GENETIC VARIATION, CORRELATION AND METROGLYPH ANALYSIS IN RICE (*ORYZA SATIVA* L.)FOR GRAIN YIELD CHARACTERS

ABSTRACT

Rice is the only cereal crop cooked and consumed mainly as whole grains, and quality considerations are more important. Rice has been reported to possess diverse therapeutic properties capable of treating diabetics to neurotic ailments as evidenced by ancient literatures apart from its nutritional importance as a major source of calories for a majority of the world population. The present investigation was taken up to study the total of 20 lines of rice including a check variety were evaluated in randomized block design for genetic variability, heritability and genetic advance by using 13 quantitative traits by metroglyph and index score method. Analysis of variance for various quantitative characters revealed that the mean sum of squares due to genotypes showed high significant difference for all characters under study at 1% level and 5% level of significance. Scattereddiagram revealed that 20 genotypes were grouped in to 5 complexes and maximum number of genotypes 11 was found in complex-1. High index score observed was 33 for a genotype SHIVA-555.

Keyword: Genetic Variability, GCV, PCV, Metroglyph, Index score, Rice (*Oryza sativa L.*)

INTRODUCTION

Rice (*Oryza sativa* L.) is one of the most important staple cereal food crop in the world and belongs to the genus *Oryza* of family Graminae (Poaceae). The genus Oryza has 24 species, 22 of which are wild and two of which are cultivated, especially Oryza sativa and Oryza glaberimma. Thebasic chromosomes number (n) of the genus *Oryza sativa* is 12 (2n=24). The cultivated varieties of *Oryza sativa* grouped in to three sub species, Indica, Japonica, and Javanica. Indica rice varieties are grown throughout the tropical and subtropical regions. Japonica varieties are grown throughout the temperate zone, and Javanica varieties are grown mainly in parts of Indonesia.

Rice (O*ryza sativa* L.) is one of the staple cereal crops of the world and it is one of the main sources of carbohydrate for nearly one half of the world population. It meets the calorie requirement of 50 percent of the population and provides livelihood to 160 million of rural poor (Santha *et al.,* 2016).

Rice is life' was the theme of the International Year of Rice in 2004, highlighting its enormous importance as a food and commerce item (Pandey *et al*., 2010). Rice has been inextricably linked to our daily lives from the dawn of time, as seen by its inclusion in nearly all of our cultural traditions. The crop is grown in a wide range of geographical and climatic circumstances, from sea level in Kuttanad (Kerala) to high altitude in Kashmir valley. Rice is grown in a variety of hydrologies, from high-moisture highland conditions to swampy environments.

The crop is cultivated round the year in one or the other parts of the country under diverse ecologies spread about 44 million hectares. About 40 percent of the rice area in India is rainfed, more than 70 percent of which is in eastern India. About 23 percent of rainfed rice area is upland and 77 percent is lowland. Rice is grown under irrigated conditions in the states of Punjab, Haryana, Uttar Pradesh, Jammu & Kashmir, Andhra Pradesh, Tamil Nadu, Sikkim,Karnataka, Himachal Pradesh and Gujarat. In India, Low land rice area is about 14.4 million hectares, which accounts 32.4% of total area under rice crop. In India, flood prone rice area is 11.01 million hectares which accounts 26% of the total area under rice. Flood prone rice are prevalent in South and South- East Asia. The crop contributes about 17 percent of total crop value of the country with an annual export of about rupees 45 thousand crores. About 6.7 crore farm-families are dependent on rice cultivation and 16 crore laborers (more than 50% female) are employed in cultivating about 44 million ha of rice in the country (FAO Statistics, 2017).

Globally, rice is cultivated now in 162.41 million hectares with annual production of around 728 million tones and average productivity of 4.65 tons/ha (USDA-2018). Asia is considered to be ‘rice bowl’ of the world, and it produces and consumes more than 90% of world rice. In World, China, India, Indonesia, Bangladesh, Vietnam and Thailand are the major rice producing countries. China is the largest rice producing country of the world. It has 33% share in the rice production of the world. Thailand is the largest rice exporting country of the world. It has 8% share in the rice export of the world.

In India, rice is staple food of 65% of the total population. It constitutes about 42% of the total food grain production and 45% of total cereal production. In India, rice is grown in 44.78 million ha, the production level is 115.65 million tons and the productivity is about 2.7tons/ha during 2018-19 (NRRI-2019). The largest rice-producing states in India include West Bengal, Uttar Pradesh, Andhra Pradesh, Punjab, Bihar, and Orissa. The state of Chhattisgarh is recognised as India's "rice bowl." In 2017, it was cultivated on 3.7 million hectares, with an average yield of 1.3 tonnes per hectare (Anonymous, 2018).

Rice is the major crop in Uttar Pradesh and is grown in about 5.91 million hectares (accounting for 13.28% of entire area). The state ranks second in the country in production of rice. The production is 13.27 million tons (accounting for 11.75% of entire production) and productivity of the state is around 2.2 t/ha (Agriculture statistics at a glance-2018).

Rice production must keep pace with rising demand in order to feed the world's growing population, as rice is the primary food crop. Rice agriculture in irrigated and suitable rainfed lowland areas has advanced technologically in the last fifty years, resulting in increased yield. Irrigated rice production supplies 75 to 80 percent of global rice requirements. However, the yield in irrigated area has reached a plateau and it is time to break the yield ceiling in those areas to feed the growing population. As the land frontiers for many countries have been exhausted, diversification of land to other crops is taking place dueto higher returns and consumer demand, and more land is being diverted for non-agricultural purposes, the growth in many countries has to come from increase in productivity of arable land.

Genetic variability is the foremost important breeding tool in order to break yield stagnation and developing high yielding varieties. The quantity of genetic diversity among genotypes determines the range of genetic variability in segregating populations, which provides more selection opportunities. The degree of heritable variation in the variables evaluated is extremely important for determining the genotype's breeding potential.

Yield is a complex character, which is influenced by several quantitative traits and is governed by polygenes. Application of biometrical techniques in plant breeding has led to thegreater understanding of genetics of quantitative characters and proved to be extremely usefulto the plant breeder for systematic genetic analysis.

Selection criteria like as heritability and genetic progress are significant. Heritability estimates combined with genetic progress are usually more useful than heritability estimates alone in estimating the gain under selection. As a result, understanding genetic progress in conjunction with heritability is quite beneficial. A high heritability character does not always imply a great genetic progress. To arrive at a more trustworthy result, high heritability should be accompanied with substantial genetic progress. The expected genetic progress expressed as a percentage of the mean illustrates the manner of gene activity in the manifestation of a characteristic, which aids in the selection of a suitable breeding approach (Kumar *et al*., 2014).

For a successful breeding effort, a full understanding of the nature and extent of genetic diversity as well as the relationship of traits in a crop species is required. The ability to see the direct and indirect effects that each character has on yield will be a huge help in the choosing process. The measure of the mutual relationship between two variables is correlation. The study of correlations may aid plant breeders in understanding how improving one feature leads to improvements in other characters. A path coefficient analysis is a standardized regression coefficient that assesses the direct impact of one variable on another. Because it is impacted by the environment, direct yield selection is not a reliable method.

As a result, it's critical to determine the component qualities that might help boost yield. Selection would be more successful for a characteristic with a high genetic progress and a strong link to grain output. The correlation coefficient is used to determine the degree of link between yield and yield components, as well as other characteristics that have a significant impact on yield (Singh, 2009).

Recognizing the importance of this crop, the current research was carried out to gather data on the following particular objectives:

1.To assess the genetic variability parameters for yield and its contributing factors in rice genotypes.

2.To investigate the relationship between grain yield characteristics of rice.

3.To assess genetic diversity among rice germplasm.

MATERIALS AND METHODS

The Experimental materials for the present study entitled **"Assessment of Genetic Variability and Correlation Studies for Yield and Yield Components in Elite Rice (*Oryza sativa* L.) Germplasm"** were obtained from the Department of Genetics and Plant Breeding, Naini Agricultural Institute, SHUATS, Prayagraj. U.P. The material and methods used in the present experiment, soil properties, climatic condition, where experiment was conducted, experimental details and the design of experiment adopted, statistical analysis and sampling techniques adopted aredeal in this chapter under the following heads:

3.1 Experimental site
3.2 Weather condition during crop season
3.3 Layout of the experiment
3.4 Experimental materials
3.5 Recording of observations
3.6 Statistical analysis

3.1 Experimental site

The present experiment was carried out at Field Experimentation centre, Department of Genetics and Plant Breeding, Naini Agricultural Institute, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj, U.P. during Rabi 2021- 2022.

Soil texture:

Prayagraj comes under middle gangetic plains (Agro climatic zone IV). The experimental plot had sandy loam soil with fairly uniform topography and normal fertilitystatus. The plot is well drained and assured irrigation facility.

3.2 Weather condition during crop season:

Prayagraj has sub-tropical and semi-arid climate. Lies 102m above sea level. The average annual rainfall is 1042 mm. The meteorological data including the weekly average of maximum and minimum temperature, relative humidity and rainfall recorded at Prayagraj during the period of experiment is presented.

3.3 Layout description

The experiment layout comprising of 19 genotypes with one check variety was grown under Randomized Block Design (RBD) with three replications. The experimental field was divided into blocks of equal size in three replications and each block containing single genotype.

Crop : Rice

Season : *kharif*, 2021

Experimental desi : Randomized Block Design

No. of Replications : 3

No. of Genotype : 20

Gross Area : 128 m^2

Net cultivated area : 120 m^2

Row to Row distance :20 cm

Plant to Plant distance :15 cm

Date of Sowing : 20/06/2021

Date of Transplanting : 21/07/2021

Fertilizer dose : N:P:K @ 120:60:60 kg/ha

3.4 Experiment materials:

The experimental material for the present study consists of 21 genotypes of chickpea including a check variety received from SHUATS Prayagraj, Uttar Pradesh.

List 1: List of genotypes used in present investigation

S.NO	NAME OF GENOTYPES
1	UNNAO DHAN SHARABATI
2	UNNAODHAN PUSA
3	UNNAO DHAN 1509

S.NO	NAME OF GENOTYPES
11	RGL 2539
12	MTU 1318
13	SAMPAK SWARNA (NP 9558)

4	UNNAO DHAN BASMATI CSR 13
5	UNNAO DHAN MOTHI
6	UNNAO DHAN 1121
7	UNNAO DHAN 1718
8	SAMBAMASURI (BPT 204)
9	BPT 74
10	BPT 1768

14	BPT 01
15	MTU 1271
16	SHIVA 555
17	SWARNA (MTU 7029)
18	BPT 02
19	NLR
20	NDR 359 (check)

3.4 Observations recorded

The observations were recorded on plot basis for days to 50% flowering, days to physiological maturity and grain yield per plot. For rest of the characters the data was recorded on five randomly selected plants from each genotype in each replication leaving first two border rows from all the four sides in order to avoid sampling error. The observation recorded as per the following procedure Recording from five plants were averaged replication wise and the mean data wasused for statistical analysis for fifteen quantitative traits and seven quality traits.

Coefficient of variation (C.V.)

It is the measure of variability evolved. Coefficient of variation is the ratio of standard deviation of a sample to its mean and expressed in percentage. In the present investigation three types of coefficient of variation were estimated *viz.*, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/environmental coefficient of variation (ECV). The formulae used to calculate PCV, GCV and ECV were given by Burton (1952).

$$\text{PCV (\%)} = \frac{\text{Phenotypic standard deviation}}{\text{Grand mean}} \times 100$$

Genotypic standard deviation

GCV (%) = _ x 100

Grand mean

Error standard deviation

ECV (%) = _ x 100

Grand mean

The GCV and PCV values were classified as described by Sivasubramanian and Menon (1973).

Classification	GCV/PCV
Low	Less than 10%
Moderate	10-20%
High	More than 20%

3.6.2.1 Heritability

Heritability is the heritable portion of the total phenotypic variance. It is a good index of transmission of characters from parents to their off spring. The estimates of heritability help the plant breeder in selection of elite genotypes from diverse genetic populations.

Heritability in broad sense (h^2) is the ratio of genotypic variance to the total variance and calculated by using the formula suggested by Burton and De Vane (1953).

$$h^2 = \sigma^2 g / \sigma^2 p \quad \text{or} \quad \sigma^2 g / \sigma^2 g + \sigma^2 e$$

Where, $\sigma^2 g$ = Genotypic variance

$\sigma^2 e$ = Environmental variance

$\sigma^2 p$=Phenotypic (Total variance)

Heritability in broad sense was categorized as per the classification given by (Johnson *et al.*,1955).

Classification	Heritability

3.6.2 **3.6.3** Low	Less than 30%
Moderate	30-60%
High	More than 60%

3.6.4 Genetic advance (GA):

Genetic advance was estimated as per the formula proposed by Lush (1940) andJohnson *et al*. (1955).

G A = K□x □p x *h* (bs)

Where, K = Selection differential at 5 per cent selection intensity which accountsto a constant value 2.06

h (bs) = Heritability in broad sense

□p = Phenotypic standard deviation

Genetic advance as percentage of mean was calculated and the range of genetic advanceas percent of mean was classified by using the formulae given by Johnson *et al*. (1955).

$$\text{GAM} = \frac{\text{Genetic advance (GA)}}{\text{Grand mean }(\bar{X})} \times 100$$

The GA as percent of mean was categorized by (Johnson *et al*., 1955) as:

Low = Less than 10%

Moderate = 10-20% High = More than 20%

3.6.5 Metroglyph and Index score analysis:

This technique was developed by Anderson (1957) to investigate the pattern of morphological variation in chickpea genotypes.

The main features of Metroglyph analysis are given below:

  - Analysis is based on first order statistics and therefore, results are statistically more reliable

    and robust.
  - Analysis is possible from both replicated as well as non-replicated data.
  - The analysis is simple.
  - The pattern of variability is depicted by glyph on thegraph.
- Assessment of variability using Metroglyph analysis and index score analysis involvedin the following steps (Singh and Narayanan, 2000).
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- **A. Plotting of glyph on the graph:**
- A small circle by which the position of a genotype or species is represented on the graph is called glyph. For plotting of glyph on the graph two characters having high variability are chosen. One of them is used on the x-axis and the other on Y-axis. The mean values of X for each genotype are plotted on the graph against the mean values.
- **B. Depiction of variation:**
- Variation for remaining characters of each genotype is displayed on the respective glyph by rays. Each character occupies a definite ray position. Variation for each character is depicted by the length of ray. Thus the length of ray for a particular character on the glyph may be shorter, medium or long depending on the index value ofa genotype.
- **C. Construction of Index Score:**
- For this purpose, the variation for each character is divided into three groups, viz. low, medium and, high. The genotypes with low, medium and high value are givenindex score 1, 2 and 3 respectively. The worth of a genotype is calculated by adding theindex values of all the characters. Thus, the maximum and minimum score of and individual will be 3n and n. where n is the total number of characters included in the study.

RESULTS AND DISCUSSION

Rice is the second largest produced cereal in the world and also the staple food for over one third of the world’s population and more than 90% to 95% of rice is produced and consumed in Asia. Yield enhancement is the major breeding objective in rice breeding programmes and knowledge on the nature and magnitude of the genetic variation governing the inheritance of quantitative characters like yield and its components is essential for effective genetic improvement.

A critical analysis of the genetic variability parameters namely, Genotypic Coefficient of Variability (GCV), Phenotypic Coefficient of Variability (PCV), heritability and genetic advance for different traits of economic importance is a major pre-requisite for any plant breeder to work with crop improvement programs. Further, information on correlation coefficients between grain yield and its component characters is essential for yield improvement, since grain yield in rice is a complex entity and is highly influenced by several component characters. The present investigation was undertaken in this context to elucidate information on variability, heritability, genetic advance in promising rice genotypes. A good knowledge of genetic resources might also help in identifying desirable genotypes for future hybridization program.

This chapter deals with result obtained by using the methodology given in chapter III and their probable discussion. The results obtained on various aspects are being discussed in the light ofrelevant literature available in chickpea under the following headings.

4.1 Analysis of Variance
4.2 Mean Performance
4.3 Coefficient of Variation
4.4 Heritability and Genetic Advance
4.5 Metroglyph Analysis

4.1 Analysis of Variance

Analysis of variance for all parameters recorded in twenty-five rice genotypes is presentedin Table 3 indicating the mean sum of squares due to replications, varieties and error for thirteen characters studied. The analysis of variance indicated the presence of sample variability in the experiment material and disclosed significant differences among the genotypes for all characters studied *viz.*, days to fifty percent flowering, plant height(cm), flag leaf length (cm), flag leaf width (cm), number of tillers per plant, number of panicles per plant, number of spikelets per panicle, panicle length (cm), grains per panicle, days to maturity, biological yield per hill (g), test weight(g), harvest index (%) and grain yield per plant(g). Highly significant mean squares due to genotypes were observed for all traits, indicating the existence of sufficient variation among the genotypes for yield and yield component characters studied in the present investigation, and therefore, there is a scope for effective selection. These findings are in similar with the findings of Mishu *et al*. (2016); Islam *et al*. (2016);Srujana *et al*. (2017) and Ali *et al*. (2018).

4.2 Mean performance of genotypes

A wide range of mean for yield and some of its contributing traits indicated good chance for improvement of yield through direct selection or by transferring desired traits. The mean squares due to varieties were highly significant for all the characters indicating that the presence of genetic variability in the material. The mean performance of twenty rice genotypes over three replications for the various characters studied is presented in Tables 4 and 5.

4.2.1 Days to fifty percent flowering

The data corresponding to days to fifty percent flowering (Table 4) was ranged from 81.00 (UNNAO DHAN-1509) to 121.73 (BPT-74) with overall mean value of 109.79. The maximum days to fifty percent flowering was observed in BPT-74 (121.73) followed by BPT- 01 (120.87) while, the minimum days to fifty percent flowering was observed in UNNAO DHAN-1509 (81.00).

This variation might be due to differences in genetic characters or due to environmental interaction. The present findings confirm the earlier reports of variability for various characters provided by (Alam *et al*.,2003; Singh *et al*., 2004 and Malik *et al*., 2009).

4.2.2 Days to maturity

Days to maturity ranged from 104.47 (UNNAO DHAN-1509) to 147.73 (BPT-74) with a general mean of 135.44. Ten genotypes surpassed the general mean of the days to maturity. The maximum days to maturity was observed in the genotype BPT-74 (147.73) followed by BPT-01(145.87) and minimum days to maturity was observed in UNNAO DHAN-1509 (104.47).

4.2.3 Plant height (cm)

Among all the genotypes UNNAO BASMATHI CSR-13 recorded the highest plant height (162.07cm) followed by UNNAO DHAN SHARABATHI (155.67cm) while, KNM- 118 had the lowest height (104.64cm) with a general mean height of 128.00cm. Eight genotypes had significantly taller when compared to general mean height. Among all genotypes the plant height ranged from 104.67cm (KNM-118) to 162.07cm (UNNAO BASMATHI CSR-13).

4.2.4 Flag leaf length (cm)

Flag leaf length ranged from 28.72 (MTU-7029) to 51.99 cm (UNNAO DHAN SHARABATHI) with a general mean of 36.89 cm. Seven genotypes surpassed the general mean of the flag leaf length. The maximum flag leaf length was observed in the genotype UNNAO DHAN SHARABATHI (51.99) followed by RGL-2332 (50.82cm) and minimum flag leaf length was observed in 20 MTU-7029 (28.72cm).

4.2.5 Flag leaf width(cm)

Flag leaf width ranged from 0.86cm (UNNAO DHAN-1121) to 1.80cm (NDR-359) with a general mean of 1.18 cm. Nine genotypes surpassed the general mean of the flag leaf width. The maximum flag leaf width was observed in the genotype NDR-359 (1.80cm) followed by UNNAO DHAN MOTHI (1.43cm) and minimum flag leaf width was observed in UNNAO DHAN-1121 (0.86cm).

4.2.6 Number of total tillers per plant

Among all the genotypes NDR-359 recorded the highest number of total tillers per plant(15.60) followed by KNM-118 (14.07) while, UNNAO DHAN PUSA had the lowest numberof total tillers per plant (7.33) and mean number of tillers per plant is 9.19. Six genotypes had significantly a greater number of total tillers per plant when compared to general mean.

4.2.7 Number of productive tillers per plant

The data corresponding to number of panicles per plant ranged from 7.33 (UNNAO DHAN PUSA) to 15.73 (KNM-118) with overall mean value of 9.20. The maximum number of panicles per plant was observed in KNM-118 (15.73) followed by NDR-359 (14.00) while, the minimum number of panicles per plant was observed in UNNAO DHAN PUSA (7.33). Six genotypes had significantly a greater number of panicles per plant when compared to general mean.

4.2.8 Panicle length (cm)

Panicle length ranged from 22.09cm (BPT-01) to 34.89cm (UNNAO DHAN-1509) with a general mean of 26.68 cm. Ten genotypes surpassed the general mean of the panicle length. The maximum panicle length was observed in the genotype UNNAO DHAN-1509 (34.89cm) followed by UNNAO DHAN PUSA (32.45cm).

4.2.9 Biological yield per hill (g)

The highest biological yield per hill was recorded in the genotype MTU-1271 (95.40g) followed by NP-9558 (82.91g) while, the lowest biological yield per plant was recorded in BPT-1768 (47.67g) and mean biological yield per hill was 63.62g where, seven genotypes were above the average biological yield per hill.

4.2.10 Harvest index (%)

The data corresponding to harvest index ranged from 40.46 (MTU-1271) to 56.69 (UNNAO DHAN-1509) with overall mean value of 50.31. The maximum harvest index was observed in UNNAO DHAN-1509 (59.69) followed by BPT-1768 (59.18) while, the minimum harvestindex was observed in MTU-1271 (40.46). Nine genotypes had significantly a greater harvest index when compared to general mean.

4.2.11 Number of spikelets per plant

Among all the genotypes SHIVA-555 recorded the highest number of spikelets per plant (309.33) followed by MTU-1271(287.67) while, UNNAO DHAN PUSA had the lowest number of total tillers per plant (127.40) and mean number of tillers per plant is 187.54. Thirteen genotypes had significantly a greater number of spikelets per plant when compared to general mean.

4.2.12 Test weight (g)

Among all the genotypes NLR recorded the highest test weight (30.00g) followed by UNNAO DHAN-1718(26.47g) while, BPT-01 had the lowest test weight (14.00g) with the mean test weight of 19.92. Ten genotypes had significantly highest test weight when compared to mean test weight. Among all genotypes the test weight ranged from 14.00g (BPT-01) to 30.00g (NLR).

4.2.13 Grain yield per plant (g)

Among all the genotypes NLR recorded the highest grain yield per plant (47.44g) followed by KNM-118(43.67) while, NDR-359 had the lowest number of total tillers per plant (22.37) and mean number of total tillers per plant is 31.46. Six genotypes had significantly a greater number of spikelets per plant when compared to general mean. The yield performance of thesegenotypes along with other metric traits is presented for ease of better comprehension. The most promising genotypes identified during the present investigation are NLR, KNM-118, SHIVA-555, MTU-1271, UNNAO DHAN PUSA, NDR-359. The high grain yield in these genotypes is due to high performance in yield attributing traits. These characters may serve asselection criteria for prediction and realization of higher yield, greater stability and better adaptation in rice. (Patel *et al*. (2018); Gyawali *et al*. (2018); Parimala and Devi (2019).

4.3 Variability studies

The data concerning phenotypic and genotypic coefficients of variation, heritability (broad sense), genetic advance and genetic advance as per cent of mean are presented in Table 6 which showed considerable variation among varieties for each character.

4.3.1 GCV, PCV, Heritability and expected genetic advance

Effectiveness of selection depends on the magnitude of genetic variability in a particular character. The absolute values of differences in genotypic variance cannot be used for comparing magnitude of variability for different characters since the mean and units of measurement of the two characters may be different. Hence the coefficients of variation expressed at phenotypic and genotypic levels were compared for assessing the variability observed for different characters.

Heritability of an attribute provides an idea about transmissibility of acharacter from parents to off-springs. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. If heritability of a character is high, selection for such a character should be fairly easy because there would be close correspondencebetween genotypic and phenotypic variation due to relatively smaller contribution of environment to the phenotype, but for a character with a low heritability, selection may be considerably difficult or virtually impractical due to masking effect of environment on the genotypic performance. Heritability estimates along with genetic advance are more effective and reliable in predicting the improvement through selection (Johnson *et al*., 1955). Estimate ofgenetic advance helps to predict the extent of improvement that can be achieved for improvingdifferent characters.

4.3.1.1 Days to fifty percent flowering

Low estimates of genotypic (8.637%) and moderate phenotypic coefficient of variation were observed and 11.484 per cent respectively for days to fifty percent flowering. Heritability was moderate (56.56%) along with moderate genetic advance expressed as percentage of mean (13.38%).

4.3.1.2 Days to maturity

Low estimates of genotypic and phenotypic coefficient of variation were observed *i.e.*, 6.029 and 9.633 per cent respectively for days to maturity. Heritability was moderate (39.175%) along with low genetic advance expressed as percentage of mean (7.774%).

4.3.1.3 Plant height (cm)

Moderate estimates of genotypic and phenotypic coefficient of variation were observed *i.e.,* 13.635 and 15.512 per cent respectively for plant height. Heritability was high (77.271%) along with high genetic advance expressed as percentage of mean (24.691%).

4.3.1.4 Flag leaf length (cm)

Moderate estimates of genotypic and phenotypic coefficient of variation were observed *i.e.,* 16.365 and 17.35 per cent respectively for plant height were observed for flag leaf length. Heritability was high (88.966%) along with high genetic advance expressed as percentage of mean (31.797%).

4.3.1.5 Flag leaf width (cm)

Moderate estimates of genotypic coefficient of variation (18.126%) and phenotypic coefficient of variation (19.308%) were observed for flag leaf width. Heritability was high (88.125%) along with high genetic advance expressed as percentage of mean (35.052%).

4.3.1.6 Number of total tillers per plant

High estimates of genotypic coefficient of variation (22.661%) and high estimates of phenotypic coefficient of variation (23.534%) were observed for number of tillers per plant. Heritability was high (92.719%) along with high genetic advance expressed as percentage of mean (44.951%).

4.3.1.7 Number of productive tillers per plant

High estimates of genotypic and phenotypic coefficient of variation were observed *i.e.,* 22.731 and 23.944 per cent respectively for number of tillers per plant. Heritability was high (90.123%) along with high genetic advance expressed as percentage of mean (44.453%).

4.3.1.8 Panicle length (cm)

Moderate estimates of genotypic coefficient of variation (13.055%) with moderate estimates of phenotypic coefficient of variation (14.852%) were observed for panicle length. Heritability was high (77.271%) along with high genetic advance expressed as percentage of mean (23.641%).

4.3.1.9 Biological yield per plant

High estimates of genotypic coefficient of variation (20.543%) and high estimates of phenotypic coefficient of variation (22.104%) were observed for biological yield per plant. Heritability was high (86.371%) along with high genetic advance expressed as percentage of mean (39.329%).

4.3.1.10 Harvest index (%)

Moderate estimates of genotypic coefficient of variation (12.57%) and moderate estimates of phenotypic coefficient of variation (14.143%) were observed for harvest index. Heritability was high (78.985%) along with high genetic advance expressed as percentage of mean (23.012%).

4.1.1.1 Number of spikelets per panicle

High estimates of genotypic coefficient of variation (37.734%) and high estimates of phenotypic coefficient of variation (38.926%) were observed for number of spikelets per panicle. Heritability was high (93.969%) along with high genetic advance expressed as percentage of mean (75.351%).

4.1.1.2 Test weight

High estimates of genotypic and phenotypic coefficient of variation were observed *i.e.*, 22.509 and 23.552 per cent respectively for test weight. Heritability was high (91.344%) along with high genetic advance expressed as percentage of mean (44.317%).

4.1.1.3 Grain yield per plant

High estimates of genotypic coefficient of variation (20.396%) and high phenotypic coefficient of variation (21.496%) were observed for grain yield per plant. Heritability was moderate (90.03%) along with high genetic advance expressed as percentage of mean (39.867%).

In the present findings phenotypic coefficient of variation was observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however, the differences were narrow which implied their relative resistance to environmental variation. It also describes that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance (Gyanendra *et al*., 2006).

The perusal of the variability estimates (Table 1) for yield and its contributing traits exhibited that estimates of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were high for number of tillers per plant, number of spikelet's per plant, biological yield per hill(g), harvest index (%), test weight(g), grain yield per hill(g) suggesting that these traits are under genetic control, and simple selection can be practiced for further improvement.

The characters such as number of panicles per plant, biological yield per hill, flag leaf length, flag leaf width and panicle length exhibited moderate phenotypic coefficient of variation and low coefficient of variation was found for the characters *viz*., days to 50% flowering, days to maturity and plant height which indicated that selection based on phenotypic performance would be rewarding. These results are in agreement with the findings obtained by Akinwale *et al*. (2011) Rice workers, and Ramanjaneyulu *et al*. (2014), Mohan *et al*. (2015), Sameera *et al*. (2015), Bhati *et al*. (2015), Allam *et al*. (2015), Srinivas *et al*. (2016), Ajmera *et al*. (2017), Behera *et al*. (2018) and Saha *et al*. (2019) reported moderate GCV and high PCV values for grain yield which are in accordance with present findings. Low estimates of PCV and GCV were observed for 1000-grain weight, days to 50% flowering and panicle length indicated that these traits are under high influence of environment suggesting need for creation of variability with hybridization followed by selection. Similar reports have been obtained for panicle length by Adhikari *et al*. (2018). In contrary to this, Dhanwani *et al*.(2013) and Ajmera *et al*. (2017) reported moderate estimates for panicle length, and also Dhanwani *et al*. (2013) showed high GCV and PCV for plant height.

High estimates of PCV than GCV were observed for all the traits studied which may be due to the high degree of interaction of genotypes with environments. A similar finding has been noted by Vanisree *et al*. (2013), Mohan *et al*. (2015), Srinivas *et al*. (2016), Ajmera *et al*. (2017) and Gyawali *et al*. (2018). It was observed that PCV was slightly higher than GCV for all the traits reflecting less influence of environment in the expression of traits and greater role of genetic control governing the characters is in agreement with the results explained by Mohan *et al*. (2015), Ajmera *et al*. (2017), Behera *et al*. (2018) and Saha *et al*. (2019).

However, estimates of PCV were considerably higher than GCV for flag leaf length, flag leaf width, number of tillers per plant, number of panicles per plant, number of spikelet's per plant, biological yield per hill, harvest index, grain yield per hill indicating the sensitive nature of these traits to environmental fluctuations and predominance of non-additive gene effects. Similar findings are in accordance with the earlier reports of Mohan *et al*. (2015),Thippaswamy *et al*. (2016) and Adhikari *et al*. (2018) for effective bearing tillers, number of grains per panicle and grain yield.

4.3.3. Heritability

Knowledge on the heritability of genetic trait is essential to the plant breeders in determining the response to selection and to provide the information on the extent of transmissibility of that selected trait of interest to the progenies in the subsequent generations (Saha *et al*., 2019). In addition, high genetic advance estimates in conjunction with high heritability values are more accurate for breeders in calculating the genetic gain under selection and offers the effective conditions for selection for the specific traits. Further, rice grain yield being a complex trait, depends upon the various yield contributing traits like test weight, number of grains per panicle, panicle length and effective bearing tiller number. Hence, the information about the relationship between yield and other yield components would be helpful in selecting proper rice genotypes as parents in breeding programmes.

High estimates of heritability were recorded for days to 50% flowering, plant height, number of panicles per plant, panicle length, number of tillers per plant, days to maturity, biological yield per hill and test weight. Whereas, flag leaf length, flag leaf width, number of spikelets per panicle, harvest index and grain yield per had relatively moderate estimates; hence, improvement through selection could be low due to masking effect of environment on the expression of these traits (Table 1). Similarly, moderate heritable values were reported by Sangram kumar *et al*. (2011), Thomas and Gabriel (2012) for test weight, Seyoum *et al*. (2012) for days to maturity, Ramanjaneyulu *et al*. (2014) for days to flowering and panicle length.

In the present investigation, number of tillers per plant, number of panicles per plant, biological yield per hill and test weight showed high heritability combined with high genetic advance values reflecting the existence of additive gene action in the expression of these traits and hence selection would be effective as investigated by Karande *etal*. (2015), Ajmera *et al*. (2017) and Saha *et al*. (2019) for number of grains per panicle; Toshimenla and Changkija (2013), Chandramohan *et al*. (2016), Islam *et al*. (2016), Srinivas *et al*. (2016) and Ajmera *et al*. (2017) for 1000- grain weight; Rahman *et al*. (2014), Karande *et al*. (2015) and Ajmera *et al*. (2017) for grain yield. Similarly, high heritability coupled with moderate genetic advance estimates were recorded for days to 50% flowering and panicle length. Ketan and Sarkar (2014), Chandramohan *et al.* (2016) and Behera *et al*. (2018) also found the same result for panicle length suggesting the role of both additive and non-additive gene effects in their inheritance, therefore, adoption of breeding procedures which could exploit both the gene actions would be an effective approach. In contrary to this, high heritability coupled with high genetic advance was reported for panicle length by Sameera *et al*. (2015).

4.4 Correlation Studies

Yield is a complex product being influenced by several interdependent quantitative characters. Selection for yield may not be effective unless the other yield components influencing it directly or indirectly are taken into consideration. Genotypic and phenotypic correlation coefficients between pairs of characters of the present study in rice are presented in Table 4. It is evident that in most cases, genotypic correlation coefficients are higher than the corresponding phenotypic correlations might be due to modifying or masking effect of environment in the expression of the character under study (NANDPURI, 1973).

4.4.1 Days to fifty percent flowering

Days to fifty percent flowering had highly significant and positive correlation with days to maturity (0.618) and non-significant positive correlation with flag leaf width (0.147) and number of spikelets perpanicle (0.230) at phenotypic level. The correlation of days to fifty percent flowering with panicle length (-0.523), harvest index (-0.343), test weight (-0.541), grain yield per plant (-0.296) found negative significant correlation whereas plant height

(-0.165), flag leaf length (-0.091), number of total tillers perplant (- 0.229), number of productive tillers per plant (-0.226), biological yield (-0.063) was found negative but nonsignificant.

At genotypic level days to fifty percent flowering showed highly significant positive association with days to maturity (0.521) followed by flag leaf width (0.245) and number of spikelet's per panicle (0.318) had non-significant positive correlation. Number of productive tillers per plant (-0.283), harvest index (-0.406), panicle length (-0.897), test weight (-0.747) and grain yield per plant (-0.429 had negative significant correlation (0.796) whereas plant height (-0.204), flag leaf length (-0.140), number of total tillers per plant (-0.239), biological yield (-0.069) had negatively nonsignificant association with days to fifty per cent flowering. However, negative relationship between days to 50% flowering and grain yield was reported by Chandan Kumar and Nilanjaya (2014), Saha *et al*. (2019).

4.4.2 Days to maturity

At phenotypic level days to maturity showed highly significant positive association with days to fifty percent flowering (0.618). Flag leaf width (0.173), test weight (-0.406), biological yield per plant (0.024), flag leaf length (-0.160) and panicle length (-0.485) had non-significant positive correlation. Number of spikelets per panicle (0.282) had negative significant correlation whereas plant height (-0.182), grain yield per plant (-0.140), number of productive tillers per plant (-0.178), harvest index (-0.244) and number of total tillers per plant (-0.179) had negatively nonsignificant association with days to maturity.

Days to maturity had highly significant and positive correlation with days to fifty percent flowering (0.521) and non-significant positive correlation with flag leaf width (0.289), test weight (-0.327), biological yield per plant (0.002), flag leaf length (-0.318) and number of total tillers per plant (-0.219) at genotypic level. The correlation of days to maturity with number of spikelets per panicle (0.431), plant height (-0.295), harvest index (-0.392), number of productive tillers per plant (-0.271) and panicle length (-0.956) found negative but non-significant correlation

Days to maturity had highly significant correlation with days to fifty percent flowering which indicated that early flowering leads to early maturity of Rice grains. Hossain *et al*. (2015), Mohan *et al*. (2015), Ratna *et al*. (2015) and Kalyan *et al*. (2017).

4.4.3 Plant height (cm)

At phenotypic level plant height showed highly significant positive association with flag leaf length (0.545), panicle length (0.442), test weight (0.411) and number of total tillers per plant (-0.275), number of productive tillers per plant (-0.318) and number of spikelets per plant

(-0.438) had significant negative correlation and flag leaf width (0.026) and had positively nonsignificant association with plant height. Harvest index (-0.167). biological yield per hill

(-0.003), days to maturity (-0.182) andgrain yield per plant (-0.119) had negative but non-significant correlation.

At genotypic level plant height (cm) had highly significant and positive correlation with flag leaf length (0.665), panicle length (0.537) and test weight (0.447). Flag leaf width (0.026) had positive non-significant correlation at genotypic level. The correlation of number of total tillers per plant(-0.325), number of productive tillers per plant (-0.369), number of spikelets per panicle (-0.506), harvest index (-0.266) and days to maturity (-0.295) was found significantly negative. Days to fifty percent flowering (-0.2042), biological yield per hill (-0.043) and grain yield per plant (-0.178) had negative but non-significant correlation with plant height.

Results indicated that the taller genotypes possessed greater flag leaf length and panicle length besides having late flowering, which appears logical. Janardanam *et al*., (2002) have also reported positive associations between these characters. However, negative association for the plantheight with tillers per plant was obtained by Chandan Kumar and Nilanjaya (2014).

4.4.4 Flag leaf length

Flag leaf length had highly significant positive correlation with test weight (0.357) at phenotypic level. Further this character exhibited positive but non-significant correlation with panicle length (0.250). Number of productive tillers per plant (-0.256) and number of spikelets per panicle (-0.319) had significantly positive. Number of total tillers per plant (-0.226), flag leaf width (-0.127), harvest index (-0.101), days to maturity (-0.160), plant height (-0.182),), biological yield per hill (-0.157), grain yield per plant (-0.226) and days to fifty percent flowering (-0.091) but this character had negative non- significant association with At genotypic level the plant height (0.665), panicle length (0.287) and test weight (0.377) showed significantly positive association with flag leaf length. Further number of productive tillers per plant (- 0.269), number of spikelets per panicle (-0.336) and days to maturity (-0.318) had negative but significant correlation. Flag leaf width (-0.145), days to fifty percent flowering (-0.140), number of totaltillers per plant (-0.245), grain yield per plant (0.201), biological yield per plant (-0.184) and harvest index (-0.149) had negative non-significant association with flag leaf length.

These results indicated that flag leaf length increased with plant height and also showed positive association with biological yield per hill and grain yield per hill. These findings are in accordance with Singh *et al*., (2015), TuhinaKhatun *et al*., (2015), Anis *et al*., (2016), Sneha gupta *et al*., (2020), parween *et al*., (2020) and Priyanka *et al*., (2020).

4.4.5 Flag leaf width

Flag leaf width had significantly positive correlation with number of total tillers per plant (0.477), number of productive tillers per plant (0.313) and number spikelets per panicle (0.511). Significantly negative had shown in harvest index (-0.301). Days to fifty percent flowering (0.147), plant height (0.045), days to maturity (0.173) and biological yield per plant (0.008) exhibit positive non-significant at phenotypic level. Further this character exhibited negative non - significant association with grain yield per plant (-0.128), flag leaf length (-0.125), panicle length (-0.209) and test weight (-0.203).

At genotypic level the days to maturity (0.289), number spikelets per panicle (0.571), number of total tillers per plant (0.503) and number of productive tillers per plant (0.362) showed significantly positive association with flag leaf width. Further days to fifty percent flowering (0.245), plant height (0.261) andbiological yield per hill (0.042) had positive but non- significant correlation. and harvest index (-0.355)had negative significant association with flag leaf width whereas panicle length (-0.246), test weight (- 0.211), grain yield per hill (-0165), flag leaf length (0-0.145), had negative but non-significant association with flag leaf width. These findings are in accordance with Singh *et al*., 2015 and Tuhina- Khatun *et al*., 2015.

4.4.6 Number of total tillers per plant

Number of total tillers per plant had highly significant positive correlation with number of productive tillers per plant (0.918), number of spikelets per panicle (0.334) and flag leaf width (0.477) at phenotypic level. Further this character exhibited positive but non-significant correlation with biological yield per plant (0.211), grain yield per plant (0.198) and test weight (0.102). But this character had negative non-significant association with flag leaf length (-0.226), panicle length (-0.139), days to maturity (-0.178), days to fifty percent flowering (-0.229) and harvest index (-0.149). But plant height (-0.275) shows significantly negative.

At genotypic level the number of productive tillers per plant (0.886), flag leaf width (0.503) number of spikelets per panicle (0.355) and biological yield per plant (0.264) showed significantly positive association with number of total tillers per plant. Further test weight (0.117) and grain yield per plant (0.205) had positive but non-significant correlation. Plant height (-0.325) shows significantly negative. Flag leaf length (-0.269), harvest index (-0.179), panicle length (0.014), days to maturity (-0.219) and days to fifty percent flowering (-0.239) had negative non-significant association with number of total tillers per plant.

Number of tillers per plant recorded significantly positive correlation with number of panicles per plant, biological yield per hill and grain yield per plant at both genotypic and phenotypic levels suggested that genotypes with more tillers and good number of panicles per plant contribute for more grain yield. The results are in agreement with Saha *et al*. (2019), Gopikannan and Ganesh (2013), Ratna *et al*. (2015) and Kumar *et al*. (2017).

4.4.7 Biological yield per plant

Biological yield per plant had highly significant positive correlation with grain yield per plant (0.694), number of productive tillers per plant (0.320), and number of spikelets per panicle (0.371) and at phenotypic level. Further this character exhibited positive but non-significant correlation with flag leaf width (0.008), number of total tillers per plant (0.211), test weight (0.138), panicle length (0.017), days to maturity (0.024) and. But this character had negative but non-significant association with plant height (-0.03) and days to fifty percent flowering (-0.06) flag leaf length (-0.157) whereas, harvest index (- 0.311) had negative significant association with biological yield per plant.

At genotypic level the grain yield per plant (0.809), number of spikelets per panicle (0.403), number of productive tillers per plant (0.348), and number of total tillers per plant (0.264) showed significantly

4.4.8 Number of productive tillers per plant

Number of productive tillers per plant had highly significant positive correlation with number of total tillers per plant (0.918), number of spikelets per panicle (0.325), flag leaf width

(-0.313), biological yield per plant (0.320) and grain yield per plant (0.332) at phenotypic level. Further this character exhibited positive but non-significant correlation with test weight (0.062). But this character had negative non-significant association with harvest index (-0.094), days to maturity (-0.178) and panicle length (- 0.145). But plant height (- 0.318) and flag leaf length (-0.256) show negatively significant.

At genotypic level the number of total tillers per plant (0.996), number of spikelets per panicle (0.355), grain yield per plant (0.350), flag leaf width (0.362) and biological yield per plant (0.264) showed significantly positive association with number of productive tillers per plant. Further, test weight (0.072) had positive but non-significant correlation. Plant height (-0.369), flag leaf length (-0.245), days to fifty percent flowering (-0.283) and days to maturity (-0.271) had negative significant association whereas, harvest index (-0.092) and panicle length (-0.228) had negative non-significant association with numberof panicles per plant.

Number of grains per panicle showed significant positive correlation with grain yield and negative correlation with 1000-grain weight indicating the practice of selecting medium slender grain genotypes would enhance the yield levels. The positive association of grain yield with filled grains per panicle was observed by Akinwale *et al*. (2011), Ruth Elizabeth *et al*. (2011), Ravindra Babu *et al*. (2012), Gopikannan and Ganesh (2013), Ratna *et al*. (2015) and Kumar *et al*. (2017).

4.4.9 Panicle length

Panicle length had highly significant positive correlation with test weight (0.667) and plant height (0.442) at phenotypic level. Further this character exhibited positive but non- significant correlation with harvest index (0.127), flag leaf length (0.250), biological yield per plant (0.017) and grain yield per plant(0.128). But this character had negative significant association with days to fifty percent flowering (- 0.523), days to maturity (-0.485) and number of spikelets per plant (-0.512) whereas negative non- significant association with, number of total tillers per plant (-0.139) number of productive tillers per plant (-0.145).

At genotypic level flag leaf length (0.287), test weight (0.724) and plant height (0.537) showed significantly positive association with panicle length. Further biological yield per plant (0.015), harvestindex (0.204), grain yield per plant (0.144), had positive but non-significant correlation. Number of spikelets per plant (- 0.588), days to maturity (-0.956) and days to fifty percent flowering (-0.897) had negative significant association whereas, number of productive tillers per plant (-0.228) and number of total tillers per plant (-0.151) flag leaf width (-0.246) and had negative but non-significant association with panicle length. Similarly, positive correlation of panicle length, 1000-grain weight and straw yield on grain yield was also reported by Kumar *et al*. (2018). Janardanam *et al*., (2002) have also reported positive associations between these characters.

The positive association with biological yield per plant. Further panicle length (0.015), days to maturity (0.002), and flag leaf width (0.042) and test weight (-0.131) had positive but non-significant correlation. Harvest index (-0.356) had negative significant association with biological yield per plant. Further flag leaf length (-0.184), plant height (-0.04) and days to fifty percent flowering (-0.06) had negative non-significant association with biological yield per plant.

These results revealed that biological yield per plant had highly significant correlation with grain yield per plant. These findings are in accordance with Singh *et al*., (2015), Tuhina- Khatun *et al*., (2015), Anis *et al*., (2016), Sneha gupta *et al*., (2020), parween *et al*., (2020) and Priyanka *et al*., (2020).

4.4.10 Harvest index

Harvest index had highly significant and positive correlation with grain yield per plant (0.276) and non-significant positive correlation with plant height (-0.167) and test weight (0.012) at phenotypic level. The correlation of biological yield per plant (-0.311), days to fifty percent flowering (-0.343) and flag leaf width (-0.301) had negative non-significant association whereas, number of spikelets per panicle (-0.060), number of productive tillers per plant

(-0.094), number of total tillers per plant (-0.149), panicle length (0.127), flag leaf length (0.101) and days to maturity (-0.244) found negative but non-significantcorrelation

At genotypic level harvest index showed highly significant positive association with and grain yield perplant (0.353). Panicle length (0.204) and test weight (0.036), had non-significant positive correlation. Number of productive tillers per plant (-0.092), flag leaf length (-0.149), number of spikelets per panicle(-0.048) and number of total tillers per plant (-0.179) had negative non-significant correlation whereas, days to fifty percent flowering (-0.406), days to maturity (-0.392), biological yield per plant (- 0.356), plant height (-0.266) and flag leaf width (-

0.355) had negatively significant association with harvest index. Harvest index is highly associated with grain yield per plant showing high contribution towards yield of the plant. Similar findings were observed by Singh *et al*., (2015), TuhinaKhatun *et al*., (2015) and Anis *et al*., (2016).

4.4.11 Number of spikelets per panicle

At phenotypic level the number of spikelets per panicle showed significantly positive association with biological yield per plant (0.371), grain yield per plant (0.364), flag leaf width (0.511), number of productive tillers per plant (0.325), number of total tillers per plant (0.334) and days to maturity (-0.244). Further days to fifty percent flowering (0.230) had positive but non-significant correlation. Panicle length (-0.512), plant height (-0.438) test weight (-0.419) and flag leaf length (-0.319) had negative significant association whereas, harvest index
(-0.060) had negative non-significant association with number of spikelets per panicle.

Number of spikelets per panicle had highly significant positive correlation with grain yield per plant (0.384), biological yield per plant (0.403), number of productive tillers per plant (0.382) and number of total tillers per plant (0.355), days to fifty percent flowering (0.318), days to maturity (0.431) and flag leaf width (0.571) at genotypic level. Further this character exhibited negative but nonsignificant correlation with harvest index (-0.048). But this character had negative significant association with panicle length (- 0.588), plant height (-0.506), test weight (-0.447) and flag leaf length (-0.336).

Number of spikelets per panicle is the most prominent yield attributing trait which showed positive correlation with grain yield per plant along with biological yield per plant number of tillers and panicles per plant. All these characters are inter correlated with each other and contribute to total yield. Singh *et al*., (2015), Tuhina-Khatun *et al*., (2015), Anis *et al*., (2016), Sneha gupta *et al*., (2020), Parween *et al*., (2020) and Priyanka *et al*., (2020), Madimita *et al*., (2020) and Kalid *et al*., (2020).

4.4.12 Test weight

Test weight had highly significant and positive correlation with plant height (0.411), panicle length (0.667) and flag leaf length (0.357) and nonsignificant positive correlation with harvest index (0.012), number of productive tillers per plant (0.062), biological yield per plant (-0.138) and number of total tillers per plant (0.102) at phenotypic level. Further days to maturity (-0.406), grain yield per plant (0.199) days to fifty percent flowering (-0.541) and number of spikelets per panicle (-0.419) at phenotypic level associated with negative significant. The correlation of flag leaf width (-0.203) and found negative but non-significant correlation with test weight.

At genotypic level test weight showed highly significant positive association with flag leaf length (0.377), Plant height (0.447) and panicle length (0.724). Biological yield per plant (0.131), harvest index(0.036), number of total tillers per plant (0.117), number of productive tillers per plant (0.072), grain yield per plant (0.217), had nonsignificant positive correlation. Number of spikelets per panicle (-0.447) days to maturity (-0.780) and days to fifty percent flowering (-0.747) had negative significant correlation whereas, flag leaf width (-0.211) had negatively nonsignificant association with test weight. The positiveassociation of test weight with harvest index was observed by Akinwale *et al*. (2011), Ruth Elizabeth Ekka *et al*. (2011), Ravindra Babu *et al*. (2012), Gopikannan and Ganesh (2013), Ratna *et al*. (2015)and Kumar *et al*., (2017).

4.4.13 Grain yield per plant

Grain yield per plant had highly significant and positive correlation with biological yield per plant (0.694), harvest index (0.276), number of spikelets per panicle (0.364), number of productive tillers perplant (0.291) and non-significant positive correlation with number of total tillers per plant (0.332), panicle length (0.128) and test weight (0.199) at phenotypic level. flag leaf width (-0.128), flag leaf length (-0.226), plant height (-0.119) and days to maturity (-0.140) found negative but non-significant correlation with grain yield per plant. The correlation of days to fifty percent flowering (-0.296) found negative significant correlation with grain yield per plant.

At genotypic level harvest index showed highly significant positive association with number of productive tillers per plant (0.350), number spikelets per panicle (0.384), biological yield per plant (0.809) and harvest index (0.353). Test weight (0.217), panicle length (0.144) and number of total tillers per plant (0.205) had non-significant positive correlation.3 flag leaf length (-0.224), flag leaf width (- 0.165), had negatively nonsignificant association with grain yield per plant and negatively significant days to fifty percent flowering (-0.747) and days to maturity (-0.780)

Trait association studies between yield and other traits and among the traits were studied for 20 genotypes revealed high magnitude of genotypic correlation coefficients in most of the cases as compared with the corresponding phenotypic correlation coefficients indicating the negligible influenceof environmental factors. Similar results were reported by Hossain *et al*. (2015), Mohan *et al*. (2015), Ratna *et al*. (2015) and Kalyan *et al*. (2017). In some cases, phenotypic correlation coefficients were higher than their genotypic correlation coefficients, which indicate the suppressing effect of the environment that can alter the expression of the characters at the phenotypic level.The measure of degree of symmetrical association between two variables or characters revealed that grain yield per plant had highly significant and positive correlation with biological yield per hill, harvest index, plant height, number panicles per plant and number of tillers per plant. Therefore, these charactersemerged as most important associates of grain yield in rice. The TW exhibited strong positive associationwith harvest index besides having strong positive association with grain yield per plant.

The above observations of strong positive associations between yield and yield components are in agreement with the available literature in rice. Similar findings were done by Singh *et al*., (2015), Tuhina-Khatun *et al*., (2015), Anis *et al*. 2016, Parween *et al*., (2020) and Sneha gupta *et al*., (2020).

Metroglyph Analysis:

Metroglyph analysis is a semi graphical method for assessing the pattern of morphological variation in germplasm lines. The results obtained on Metroglyph analysis in twenty rice germplasm lines are presented in following lines.

The range of variability, index scores and signs used for 13 characters for metroglyph analysiswere presented in Table 4. It was observed that maximum variability was in number of spikelets per panicle (63.13-309.33) followed by biological yield (47.67-95.4), plant height (104.64-162.07), days to 50% flowering (81.0-121.73), days to maturity (104.47-147.73), grainyield per plant (22.67-47.44), harvest index (40.46-59.69). The range of mean values were utilized to assess the index score 1, 2 and 3 for all the characters studied. The simple circle without rays represents index score 1, while other with values for index score 2 and 3 have shortand long rays on respective circle in different directions, respectively.

The mean performance and total index score of 20 genotypes are presented in Table 5. The total index score was varied from 23 (UNNAO DHAN-1121) to 30 (SHIVA-555). The highesttotal index score of 30 was recorded in only one germplasm line (SHIVA-555) followed by total index score 29 recorded in (NLR) and Total index score of 28 was recorded in UNNAO DHANPUSA, MTU-1271, RGL-2332 and NDR-359. Minimum frequency of genotypes 1occured forindex score 29 and 30. The scatter diagram has been prepared by taking number of pods per plant on x-axis and number seeds per plant on y-axis and three complexes could be distinguishedon the basis of morphological variation. (table 6 and figure 2)

Complex-1: High number of spikelets per panicle with moderate plant height

This complex was represented by 11 (BPT -1768, BPT-204, MTU-7029, NP-9558, BPT-01, BPT-02, KNM - 118, MTU-1271, NLR and NDR-359 (Check) genotypes with High numberof spikelets per panicle with moderate plant height with range of 24-29 and average score of26.36.

Complex-2: Low number of spikelets per panicle with higher plant height

This complex was represented by 5 (UNNAO DHAN SHARABATHI, UNNAO DHAN PUSA, UNNAO DHAN-1718, UNNAO DHAN-1121, UNNAO DHAN BASMATHI CSR-30) genotypes with Low number of spikelets per panicle with higher plant height with range of 22-28 and average score of 26.20.

- **Complex-3:** Moderate number of spikelets per panicle with moderate plant height
- Complex-3 was represented by 2 (UNNAO DHAN MOTI and RGL-2332) genotypes with Moderate number of spikelets per panicle with moderate plant height with range of 24-28 and average score of26.
- **Complex-4:** Moderate number of spikelets per panicle with moderate plant height
- Complex-4 was represented by 1 (UNNAO DHAN-1509) genotypes with Moderate number of spikelets per panicle with moderate plant height with index score 25.
-
- **Complex-5**: Low number of spikelets per panicle with shorter plant height
- Complex-5 was represented by 1 (SHIVA-555) genotypes with Low number of spikelets per paniclewith shorter plant height with index score 30.
- The frequency diagram (figure 3) showed index score for 13 characters of 20 genotypes revealed that the index scores ranged from 23-30. maximum frequency of genotypes 4 occurred for index score of 26 and 28 followed by minimum frequency of genotypes 1 occurred for index score of 23, 29 and 30.
- Highest index score of 30 recorded by only one line (SHIVA-555) followed by index score of 29, 28,and 26 by 1, 4, and 4 lines.

CONCLUSION

- According to the findings of this study, NLR outperformed KNM-118 in terms of grain output per plant, while UNNAO DHAN-1509 has the earliest days to maturity among the 20 rice genotypes tested. Number of spikelets per panicle, productive tillers, and tillers per hill have showed substantial variance among all other features, with high PCV, GCV, and heritability, as well as genetic progress as a percent mean. A scatter diagram was created for 20 genotypes that formed five complexes with 11,5,2,1, and 1 genotypes in each complex. The genotypes SHIVA-555, NLR, NDR -359, and BPT-01, which have a high index score and fall into various clusters, can be utilised as parents in hybridization to get the most variety in character combinations.

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TABLES

Table 1: Analysis of Variance for 13 quantitative traits of rice genotypes

S.No.	Source	Replication	Treatment	Error
	Degrees of freedom	2	19	38
1	Days to fifty percent flowering	87.2950	338.802**	69.058
2	Days to Maturity	97.4720	303.584**	103.534
3	Plant height	71.2050	1003.51**	89.606
4	Flag Leaf Length	8.4830	113.87**	4.52
5	Flag Leaf Width	0.0010	0.144**	0.006
6	Number of Total Tillers	0.3380	13.352**	0.341
7	Number of Productive Tillers	0.1010	13.609**	0.48
8	Panicle Length	0.4120	39.979**	3.57
9	Biological yield	8.3980	539.328**	26.951
10	Harvest Index	15.1250	130.589**	10.638

11	Number of spikelets per panicle	103.2220	15345.37**	321.431
12	Test Weight	2.5860	62.238**	1.906
13	Grain Yield per Plant	0.1730	128.102**	4.56

*** Significant at P<0.5, respectively**
**** Significant at P<0.01, respectively**

Table 2: Genotypic variation

Genotypes	Days to fifty percent flowering	Days to Maturity	Plant height (cm)	Flag Leaf Length (cm)	Flag Leaf Width (cm)	Number of Total Tillers	Number of Productive Tillers	Panicle Length (cm)	Biological yield	Harvest Index (%)	Number of spikelets per panicle	Test Weight (g)	Grain Yield per Plant (g)
Unnao Dhan sharabathi	102.2	124.667	155.673	51.993	1.139	8.333	8.333	28.473	55.58	49.864	142.2	22	28.233
Unnao Dhan-1509	81	104.467	118.46	36.78	0.866	8	8	34.887	50.613	59.693	92.333	25.52	30.275
Unnao Dhan Pusa	110.067	135.133	135.367	40.38	1.064	7.333	7.333	32.453	60.44	58.604	127.4	18.6	34.56
Unnao Dhan Moti	110.267	135.6	145.847	36.6	1.432	7.933	7.933	25.273	49.66	46.476	204.733	15.133	22.947
Unnao Dhan-1718	111.267	135.867	148.728	42.313	0.879	7.733	7.733	30.733	57.313	44.757	63.133	26.467	25.56
Unnao Dhan-1121	110.067	135.133	144.547	42.253	0.858	8.067	8.067	27.227	65.22	42.611	74.8	22.6	26.753

Basmathi CSR 30	110.267	135.6	162.073	31.853	1.223	8	8	28.927	60.513	51.56	71.467	20	29.54
BPT-1768	119.467	145.667	109.947	35.572	1.155	8	8	22.953	47.667	59.183	240.333	14.067	28.22
BPT-204	117.933	143.933	110.04	34.727	1.024	7.867	7.867	22.947	51.4	57.843	183.8	16.733	29.527
BPT - 74	121.733	147.733	109.947	34.727	1.155	7.867	7.867	22.953	59.113	49.982	193.533	15.133	29.193
MTU-7029	116.067	141.267	113.54	28.72	1.208	8.8	8.8	23.92	58.12	55.851	207	20	32.38
NP-9588	113.933	139	120.42	36.133	1.329	9.733	9.733	26.187	82.913	40.76	196.8	19	33.773
SHIVA-555	108	134	141.12	38.913	1.413	8.933	8.933	26.987	78.273	50.873	309.333	17	39.74
BPT -01	120.867	145.867	105.633	31.34	1.267	9.2	9.2	22.093	53.98	49.425	274.933	14	26.493

Genotypes	**Days to fifty percent flowering**	**Days to Maturity**	**Plant height (cm)**	**Flag Leaf Length (cm)**	**Flag Leaf Width (cm)**	**Number of Total Tillers**	**Number of Productive Tillers**	**Panicle Length (cm)**	**Biological yield**	**Harvest Index (%)**	**Number of spikelets per panicle**	**Test Weight (g)**	**Grain Yield per Plant (g)**
BPT-02	119	145	106.38	31.313	1.156	9.933	9.933	23.52	69.867	41.573	214	16	28.707
KNM - 118	101	125.333	104.64	32.227	1.009	14.067	15.733	22.693	80.854	55.029	234.667	17.1	43.673
MTU-1271	117	141.533	129.313	33.233	1.275	8.933	8.933	26.947	95.4	40.461	287.667	20	38.42
RGL -2332	113.667	136.933	146	50.82	1.244	9	9	24.94	63.047	49.062	202.8	26	31.153
NLR	87	125	127.42	32.147	1.128	10.467	10.667	31.6	80.867	58.538	219.333	30	47.44
NDR-359	105	131	125	35.81	1.797	15.6	14	27.967	51.5	43.97	210.6	23.103	22.667
Mean	109.79	135.44	128	36.89	1.18	9.19	9.2	26.68	63.62	50.31	187.54	19.92	31.46
Minimum	81	104.47	104.64	28.72	0.86	7.33	7.33	22.09	47.67	40.46	63.13	14	22.67
Maximum	121.73	147.73	162.07	51.99	1.8	15.6	15.73	34.89	95.4	59.69	309.33	30	47.44

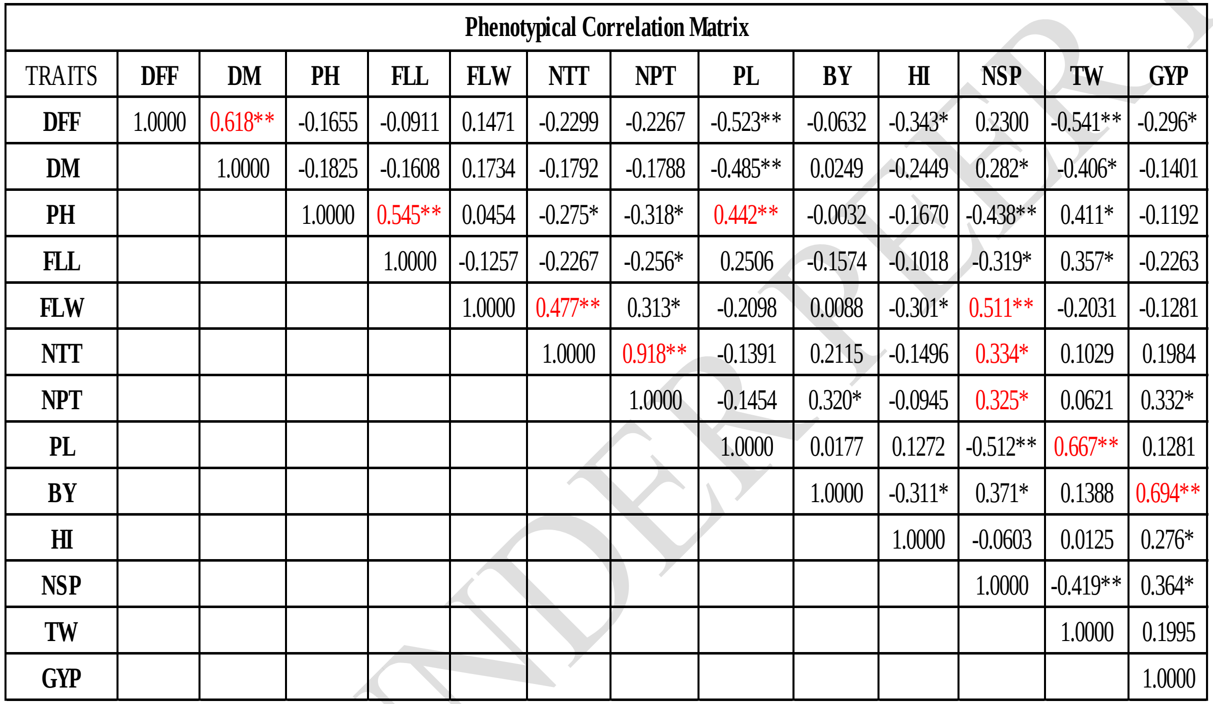
CV	7.57	7.51	7.4	5.76	6.65	6.35	7.52	7.08	8.16	6.48	9.56	6.93	6.79
CD at 5%	13.74	16.82	15.65	3.51	0.13	0.96	1.14	3.12	8.58	5.39	29.63	2.28	3.53
CD at 1%	18.4	22.53	20.96	4.71	0.17	1.29	1.53	4.18	11.49	7.22	39.69	3.06	4.73
SEm	4.8	5.87	5.47	1.23	0.05	0.34	0.4	1.09	3	1.88	10.35	0.8	1.23
Replication	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS
Treatment	S	S	S	S	S	S	S	S	S	S	S	S	S

Table 3 Genetic Parameters for 13 Quantitative Characters in Rice Genotypes

S. No	Genetic parameters	GCV	PCV	H2	GAM%
1	Days to fifty percent flowering	8.637	11.484	56.56	13.381
2	Days to Maturity	6.029	9.633	39.18	7.774
3	Plant height	13.635	15.512	77.271	24.691
4	Flag Leaf Length	16.365	17.35	88.966	31.797
5	Flag Leaf Width	18.126	19.308	88.125	35.052
6	Number of Total Tillers	22.661	23.534	92.719	44.951
7	Number of Productive Tillers	22.731	23.944	90.123	44.453
8	Panicle Length	13.055	14.852	77.271	23.641

9	Biological yield	20.543	22.104	86.371	39.329
10	Harvest Index	12.57	14.143	78.985	23.012
11	Number of spikelets per panicle	**37.734**	**38.926**	**93.97**	**75.351**
12	Test Weight	22.509	23.552	91.344	44.317
13	Grain Yield per Plant	20.396	21.496	90.03	39.867

Table 4: Phenotype Correlation Matrix



Phenotypical Correlation Matrix													
TRAITS	**DFF**	**DM**	**PH**	**FLL**	**FLW**	**NTT**	**NPT**	**PL**	**BY**	**HI**	**NSP**	**TW**	**GYP**
DFF	1.0000	0.618**	-0.1655	-0.0911	0.1471	-0.2299	-0.2267	-0.523**	-0.0632	-0.343*	0.2300	-0.541**	-0.296*
DM		1.0000	-0.1825	-0.1608	0.1734	-0.1792	-0.1788	-0.485**	0.0249	-0.2449	0.282*	-0.406*	-0.1401
PH			1.0000	0.545**	0.0454	-0.275*	-0.318*	0.442**	-0.0032	-0.1670	-0.438**	0.411*	-0.1192
FLL				1.0000	-0.1257	-0.2267	-0.256*	0.2506	-0.1574	-0.1018	-0.319*	0.357*	-0.2263
FLW					1.0000	0.477**	0.313*	-0.2098	0.0088	-0.301*	0.511**	-0.2031	-0.1281
NTT						1.0000	0.918**	-0.1391	0.2115	-0.1496	0.334*	0.1029	0.1984
NPT							1.0000	-0.1454	0.320*	-0.0945	0.325*	0.0621	0.332*
PL								1.0000	0.0177	0.1272	-0.512**	0.667**	0.1281
BY									1.0000	-0.311*	0.371*	0.1388	0.694**
HI										1.0000	-0.0603	0.0125	0.276*
NSP											1.0000	-0.419**	0.364*
TW												1.0000	0.1995
GYP													1.0000

Table 5: Genotype Correlation Matrix

Genotypical Correlation Matrix													
TRAITS	**DFF**	**DM**	**PH**	**FLL**	**FLW**	**NTT**	**NPT**	**PL**	**BY**	**HI**	**NSP**	**TW**	**GYP**
DFF	1.0000	**0.521****	-0.2042	-0.1409	0.2459	-0.2391	-0.283*	-0.897**	-0.0693	-0.406*	0.318*	-0.747**	-0.429**
DM		1.0000	-0.295*	-0.318*	0.289*	-0.2198	-0.271*	-0.956**	0.0002	-0.392*	**0.431****	-0.780**	-0.327*
PH			1.0000	**0.665****	0.0261	-0.325*	-0.369*	**0.537****	-0.0434	-0.266*	-0.506**	**0.447****	-0.1786
FLL				1.0000	-0.1450	-0.2453	-0.269*	0.287*	-0.1849	-0.1492	-0.336*	0.377*	-0.2244
FLW					1.0000	**0.503****	0.362*	-0.2463	0.0428	-0.355*	**0.571****	-0.2116	-0.1651
NTT						1.0000	**0.996****	-0.1515	0.264*	-0.1796	0.355*	0.1173	0.2055
NPT							1.0000	-0.2289	0.348*	-0.0927	0.382*	0.0729	0.350*
PL								1.0000	0.0152	0.2049	-0.588**	**0.724****	0.1445
BY									1.0000	-0.356*	0.403*	0.1313	**0.809****
HI										1.0000	-0.0485	0.0369	0.353*
NSP											1.0000	-0.447**	0.384*
TW												1.0000	0.2170
GYP													1.0000

Table 6 Index scores and signs used for characters for metroglyph analysis of 20 genotypes of rice

Sl.No.	**Character**	**Range of Mean**	**Score 1**	**Sign**	**Score 2**	**Sign**	**Score 3**	**Sign**
			Value <		**Value from - to**		**Value >**	
1	DFF	81-121.73	99.16	○	99.16-120.42		120.42	
2	DM	104.47-147.73	125.38	○	125.38-145.5		145.50	
3	PH	104.64-162.07	109.72	○	109.72-146.29		146.29	
4	FLL	28.72-51.99	30.73	○	30.73-43.05		43.05	
5	FLW	0.86-1.8	0.96	○	0.96-1.4		1.40	
6	NTT	7.33-15.6	7.08	○	7.08-11.3		11.30	

7	NPT	7.33-15.73	7.07	○	7.07-11.33	○╱	11.33	○╱
8	PL	22.09-34.89	23.03	○	23.03-30.33	○╱	30.33	○╱
9	BY	47.67-95.4	50.21	○	50.21-77.03	╲○	77.03	╲○
10	HI	40.46-59.69	43.71	○	43.71-56.9	○—	56.90	○—
11	NSP	63.13-309.33	116.02	○	116.02-259.06	—○	259.06	—○
12	TW	14-30	15.37	○	15.37-24.48	○_	24.48	○_
13	GYP	22.67-47.44	24.93	○	24.93-38	○	38.00	○

Complex	**Name of complex**	**No. of lines**	**Name of lines**	**Range and average score**
I	High number of spikelets per plant with moderate plant height	11	BPT -1768, BPT-204, BPT -74, MTU-7029, NP9558, BPT -01, BPT-02, KNM -118, MTU-1271, NLR and NDR-359 (Check)	24.00-29.00 (26.36)
II	Low number of spikelets per plant with higher plant height	5	Dhan sharabathi, Dhan Pusa, Dhan-1718, Dhan1121 and Basmathi CSR 30	23.00-28.00 (26.20)
III	Moderate number of spikelets per plant with moderate plant height	2	Dhan Moti and RGL -2332	24.00-28.00 (26.00)
IV	High number of spikelets per plant with moderate plant height	1	Dhan-1509	25
V	Low number of spikelets per plant with shorter plant height	1	SHIVA-555	30

Table 8: Genotypes in different complex in metroglyph analysis

Sl.No.	Genotypes	DFF	DM	PH	FLL	FLW	NTT	NPT	PL	BY	HI	NSP	TW	GYP	Total Index Score
1	Unnao Dhan sharabathi	102.2 (2.00)	124.67 (1.00)	155.67 (3.00)	51.99 (3.00)	1.14 (2.00)	8.33 (2.00)	8.33 (2.00)	28.47 (2.00)	55.58 (2.00)	49.86 (2.00)	142.2 (2.00)	22 (2.00)	28.23 (2.00)	27.00
2	Unnao Dhan-1509	81 (1.00)	104.47 (1.00)	118.46 (2.00)	36.78 (2.00)	0.87 (1.00)	8 (2.00)	8 (2.00)	34.89 (3.00)	50.61 (2.00)	59.69 (3.00)	92.33 (1.00)	25.52 (3.00)	30.28 (2.00)	25.00
3	Unnao Dhan Pusa	110.07 (2.00)	135.13 (2.00)	135.37 (2.00)	40.38 (2.00)	1.06 (2.00)	7.33 (2.00)	7.33 (2.00)	32.45 (3.00)	60.44 (2.00)	58.6 (3.00)	127.4 (2.00)	18.6 (2.00)	34.56 (2.00)	28.00
4	Unnao Dhan Moti	110.27 (2.00)	135.6 (2.00)	145.85 (2.00)	36.6 (2.00)	1.43 (3.00)	7.93 (2.00)	7.93 (2.00)	25.27 (2.00)	49.66 (1.00)	46.48 (2.00)	204.73 (2.00)	15.13 (1.00)	22.95 (1.00)	24.00
5	Unnao Dhan-1718	111.27 (2.00)	135.87 (2.00)	148.73 (3.00)	42.31 (2.00)	0.88 (1.00)	7.73 (2.00)	7.73 (2.00)	30.73 (3.00)	57.31 (2.00)	44.76 (2.00)	63.13 (1.00)	26.47 (3.00)	25.56 (2.00)	27.00
6	Unnao Dhan-1121	110.07 (2.00)	135.13 (2.00)	144.55 (2.00)	42.25 (2.00)	0.86 (1.00)	8.07 (2.00)	8.07 (2.00)	27.23 (2.00)	65.22 (2.00)	42.61 (1.00)	74.8 (1.00)	22.6 (2.00)	26.75 (2.00)	23.00
7	Unnao Basmathi CSR 30	110.27 (2.00)	135.6 (2.00)	162.07 (3.00)	31.85 (2.00)	1.22 (2.00)	8 (2.00)	8 (2.00)	28.93 (2.00)	60.51 (2.00)	51.56 (2.00)	71.47 (1.00)	20 (2.00)	29.54 (2.00)	26.00
8	Unnao BPT -1768	119.47 (2.00)	145.67 (3.00)	109.95 (2.00)	35.57 (2.00)	1.16 (2.00)	8 (2.00)	8 (2.00)	22.95 (1.00)	47.67 (1.00)	59.18 (3.00)	240.33 (2.00)	14.07 (1.00)	28.22 (2.00)	25.00
9	BPT-204	117.93 (2.00)	143.93 (2.00)	110.04 (2.00)	34.73 (2.00)	1.02 (2.00)	7.87 (2.00)	7.87 (2.00)	22.95 (1.00)	51.4 (2.00)	57.84 (3.00)	183.8 (2.00)	16.73 (2.00)	29.53 (2.00)	26.00
10	BPT - 74	121.73 (3.00)	147.73 (3.00)	109.95 (2.00)	34.73 (2.00)	1.16 (2.00)	7.87 (2.00)	7.87 (2.00)	22.95 (1.00)	59.11 (2.00)	49.98 (2.00)	193.53 (2.00)	15.13 (1.00)	29.19 (2.00)	26.00
11	MTU-7029	116.07 (2.00)	141.27 (2.00)	113.54 (2.00)	28.72 (1.00)	1.21 (2.00)	8.8 (2.00)	8.8 (2.00)	23.92 (2.00)	58.12 (2.00)	55.85 (2.00)	207 (2.00)	20 (2.00)	32.38 (2.00)	25.00
12	NP-9558	113.93 (2.00)	139 (2.00)	120.42 (2.00)	36.13 (2.00)	1.33 (2.00)	9.73 (2.00)	9.73 (2.00)	26.19 (2.00)	82.91 (3.00)	40.76 (1.00)	196.8 (2.00)	19 (2.00)	33.77 (2.00)	26.00
13	SHIVA-555	108 (2.00)	134 (2.00)	141.12 (2.00)	38.91 (2.00)	1.41 (3.00)	8.93 (2.00)	8.93 (2.00)	26.99 (2.00)	78.27 (3.00)	50.87 (2.00)	309.33 (3.00)	17 (2.00)	39.74 (3.00)	30.00
14	BPT -01	120.87 (3.00)	145.87 (3.00)	105.63 (1.00)	31.34 (2.00)	1.27 (2.00)	9.2 (2.00)	9.2 (2.00)	22.09 (1.00)	53.98 (2.00)	49.43 (2.00)	274.93 (3.00)	14 (1.00)	26.49 (2.00)	26.00
15	BPT-02	119 (2.00)	145 (2.00)	106.38 (1.00)	31.31 (2.00)	1.16 (2.00)	9.93 (2.00)	9.93 (2.00)	23.52 (2.00)	69.87 (2.00)	41.57 (1.00)	214 (2.00)	16 (2.00)	28.71 (2.00)	24.00
16	KNM - 118	101 (2.00)	125.33 (1.00)	104.64 (1.00)	32.23 (2.00)	1.01 (2.00)	14.07 (3.00)	15.73 (3.00)	22.69 (1.00)	80.85 (3.00)	55.03 (2.00)	234.67 (2.00)	17.1 (2.00)	43.67 (3.00)	27.00
17	MTU-1271	117 (2.00)	141.53 (2.00)	129.31 (2.00)	33.23 (2.00)	1.28 (2.00)	8.93 (2.00)	8.93 (2.00)	26.95 (2.00)	95.4 (3.00)	40.46 (1.00)	287.67 (3.00)	20 (2.00)	38.42 (3.00)	28.00
18	RGL -2332	113.67 (2.00)	136.93 (2.00)	146 (2.00)	50.82 (3.00)	1.24 (2.00)	9 (2.00)	9 (2.00)	24.94 (2.00)	63.05 (2.00)	49.06 (2.00)	202.8 (2.00)	26 (3.00)	31.15 (2.00)	28.00
19	NLR	87 (1.00)	125 (1.00)	127.42 (2.00)	32.15 (2.00)	1.13 (2.00)	10.47 (2.00)	10.67 (2.00)	31.6 (3.00)	80.87 (3.00)	58.54 (3.00)	219.33 (2.00)	30 (3.00)	47.44 (3.00)	29.00

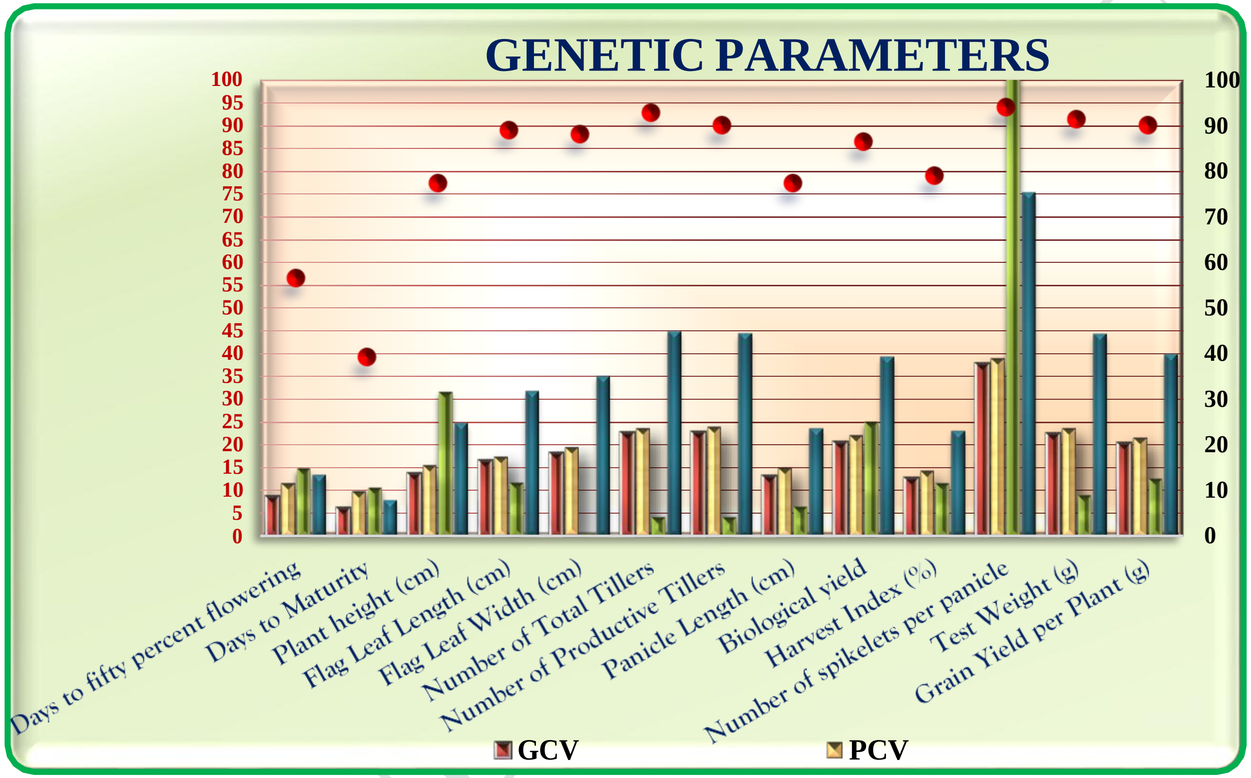
20	NDR-359 (Check)	105 (2.00)	131 (2.00)	125 (2.00)	35.81 (2.00)	1.8 (3.00)	15.6 (3.00)	14 (3.00)	27.97 (2.00)	51.5 (2.00)	43.97 (2.00)	210.6 (2.00)	23.1 (2.00)	22.67 (1.00)	28.00

Sl.No.	Genotypes	DFF	DM	PH	FLL	FLW	NTT	NPT	PL	BY	HI	NSP	TW	GYP	Total Index Score
1	Unnao Dhan sharabathi	102.2 (2.00)	124.67 (1.00)	155.67 (3.00)	51.99 (3.00)	1.14 (2.00)	8.33 (2.00)	8.33 (2.00)	28.47 (2.00)	55.58 (2.00)	49.86 (2.00)	142.2 (2.00)	22 (2.00)	28.23 (2.00)	27.00
2	Unnao Dhan-1509	81 (1.00)	104.47 (1.00)	118.46 (2.00)	36.78 (2.00)	0.87 (1.00)	8 (2.00)	8 (2.00)	34.89 (3.00)	50.61 (2.00)	59.69 (3.00)	92.33 (1.00)	25.52 (3.00)	30.28 (2.00)	25.00
3	Unnao Dhan Pusa	110.07 (2.00)	135.13 (2.00)	135.37 (2.00)	40.38 (2.00)	1.06 (2.00)	7.33 (2.00)	7.33 (2.00)	32.45 (3.00)	60.44 (2.00)	58.6 (3.00)	127.4 (2.00)	18.6 (2.00)	34.56 (2.00)	28.00
4	Unnao Dhan Moti	110.27 (2.00)	135.6 (2.00)	145.85 (2.00)	36.6 (2.00)	1.43 (3.00)	7.93 (2.00)	7.93 (2.00)	25.27 (2.00)	49.66 (1.00)	46.48 (2.00)	204.73 (2.00)	15.13 (1.00)	22.95 (1.00)	24.00
5	Unnao Dhan-1718	111.27 (2.00)	135.87 (2.00)	148.73 (3.00)	42.31 (2.00)	0.88 (1.00)	7.73 (2.00)	7.73 (2.00)	30.73 (3.00)	57.31 (2.00)	44.76 (2.00)	63.13 (1.00)	26.47 (3.00)	25.56 (2.00)	27.00
6	Unnao Dhan-1121	110.07 (2.00)	135.13 (2.00)	144.55 (2.00)	42.25 (2.00)	0.86 (1.00)	8.07 (2.00)	8.07 (2.00)	27.23 (2.00)	65.22 (2.00)	42.61 (1.00)	74.8 (1.00)	22.6 (2.00)	26.75 (2.00)	23.00
7	Unnao Basmathi CSR 30	110.27 (2.00)	135.6 (2.00)	162.07 (3.00)	31.85 (2.00)	1.22 (2.00)	8 (2.00)	8 (2.00)	28.93 (2.00)	60.51 (2.00)	51.56 (2.00)	71.47 (1.00)	20 (2.00)	29.54 (2.00)	26.00
8	Unnao BPT -1768	119.47 (2.00)	145.67 (3.00)	109.95 (2.00)	35.57 (2.00)	1.16 (2.00)	8 (2.00)	8 (2.00)	22.95 (1.00)	47.67 (1.00)	59.18 (3.00)	240.33 (2.00)	14.07 (1.00)	28.22 (2.00)	25.00
9	BPT-204	117.93 (2.00)	143.93 (2.00)	110.04 (2.00)	34.73 (2.00)	1.02 (2.00)	7.87 (2.00)	7.87 (2.00)	22.95 (1.00)	51.4 (2.00)	57.84 (3.00)	183.8 (2.00)	16.73 (2.00)	29.53 (2.00)	26.00
10	BPT - 74	121.73 (3.00)	147.73 (3.00)	109.95 (2.00)	34.73 (2.00)	1.16 (2.00)	7.87 (2.00)	7.87 (2.00)	22.95 (1.00)	59.11 (2.00)	49.98 (2.00)	193.53 (2.00)	15.13 (1.00)	29.19 (2.00)	26.00
11	MTU-7029	116.07 (2.00)	141.27 (2.00)	113.54 (2.00)	28.72 (1.00)	1.21 (2.00)	8.8 (2.00)	8.8 (2.00)	23.92 (2.00)	58.12 (2.00)	55.85 (2.00)	207 (2.00)	20 (2.00)	32.38 (2.00)	25.00
12	NP-9558	113.93 (2.00)	139 (2.00)	120.42 (2.00)	36.13 (2.00)	1.33 (2.00)	9.73 (2.00)	9.73 (2.00)	26.19 (2.00)	82.91 (3.00)	40.76 (1.00)	196.8 (2.00)	19 (2.00)	33.77 (2.00)	26.00
13	SHIVA-555	108 (2.00)	134 (2.00)	141.12 (2.00)	38.91 (2.00)	1.41 (3.00)	8.93 (2.00)	8.93 (2.00)	26.99 (2.00)	78.27 (3.00)	50.87 (2.00)	309.33 (3.00)	17 (2.00)	39.74 (3.00)	30.00
14	BPT -01	120.87 (3.00)	145.87 (3.00)	105.63 (1.00)	31.34 (2.00)	1.27 (2.00)	9.2 (2.00)	9.2 (2.00)	22.09 (1.00)	53.98 (2.00)	49.43 (2.00)	274.93 (3.00)	14 (1.00)	26.49 (2.00)	26.00
15	BPT-02	119 (2.00)	145 (2.00)	106.38 (1.00)	31.31 (2.00)	1.16 (2.00)	9.93 (2.00)	9.93 (2.00)	23.52 (2.00)	69.87 (2.00)	41.57 (1.00)	214 (2.00)	16 (2.00)	28.71 (2.00)	24.00
16	KNM - 118	101 (2.00)	125.33 (1.00)	104.64 (1.00)	32.23 (2.00)	1.01 (2.00)	14.07 (3.00)	15.73 (3.00)	22.69 (1.00)	80.85 (3.00)	55.03 (2.00)	234.67 (2.00)	17.1 (2.00)	43.67 (3.00)	27.00
17	MTU-1271	117 (2.00)	141.53 (2.00)	129.31 (2.00)	33.23 (2.00)	1.28 (2.00)	8.93 (2.00)	8.93 (2.00)	26.95 (2.00)	95.4 (3.00)	40.46 (1.00)	287.67 (3.00)	20 (2.00)	38.42 (3.00)	28.00
18	RGL -2332	113.67 (2.00)	136.93 (2.00)	146 (2.00)	50.82 (3.00)	1.24 (2.00)	9 (2.00)	9 (2.00)	24.94 (2.00)	63.05 (2.00)	49.06 (2.00)	202.8 (2.00)	26 (3.00)	31.15 (2.00)	28.00
19	NLR	87 (1.00)	125 (1.00)	127.42 (2.00)	32.15 (2.00)	1.13 (2.00)	10.47 (2.00)	10.67 (2.00)	31.6 (3.00)	80.87 (3.00)	58.54 (3.00)	219.33 (2.00)	30 (3.00)	47.44 (3.00)	29.00

20	NDR-359 (Check)	105 (2.00)	131 (2.00)	125 (2.00)	35.81 (2.00)	1.8 (3.00)	15.6 (3.00)	14 (3.00)	27.97 (2.00)	51.5 (2.00)	43.97 (2.00)	210.6 (2.00)	23.1 (2.00)	22.67 (1.00)	28.00

Table 7 Mean and index score for 13 quantitative traits for 20 rice genotypes

Fig 1. Histogram depicting GCV, PCV, Genetic advance and h^2 for 13 quantitative characters of rice genotypes.



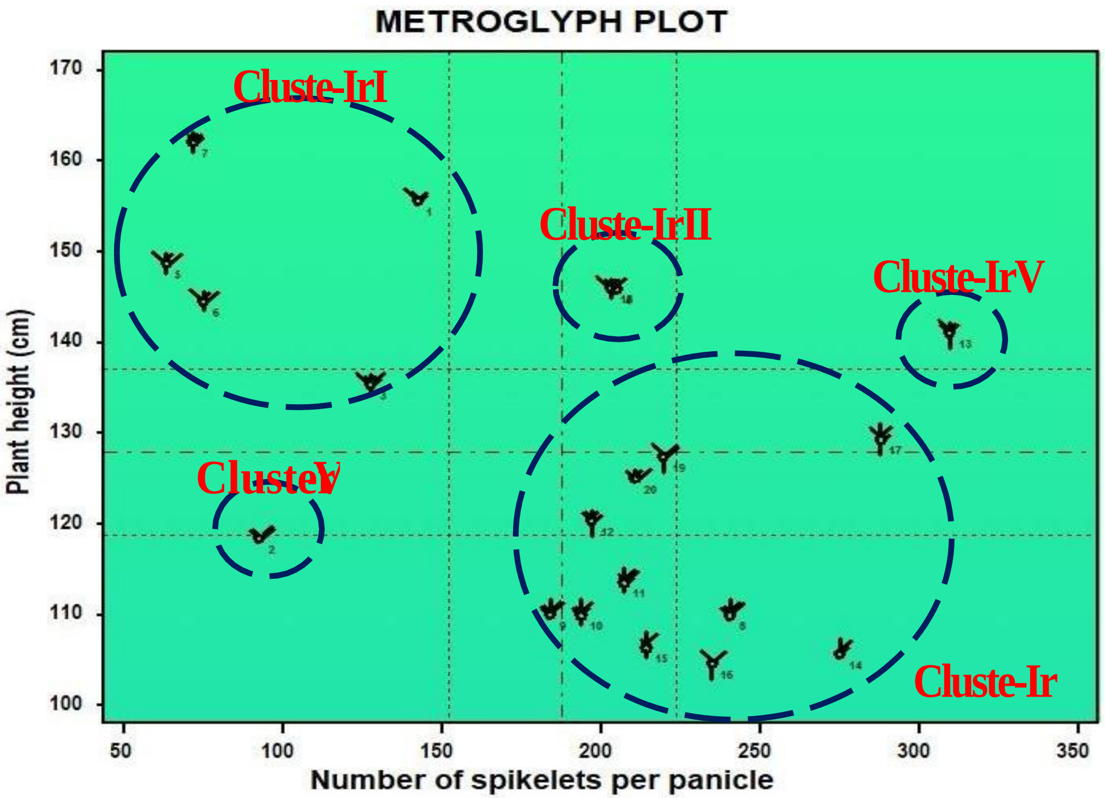


Fig.2 Scattered diagram of Metroglyph analysis showing 20 genotypes of rice

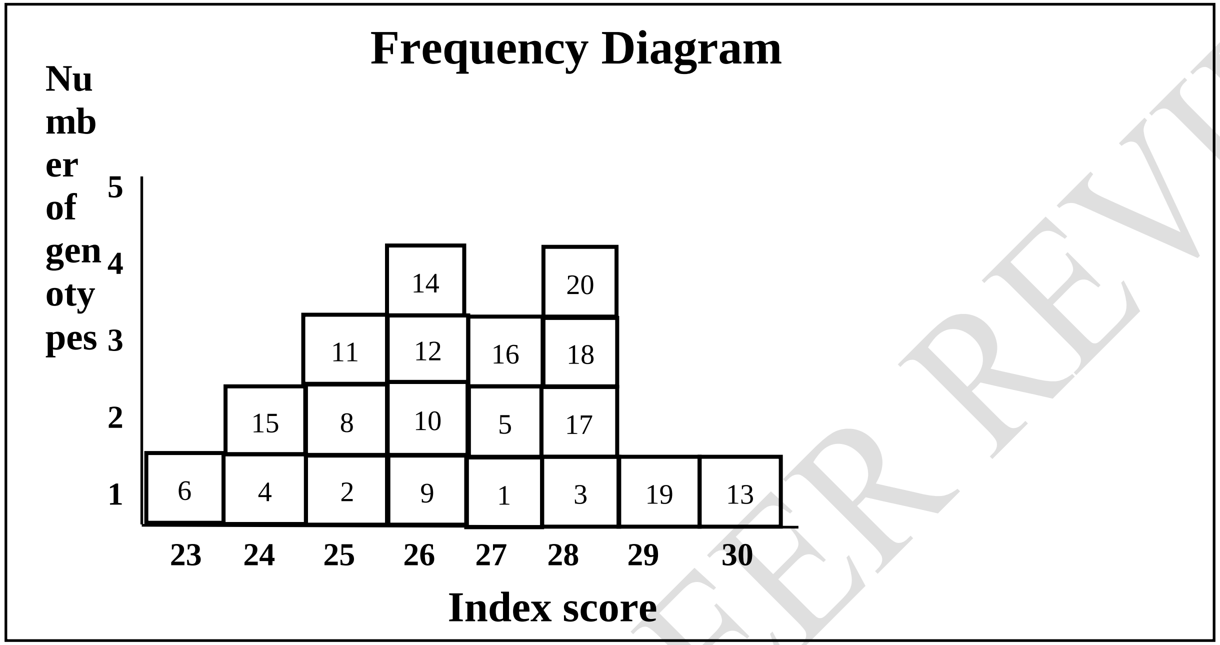


Fig 3. Metroglyph frequency diagram showing 20 genotypes of rice