



Combining Ability and Heritability Analysis for Early Maturity and Yield Traits in Contemporary Spring Wheat (*Triticum aestivum* L.)

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Authors' contributions

This work was carried out in collaboration among all authors. All authors read and approved the final manuscript.

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ABSTRACT

An experiment was carried out with North Carolina Mating Design II (NC II) derived F₁ progenies along with parents to know nature of gene action in regulating early maturity, yield and yield contributing traits. The principal objective of this research was to identify best parents and specific cross combinations based on combining ability analysis and estimation of heritability. Hybrids and their parents were arranged in a 8 by 8 partially balanced lattice design with two replicates. Kanchan, BARI Gom-25 x BARI Gom-21, BARI Gom-26 x Kanchan, Rawal x Kanchan, Rawal x

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BARI Gom-22 and BARI Gom-23 × Kheri showed earliness and BARI Gom-25 × BARI Gom-21 showed highest yield potentiality. The genotypes BARI Gom-28 and BARI Gom-30 were used as checks and the selected genotypes performed comparatively better than the checks. The genetic analysis exhibited significant additive and non-additive genetic variations for all the traits. For earliness and yield potentiality the variance due to SCA was highly significant than GCA. Heritability estimates revealed low broad sense heritability except the traits i.e. days to 50% flowering, days to 100% flowering, plant height and 100-grain weight, which exhibited medium heritability. Narrow sense heritability was low for all the traits. The GCA effect of 15 parental genotypes was insignificant for all the traits that were assessed. BARI Gom-25 × BARI Gom-21, BARI Gom-23 × BARI Gom-21, BARI Gom-25 × BARI Gom-27, BARI Gom-26 × Kanchan, BARI Gom-26 × BARI Gom-28, BARI Gom-25 × BARI Gom-27 showed significant SCA effects for earliness. BARI Gom-25 × BARI Gom-22, BARI Gom-26 × CB51 showed significant SCA effects for yield potentiality.

Keywords: *Wheat; combining ability; heritability; GCA; SCA; early maturity; yield.*

1. INTRODUCTION

Wheat (*Triticum aestivum* L.) is the world ranking first cereal crop both in acreage and production (Hanson et al. 1982). Wheat production has been increased worldwide for its sustainability in wide environmental conditions, for its abundant health benefits and due to its higher yield potential. Wheat has been produced on 215 million hectares throughout the world with an average grain yield (GY) of 3.43 t ha⁻¹ [1].

Wheat is the second most important cereal crop in Bangladesh after rice [2]. The dietary habit of the people of this country has changed to a considerable extent and now wheat has become an indispensable food item filling the food gap, also providing good quality fiber and slow digestible carbohydrate. In 2017-18, the total crop area under wheat crop cultivation was 0.35 million ha with 3.13 m ton yield/ha which contributed 0.84% decrease in total volume of production compared to previous 2016-17 year [3]. Spring wheat has commercially grown in Bangladesh besides winter wheat. Bangladesh is still not in the top ranking wheat production country all over the world [4]. So we need to uplift our worse condition as it is our second most important cereal crops. We have to import 5.0million metric tons of wheat every year [4] due to inadequate production of this crop and to fulfill our local consumption. So, different crop improvement and crop production program should be undertaken to fulfill the current demand so that we can minimize our import through maximizing our domestic production.

The most important objective of any wheat breeding program is to enhance grain yield

without adversely affecting other desirable traits and to reduce the time to maturity that may increase the chances of production failure. The success of any plant breeding programs primarily depends not only on the selection of parents but also breeding methods [5]. The combining ability analysis is one of the quantitative genetic parameter to study genetic architecture of quantitative characters. It enables the plant breeders to decide pure line or hybrid breeding to choose on as a technique for further improvement of specific crop [6]. Additionally the effect of general and specific combining abilities and their variances are very useful genetic parameters in this breeding program [7]. Combining ability helps to identify the potential parents or crosses for breeding high potential cultivars [8]. Normally in conventional breeding program parents with high general combining ability (GCA) are used while in hybrid variety development the crosses with significant specific combining ability (SCA) effect used. Information on inheritance of grain yield and associated characters are important in launching successful breeding program. The inheritance of yield and most yield contributing characters are quantitative and polygenic in nature. Combining ability analysis can be used to evaluate the relative importance and amount of additive and non additive forms of gene activity in the production of features [9,10]. A genotype with greater additive gene action is more responsive to selection with higher non-additive gene action. Therefore, the present research work was undertaken to identify the best combiners, crosses, gene action nature and heritability for earliness, yield and yield contributing traits of spring wheat genotypes.

2. MATERIALS AND METHODS

2.1 Experimental Site and Duration

The experiment work was carried out at the Experimental Farm of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh during the period from 29th November, 2015 to 24th March, 2016. The experimental site was located at 24°75'N latitude and 90°5'E longitude at an elevation of 18m above the mean sea level. This area was characterized by non-calcareous dark grey floodplain soil belonging to the Sonatola Soil Series under the Old Brahmaputra Floodplain which considered as the Agro-Ecological Zone 9 [11].

2.2 Soil and Climate

The soil of the experimental site was slightly acidic with a pH value of 6.17, low in organic matter and fertility level. The land type was medium high with silty loam texture. The chemical characteristics of the soil of the experimental site are soil p^H 6.67%, organic carbon 1.52%, organic matter 4.15%, total nitrogen 0.10%, available potassium 0.076me, available phosphorus 2.35 ppm and available sulphur 11.43 ppm. The climate of the experimental site is characterized by wet summer and dry winter. Meteorological data of experimental period recorded during the concerned period at Weather Yard, Department of Irrigation and Water Management, Bangladesh Agricultural University, Mymensingh are presented in Table 1.

2.3 Materials

Nine male and six female parents were used as parent material for this study. BARI Gom-21, BARI Gom-22, Akbar, BARI Gom-27, Kheri,

Kanchan, BARI Gom-28, BARI Gom-30, CB 51 were used as male parents which renamed as 1, 2, 3, 4, 5, 6, 7, 8, and 9 respectively. BARI Gom-26, BARI Gom-25, Rawal, BARI Gom-24, BAW 1008, BARI Gom-23 were used as female parents which renamed as A, B, C, D, E and F respectively. Parents were selected for their potentials and relevance to the breeding objectives of the study. The country of origin of the parental genotype is given in Table 2 and other information on the link of <http://wheatatlas.org/country/varieties/BGD/0> access on 15 November, 2022.

2.4 Crossing Procedure and Field Trial

North Carolina Mating Design II (NC II) crosses [12] were made to develop genetic materials (F₁) in 2014-15 wheat growing season at Bangladesh Agricultural University, Mymensingh. We could not obtain the entire cross combinations due to lack of synchronization and poor seed setting in some of the parents. Seed setting mostly took place during later part of January to most part of February. At maturity hybrid seeds were harvested and threshed manually and then sun dried. The dry hybrid seeds were stored in the refrigerator under low temperature (-5°C). The F₁ along with their respective parents were used to assess their performance in the field trial from November 2015 to March 2016. Experiment was arranged in a 8 by 8 partially balanced lattice design with two replicates. Seeds of each genotype were sown in a 2 m long row representing a plot with 0.40 m spacing between row-row. Plant to plant distance was approximately 5 cm. Two parental inbreds, BARI Gom- 28 and BARI Gom- 30 were used as check varieties for this trial.

2.5 Land Preparation and Fertilizer Dose

The land was prepared by ploughing with power tiller followed by harrowing and laddering.

Table 1. Pattern of monthly average rainfall, humidity and temperature at GPB farm, BAU Campus, Mymensingh during the experimental period (November, 2015-April, 2016)

Months	Year	Air temperature (°C)			Relative Humidity (%)	Rainfall (mm)
		Max.	Min.	Mean		
November	2015	30.00	18.10	23.40	82.20	4.30
December	2015	25.20	13.30	19.30	83.40	0.00
January	2016	26.30	12.80	19.20	85.10	0.06
February	2016	24.20	11.20	18.60	87.70	2.35
March	2016	23.70	11.50	19.30	86.10	3.56

Source: Weather Yard, Department of Irrigation and Water Management, BAU, Mymensingh-2202.

Table 2. List of the parental genotypes of wheat with their country of origin and Institute used in this research work

Parents	Genotypes	Developing institute	Country of origin
1	BARI Gom-21	BARI	CIMMYT, Mexico
2	BARI Gom-22	BARI	CIMMYT, Mexico
3	Akbar	BARI	CIMMYT, Mexico
4	BARI Gom-27	BARI	CIMMYT, Mexico
5	Kheri	BARI	CIMMYT, Mexico
6	Kanchan	BARI	CIMMYT, Mexico
7	BARI Gom-28	BARI	CIMMYT, Mexico
8	BARI Gom-30	BARI	CIMMYT, Mexico
9	CB 51	BARI	CIMMYT, Mexico
A	BARI Gom-26	BARI	CIMMYT, Mexico
B	BARI Gom-25	BARI	CIMMYT, Mexico
C	Rawal	BARI	CIMMYT, Mexico
D	BARI Gom-24	BARI	CIMMYT, Mexico
E	BAW 1008	BARI	CIMMYT, Mexico
F	BARI Gom-23	BARI	CIMMYT, Mexico

Here, 1-9 represents male parents and A-F represents female parents

All the stubbles and weeds were removed carefully. Urea, Triple super phosphate (TSP), Muriate of potash (MoP) and Gypsum were used as source of nitrogen, phosphorous, potassium and Sulphur respectively. Compost manure (9 t ha⁻¹), urea (220 kg ha⁻¹), TSP (180 kg ha⁻¹), MoP (50 kg ha⁻¹), Gypsum (110 kg ha⁻¹) was applied in the soil. At the time of final land preparation one third urea and all manures and fertilizers were applied to the soil. The remaining urea was applied in two splits at tillering and panicle initiation stage.

2.6 Sowing and Intercultural Operations

The seeds of the parental genotypes were sown in the same environmental condition on 29th November, 2015. Weeding was done twice, 22 and 38 days after sowing. Thinning was not required for this experiment. 1st and 2nd irrigation was applied during crown root initiation and panicle initiation respectively.

2.7 Harvesting

Harvesting of the crop started when all the crop plants withered and turned dark brown. Different genotypes matured at different times. So, harvesting was performed on 24th march, 2016 considering the optimum physiological maturity of all genotypes successfully.

2.8 Recording of Data

Data were taken from five plants representing the each genotype considering it's breeding

objectives. Then the mean value of each parameter was used for the statistical analysis. The data were taken for the following traits:

Days to 1st flowering: Data were recorded from date to sowing to date when first flowering was observed. This parameter was recorded in days.

Days to 50% flowering: The 50% flowering data were recorded when almost all the plants of the respected plot remained in 50% flowering condition and it was in days unit.

Days to 100% flowering: The 100% flowering data were recorded when almost all the plants of the respected plot remained in 100% flowering condition. This parameter was recorded in days.

Spikes plant⁻¹: The spikes of five sampling plants were counted manually and it was converted for respective plot.

Plant height: This parameter was recorded in cm of the main culm from collar region to the tip of the spike excluding awn.

Spikes length: Length of main spikes excluding awn was measured from spikes in cm.

Spikelets spike⁻¹: The number of spikelet was counted from sampling plants and the estimation of mean value was completed.

Grains spike⁻¹: The grain formation of each spikes were counted and the mean

value of this parameter was estimated in numbers.

100 grain weight: This parameter was weighted in electronic balance and recorded in gm.

Yield plant⁻¹: The yields of five sample plants were calculated firstly and then the mean value of each plant was estimated in gm.

Yield plot⁻¹: The estimated value of Yield plant⁻¹ was converted for whole plot in gm by multiplying the total plant no. of the respected plot.

Yield ha⁻¹: This parameter was calculated by multiplying the total area of 1 hectare land from the estimated value of yield plot⁻¹. The calculated value was in ton unit.

Straw grain weight: This parameter was weighted in weight machine in gm.

Harvest index: It is ratio of economic yield and biological yield estimated in percentage.

$$HI = \frac{\text{Economic yield}}{\text{Biological yield}} \times 100$$

2.9 Statistical Analysis

2.9.1 Combining ability analysis

General and specific combining ability variances and effects were calculated using SAS software version 9.3 [13] following NC II (model II) as described by Hallauer and Miranda [14]. The GCA is the male and female expatiations and SCA is the male by female interaction expectation. The assumptions were random parents, no epistasis, no linkage disequilibrium and no maternal effects exist on the material we used. The GCA female and male variances were pooled together to have a single GCA variances.

2.9.2 Estimation of heritability

Heritability in broad sense (h²b) was estimated according to the formula suggested by Johnson et al. [15] and Hanson [16].

$$\text{Heritability in broad sense, } (h^2_b) = \frac{\sigma^2_g}{\sigma^2_p} \times 100$$

Where,

σ^2_g = Genotypic variance
 σ^2_p = Phenotypic variance

Heritability in narrow sense (h²n) was estimated according to the formula suggested by Johnson et al. (1955) and Hanson (1961).

$$\text{Heritability in narrow sense, } (h^2_n) = \frac{\sigma^2_A}{\sigma^2_p} \times 100$$

Where,

σ^2_A = Additive genetic variance

σ^2_p = Phenotypic variance

3. RESULTS AND DISCUSSION

3.1 Analysis of Variance (ANOVA) for Agronomic Traits

The analysis of variance (ANOVA) of different yield and yield contributing traits of parental genotypes and their F₁ are presented in the Table 3. Highly significant (P<0.001) differences due to genotypes were observed (Table 4) for the trait 100-grain weight (g). Moderately significant (P<0.01) differences were found for the traits days to 50% flowering (days), days to 100% flowering (days) and plant height (cm). Significant (P<0.05) differences were observed for the trait days to first flowering (days), yield plant⁻¹ (g), yield plot⁻¹ (g), yield ha⁻¹ (ton) and harvest index. The traits spike plant⁻¹ (no.), spikes length (cm), spikelet's spike⁻¹ (no.) and grains spike⁻¹ (no.) were found to be insignificant for this analysis. Such findings revealed that the traits showed significant variations among the 64 genotypes with wide genetic diversity which could provide sufficient scope for selection of these traits. Khan et al. [17] reported highly significant variations for the evaluated traits of the experimented eight wheat genotypes under study.

3.2 Combining Ability Analysis

Analysis of variance for combining ability was carried out in North Carolina Mating Design II (NC II) for the evaluation of GCA and SCA variances and effects involving 13 traits were presented in Table 4.

3.2.1 Days to first flowering

The variance due to GCA was significant at 5% level of probability for the trait days to first flowering. It indicates that the additive genetic variance prevails for the trait days to first flowering. SCA was highly significant for this trait at 0.01% level of probability. This finding also is the indicator of non-additive genetic variation

effects. Dominance genetic variance (5.95) was higher than additive genetic variance (0.91). Estimated degree of dominance (1.58) showed over-dominance inheritance for expressing the trait.

3.2.2 Days to 50% flowering

The variance due to GCA was moderately significant at 1% level of probability for the trait days to 50% flowering whereas SCA was highly significant at 0.01% level of probability for this trait. As a result it can be concluded that both additive and non-additive genetic variation were important for the expression of the trait days to 50% flowering. In this case non-additive gene action was more effective than the additive effects. Dominance genetic variance (4.88) was higher than additive genetic variance (1.24). Estimated degree of dominance (1.53) showed over-dominance for the trait.

3.2.3 Days to 100% flowering

The variance due to GCA and SCA were highly significant at 0.01% level of probability for this trait. As a result it is the clearly indication of both additive and non-additive genetic components were important to control the character days to 100% flowering for the genotypes we analyzed. Additive genetic variance (1.11) was lower than dominance genetic variance (3.56). Estimated degree of dominance (1.44) showed over-dominance for the trait.

3.2.4 Spikes plant⁻¹

The variance due to GCA was moderately significant at 1% level of probability for the trait spikes plant⁻¹. SCA was highly significant at 0.01% level of probability for this trait. From the findings we concluded that the non-additive genetic variation was more effective for the trait spikes plant⁻¹ than additive genetic variation. Dominance genetic variance (0.38) was higher than additive genetic variance (0.10). Estimated degree of dominance (1.75) showed over-dominance for the trait.

3.2.5 Plant height

The analysis of variance for combining ability showed that GCA was significant at 5% level of probability which revealed that additive genetic variation was effective for controlling the trait plant height. SCA was highly significant at 0.01% level of probability for this trait. From the findings we concluded that non-additive genetic variation

was involved for the regulation of the trait plant height. Dominance genetic variance (15.66) was higher than additive genetic variance (2.22). Estimated degree of dominance (1.39) showed over-dominance for the trait.

3.2.6 Spikes length

The variance due to GCA was significant at 5% level of probability for the trait spikes length whereas the SCA was insignificant for the trait. So, we can say that the additive genetic variation was involved in controlling the trait spikes length for the genotypes we analyzed. Additive genetic variance (0.09) was lower than dominance genetic variance (0.20). Estimated degree of dominance (1.29) showed over-dominance for the trait.

3.2.7 Spikelets spike⁻¹

The analysis of variance for combining ability showed that GCA was moderately significant at 1% level of probability for the trait spikelets spike⁻¹ which revealed that the effect of additive genetic variation on this trait. SCA was highly significant at 0.01% level of probability for this trait. From the findings we concluded that non-additive genetic variation was also involved for the regulation of the trait spikelets spike⁻¹. Dominance genetic variance (1.53) was higher than additive genetic variance (0.44) for the trait spikelets spike⁻¹. Estimated degree of dominance (1.76) showed over-dominance for the trait.

3.2.8 Grains spike⁻¹

The analysis of variance for combining ability showed that GCA was moderately significant at 1% level of probability for the trait grains spike⁻¹ which revealed that the effect of additive genetic variation on this trait. SCA was highly significant at 0.01% level of probability for this trait. From the findings we concluded that non-additive genetic variation was also involved for the regulation of the trait grains spike⁻¹. Additive genetic variance (2.20) was lower than dominance genetic variance (7.56). Estimated degree of dominance (1.73) showed over-dominance for the trait.

3.2.9 100-grain weight

The variance due to GCA was moderately significant at 1% level of probability for the trait 100-grain weight which revealed that the effect of additive genetic variation on this trait. The SCA was highly significant at 0.01% level of

Table 3. Analysis of variance (mean squares) for different characters of 64 genotypes of wheat

SOV	d.f.	FF(d)	SF(d)	HF(d)	SP(no.)	PH(cm)	SL (cm)	SS(no.)	GS(no.)	HGW(g)	YP(g)	YPL(g)	YH (ton)	HI
Replicates	1	2.26	3.13	1.76	0.03	37.64	1.00	0.13	0.38	0.01	3.17	79.52	0.01	11.26
Block (Rep.)	14	7.97	6.76	4.69	1.22	40.47	6.56	4.90	24.00	0.16	6.66	166.41	0.03	9.89
Treatments	63	21.47*	17.49**	12.07**	1.82	57.99**	5.20	7.29	36.68	0.62***	18.98*	474.59*	0.07*	28.43*
Error	49	12.01	9.13	5.21	1.33	25.48	4.73	5.31	26.55	0.16	10.91	272.72	0.04	16.59

***, ** and * indicates at 0.001%, 0.01% and 0.05% level of probability respectively Here, **FF**= Days to first flowering, **SF**= Days to 50% flowering, **HF**= Days to 100% flowering, **SP**= Spike plant⁻¹, **PH**= Plant height, **SL**= Spikes length, **SS**= Spikelets spike⁻¹, **GS**= Grains spike⁻¹, **HGW**= 100 grain weight, **YP**= Yield plant⁻¹, **YPL**= Yield plot⁻¹, **YH**= Yield ha⁻¹, **SGW**= Straw grain weight, **HI**= Harvest index

Table 4. North Carolina design II derived variances and genetic parameters obtained in 64 spring wheat genotypes

SOV	FF	SF	HF	SP	PH	SL	SS	GS	HGW	YP	YPL	YH	HI
Replicates	17.60	25.34	12.89	0.21	20.85	0.50	0.83	5.06	0.0014	3.38	84.87	0.0132	20.43
GCA (M+F)	1.56*	2.11**	2.81***	1.96**	1.63*	1.69*	1.96**	2.00**	2.00**	0.96*	0.96*	0.97*	3.1***
SCA (M*F)	23.85***	18.50***	12.74***	2.29***	61.05***	1.11	9.17***	45.46***	0.83***	31.86***	796.59***	0.12***	25.19***
Residual	11.37	8.26	5.28	1.49	28.17	0.70	5.97	29.58	0.22	10.20	255.12	0.04	13.39
σ^2A	0.91	1.24	1.11	0.10	2.22	0.09	0.44	2.20	0.05	3.40	84.92	0.01	3.31
σ^2D	5.95	4.88	3.56	0.38	15.66	0.20	1.53	7.56	0.29	10.32	257.96	0.04	5.62
<i>d</i>	1.58	1.53	1.44	1.75	1.39	1.29	1.76	1.73	1.58	2.26	2.26	2.43	1.38
h^2b (%)	28.24	31.42	39.71	15.67	38.95	4.75	15.67	16.02	58.39	27.01	27.01	24.45	26.31
h^2n (%)	7.25	12.09	15.25	8.30	6.95	13.50	8.83	8.95	10.66	18.05	18.05	18.06	21.20

***, ** and * indicates at 0.1%, 1% and 5% level of probability respectively Here, **FF**= Days to first flowering (d), **SF**= Days to 50% flowering (d), **HF**= Days to 100% flowering (d), **SP**= Spike plant-1 (no.), **PH**= Plant height (cm), **SL**= Spikes length (cm), **SS**= Spikelets spike-1 (no.), **GS**= Grains spike-1 (no.), **HGW**= 100 grain weight (g), **YP**= Yield plant-1 (g), **YPL**= Yield plot-1 (g), **YH**= Yield ha-1 (ton), **HI**= Harvest index, **GCA**= General combining ability, **SCA**= Specific combining ability, σ^2A = Additive genetic variance, σ^2D = Dominance genetic variance, *d* = Degree of dominance, h^2n = Heritability in narrow sense, h^2b = Heritability in broad sense

probability for this trait. From the findings we concluded that non-additive genetic variation was also involved for the regulation of the trait 100-grain weight. Dominance genetic variance (0.29) was higher than additive genetic variance (0.05). Estimated degree of dominance (1.58) showed over-dominance for the trait.

3.2.10 Yield plant⁻¹

The analysis of variance for combining ability showed that GCA was significant at 5% level of probability which revealed that additive genetic variation was effective for controlling the trait yield plant⁻¹. The SCA was highly significant at 0.01% level of probability for this trait. From the findings we concluded that non-additive genetic variation was involved for the regulation of the trait yield plant⁻¹. Additive genetic variance (3.40) was lower than dominance genetic variance (10.32). Estimated degree of dominance (2.26) showed over-dominance for the trait.

3.2.11 Yield plot⁻¹

The variance due to GCA was significant at 5% level of probability which revealed that additive genetic variation was effective for controlling the trait yield plot⁻¹. The SCA was highly significant at 0.01% level of probability for this trait. From the findings we concluded that non-additive genetic variation was involved for the regulation of the trait yield plot⁻¹. Dominance genetic variance (257.96) was higher than additive genetic variance (84.92). Estimated degree of dominance (2.26) showed over-dominance for the trait.

3.2.12 Yield ha⁻¹

The analysis of variance for combining ability showed that GCA was significant at 5% level of probability which revealed that additive genetic variation was effective for controlling the trait yield ha⁻¹. SCA was highly significant at 0.01% level of probability for this trait. From the findings we concluded that non-additive genetic variation was involved for the regulation of the trait yield ha⁻¹. Additive genetic variance (0.01) was lower than dominance genetic variance (0.04). Estimated degree of dominance (2.43) showed over-dominance for the trait.

3.2.13 Harvest index

The variance due to GCA and SCA were highly significant at 0.01% level of probability for the

trait harvest index. As a result it was the clearly indication of both additive and non-additive genetic components were important to control the character harvest index for the genotypes we analyzed. Dominance genetic variance (5.62) was higher than additive genetic variance (3.31). Estimated degree of dominance (1.38) showed over-dominance for the trait.

Mean square variances value from analysis of variance for combining ability showed that GCA and SCA were significant for almost all traits that were assessed. So, it was clear indication of additive and non-additive genetic variation in determining the traits. Ali et al. [18] reported similar results in wheat where plant height, spike length, spikelet's spike⁻¹, grains spike⁻¹, seed weight and grain yield plant⁻¹ showed significant GCA and SCA variation. In this analysis SCA variances was highly significant and its value was higher than GCA for almost all traits. So, it revealed that non-additive gene action had more influence than additive gene action for regulating the traits. Akram et al. [19] reported variance due to SCA was greater than GCA for almost all traits under study. Similar result also reported by Farooq et al. [20] where higher SCA variances was prevalent in case of plant height, tillers plant⁻¹, 1000-grain weight and grain yield plant⁻¹ than GCA variances. The effect of additive genetic variance was lower than dominance genetic variance for all the traits we studied. The performance of degree of dominance resulted over-dominance for all the traits.

3.3 Heritability Analysis in Spring Wheat Genotypes

Heritability in narrow sense was 7.25% for the trait days to first flowering (Table 4). In case of the trait days to 50% flowering, the narrow sense heritability was 12.09%. Heritability in narrow sense was 15.25% for the trait days to 100% flowering. Spikes plant⁻¹ showed 8.30% narrow sense heritability. In case of plant height trait the narrow sense heritability was 6.95% and in case of spikes length 13.50%. The trait spikelets spike⁻¹ showed narrow sense heritability 8.83% and grains spike⁻¹ showed 8.95% narrow sense heritability. The trait 100-grain weight showed 10.66% narrow sense heritability. The traits yield plant⁻¹, yield plot⁻¹ and yield ha⁻¹ showed narrow sense heritability 18.05%, 18.05% and 18.06% respectively. The trait harvest index showed narrow sense heritability 21.20% for the genotypes we analyzed (Table 6).

Table 5. Estimation of GCA effects of the parental genotypes for yield and yield contributing traits

Genotypes	FF	SF	HF	SP	PH	SL	SS	GS	HGW	YP	YPL	YH	HI
BARI Gom-21	0.63	-0.01	0.30	0.24	0.26	-0.12	0.47	1.10	-0.46	-242.71	-603.28	-8.98	0.22
BARI Gom-22	-0.40	-0.02	0.28	-0.01	0.12	-0.02	-0.03	-0.07	-0.32	4.26	21.08	0.19	-0.11
Akbar	0.40	0.29	0.34	-0.31	-1.50	0.03	-0.61	-1.42	-0.38	102.61	509.41	5.29	-0.09
BARI Gom-27	-0.89	-0.41	-0.89	0.15	0.00	0.14	0.30	0.67	0.25	32.81	162.55	1.58	0.17
Kheri	0.01	-0.48	0.10	-0.27	0.74	0.12	-0.54	-1.21	-0.23	32.27	159.81	1.58	-0.03
Kanchan	1.16	1.36	0.40	0.21	0.43	-0.22	0.42	0.99	0.72	8.25	40.82	0.38	-0.15
BARI Gom-28	-0.55	-0.48	-0.07	0.08	1.54	-0.09	0.16	0.36	0.46	31.95	158.35	1.52	0.20
BARI Gom-30	-0.55	-0.48	-0.46	-0.02	-1.32	0.12	-0.05	-0.07	-0.07	29.53	146.14	1.39	-0.10
CB51	0.20	0.23	0.02	-0.07	-0.28	0.05	-0.14	-0.34	0.01	1.03	5.11	0.06	-0.11
BARI Gom-26	0.13	-0.26	-0.08	0.01	0.04	-0.35	0.02	-0.01	0.00	1.96	9.75	0.11	-0.47
BARI Gom -25	-0.16	0.80	1.19	-0.01	0.13	0.12	-0.03	0.01	0.00	1.43	7.07	0.07	0.94
Rawal	0.12	-0.49	-0.59	0.00	-0.32	-0.10	0.00	0.00	-0.03	-5.74	-28.49	-0.30	-1.08
BARI Gom-24	-0.04	-0.12	-0.19	0.00	0.09	0.15	0.00	0.00	0.00	2.85	14.15	0.15	0.29
BAW 1008	-0.06	0.00	-0.06	-0.01	0.29	0.28	-0.02	0.01	0.02	0.95	4.66	0.03	-1.64
BARI Gom-23	0.02	0.06	-0.28	0.01	-0.23	-0.11	0.02	-0.01	0.01	-1.45	-7.13	-0.05	1.96

Here, **FF**= Days to first flowering (d), **SF**= Days to 50% flowering (d), **HF**= Days to 100% flowering (d), **SP**= Spike plant-1 (no.), **PH**= Plant height (cm), **SL**= Spikes length (cm), **SS**= Spikelets spike-1 (no.), **GS**= Grains spike-1 (no.), **HGW**= 100 grain weight (g), **YP**= Yield plant-1 (g), **YPL**= Yield plot-1 (g), **YH**= Yield ha-1 (ton), **HI**= Harvest index.

Table 6. Estimation of SCA effects of the crossing genotypes for yield and yield contributing traits

Genotypes	FF	SF	HF	SP	PH	SL	SS	GS	HGW	YP	YPL	YH	HI
BARI Gom-26 x BARI Gom-21	-3.25	-1.83	-1.53	0.55	3.05	0.55	1.11	2.58	1.07	165.04	818.38	8.24	-1.63
BARI Gom-25 x BARI Gom-21	-3.61*	-1.05	-1.68	0.56	0.55	-0.06	1.12	2.58	0.44	165.52	820.78	8.28	-2.22
Rawal x BARI Gom-21	-0.74	-0.11	-1.21	0.41	-2.21	0.17	0.82	1.83	0.51	200.80	995.63	10.00	-2.31
BARI Gom-24 x BARI Gom-21	0.16	-0.82	-0.61	-0.35	1.61	-0.45	-0.69	-1.65	0.63	156.80	777.20	7.73	1.16
BAW 1008 x BARI Gom-21	1.96	1.55	1.04	-0.42	-7.19**	-0.67	-0.84	-1.99	-0.52	156.28	774.58	7.70	-0.96
BARI Gom-23 x BARI Gom-21	0.68	2.32*	0.94	0.09	1.89	-0.05	0.18	0.45	0.37	192.49	954.13	9.49	1.19
BARI Gom-25 x BARI Gom-22	1.75	1.63	0.73	0.36	-0.52	-0.02	0.71	1.65	2.17	-4.82***	-23.89	-0.23**	1.12
Rawal x BARI Gom-22	-1.69	-1.70	-1.80	0.47	1.77	-0.01	0.95	2.13	0.58	5.07	25.45	0.35	-0.15
BARI Gom-24 x BARI Gom-22	1.46	0.54	0.56	-0.16	-3.62	-0.12	-0.31	-0.75	-0.60	-8.63	-42.87	-0.45	0.15
BAW 1008 x BARI Gom-22	-0.32	-1.42	-1.81	-0.31	-0.93	0.10	-0.63	-1.42	1.00	-3.78	-18.60	-0.15	1.26
BARI Gom-23 x BARI Gom-22	1.88	1.09	-0.45	-0.41	2.24	-0.03	-0.82	-1.87	-1.41	-6.06	-30.17	-0.33	0.02
BARI Gom-26 x Akbar	-0.32	-0.09	-0.12	-0.34	1.12	0.19	-0.67	-1.47	0.23	-70.33	-349.11	-3.63	-1.74
BARI Gom-25 x Akbar	0.34	0.69	-0.55	-0.27	2.52	-0.22	-0.54	-1.14	0.25	-72.80	-361.42	-3.78	1.60
Rawal x Akbar	-0.83	-0.78	-0.11	-0.56	0.36	-0.35	-1.11	-2.49	0.45	-69.15	-343.38	-3.60	0.83
BARI Gom-24 x Akbar	1.04	0.65	-0.05	-0.10	3.70	-0.38	-0.21	-0.46	0.56	-73.28	-363.83	-3.80	2.26
Baw 1008 x Akbar	-2.27	-1.86	-1.85	0.24	4.71	0.12	0.47	1.06	0.36	-69.08	-342.82	-3.54	-1.74
BARI Gom-23 x Akbar	-1.03	-0.70	-0.73	-0.08	0.72	0.77*	-0.15	-0.43	0.23	-83.73	-415.78	-4.35	0.86
BARI Gom-26 x BARI Gom-27	-0.43	-1.07	-0.27	-0.54	-0.91	0.59	-1.09	-2.35	0.54	-26.42	-130.99	-1.31	1.70
BARI Gom-25 x BARI Gom-27	6.11	5.67*	6.18***	0.08	-0.78	0.05	0.17	0.35	-1.48	-26.93	-133.53	-1.34	0.19
Rawal x BARI Gom-27	0.34	0.14	1.74	0.25	3.36	0.16	0.50	1.03	-0.15	-17.88	-88.49	-0.82	-2.02
BARI Gom-24 x BARI Gom-27	0.17	-0.60	0.37	0.15	-1.65	0.28	0.31	0.70	0.13	-23.76	-117.66	-1.13	0.16
BAW 1008 x BARI Gom-27	0.69	-0.67	1.16	0.35	-1.65	-0.42	0.69	1.54	-0.27	-22.21	-109.91	-1.04	-2.01
BARI Gom-23 x BARI Gom-27	-0.11	-0.43	-0.15	0.25	1.64	-0.10	0.49	1.04	-0.18	-22.96	-113.87	-1.14	-1.79

***, ** and * indicates at 0.1%, 1% and 5% level of probability respectively ; Here, **FF**= Days to first flowering (d), **SF**= Days to 50% flowering (d), **HF**= Days to 100% flowering (d), **SP**= Spike plant-1 (no.), **PH**= Plant height (cm), **SL**= Spikes length (cm), **SS**= Spikelets spike-1 (no.), **GS**= Grains spike-1 (no.), **HGW**= 100 grain weight (g), **YP**= Yield plant-1 (g), **YPL**= Yield plot-1 (g), **YH**= Yield ha-1 (ton), **HI**=Harvestindex

Table 6. Estimation of SCA effects of the crossing genotypes for yield and yield contributing traits (Continued)

Genotypes		FF	SF	HF	SP	PH	SL	SS	GS	HGW	YP	YPL	YH	HI
BARI Gom-26	x Kheri	-0.89	-0.22	-1.13	-0.29	0.64	0.39	-0.58	-1.20	0.14	-25.82	-127.93	-1.30	-1.04
BARI Gom-25	x Kheri	2.07	2.45	1.02	0.39	0.17	-0.07	0.79	1.66	-0.26	-23.57	-116.67	-1.15	-0.47
Rawal x Kheri		-0.63	-0.10	-0.55	-0.40	-1.16	0.39	-0.80	-1.71	0.80	-19.79	-97.97	-0.97	3.28
BARI Gom-24	x Kheri	-1.31	0.25	-0.20	-0.40	-1.78	-0.20	-0.80	-1.71	0.40	-24.50	-121.34	-1.21	-0.78
Baw 1008 x Kheri		2.53	2.62	1.73	-0.24	-3.33	0.03	-0.49	-1.04	-0.02	-24.29	-120.27	-1.19	-0.66
BARI Gom-23	x Kheri	-1.85	-1.48	-1.87	-0.03	-1.07	-0.05	-0.05	-0.19	0.21	-19.92	-98.58	-0.97	0.24
BARI Gom-26	x Kanchan	-3.01	-3.11*	-1.58	0.05	-1.22	-0.06	0.11	0.25	-0.92	-7.14	-35.29	-0.33	-2.05
BARI Gom-25	x Kanchan	-0.05	-1.79	-0.01	-0.14	-4.10	-0.37	-0.29	-0.60	-0.87	-9.38	-46.45	-0.47	1.99
Rawal x Kanchan		-2.75	-2.45	-1.58	0.06	8.81	-0.23	0.12	0.25	-0.04	-1.39	-6.71	-0.02	1.25
BARI Gom-24	x Kanchan	-0.62	-0.75	-0.66	0.57	-3.00	0.18	1.13	2.45	-1.15	-9.88	-48.98	-0.49	2.12
Baw 1008 x Kanchan		-2.40	-1.90	-0.16	0.23	-4.31	-0.42	0.46	1.09	-1.02	-7.48	-36.95	-0.34	-0.07
BARI Gom-26 x BARI Gom-28		3.49	3.84**	3.56**	-0.13	-7.73	0.03	-0.26	-0.55	-1.04	-27.47	-136.30	-1.37	-0.24
BARI Gom-25 x BARI Gom-28		0.06	-0.26	-0.32	0.45	-1.28	0.02	0.89	1.98	0.10	-18.85	-93.21	-0.82	-1.35
Rawal x BARI Gom-28		1.45	0.98	0.41	-0.27	-1.19	-0.02	-0.55	-1.23	-0.72	-21.05	-104.41	-1.02	-1.55
BARI Gom-24 x BARI Gom-28		0.51	-0.56	-1.25	-0.12	-2.05	-0.13	-0.25	-0.55	-0.29	-25.61	-126.99	-1.25	-1.57
BAW 1008 x BARI Gom-28		-0.25	-0.36	-1.32	0.61	-1.01	-0.29	1.23	2.66	-0.40	-20.20	-99.95	-0.91	-0.61
BARI Gom-23 x BARI Gom-28		-1.05	-0.13	-0.34	-0.24	-0.29	0.00	-0.48	-1.06	-0.21	-23.31	-115.67	-1.15	0.96
BARI Gom-26 x BARI Gom-30		-0.09	1.95	0.92	-0.37	1.28	-0.08	-0.75	-1.59	0.06	-24.10	-119.39	-1.18	1.74
BARI Gom-25 x BARI Gom-30		0.83	-0.53	0.19	-0.08	-1.09	0.05	-0.17	-0.41	-0.31	-24.21	-119.93	-1.18	0.85
Rawal x BARI Gom-30		-0.59	-0.10	0.35	-0.09	1.73	0.38	-0.18	-0.41	0.45	-16.31	-80.60	-0.73	-1.31
BARI Gom-24 x BARI Gom-30		0.51	0.25	0.98	0.48	3.45	0.03	0.95	2.13	0.13	-21.08	-104.28	-0.98	-2.97
BAW 1008 x BARI Gom-30		2.82	2.07	0.91	0.48	3.27	0.07	0.96	2.13	-0.08	-19.23	-95.01	-0.86	1.78
BARI Gom-23 x BARI Gom-30		0.74	-0.13	1.32	-0.49	2.98	0.03	-0.98	-2.10	0.12	-21.23	-105.15	-1.04	2.14
BARI Gom26	x CB51	-1.49	-1.69	-0.22	-0.25	2.49	0.19	-0.49	-1.16	-0.05	-4.39	-21.83	-0.24***	2.40

***, ** and * indicates at 0.1%, 1% and 5% level of probability respectively ; Here, **FF**= Days to first flowering (d), **SF**= Days to 50% flowering (d), **HF**= Days to 100% flowering (d), **SP**= Spike plant-1 (no.), **PH**= Plant height (cm), **SL**= Spikes length (cm), **SS**= Spikelets spike-1 (no.), **GS**= Grains spike-1 (no.), **HGW**= 100 grain weight (g), **YP**= Yield plant-1 (g), **YPL**= Yield plot-1 (g), **YH**= Yield ha-1 (ton), **HI**= Harvest index

Heritability in broad sense was 28.24% for the trait days to first flowering. In case of trait days to 50% flowering, the broad sense heritability was 31.42%. Heritability in broad sense was 39.71% for the trait days to 100% flowering. Spikes plant⁻¹ showed 15.67% broad sense heritability. In case of plant height trait the broad sense heritability was 38.95% and in case of spikes length 4.75%. The trait spikelets spike⁻¹ showed broad sense heritability 15.67% and grains spike⁻¹ showed 16.02% broad sense heritability. The trait 100-grain weight showed 58.39% broad sense heritability. The traits yield plant⁻¹, yield plot⁻¹ and yield ha⁻¹ showed broad sense heritability 27.01%, 27.01% and 24.45% respectively. The trait harvest index showed broad sense heritability 26.31% for the genotypes we analyzed (Table 6).

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular trait. Johnson et al. [15] classified heritability as low (below 30%), medium (30-60%) and high (above 60%). All the traits studied in case of narrow sense heritability expressed low heritability estimates ranging from 6.95 to 18.06% (Table 6). Aycicek and Yildirim [21] reported low heritability for 20 bread wheat genotypes under the traits grain yield, spike no. per square meter, plant height, grains spike⁻¹, grain weight spike⁻¹, 1000 kernel weight and time to heading. In case of broad sense heritability the traits days to 50% flowering, days to 100% flowering, plant height and 100-grain weight expressed medium heritability (Table 5). The remaining traits exhibited low broad sense heritability. Mohsin et al. [22] estimated broad sense heritability and found high heritability in their experimental work on synthetic elite lines of wheat.

3.4 Estimation of GCA and SCA Effects

3.4.1 GCA effects

The GCA effect of 15 parental genotypes for different traits was presented in Table 5. GCA effects were insignificant for all the traits we analyzed.

3.4.2 SCA effects

SCA effects of crossing genotypes for different traits was presented in Table 5. BARI Gom-25 x BARI Gom-21 showed significant SCA effects for the trait days to first flowering. BARI Gom-23 x BARI Gom-21, BARI Gom-25 x BARI Gom-27,

BARI Gom-26 x Kanchan showed significant effects for the trait days to 50% flowering whereas BARI Gom-26 x BARI Gom-28 showed moderately significant SCA effects for the trait days to 50% flowering and days to 100% flowering. BARI Gom-25 x BARI Gom-27 showed highly significant SCA effects for the trait days to 100% flowering. BAW 1008 x BARI Gom-21 showed moderately significant effects for the trait plant height. BARI Gom-23 x Akbar showed significant effects for spikes length trait. BARI Gom-25 x BARI Gom-22 showed highly significant SCA effects for the trait yield plant⁻¹ and moderately significant effects for the trait yield ha⁻¹. BARI Gom-26 x CB51 showed highly significant SCA effects for the trait yield ha⁻¹.

4. CONCLUSIONS

Combining ability was analyzed and it revealed significant GCA variances for days to first flowering, plant height, spikes length, yield plant⁻¹, yield plot⁻¹ and yield ha⁻¹. Moderately significant GCA variances were found in days to 50% flowering, spikes plant⁻¹, spikelets spike⁻¹, grains spike⁻¹ and 100-grain weight. Highly significant GCA variances were found in days to 100% flowering and harvest index revealed that additive genetic action influenced greatly for those traits. However, highly significant variances were observed for SCA refers preponderance of non-additive variances for regulating almost all traits. The findings revealed that non-additive genetic variance was more effective than additive genetic variances. The degree of dominance implied over-dominance for all the traits we studied. Broad sense heritability performed was also low except days to 50% flowering, days to 100% flowering, plant height and 100-grain weight exhibited medium heritability. Estimated values revealed low heritability for all the traits we analyzed in case of narrow sense heritability. The GCA effect of 15 parental genotypes was insignificant for all the traits we analyzed. BARI Gom-25 x BARI Gom-21, BARI Gom-23 x BARI Gom-21, BARI Gom-25 x BARI Gom-27, BARI Gom-26 x Kanchan, BARI Gom-26 x BARI Gom-28, BARI Gom-25 x BARI Gom-27 showed significant SCA effects for earliness. BARI Gom-25 x BARI Gom-22, BARI Gom-26 x CB51 showed significant SCA effects for yield potentiality.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. FAOSTAT; 2020
Available:<http://faostat.fao.org>
2. Banglapedia. National Encyclopedia of Bangladesh. Major and Minor crops in Bangladesh.
Accepted on 15 February 2015.
Available:<http://en.banglapedia.org/index.17433>.
3. BBS. Bangladesh Bureau of Statistics, Estimates of wheat 2017-18, Planning division, Ministry of Planning, Government of the People's Republic of Bangladesh. 2018;78-79.
4. USDA. United States Department of Agriculture, Agricultural Statistics Annual, National Agricultural Statistics Service; 2019.US.
5. Torres EA, Geraldi IO. Partial diallel analysis of agronomic characters in rice (*Oryza sativa* L.). Genetics and Molecular Biology. 2007;30(3): 605-613.
6. Sharma V, Dodiya N, Dubey, R, Khan R. Combining ability analysis in bread wheat (*Triticum aestivum* (L.) Em. Thell) under different environmental conditions. Bangladesh Journal of Botany. 2019;48(1):85–93.
DOI:<https://doi.org/10.3329/bjb.v48i1.47419>
7. Viana JMS, Matta FP. Analysis of general and specific combining abilities of popcorn populations, including selfed parents. Genet. Mol. Biol. 2003;26:465–471.
DOI: 10.1590/S1415-4757200300040001
8. Acquaah G. Principles of plant genetics and breeding. Oxford. Wiley-Blackwell; 2007.
9. Katiyar S, Khan R, Kumar S. Artificial bee colony algorithm for fresh food distribution without quality loss by delivery route optimization. Journal of Food Quality. 2021;2021:1-9.
DOI:<https://doi.org/10.1155/2021/4881289>
10. Khan R, Tyagi N, Chauhan N. Safety of food and food warehouse using VIBHISHAN. Journal of Food Quality. 2021;2021:1-12.
DOI:<https://doi.org/10.1155/2021/1328332>
11. UNDP/FAO. Land Resource Appraisal of Bangladesh for Agricultural Development. Report No. 2 Agro-ecological Regions of Bangladesh. 1998;15(30):212-221.
12. Comstock, RE, Robinson HF. The components of genetic variance in the populations of biparental progenies and their use in estimating the average degree of dominance. Biometrics. 1948;4:254-266.
13. SAS Institute.SAS user's guide: Statistics. 4th ed. SAS Inst., Cary, NC. Torres, EA. Geraldi OI (2007). Partial diallel analysis of agronomic characters in rice (*Oryza sativa* L.).Genetics and Molecular Biology. 2010;30(3): 605-613.
14. Hallauer, AR, Miranda, Fo JB. Quantitative genetics in maize breeding. 2nd ed. Iowa State University Press, Ames.1988;64-71.
15. Johnson HW, Robinson HF, Comstock RE. Estimation of genetic and environmental variability in soybean. Agronomy Journal.1955;47 (2):314-318.
16. Hanson, WD. Heritability. Statistical genetics and plant breeding.National academy of science. National Research Council, Washington. 1981;125-140.
17. Khan I, Khan US, Khan KM, Khan A, Gurmani AR, Shah AL, Khan SM, Ullah I, Ali I, Ali M. Evaluation of five different wheat (*Triticum aestivum* L.) genotypes under drought stress conditions at Hairpur villey. Int. J. of Biosciences. 2016.8 (5):2222-5234.
18. Ali FK, Ali AR, Ali SK, Amanullah M, Ali A, Ahmed SO, Newaz, RS, Ali F, Ali ZD. Heterosis and combining ability in F1 population of hexaploid wheat (*Triticum aestivum* L.). American Journal of Plant Sciences. 2015;6(7):1011-1026.
DOI: 10.4236/ajps.2015.67107
19. Akram Z, Ajmal SU, Khan KS, Qureshi R, Zubair M. Combining ability estimates of some yield and quality related traits in spring wheat (*Triticum aestivum* L.). Pakistan Journal of Botany. 2011;43(1): 221-231.
20. Farooq J, Habib I, Saeed A, Nawab NN, Khaliq I, Abbas G. Combining ability for yield and it's components in bread wheat (*Triticum aestivum* L.). Journal of Agriculture and Social Sciences. 2006; 2(4):207-211.
21. Aycicek M, Yildirim T. Heritability of yield and some yield components in bread wheat (*Triticum aestivum* L.) genotypes.

- Bangladesh Journal of Botany. 2006; 35(1):17-22.
22. Mohsin T, Khan N, Naqvi FN. Heritability, phenotypic correlation and path coefficient studies for some agronomic characters in synthetic elite lines of wheat. Journal of Food, Agriculture and Environment. 2009; 7(3-4):278-282.

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