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Elucidating the components of genetic variation and genetic parameters for selected quantitative attributes in F_1 rice genotypes

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Abstract
An investigation was commenced to examine the genetic aspects of yield and yield contributing characters in rice using 6×6 diallel population without reciprocal. Analysis of variance (ANOVA) revealed highly significant ($p<0.001$) variations among the genotypes for all the characters except grain width (cm) and grain test weight (g/5 ml). The estimates of components of variances demonstrated the involvement of both additive and dominant components in the inheritance of all the traits under study. The dominance component (H_1) was greater than additive component (D) for all the characters except days to 1st flowering, plant height at maturity (cm), grain length (mm) and 1000-grain weight (g), indicating preponderance of dominance component in the inheritance of these traits. The components of variation due to dominance effect of the genes (H_1) was greater than H_2 component for all the characters indicating the presence of unequal proportion of positive and negative alleles in the loci governing the characters. Differences between parents and hybrids were substantiated by significant h^2 value for the traits plant height at maturity (cm), number of tiller per hill, number of panicle per hill, panicle length (cm), number of filled grain per panicle and 1000-grain weight (g). Environmental heterogeneity about the distribution was recorded only for days to1st flowering. $\sqrt{H_1/D}$ Value) suggested partial dominance for days to 1st flowering (0.169), plant height at maturity (0.718), grain length (0.876) and 1000-grain weight (0.506) whereas over dominance was recorded for rest of the traits. Positive or negative alleles irrespective of dominance or recessive were asymmetrically distributed in the parents for the all the traits. Dominant and recessive genes were equally distributed in the parental genotypes for all the characters except days to maturity, pollen fertility (%), plant height at maturity (cm) and number of filled grain per panicle. h^2/H_2 had a value greater than unity for the characters days to 1st flowering (2.50), plant height at maturity (1.27), number of tiller per hill (1.39), number of panicle per hill (1.66) and 1000-grain weight (1.21) indicating that these characters were controlled by more than two genes or group of genes. Exclusively high narrow sense heritability was recorded for days to 1st flowering (89.2%), grain length (82.2%) and 1000-grain weight (90.1%).

Keywords: Inheritance, heritability, dominance, additive, genes, diallel and rice

Introductions
Food security is just one of the numerous issues the globe is dealing with in the twenty-first century. The world's rice consumption is expected to reach 880 million tons by 2025, which is 70% greater than the amount currently produced (IRRI, 2020) [6]. With a total need of 35.3 million tons, Bangladesh is now producing 18.04 million tons of rice grain (BBS, 2022) [1]. Because it is the primary crop consumed by the majority of Bangladeshis, increasing its productivity is therefore essential to closing the gap between supply and demand (Subbaiah *et al.*, 2011) [15]. Conversely, the potential yield of contemporary rice cultivars grown in Asia's tropical regions has lately plateaued.

Therefore, it is imperative to increase the yield potential of contemporary rice varieties, which can be done by enhancing the genotypes' genetic potential. We must alter the current high-yielding plant variety if we hope to achieve another quantum leap in rice production potential.

A polygenic trait, yield is the outcome of the interaction between traits that contribute to yield and are impacted by environmental variations. A crop development program's most crucial component is selection, however improving a crop only via direct selection based on phenotypic performance is challenging. The relative contribution of the heritable and non-heritable components would determine the value of the chosen progeny plants. Selecting parents for a hybrid breeding program solely based on phenotypic performance is not a wise idea because phenotypically superior lines may result in poor recombination in the segregating generations. For any plant breeding effort, parents should therefore be picked or selected based on their genetic worth.

Comparative analysis offers a quick and efficient way to learn about the homozygous lines' genetic characteristics. The potential of parental lines to combine in hybrid combinations and then be used to generate pure lines or hybrid variations determines which lines should be selected. Dividing the genetic component of characters into additive and non-additive components is another opportunity provided by the research of combining ability.

Furthermore, breeders can pick desired features and maximize genetic gain with minimal time and resources by using the heritability estimate (Smalley *et al*., 2004) [13]. Heritability's predictive role in quantitative character genetic studies is one of its most well-known uses; it helps determine the dependability of phenotypic value as a breeding value guide (Kumar *et al*., 2014) [8]. High heritability characters can be developed fast with simple selection. Conversely, it has been investigated and demonstrated that heritability is useless in the absence of genetic improvements. Genetic progress is the amount of heritable genes that a character acquires under a particular selection pressure. The ideal circumstances for selection are those with high heritability estimates and high genetic advancement (Bello *et al*., 2012) [2].

The coefficient of variation delineates the degree of inconstancy display in a huge number of diverse characteristics, but it does not incorporate the heritable component. A relationship considers can moreover give reliable and supportive data around the sort, scope, and course of determination (Zeeshan *et al*., 2013) [17]. The coefficient of relationships helps in deciding the level of relationship between two partitioned characteristics as well as the level at which these characteristics are commonly variable (Boćanski *et al*., 2009; Nagabhushan *et al*., 2011) [3, 12].

The objective of this study was to study genetic components couple with heritability in respect to yield and yield components.

Materials and Methods
Site selection for research materials
The experiment was carried out at the field laboratory of the Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Salna, Gazipur. The soil type of the experimental field belongs to the Shallow Red Brown Terrace type characterized by silty clay with pH value of 6.5 (Haider *et al.,* 1991) [5]. The climate of the experimental site is subtropical in nature characterized by heavy rainfall during the months from June to September and scanty in winter with gradual fall of temperature from the month of September. Six genotypes of rice viz. chinnigura, parija, BR-29, pokkali, kataktara, double rice and their 15 F_1s derived from diallel cross (without reciprocal) were included in the experiment.

Selection of the genotypes
The materials used in the experiment were obtained through the germplasm poll of the Department of Genetics and plant Breeding, BSMRAU, Salna, Gazipur-1706. The relevant details of the parental genotypes are presented in Table 1. The parents were crossed in a half diallel, thus producing 15 F_1 progenies. All the mature F_1 seeds generated from crosses were harvested and dried up to 14% moisture content and stored for evaluating the generated progeny with their parents.

Table 1: Details of the six parental genotypes of rice used in the study

|	
Kalijira	Chinnigura is a variety of aromatic rice mostly popular and cultivated in Bangladesh. This rice variety is totally black in outside color, thin and long in size with little bit round lower edge and pointy head.
Parija	Parija is a short durated Aus variety, seed can be sowed using direct seeded rice method to harvest in 90 days or transplanted 18-day old seedlings to harvest in 75 days to achieve the maximum yield under changed climate without hampering Aman cultivation.
BR-29	A popular Boro season variety of Bangladesh Rice Research Institute (BRRI). Plant height 95 cm, rice medium slender and white, moderately resistance to blight, high yielding, and most popular term as "mega variety" of Bangladesh.
Pokkali	Pokkali is a unique saline tolerant rice variety that is cultivated using extensive aquaculture in an organic way in the water-logged coastal regions. Pokkali is famed for its peculiar taste and its high protein content, grains are extra large- has several medicinal properties. In the past, pokkali provided the energy to fishermen to stay at sea all day long.
Kataktara	A moderately drought tolerant variety at seedling stage, local popular fine grain variety for regular consumption, suitable for broadcast/upland Aus rice ecosystem.
Double rice	A Chinese land race having multiple grained rice, the unique rice variety that has two grains in a single rice seed, quite similar to *'Biram sundori'* of Bangladesh or *'Laila Majnu'* of Nepal having two (sometime three) grins in a rice seed.
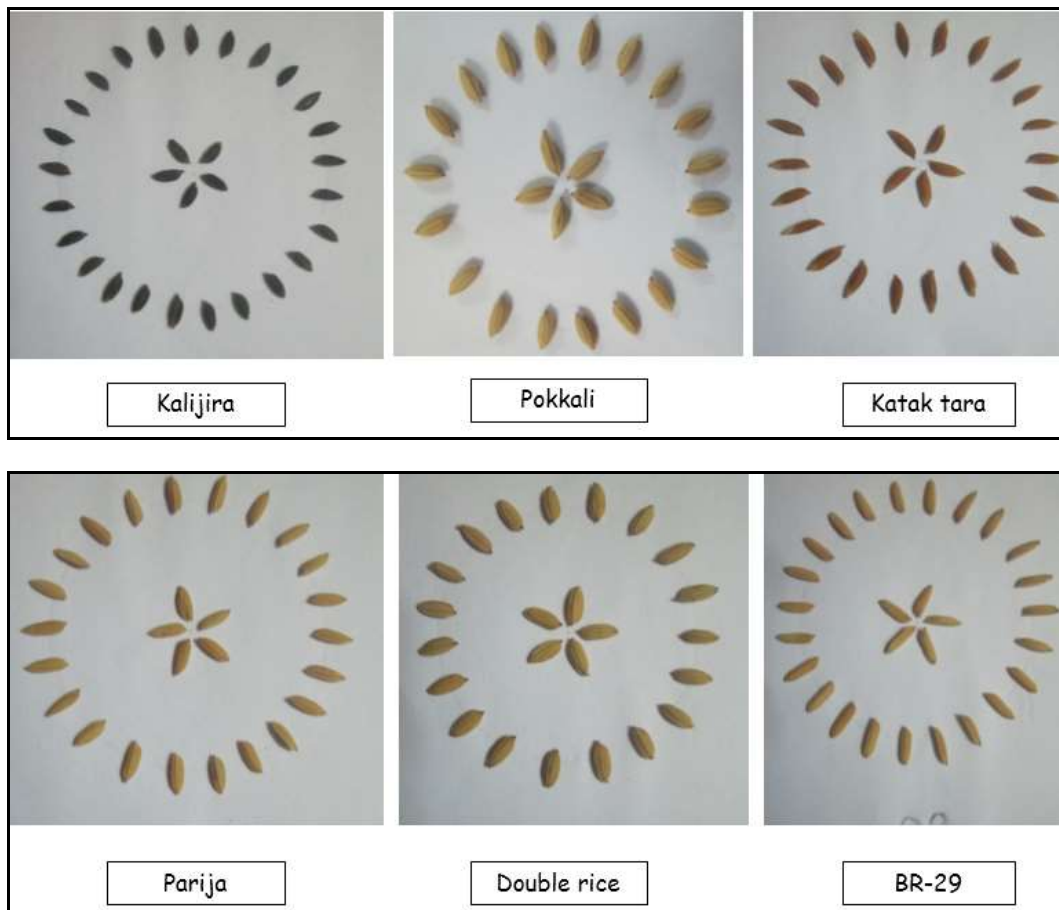
Fig 1: Grain morphology of the six parental rice genotypes used in diallele matting design

Experimental design and cultural practices for progeny evaluation

After raising seedlings in pots, single seedling per slope of all genotypes was transplanted to the test plot and five slopes were alloted for one genotype in a replication with an interspace of 20 cm. The genotypes were assessed in a Randomized Total Square Plan (RCBD) with three replications having plant to plant and line to line separate with 20 cm and 20 cm, separately. Standard intercultural hones were taken after amid trimming period for legitimate development and improvement of the plants. Weeding, amid to begin with two best dressing of urea, was done to break the soil hull, to keep the plots free from weed and to join the urea fertilizer into the soil for lessening the misfortune of urea through denitrification. Water system with customary interim was given to preserve 5-7 cm water up to difficult mixture arrange of the rice. Appropriate control measures were taken against rice stem borer amid tillering and heading arrange of rice. Gathering was done depending upon the development of diverse genotypes. Diverse genotypes achieve their development at diverse times. The date of collecting was restricted when 90% of the grain accomplished brilliant yellow color.

Data collection and observations

Data were recorded on individual plant basis from 10 randomly selected plants of each genotype. Among the studied characters plant height, length and width of flag leaf, days to 1st flowering, tillers per hill, and length of panicle, and days to physiological maturity were recorded in the field. The remaining characters were recorded in the field laboratory after harvesting. The data were collected on the traits as Days to 1st flowering, % fertile pollen, Plant height at maturity (cm), Flag leaf length (cm), Flag leaf width (cm), Tillers per hill, Panicles per hill, Panicle length (cm), Primary branches per panicle (no.), Secondary branches per panicle (no.), Filled grains per panicle (no.), Unfilled grains per panicle (no.), Grain length (mm), Grain width (mm), Milled grain length (mm), Milled grain width (mm),1000 grain weight (g), Grain test weight (g), Grain yield per hill (g) and Days to maturity

Data observation and analysis

The preliminary statistical analysis of the data was done according to standard texts and the subjects (Snedecor and Cochran, 1967; Clark, 1973) [14, 4]. For the genetic analysis of diallel population (F_1), data were subjected to Hayman's approach.

The analysis of variance for the complete diallel table was given by Hayman (1954) [7], developing in one direction that of Yates (1947) [16]. Frequently, however, reciprocal differences are assumed absent, and only one of each pair of reciprocal crosses is raised. For such situation Morley Jones (1965) [11] brought some modification of Hayman's approach (Table 1). In this modification using the same model as Hayman, the determination of the sum of squares corresponding to additive effects (a), and on the assumption of no epistasis to mean dominance (b_1), to additional dominance effects that can be accounted for by genes having one allele present in only one line (b_2) and to residual dominance effects (b_3), is in essence a straight forward application of fitting constants by least squares.

Table 2: Analysis of variance following Morley Jones' modification without reciprocal using means value of Diallel fashion

Item	d.f.	Sum of squares	Mean squares
a	n-1	$\dfrac{1}{n+2}\, dev^2 ur$	Ma
b_1	1	$\dfrac{1}{n(n^2+1)}\,[2X.. -(n+1)X.]^2$	Mb_1
b_2	n-1	$\dfrac{1}{n^2+4}\, dev^2 tr$	Mb_2
b_3	n(n-3)/2	Total SS-(a ss +b_1 ss + b_2 ss)	Mb_3
b	n(n-1)/2	b_1 ss + b_2 ss + b_3 ss	Mb
Error	(r-1) (t-1)	SSe	Me

Where,
a = Additive effects
b_1 = Mean dominance
b_2 = Additional dominance effects that can be accounted for by genes having one allele present in only one line-the remaining n-1 lines being assumed to carry the same alternative allele (=dominance deviation due to arrays)
b_3= Residual dominance effects
dev^2 = Sum of square of deviations from the mean

$Vr = X_{i.} + X_{ii}$
$tr = 2\,(X_{i.} + X_{ii})-(n+2)X_{ii}$

Hayman (1954) [7] derived the speciation for the statistics calculated from F_1 diallel table and also the expected values of the components of variations using least square technique. The genetic components as per Hayman's that was elucidated include
$D = V_0L_0 – E$ = variation due to additive effect
$F = 2V_0L_0 – 4W_0L_{01}– 2\,(n-2)\,\hat{E}/n$ = The mean of 'Fr' values over the arrays
$H_1 = V_0L_0-4W_0L_{01} + 4\,V_1\,L_1-(3n-2)\,\hat{E}/n$ =Component of variation due to the dominance effect of the genes.
$H_2 = 4V_1L_1-4V_0L_1-2E$ = Proportion of positive genes u and proportion of negative genes v in the parents
$h_2 = 4\,(ML_1-ML_0)^2-4(n-1)\,\hat{E}/n^2$=Dominance effect (as the algebraic sum over all loci in heterozygous phase in all crosses)

$E = Error = \left[\dfrac{Error\ SS + Replication\ SS}{d.f.}\right] \div number\ of\ replication$

Where,
V_0L_0 = Variance of parents
V_1L_1 = Mean variance of the arrays
W_0L_{01} = The mean covariance between the parents and the arrays
V_0L_1 = The variance of the mean of arrays
(ML_1-ML_0) = The difference between the mean of the parents and the mean of their n^2 progeny

The significance of the estimates of various components is tested by calculating their corresponding standard errors. The mean degree of dominance is calculated as $\sqrt{H_1/D}$, the relative proportion of genes with positive negative effects as $H_2/4H_1$, the relative proportion of dominant and recessive gene in the parents as $[\sqrt{4DH_1}+F]/[\sqrt{4DH_1}-F]$ and the number of genes which control the characters and exhibit dominance as h^2/H_2. Heritability in narrow sense are estimated using D, H_1, H_2, F and E components of genetic variation as outlined by Hayman (1954) [7], and Mather and Jinks (1981) [10] for F_1 population: $h^2n = \dfrac{\frac{1}{2}D+\frac{1}{2}H_1-\frac{1}{2}H_2-\frac{1}{2}F}{\frac{1}{2}D+\frac{1}{2}H_1-\frac{1}{4}H_2-\frac{1}{2}F+F}$

Results
Analysis of Variance
Analysis of variance for yield and yield contributing characters of six diverse parental genotypes and their 15 crosses of rice (*Oryza sativa* L.) are presented in Table 2. Mean squares due to genotypes were highly significant ($p<0.001$) for all the yield and yield contributing characters studied. Significant mean square due to genotypes for the characters indicated significant differences among the parents and the hybrids (F_1's) which were important for further study in Hayman's approaches of diallel analysis and also for investigation in the material chosen due to considerable genetic variability.

Components of genetic variation and genetic parameters
Components of variation and genetic parameters such as D, H_1, H_2, F, h^2, E, $(H_1/D)^{1/2}$, $H_2/4H_1$, $[\sqrt{4DH_1}+F]/[\sqrt{4DH_1}-F]$, h^2/H_2 and heritability in narrow sense (h^2_n) have estimated as well as presented in Table 3 .
Among the components of variation, D, H_1, H_2 and F are the genetic components and E is the environmental component (Mather and Jinks, 1977) [9]. D measures only additive effects of genes while H, and H_2 measure only dominance effects and one of which, H_1, has the same coefficient as D so that $(H_1/D)^{1/2}$ is a measure of degree of dominance. The relationship of H_1 and H_2 parameters is reflected in $H_2/4H_1$ index that estimates the frequency of positive and negative alleles showing dominance in parents. The sign and magnitude of F shows the relative frequencies of dominant to recessive alleles in the parental genotypes and variations in the dominance level over all loci. F is positive for an excess of dominant alleles, irrespective of whether or not the dominant alleles are increasing or decreasing in their effect on the characters and negative for an excess of recessive alleles. The $[\sqrt{4DH_1}+F]/[\sqrt{4DH_1}-F]$ ratio represents the proportion of dominant and recessive genes in the parents. The ratio of h^2 and H_2 gives information about the number of genes, which control the character and exhibit dominance.

a) Days to 1st flowering
For days to 1st flowering, D was only the genetic component which was significant indicating the importance of only additive effects of genes in the inheritance of the trait (Table 8) and H_1 was smaller in magnitude than D, indicating greater role of additive component in the inheritance of the trait. Highly significant ($p<0.001$) negative F value revealed that the recessive alleles were proportionately in excess in

its inheritance. H_2 value differed from H_1 suggesting that there was unequal frequency of increasing and decreasing alleles. The value of h^2 showed the existence of non-significant differences between parents and crosses. Apparently, there was an environmental heterogeneity, about the distribution as the value of the parameter E was highly significant ($p<0.01$). $\sqrt{H_1}/D$ estimate suggested the presence of partial dominance as the calculated value was less than unity. Positive and negative alleles were asymmetrically distributed, as indicated by $H_2/4H_1$ value which was smaller than the expected value of 0.25. The dominant and recessive alleles were equally distributed in the parents as the ratio of $\left[\sqrt{4DH_1}+F\right]/\left[\sqrt{4DH_1}-F\right]$ were less than the unity (Table 8). Since the parameter h^2/H_2 had a value greater than unity, the character appeared to be governed by more than two genes or group of genes. Heritability estimate in narrow sense (Table 8 and Figure 1) was extremely high (89.2%).
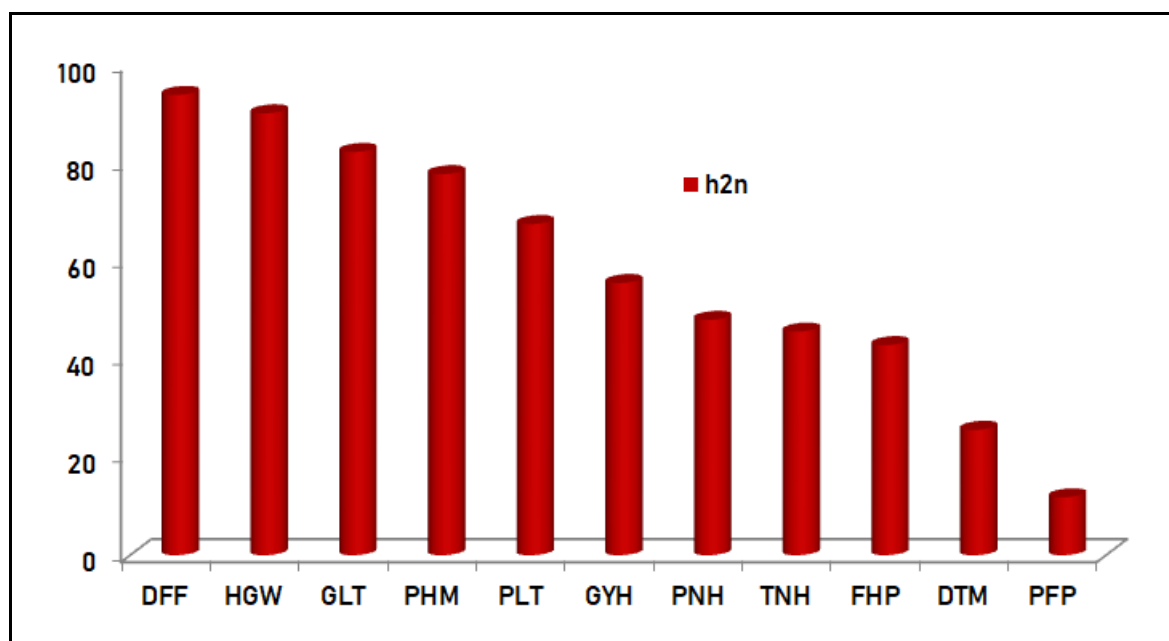
b) Days to maturity

The estimates suggested the role of both additive and dominance components (D, H_1 and H_2) for the inheritance of this trait as both of them were significant, but the dominant components had major role due to higher magnitude than the additive component (Table 8). The result of dominance effect (h^2) suggesting that there were non-significant differences between parents and crosses. Environmental component (E) was only (value) and statistically non-significant. By being greater than unity, $\sqrt{H_1}/D$ suggested the presence of over dominance condition for the expression of this trait. Positive and negative alleles were asymmetrically distributed which was indicated by $H_2/4H_1$ value as the value was smaller (0.21) than the expected value (0.25).

Fig 2: Magnitude of estimated heritability in narrow sense for the considered traits as arranged chronological order

c) Pollen fertility (%)

H_2 value differed from H_1 suggesting that there was unequal frequency of increasing and decreasing alleles. Positive F value revealed that the dominance was predominantly in excess in its inheritance, but then the estimate was non-significant. Over dominance was considered for the character expression since $\sqrt{H_1}/D$ parameter is higher than unity (Table 8). An asymmetrical distribution of positive and negative alleles was indicated as $H_2/4H_1$ value (0.193) was not equal to 0.25. The ratio of $\left[\sqrt{4DH_1}+F\right]/\left[\sqrt{4DH_1}-F\right]$ was greater than unity, suggesting an unequal distribution of dominant and recessive genes in the parents. Heritability estimate in narrow sense was 11.8%.

d) Plant height at maturity (cm)

The components D, H_1 and H_2 were highly significant ($p<0.001$) for this character (Table 8) indicating the importance of both additive and dominance effects of genes in the inheritance of the trait. But D was greater than H_1 indicating greater role of additive component in the

inheritance of this trait. Significant and positive value of F suggested the presence of more dominant alleles in the parents. The significant value of h^2 showed the existence of differences between the parents and hybrids. $\sqrt{H_1}/D$ value was less than unity suggesting the partial dominance condition in expressing the trait. The $H_2/4H_1$ value (0.216) was not equal to the expected value (0.25), which indicated that there was asymmetrical distribution of positive and negative alleles in the parents. Since the ratio $\left[\sqrt{4DH_1}+F\right]/\left[\sqrt{4DH_1}-F\right]$ was greater (1.36) than unity, there was unequal distribution of dominant and recessive genes. The character was controlled by more than two genes or group of genes as the parameter h^2/H_2 had a value than the unity. Heritability estimate in narrow sense was very high (76.4%).

e) Tillers per hill (no.)

The presence of more recessive alleles was recommended by the negative value of F while the estimate was non-significant. The highly significant ($p<0.001$) value of h^2 explored the existence of differences between parents and

crosses. Moreover, over dominance was considered for the character expression since $\sqrt{H_1}$/D parameter (2.467) was much higher than unity. $H_2/4H_1$ value (0.22) was less than the desired value of 0.25 indicating asymmetrically distribution of the positive and negative alleles in the parents. An equal distribution of dominant and recessive genes was also indicated by $\left[\sqrt{4DH_1} + F\right]/\left[\sqrt{4DH_1} - F\right]$ value (0.796) which was less than unity. The character appeared to be governed by more than two genes or group of genes as h^2/H_2 parameter was greater than unity. The heritability estimate in narrow sense was 45.6%.

f) Panicles per hill (no.)
The magnitude of H_1 was much higher than D, signifying the preponderance of dominance component. H_2 value differed from H_1 suggesting that there was unequal frequency of increasing and decreasing alleles. The negative F value indicated the excess of recessive genes in their effects but the value was non-significant. Besides, significant differences between parents and crosses were indicated by the h^2 value for this trait. Moreover, $\sqrt{H_1}$/D value was higher than unity revealing that there was over dominance for the expression of this trait in rice. Positive and negative alleles were asymmetrically distributed, as indicated by smaller value (0.228) of $H_2/4H_1$ than the expected value (0.25). The dominant and recessive alleles were equally distributed in the parents as the ratio of $\left[\sqrt{4DH_1} + F\right]/\left[\sqrt{4DH_1} - F\right]$ were less than unity. The character was governed by more than two genes or group of genes since h^2/H_2 parameter was greater than unity.

g) Panicle length (cm)
The result of dominance effect (h^2) was significant suggesting there were substantial differences between parents and crosses. The estimates (E) suggested that there was not an environmental heterogeneity. On an average over dominance was considered for this trait since the value of the parameter $\sqrt{H_1}$/D was higher (1.106) than unity. An asymmetrical distribution of positive and negative alleles was indicated by $H_2/4H_1$ value (0.212) which is not equal to the desired value of 0.25. The dominant and recessive genes were more or less equally distributed since the relevant parameter had a value (1.10) very close to unity. Heritability estimate in narrow sense was 67.5%.

h) Filled grains per panicle (no.)
Both additive and non-additive components (D, H_1 and H_2) played important role in the expression of the trait number of filled grains per panicle. The excess of dominant alleles in the parents was recorded due to positive F value but the value was non-significant. The value of H_2 differed from H_1 which indicated that there was unequal frequency of increasing and decreasing alleles. Highly significant h^2 value ($p<0.01$) substantiated the differences between parents and hybrids. On an average overdominance was considered for this trait since the value of the parameter $\sqrt{H_1}$/D was greater than unity. Positive and negative alleles were asymmetrically distributed, as indicated by lower value (0.218) of $H_2/4H_1$ than the desired value of 0.25. As $\left[\sqrt{4DH_1} + F\right]/\left[\sqrt{4DH_1} - F\right]$ value exceeded unity, it was obvious that the dominant and recessive genes did not

distributed equally. Heritability estimate in narrow sense was 42.4%.

i) Grain length (mm)
Both additive and dominance components were significant for this trait (Table 8). This indicated the importance of both additive and dominance effect of genes in the inheritance of the trait. However, the magnitude of D was much higher than H_1, indicating the preponderance of additive component. The positive F value indicated the excess of dominant genes in their effects, but the value was non-significant. Non-significant differences between parents and crosses were indicated by the h^2 values for this trait. $\sqrt{H_1}$/D value was less than unity, revealing the partial dominance for the expression of this trait in rice. Positive and negative alleles were asymmetrically distributed, as indicated by lower value (0.174) of $H_2/4H_1$ than the desired value of 0.25. There was also an equal distribution of dominant and recessive genes in the parents, since the ratio $\left[\sqrt{4DH_1} + F\right]/\left[\sqrt{4DH_1} - F\right]$ was very close to unity (1.004). Heritability estimate in narrow sense was very high (82.2%).

j) 1000-grain weight (g)
Additive and dominance components were significant for the trait 1000-grain weight (g) where H_1 was smaller in magnitude than D, indicating greater role of additive component in the inheritance of the trait.. Differences between parents and hybrid were indicated by the highly significant ($p<0.001$) h^2 value for this trait. Partial dominance condition was found in expressing the trait by the $\sqrt{H_1}$/D value which was less than unity. Asymmetrical distribution of positive and negative alleles in the parents was indicated by the $H_2/4H_1$ value (0.178).. It was obvious that the dominant and recessive genes did not distribute equally as suggested by $\left[\sqrt{4DH_1} + F\right]/\left[\sqrt{4DH_1} - F\right]$ value that exceeded unity. More than two genes or group of genes controlled the character as the parameter h^2/H_2 had a value than the unity. Heritability estimate in narrow sense was very high 90.1%.

k) Grain yield per hill (g)
The genetic parameters (D, H_1 and H_2) were significant for the character grain yield per hill that means both additive and dominant effects of genes were important for the character expression (Table-8). D<H_1 indicated the greater role of dominance component in the inheritance. There was unequal frequency of increasing and decreasing alleles since the value of H_2 differed from H_1. Non-significant differences between parents and crosses were indicated by the h^2 value for this trait. Environmental component (E) for this trait was statistically non-significant. On an average overdominance was explored for this trait as the calculated value of $\sqrt{H_1}$/D was greater than unity. The value of $H_2/4H_1$ was smaller (0.202) than the expected value (0.25) indicating an asymmetrical distribution of positive and negative alleles in the parents. The dominant and recessive genes distributed equally as $\left[\sqrt{4DH_1} + F\right]/\left[\sqrt{4DH_1} - F\right]$ value was equal to unity. However, narrow sense heritability for this trait was 54.2%.

Discussion

Cereal crops, especially rice, play a crucial part in worldwide nourishment security. Understanding the hereditary variety and parameters that oversee quantitative traits in rice genotypes is basic for making strides edit abdicate, quality, and versatility. This ponder points to investigate the components of hereditary variety and hereditary parameters for chosen quantitative characteristics in F_1 rice genotypes, utilizing different hereditary investigation approaches such as diallel investigation and Morley-Jones adjustment. Diallel examination could be a capable instrument for examining the hereditary premise of quantitative characteristics in cereal crops. In this consider, the mating of different rice genotypes in a full diallel design permits for the estimation of common combining capacity (GCA) and particular combining capacity (SCA). GCA reflects added substance hereditary impacts, whereas SCA speaks to non-additive impacts. Understanding these components makes a difference in recognizing the mode of quality activity for the characteristics beneath thought. Griffing's strategies, counting Strategy 1 and Strategy 2, are broadly utilized for diallel examination in cereal crops. Hayman's approach amplifies the diallel examination by breaking down the hereditary fluctuation into distinctive components, such as added substance, dominance, and epistatic changes. This makes a difference in observing the particular hereditary mechanisms contributing to the phenotypic variety watched within the chosen quantitative properties in F_1 rice genotypes. Such data is pivotal for focused on breeding endeavors pointed at progressing these characteristics. Moreover, the Morley-Jones adjustment of diallel examination gives an expansion to Griffing's strategies, consolidating the impacts of complementary crosses. Considering the potential affect of maternal impacts on quantitative characteristics in cereal crops, this alteration improves the exactness of hereditary parameter estimation. It is especially important when examining characteristics affected by cytoplasmic and maternal hereditary variables.

Understanding the genetic variety and parameters for quantitative traits in F_1 rice genotypes has critical suggestions for trim enhancement programs. The information picked up from diallel examination, Griffing approaches, Hayman's approach, and Morley-Jones alteration can direct breeders in selecting fitting parental combinations, planning viable breeding techniques, and optimizing the misuse of added substance and non-additive hereditary impacts for wanted characteristic changes. Illustrating the components of hereditary variety and hereditary parameters for chosen quantitative qualities in F_1 rice genotypes through comprehensive hereditary investigations is imperative for progressing our understanding of the hereditary premise of these characteristics. The experiences picked up from diallel examination, Griffing approaches, Hayman's approach, and Morley-Jones adjustment contribute to the advancement of more effective and focused on breeding procedures for improving the efficiency and quality of cereal crops, in this manner tending to worldwide nourishment security challenges.

Morley-Jones alteration has been effectively connected in different crops to dismember the hereditary design of quantitative characteristics. For occurrence, in maize, the alteration was utilized to look at the part of maternal and cytoplasmic impacts in deciding grain surrender. The experiences picked up encouraged the recognizable proof of key hereditary components impacting the characteristic, supporting breeders in concocting focused on methodologies for advancement.

In rice breeding, where characteristics like abdicate, grain quality, and stretch resistance are vital, Morley-Jones alteration offers a nuanced viewpoint. By considering the corresponding crosses, breeders can unravel the impacts of maternal and cytoplasmic variables from the hereditary variety, empowering a more exact estimation of hereditary parameters. This data is urgent for selecting reasonable guardians and planning compelling breeding programs. As rice breeding endeavors ended up more advanced and request accuracy, Morley-Jones alteration stands as a promising instrument. Future inquire about ought to investigate its application in unraveling the hereditary complexities of particular quantitative characteristics in rice, such as resistance to biotic and abiotic stresses. Coordination this adjustment into atomic breeding approaches may assist the advancement of progressed rice assortments with upgraded flexibility and efficiency.

F_1 rice genotypes, coming about from the crossing of different parental lines, include a wealthy range of hereditary variety. This variety emerges from both added substance and non-additive hereditary impacts. Added substance impacts speak to the commitment of person alleles, whereas non-additive impacts incorporate dominance and epistatic intelligent. The investigation of these hereditary components is basic for understanding the heritability of quantitative characteristics and concocting viable breeding methodologies.

Illustrating the components of hereditary variety and hereditary parameters in F_1 rice genotypes has significant suggestions for rice breeding. The knowledge gained from this think about can direct breeders in selecting parent lines deliberately, optimizing the potential for added substance and non-additive hereditary impacts within the improvement of predominant rice assortments. Moved forward quantitative qualities, such as expanded surrender and improved push resilience, are basic for tending to worldwide As progressions in genomics and atomic breeding proceed, the integration of atomic methods with conventional hereditary investigations holds great promise for the long run of rice breeding. Understanding the components of hereditary variety at the atomic level can advance refine the choice of parental lines, quickening the advancement of high-performing and strong rice assortments.

Conclusion

The estimates of components of variances demonstrated the involvement of both additive and dominant components in the inheritance of all the traits under study. The dominance component (H1) was greater than additive component (D) for all the characters except days to 1st flowering, plant height at maturity (cm), grain length (mm) and 1000-grain weight (g), indicating preponderance of dominance component in the inheritance of these traits. High narrow sense heritability was recorded for days to 1st flowering, plant height at maturity (cm), panicle length (cm), grain length (mm) and 1000-grain weight (g). Moderate heritability was found for number of tiller per hill, number of panicle per hill, number of filled grain per panicle and grain yield (g) whereas limited heritability was observed for days to maturity and pollen fertility (%).

References
1. Bangladesh Bureau of Statistics. Monthly Statistical Bulletin, October. Dhaka: Bangladesh Bureau of Statistics, Statistics Division, Ministry of Planning, Government of the People's Republic of Bangladesh; c2022. p. 57.
2. Bello OB, Ige SA, Azeez MA, Afolabi MS, Abdulmaliq SY, Mahamood J. Heritability and genetic advance for grain yield and its component characters in maize (*Zea mays* L.). International Journal of Plant Research. 2012;2(5):138-145.
3. Boćanski J, Srećkov Z, Nastasić A. Genetic and phenotypic relationship between grain yield and components of grain yield of maize (*Zea mays* L.). Genetika-Belgrade. 2009;41(2):145-154.
4. Clark GM. Statistics and Experimental Design. London: Edward Arnold; c1973.
5. Haider R, Rahman AA, Huq S (eds.). Cyclone '91: An Environmental and Perceptional Study. Dhaka: Bangladesh Centre for Advanced Studies; c1991.
6. International Rice Research Institute (IRRI). International Rice Institute and International Rice Information System (IRIS); IRIS database. Available from: https://www.irri.org/; c2020.
7. Hayman BI. The analysis of variance of diallel tables. Biometrics. 1954;10(2):235-244.
8. Kumar A, Roy B, Lakhani GP, Jain A. Evaluation of dried bread waste as feedstuff for growing crossbred pigs. Veterinary World. 2014;7(9):698-701.
9. Mather K, Jinks JL. Biometrical Genetics. 2nd ed. London: Chapman and Hall; c1977.
10. Mather K, Jinks JL. Biometrical Genetics. 2nd ed. London: Chapman and Hall; c1981.
11. Morley-Jones R. The analysis of variance of the half diallel. J Maharashtra Agril Uni. 1965;14:30-33.
12. Nagabhushan NM, Mallikarjuna CH, Shashibhaskar MS, Prahalada GD. Genetic variability and correlation studies for yield and related characters in single cross hybrids of maize (*Zea mays* L.). Current Biology. 2011;5:157-163.
13. Smalley MD, Daub JL, Hallauersa AR. Estimation of heritability in maize by parent-offspring regression; c2004.
14. Snedecor GW, Cochran W. Statistical Methods. Ames: Iowa State College Press; c1967.
15. Subbaiah PV, Sekhar MR, Reddy KHP, Reddy NP. Variability and genetic parameters for grain yield and its components and kernel quality attributes in CMS based rice hybrids (*Oryza sativa* L.). Int J of App Biol and Phar Tech. 2011;2(3):603-609.
16. Yeats P. Analysis of data from all possible reciprocal crosses between a set of parental lines. Heredity. 1947;1:287-301.
17. Zeeshan M, Ahsan M, Arshad W, Ali S, Hussain M, Khan MI. Estimate of correlated responses for some polygenic parameters in yellow maize (*Zea mays* L.) hybrids. International Journal of Advanced Research. 2013;1(5):24-29.