]. The coefficient of variation is the measurement of variability present in the traits of which genotypic co-efficient of variation projects heritable variability and phenotypic co-efficient of variation assesses the effect of environment on the genotype. Environmental effects on traits are indicated by the differences between PCV and GCV *viz.*, small differences indicate low genetic difference, and large differences indicate high environmental effects. Hence small differences between GCV and PCV must be considered for yield improvement in further breeding programs [13]. The present study was taken to determine variability, heritability, genetic advance as a percent of the mean, skewness, and kurtosis in BC_2F_2 generation.

2. Materials and Methods

2.1 Plant materials and crossing strategy

The experimental study was conducted at the Agricultural College and Research Institute, Killikulam. ADT43, a popular, medium slender, and short duration variety, further highly susceptible to blast and bacterial blight diseases was taken as a recurrent parent. RP-Bio-Patho-2, a near-isogenic line of Samba Mahsuri, possesses both blast and bacterial blight disease resistance genes and was used as the donor parent in the backcross breeding program along with marker-assisted selection. The heterozygous F_1's with both blast and bacterial blight resistance genes were selected through foreground selection using both gene-specific STS markers. The double positive F_1's were further backcrossed with recurrent parent ADT43 to develop BC_1F_1 generation. Heterozygosity for both genes were confirmed further and the double positive were subjected to background selection for maximum recurrent parent genome recovery. The double positive line with maximum RPG was selected and further backcrossed with the recurrent parent to develop the BC_2F_1 population. The BC_2F_1 population was again exposed through the above same program for the selection of double positive lines with maximum RPG. The selected lines were selfed to produce BC_2F_2 generation.

2.2 Data assortment

Single plants were selected randomly and observations on plant height (cm), number of productive tillers, panicle length (cm), number of grains per panicle, filled grains per panicle, thousand-grain weight (g), grain length (mm), grain width (mm), grain length/breadth ratio, kernel length before cooking (mm), kernel length after cooking (mm), kernel length/breadth before cooking, kernel length after cooking (mm), kernel length after cooking (mm), kernel elongation ratio after cooking and grain yield per plant (g) were taken.

2.3 Quantitative genetic parameters and statistical analysis

Mean, range, genotypic and phenotypic variances, genotypic coefficient of variation, heritability, genetic advance, skewness and kurtosis were computed employing Microsoft Excel and TNAUstat statistical software.

2.3.1 Genotypic and phenotypic variance

According to Johnson *et al.*, (1955) [14] the phenotypic and genotypic variances were calculated as given below:

Genotypic variance (σ_g^2) = $\frac{MSt-MSe}{r}$

Phenotypic variance (σ_p^2) = $\sigma_g^2 + \sigma_e^2$

Where,
MST = Mean sum of squares for a trait of genotype
MSe = Mean sum of square for error of genotype
r = number of replications
σ_g^2 = Genotypic variance for each trait of genotype
σ_p^2 = Phenotypic variance for each trait of genotype
σ_e^2= Environmental variation among the tested traits of genotype

2.3.2 Genotypic coefficient of variance and phenotypic co-efficient of variance

Also, Burton and Vane (1953) [15] suggested GCV and PCV as below:

Genotypic Co-efficient of Variation (GCV) =

$$\frac{\sqrt{Genotypic\ Variance}}{Mean}\ X\ 100$$

Phenotypic Co-efficient of Variation (PCV) =
$$\frac{\sqrt{Phenotypic\ Variance}}{Mean}\ X\ 100$$

GCV and PCV are categorized as low (<10%), moderate (10-20%) and high (>20%) by Robinson *et al.*, (1949) [16].

2.3.3 Broad sense heritability

Burton (1952) estimated the heritability in broad sense as below:

Broad sense heritability (H^2)
$$=\frac{\text{Genotypic Variance}}{\text{Phenotypic Variance}}\ X\ 100$$

Robinson *et al.*, (1949) [16] classified H^2 as low (0-30%), medium (31-60%) and high (>60%).

2.3.4 Genetic Advance

Genetic advance (GA) was calculated as given by Johnson *et al.*, (1995) [14] and Allard (1960) [17]:

$GA = H^2. K. \sigma_p$

Where,
H^2 = Broad sense heritability
K = Selection differential, the value of which is 2.06 at 5% selection intensity
σ_p = Phenotypic variance standard deviation
Genetic advance as a percent of the mean was suggested by Comstock and Robinson (1952) [18] as

$$GA\ \% = \frac{\text{Genetic advance}}{\text{mean}}\ X\ 100$$

As per Falconer and Mackay (1996) [19], the genetic advance as percent of the mean is categorized as low (<10%), moderate (10-20%), and high (>20%).

2.3.4 Skewness and kurtosis

Skewness and kurtosis are two statistical measures used to describe the shape of a probability distribution or a dataset. They provide insights into the characteristics of the data distribution ahead of mean and standard deviation.

2.3.4.1 Skewness

Skewness measures the asymmetry of a probability distribution of a population. It indicates whether the data is nearly symmetric, positively skewed to the right, or negatively skewed to the left.

- The data are left-skewed if the skewness is negative, which denotes a longer tail on the left side of the distribution. The mean is often lower than the median in a left-skewed distribution.
- The data are right-skewed if the skewness is positive, which denotes a longer tail on the right side of the distribution. The mean is often higher than the median in a right-skewed distribution.
- When the skewness value is 0, the data is roughly symmetric.

2.3.5.2 Kurtosis

Kurtosis assesses a probability distribution's "tailedness" or the peak/flatness of a population. It aids in determining whether the population has more or fewer outliers (extreme values) than would be expected from a normal distribution.

- Positive kurtosis (greater than 3) indicates heavy tails and a peaked distribution, which means that the population has more extreme values and is leptokurtic.
- Negative kurtosis (less than 3) indicates light tails and a flattened distribution, which means that the population has fewer extreme values than a normal distribution and is platykurtic.

Since a normal distribution is sometimes defined as having a kurtosis value of 3, variations from this value provide information about the distribution's structure.

Therefore, kurtosis focuses on the thickness of the tails and the peakness of the distribution, whereas skewness focuses on the symmetry of the population distribution.

3. Results and Discussion

3.1 Variability studies

The basis of selection of an individual is the mean data developed from the traits taken under study. The selection index is based on the high or low mean of the characters taken for the study [20]. Apart from the mean performance, the potency of a cross is also measured by the variability present in it [17]. The selection of a program for the enhancement of any traits depends on the magnitude of variability and the population chosen. The effect of environment on different traits can be studied based on the assessments of genotypic and phenotypic coefficient of variation. Also, the magnitude of the differences between the genotypic and the phenotypic coefficient of variation directs the magnitude of environmental influence on any trait [21-22].

Due to continuous selection, the accessibility of variability is inadequate. Hence it is best to adopt a recombination breeding program for added genetic enrichment [23]. A potent cross can be chosen based on genetic variability like PCV and GCV which helps further measure the genetic variability in traits and thereby differences in quantitative traits [17]. When selection is based on the mean and genetic variation created in the population, crosses will expose their potency in the further generation [24] and the crosses that apprehend homozygosity earlier are well-matched for the further breeding program. Since mean and variability are complementary, the selection is based on high mean and high variability. Further to some extent, selection can also be done in high mean and low variability due to the development of more transgressive segregants.

The variability of 58 BC_2F_2 genotypes was studied and presented in Table 1. From the study, it was observed that there was a maximum range for the number of grains per panicle, followed by the number of filled grains per panicle and plant height and a minimum range for kernel elongation ratio after cooking, kernel L/B ratio before cooking and kernel breadth before cooking. Further, traits such as plant height, thousand-grain weight, grain L/B ratio, kernel L/B ratio before cooking, kernel breadth after cooking, and grain yield per plant showed a moderate genotypic and phenotypic coefficient of variations (Fig. 1).

The highest genotypic and phenotypic coefficient of variations were observed in the number of productive tillers per plant, and number of filled grains per panicle whereas the lowest genotypic and phenotypic coefficient of variation were found in panicle length, grain length, grain breadth, kernel length before cooking, kernel length after cooking and kernel elongation ratio after cooking. Kernel breadth before cooking showed a moderate level of PCV and a low level of GCV indicating a high impact on the environment on the phenotypic expression of the trait. Further, high PCV and moderate GCV were observed in the number of grains per panicle.

The number of filled grains per panicle showed high mean and high variability, hence it is best to select plants based on the same traits. Similar reports were given by Lakshmi *et al*., (2017) [25], Abhilash *et al*., (2018) [26], Abigail *et al*., (2019) [28], Priyanka *et al*., (2019) [7], Shahid *et al*., (2019) [27], and Renuprasath *et al*., (2023) [29]. Added, high to moderate mean and variability were observed in the number of grains per panicle and number of productive tillers per plant which can be noted for the selection program. Estimates of PCV were higher than GCV with moderate to less differences which in turn displays less environmental influence on all traits except kernel length after cooking. Analogous findings were given by Adhikari *et al*., (2018) [12], Rasel *et al*., (2018) [30], Shahid *et al*., (2019) [27], and Renuprasath *et al*., (2023) [29] apart from kernel length. The segregates found in BC_2F_2 population was given in the figures 2, 3 & 4. The grain length and panicle length showed vast differences between PCV and GCV, representing a higher influence of the environment on these traits, and therefore selection based on these traits is not recommended.

However, the number of productive tillers, number of filled grains per panicle, thousand-grain weight, grain breadth, grain L/B ratio, kernel length before cooking, kernel L/B ratio before cooking, kernel elongation ratio after cooking, kernel breadth after cooking and grain yield per plant showed a small difference for PCV and GCV. Less environmental influence on the mentioned same characters is noticed. Yet, no difference was found in the trait kernel length after cooking which indicated no influence on the trait and thus resulted in higher heritability values.

3.2 Heritability and Genetic advance

Assessment of mean and variability alone for selection is not effective compared to in combination with an estimation of heritability and genetic advance as percent of mean. Expression of characters of the genes depends on the appropriate environment and the contrary, manipulation of the environment to express the character is possible only with the presence of the desirable genes [31]. Heritability indicates the inheritance of traits or variations from parents to progenies whereas genetic advance helps in the selection program with anticipation of the genotypic value of the selected lines against the base population.

High heritability and high genetic advance indicate additive gene action of the traits and selection of that trait is rewarding. But high heritability and low genetic advance indicate non-additive gene action, hence retort to selection of that trait will be inferior.

Consequently, the traits of panicle length and grain length showed low heritability compared to all the other traits. Kernel breadth before cooking is the only character that showed moderate heritability whereas plant height, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, thousand-grain weight, grain breadth, grain L/B ratio, kernel length before cooking, kernel L/B ratio before cooking, kernel length after cooking, kernel breadth after cooking, kernel elongation ratio and grain yield per plant showed highest heritability in the study (Fig. 2).

Genetic advance as percent of mean was also studied for the sixteen characters of the 58 lines of the BC_2F_2 generation. Low genetic advance was detected in panicle length and grain length characters however plant height, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, grain breadth, grain L/B ratio, kernel L/B ratio before cooking and grain yield per plant showed highest percentage in genetic advance. The genetic advance was observed moderately in traits such as thousand-grain weight, kernel length before cooking, kernel breadth before cooking, kernel length after cooking, kernel breadth after cooking, and kernel elongation ratio after cooking.

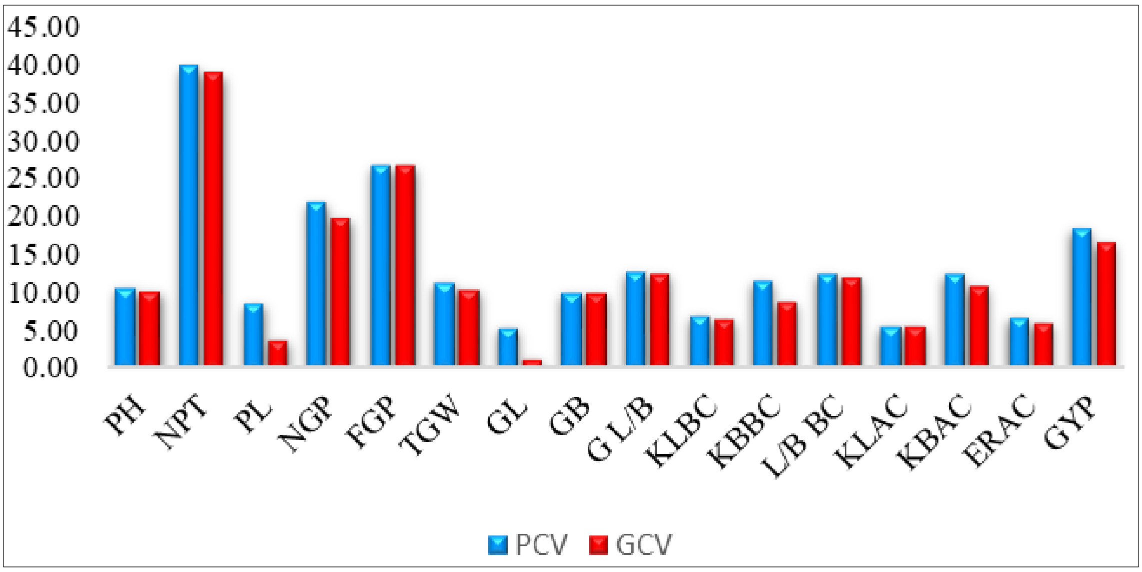


Fig 1: GCV and PCV for the sixteen traits of BC_2F_2 population

Fig 2: Segregation based on duration of flowering in BC_2F_2 population (From late flowering to early flowering)

Fig 3: Segregation based on number of tillers in BC_2F_2 population (From lowest to highest number of tillers)

Fig 4: Segregation based on height in BC_2F_2 population (From dwarf type to tall type)

Table 1: Variability parameters for 16 characters in BC_2F_2 population of ADT43 X RP-Bio-Patho-2

Parameters	Mean	Minimum	Maximum	σ_p^2	σ_g^2	PCV	GCV	Heritability (%)	GAM (%)	Skewness	Kurtosis
PH	111.73	84.00	130.00	138.45	128.64	10.53	10.15	92.92	20.16	-0.82 *	-0.18
NPT	15.69	5.00	32.00	38.64	37.21	39.62	38.88	96.30	78.60	0.57	-0.09
PL	24.27	20.50	28.00	4.27	0.77	8.51	3.62	18.12	3.18	-0.04	-1.31 *
NGP	177.19	103.00	235.00	1502.65	1213.74	21.88	19.66	80.77	36.40	-0.41	-0.98
FGP	149.31	76.00	208.00	1573.97	1571.70	26.57	26.55	99.86	54.66	-0.36	-1.22
TGW	12.82	10.80	15.90	2.06	1.75	11.19	10.33	85.20	19.65	0.52	-0.90
GL	8.05	7.00	9.10	0.18	0.01	5.29	1.31	6.15	0.67	0.15	1.89 **
GB	2.84	2.10	3.20	0.08	0.08	9.98	9.96	99.71	20.49	-1.17 **	0.32
G L/B	2.87	2.26	4.05	0.13	0.13	12.69	12.48	96.65	25.27	1.08 **	1.17
KLBC	5.65	5.00	6.20	0.15	0.14	6.83	6.56	92.16	12.97	-0.43	-1.42 *
KBBC	1.96	1.50	2.90	0.05	0.03	11.51	8.84	59.00	13.99	2.17 **	7.99 **
L/B BC	2.92	2.03	4.00	0.13	0.12	12.35	12.03	94.85	24.13	0.35	1.89 **
KLAC	8.50	7.50	9.20	0.22	0.22	5.54	5.54	99.98	11.42	-0.43	-1.01
KBAC	3.18	2.50	3.90	0.16	0.12	12.36	10.83	76.71	19.54	0.38	-1.11
ERAC	1.51	1.25	1.75	0.01	0.01	6.65	5.91	79.09	10.83	0.22	0.62
GYP	23.92	14.89	33.10	19.16	15.62	18.30	16.52	81.54	30.74	-0.53	-0.21

High heritability and high genetic advance were seen in plant height, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, grain breadth, grain L/B ratio, kernel L/B ratio before cooking, and grain yield per plant. Selection can be done based on the above-mentioned traits as it can be gratifying. Parallel findings were given by Dhanwani *et al*., (2013) [33] for the number of productive tillers per plant; Shaid *et al*., (2019) [27] for number of filled grains per panicle; Mustikarini *et al*., (2019) [34] for the number of filled grains per panicle and grain yield per plant; Somtochukwu *et al*., (2021) [32] for plant height; Renuprasath *et al*., (2023) [29] for number of productive tillers plant and grain yield per plant; Priyanka *et al*., (2019) [7] for plant height, number of grains per panicle and grain yield per plant; Manojkumar *et al*., (2022) [35] for number of grains per panicle, number of filled grains per panicle, thousand-grain weight. Since low heritability and low genetic advance were observed in panicle length and grain length, non–additive gene action is detected.

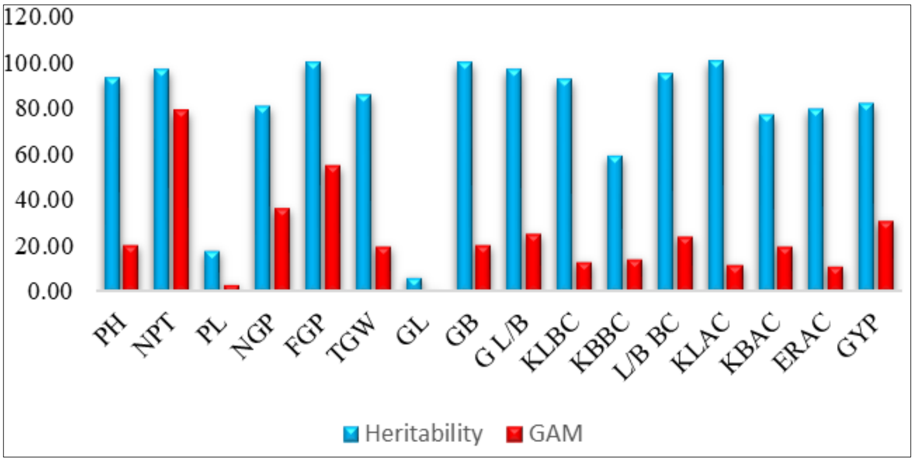
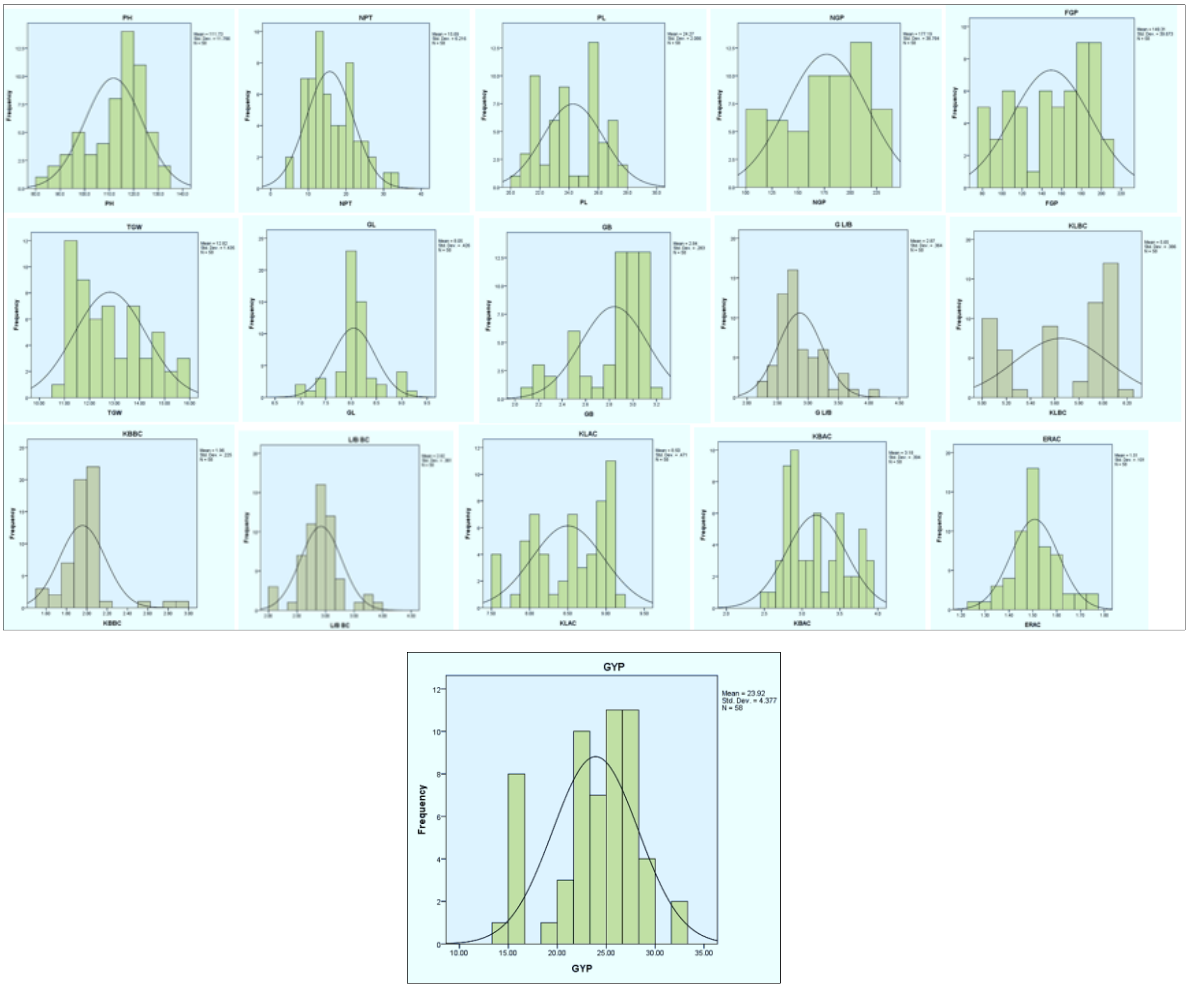


Fig 5: Heritability and GAM for the traits of BC_2F_2 population

3.3 Skewness and kurtosis

In the BC_2F_2 lines, positively significant skewness was detected in traits namely grain L/B ratio and kernel breadth before cooking whereas negatively significant skewness was found in plant height and grain breadth characters. Priyanka *et al*., (2019) [7] reported negatively significant skewness for plant height in the F_2 population of ASD16 X Improved Pusa Basmati 1. Hence, a greater number of individuals are found in the lower end of the distribution of positively skewed traits and transgressive segregants can be seen. Consequently, single plant selection from transgressive segregants will be more rewarding for positively skewed traits. Additionally, since plant height is negatively skewed, the selection of dwarf plants can be done from the lower end of the distribution (Fig. 3).



PH-Plant Height; NPT-Number of Productive tillers per plant; PL-Panicle Length; NGP-Number of Grains per panicle; FGP-Number of Filled grains per panicle; TGW-Thousand grain weight; GL-Grain Length; GB-Grain Breadth; GL/B-Grain L/B ratio; KLBC-Kernel Length before cooking; KBBC-Kerenel Breadth before cooking; L/B BC- Kernel L/B ratio before cooking; KLAC- Kerenl Length after cooking; KBAC-Kernel Breadth after cooking; ERAC- Kerenl Elongation Ratio after cooking; GYP-Grain yield per plant

Fig 6: Frequency distribution for the sixteen characters of BC_2F_2 population

In the case of kurtosis, positive significant mesokurtic was observed in characters such as grain length, kernel breadth before cooking, and kernel L/B ratio before cooking, and negative significant mesokurtic in panicle length trait. The above-mentioned traits have similar extreme characteristics as that of a normal distribution. Added, a negative significant platykurtic was found in kernel length before cooking which in turn indicated dominance-based complementary gene interaction with a large number of genes having a decreasing effect in the inheritance of the trait.

4. Conclusion

The genetic parameters of yield and qualities that contribute to yield were examined in BC_2F_2 populations of 58 backcross-derived rice genotypes (ADT43 X RP-Bio-Patho-2), recipient parent ADT43, and donor parent RP-Bio-Patho-2. Higher to moderate estimates of PCV and GCV was expressed in plant height, number of productive tillers per plant, number of grains per panicle, number of filled grains per panicle, grain L/B ratio, kernel L/B ratio before cooking, and grain yield per plant and higher estimates of heritability and genetic advance of the same traits indicate the presence of additive genes in the traits. Hence selection based on these traits will help in the crop improvement program.

5. Acknowledgment

Innovation in Science Pursuit for Inspired Research (INSPIRE), Department of Science & Technology, India, provided funding for the research project.

6. Author Contributions

The findings were shaped by the input of all authors, who also assisted with numerous laboratory and field analyses and manuscript editing.

7. Statements and declarations

7.1 Conflict of interest: No conflict of interest.

7.2 Ethical statement: None to disclose.

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