GENETIC VARIABILITY, CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS IN WHEAT (*Triticum aestivum* L.)

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By

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CERTIFICATE

This is to certify that thesis entitled, "GENETIC VARIABILITY, CHARACTER ASSOCIATION AND DIVERSITY ANALYSIS IN WHEAT (Triticum aestivum L.)" submitted to the Faculty of AGRICULTURE, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bona fide research work carried out by MD. REZAUR RAHMAN, Registration No.11-04415 under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

I further certify that such help or source of information, as has been availed of during the course of this investigation has duly been acknowledged.

Dated : December, 2016
Place : Dhaka, Bangladesh

(Prof. Dr. Md. Sarowar Hossain)
Supervisor

Dedication

It is dedicated to all the wonderful people I’ve met along the path of life including . . .

My Beloved Parents and inspiring Siblings

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ABSTRACT

Current research work was a modest attempt to screen out suitable parental group from twenty wheat genotypes with better performance and heritable characters. In this regard, twenty wheat genotypes were collected from BARI and ten characters *viz.* plant height, spikes/plant, spike length, grains/spike, 1000-grain weight, harvest index, vegetative period, grain filling period, days to maturity and grain yield/plant were selected for investigation. Significant variations were observed among the genotypes for all the characters studied. Most of the characters had shown slightly higher phenotypic coefficient of variation than corresponding genotypic coefficient of variation but spikes/plant had shown wide gap which suggested greater environmental influence in controlling this trait. Harvest index and grain yield/plant had shown high heritability with high genetic advance indicated additive gene action in controlling this trait and heritable in nature. Spikes/plant had shown low heritability with low genetic advance indicating that it was controlled by non-additive gene. Correlation coefficient analysis had shown that genotypic correlation co-efficient was slightly higher than the corresponding phenotypic correlation co-efficient for most of the characters except for grain filling period. Grain yield/plant had shown highly significant and positive correlation with harvest index, spike length, 1000-grain weight and grains/spike. Path coefficient analysis also confirmed that these characters had influenced grain yield directly in positive direction. So, these characters should be taken into consideration in selection for yield improvement. Multivariate techniques were used for diversity analysis. Twenty wheat genotypes were clustered into five diverse groups. The maximum number of genotypes were grouped in cluster I followed by cluster V, IV, III and II. The highest inter cluster distance was noticed between the clusters I and II. Therefore, the genotype G_{12} (BARI Gom 22) for longest spike length and highest percentage of harvest index from cluster III, G_{15} (BARI Gom 25) for maximum 1000-grain weight from cluster III, G_6 (Akbar) for shorter vegetative period from cluster II and G_{10} (BARI Gom 20) for shorter grain filling period from cluster V could be selected for future hybridization program.

SOME COMMONLY USED ABBREVIATIONS

Full word		**Abbreviation**
Academy	:	*Acad.*
Advanced	:	*Adv.*
Agricultural	:	*Agril.*
Agriculture	:	*Agric.*
Agro ecological zone	:	AEZ
Agronomy	:	*Agron.*
American	:	*Am.*
Analysis of variance	:	ANOVA
And others (at elli)	:	*et al.*
Annals	:	*Ann.*
Applied	:	*App.*
As follows	:	*viz.*
At the rate of	:	@
Bangladesh	:	*Bang.*
Bangladesh Agricultural Research Institute	:	BARI
Bangladesh Bureau of Statistics	:	BBS
Botany	:	*Bot.*
Breeding	:	*Breed.*
Bulletin	:	Bull.
Centimeter	:	cm
Coefficient of variation	:	CV
Communications	:	*Comm.*
Conference	:	*Conf.*
Congress	:	*Congr.*
Degree Celsius	:	^{o}C
Degree of freedom	:	df
Duncan's Multiple Range Test	:	DMRT
Ecology	:	*Ecol.*
Editor(s), Edition	:	ed.
Environmental coefficient of variation	:	ECV
Environmental variance	:	δ^{2}_{e}
Food and Agricultural Organization	:	FAO
General	:	*Gen.*
Genetic advance	:	GA
Genetics	:	*Genet.*
Genotypic coefficient of variation	:	GCV
Genotypic variance	:	δ^{2}_{g}
Gram	:	g
Gross domestic product	:	GDP

SOME COMMONLY USED ABBREVIATIONS (CONT'D)

Full word		Abbreviation
Hectare	:	ha
Heritability in broad sense	:	h^2_b
Hughes Integrated Surveillance and	:	*Hisar.*
Reconnaissance	:	pH
Hydrogen ion concentration		
International Maize and Wheat Improvement	:	CIMMYT
Centre		
Journal	:	*J.*
Least significant difference	:	LSD
Mean sum of square	:	MSS
Meter	:	m
Milliequivalent	:	meq
Molecular	:	*Mol*
Muriate of Potash	:	MP
Nature/Natural	:	*Nat.*
Number	:	No.
Percent	:	%
Phenotypic coefficient of variation	:	PCV
Phenotypic variance	:	δ^2_{ph}
Plant	:	*Pl.*
Principal component analysis	:	PCA
Proceedings	:	Proc.
Randomized Complete Block Design	:	RCBD
Research	:	*Res.*
Science/Scientific	:	*Sci.*
Sher-e-Bangla Agricultural University	:	SAU
Society	:	*Soc.*
Square meter	:	m^2
Standard deviation	:	SD
Standard Error	:	SE
Symposium	:	Symp.
Technical	:	Tech.
That is	:	*i.e.*
Theory	:	*Theor.*
Ton	:	*t*
Triple Super Phosphate	:	TSP
Tropical	:	Trop.
University	:	*Univ.*

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CHAPTER I

INTRODUCTION

World's largest cereal crop, wheat (*Triticum aestivum* L.) had been the staple food for 35% of the world's population and was grown on 17% of the cultivated area in the world (Kronstad, 1998). It was originally from the Fertile Crescent region *i.e.* Lebanon, Syria, Iraq, Northern Israel and Eastern Turkey but now cultivated worldwide. It was also described as 'King of Cereals' because of the acreage it occupies, yield it produces and the prominent position it holds in the international food grain trade.

The tribe (taxonomic rank, between genus and subfamily) 'Triticeae', from the family 'Poaceae' (formerly Gramineae), has contained a large number of genera *i.e.* *Triticum, Hordeum, Secale, Aegilops, Agropyron* and so on (Wikipedia). Among them, *Triticum* and *Aegilops* were involved in the evolution of cultivated hexaploid bread wheat (*Triticum aestivum* L.) possessing AABBDD genotype (Levy and Feldman, 2002). On the other hand, Triticale (man-made cereal), a synthetic amphidiploid obtained from durum wheat (4x) and rye (2x), has utilized the genus *Secale* as a parent in its development. This information has indicated that there was identical chromosome or part of chromosome in the genera of the tribe Triticeae (Ahn *et al.*, 1993). These genetically related chromosomes or part of chromosomes in different genomes were called partially homologus or homoeologous chromosomes. This information was highly significant in understanding of the natural phenomenon of genome evolution and speciation poly ploid wheat. Club wheat, Dinkel wheat and Bread wheat etc. were hexaploid (6x); Khorassan, Polish, Emmer and Durum wheat etc. were tetraploid (4x); Einkorn wheat was diploid (2x) in relation to ploidy level (Mohibullah *et al.*, 2011).

Wheat (*Triticum aestivum* L.) was regarded the second most important grain crop after rice in Bangladesh. The popularity behind this was due to its food value, industrial impact and high palatability. Roti (bread) was taken by every diabetic patient instead of rice due to its better response. Various delicious biscuits, baby foods, daily meals *viz.* atta, suji, flour, noodles, macaroni, muffin and breads etc. were made of it. It was observed that 20% calories and a large share of carbohydrates of daily human consumption were provided by wheat. Straw particle board used in kitchen cabinets, adhesives on postage stamps, medical swabs and paper industry had high usage of wheat apart from food grain. Besides, vegetative parts could be used as animal feed as well as green manure for recovery of soil health.

Wheat (*Triticum aestivum* L.) stood first globally in terms of acreage and third in terms of production (FAOSTAT, 2013). However, the average yield of wheat in Bangladesh was lower than other wheat growing countries around the world. The potential yield was 4.0 to 4.5 t/ha but 1.9 t/ha in farmers' field (BARI, 1989-90). BARI had released several high yielding varieties that made the total increase of production during 1970 to 2002. But thereafter production was decreased as the production area also fell (Hossain and Teixeira da Silva, 2013). The decrease in area was due to competition from other rabi-grown crops such as Boro rice, potato and maize (WRC, 2009). Moreover, there were tough challenges of neutralizing the importation of 3.1 million metric tons of wheat each year to mitigate the local demand. This situation indicated at the need for improving the technology involved in wheat production.

The main point in breeding of wheat was focused on improvement of genetic background with features that contribute to higher yield potential, more yield stability and improved product quality (Poehlman and Sleeper, 1995). The potential force of altering the genetic properties was laid in creation of variation. Various measure of genetical variability for different characters of a definite number of genotype in a population were estimated through analysis of variance (ANOVA), comparing the extent of variation (%CV) from mean performance, estimation of variance components, estimation of coefficient of variance components, heritability and genetic advance.

For improvement of the related complex character, determination of correlation coefficient between the yield and its component characters had a considerable importance in selecting breeding materials (Afroz *et al.*, 2004). On the other hand, path coefficient analysis was the partitioning of correlations into direct and indirect effects to give more specific information on the direct and indirect influence of each of the component characters upon yield. It was more likely a cause and effect relationship. It would also help in predicting the performance of selected plants in the next generation.

Information on genetic divergence has been crucial to a plant breeder for efficient choice of parents in hybridization program. In general, diverse parents were likely to contribute desirable segregants. More diversified the parents; greater would be the chances of obtaining high heterotic F_1s and broad spectrum variability in segregating generations (Murty and Arunachalam, 1966). Evaluation of diversity analysis has been significant to know the source of gene for a particular trait within the available germplasms (Tomooka, 1991). The importance of genetic diversity for the improvement of crop had been stressed in both self and cross-pollinated crops (Gaur *et al*., 1978; Murty and Arunachalam, 1966; Griffin and Lindstorm, 1954). Genetic diversity was estimated following Mahalanobis' D^2-statistics (Mahalanobis, 1936). The quantification of genetic diversity through biometrical procedure has made it possible to choose genetically diverse parents for a successful hybridization program (Anderson, 1957; Rao, 1952). The utility of multivariate analysis for measuring the degree of divergence and for assessing the relative contribution of different characters to the total divergence in self-pollinated crops has been established by several workers (Golakia and Makne, 1992; Sindhu *et al.,* 1989; Natarajan *et al.*, 1988; Das and Gupta, 1984).

Therefore, a good knowledge on genetic diversity may help in identifying desirable parents for future hybridization program for developing new varieties and to study the feasibility of utilizing all those information for the varietal improvement of wheat.

Current investigation was carried out convincingly with the following objectives:

1. To study the variability of genetic parameters for different traits in wheat genotypes.
2. To estimate the correlation and path coefficient for different yield contributing characters over grain yield among genotypes of wheat.
3. To screen out the suitable parental groups with better performance for selection in future breeding program.

CHAPTER II

REVIEW OF LITERATURE

Comprehensive studies on wheat breeding were performed in many countries for its improvement. In Bangladesh, a fair amount of research was also being carried out by various agricultural universities and research institutes. An effort has been made here to review the findings of the studies relevant to present investigation. The whole review has been sorted under following heads.

2.1. Performance of wheat varieties in Bangladesh

Sharma *et al.* (2007) performed a research along with 21 wheat genotypes selected from a regional wheat screening nursery in South Asia in six wheat growing seasons (2002-2005). There were four check cultivars (Kanchan, Sonalika, Bhrikuti and PBW 343). One or more of the experimental genotypes showed high and stable grain yield and acceptable maturity, plant height and disease resistance compared to the check cultivars. Identification of wheat genotypes with high-grain yield in individual sites highlighted their value for regional wheat breeding programs.

Joshi *et al.* (2007) studied 729 lines of diverse wheat germplasm collection in eight locations of three countries *i.e.* India, Nepal and Bangladesh for five years (1999-2000 to 2003-04) on agronomic performance and tolerance to spot blotch of wheat. Many lines yielded significantly more than the best check and possessed high levels of spot blotch resistance under warm humid environments of South Asia. The most promising 25 lines had been identified as source of strong resistance with 9 lines as better yielding than the best resistant check, PBW 343. The line EGPYT 67 and Kauz were the best for spot blotch resistance, grain yield, days to maturity and 1000-grain weight. The next 2 lines in the order of merit were EGPYT 84 and EGPYT 69.

Miah and Shamsuddin (2002) in their study evaluated source-sink and grain yield traits (dry weight of green leaf at 50% booting stage, dry weight of stem and leaf sheath at 50% booting stage, no. of tillers at 50 % booting stage, spike weight at final harvest, no. of grains per spike at final harvest, 1000-grain weight, vegetative period and grain filling period) in 16 bread wheat cultivars grown in Mymensingh, Bangladesh during winter season of 1992-93. They had observed that Akbar, BD-150 and Kanchan recorded the highest yield, spike weight, 1000-seed weight and no. of grains/spike and longest grain-filling period. Significant variation was observed among the cultivars for all traits except for one character *i.e.* dry weight of green leaf at 50% booting stage.

2.2. Variability, heritability and genetic advance

Genetic variability was a prerequisite for initiating a successful breeding program. Genetic parameters *viz.* variance components, coefficient of variance components, heritability and genetic advance were considered as measures for genetic variability.

There were three types of variance components *viz.* genotypic variance, phenotypic variance and environmental variance. If the variability in the varieties was largely due to genetic cause with least environmental effects, the probability of isolating superior genotypes would be high. How much of the phenotypic variability would transmit from parents to offspring could be measured by a parameter called heritability. Such gradual heritable change in genetic makeup of genotypes would lead to closer correspondence between phenotype and genotype. Closer the correspondence, greater would be the genetic advance. If the GA (genetic advance) value was high, selection would be rewarding for improvement of such trait. But if GA value was low, then heterosis breeding would be useful.

When the objective was to compare the variability of different characters in single population or between populations for the same character, estimation of the coefficient of variance components would be required. An overview about the magnitude of variability present in a genetic population was clarified by the relative value of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and environmental coefficient of variation (ECV). By definition, a variance component would always be positive, but negative estimate could arise due to inadequate sampling, inadequate statistical model, Sampling error or poor experimental design etc.

A good number of literatures concerning the variability for ten characters in wheat (*Triticum aestivum* L.) were presented here.

2.2.1. Plant height

Randhawa *et al.* (1975) observed wide range of variation for plant height in bread wheat. They reported high heritability associated with high genetic advance. It indicated that high GA for the character was achieved by both wider variation and high heritability. Saha and Faridi (1987) observed little environmental effect on plant height in bread wheat in a study of genetic variability and correlation. Pathak and Nema (1985) reported medium genotypic and phenotypic coefficient of variation in bread wheat. They also observed high estimates of heritability for this trait. Maloo (1984) reported moderate genotypic coefficient of variation for this trait. High heritability value was also noticed which indicated at high transmission index for plant height in bread wheat. Singh *et al.* (1978) observed the lowest coefficient of variation at both genotypic and phenotypic level for plant height in bread wheat. They discussed their results and suggested that it might be due to inter-selection pressure towards the selection of dwarf plant types. Johnson *et al.* (1955) also suggested that estimation of heritability along with genetic advance were more useful for effective improvement.

2.2.2. Spikes/plant

Mahmood and Shahid (1993) reported high heritability with high genetic advance for spikes/plant. It indicated that genetic effect was more pronounced for this character. This character could be fixed by resorting simple selection. Singh and Tewari (1990) observed low genotypic coefficient of variation and high phenotypic coefficient of variation in Triticale. They also reported low heritability and low genetic advance for this trait. They opined that poor estimates of heritability and genetic advance were due to influence of environment on this trait.

Pawar *et al.* (1988) observed higher genotypic and phenotypic coefficients of variation for this character. They also reported high heritability coupled with high genetic advance. High value of both heritability and genetic advance for spikes/plant indicated that the character was mostly controlled by additive gene effects and could be improved by simple selection. Maloo (1984) observed high genotypic coefficient of variation for spikes/plants in wheat. He reported high heritability accompanied by high genetic advance also. Tripathi *et al.* (1973) reported moderate genotypic coefficient of variation in bread wheat. Low heritability and low genetic advance for this trait were also observed. The low genetic advance in this case could be explained as the results of low heritability and moderate genotypic coefficient of variation.

2.2.3. Spike length

Both Biju and Malik (2007) and Bhutta *et al.* (2005) observed significant variation for spike length in common wheat. They also observed moderately high genotypic and phenotypic coefficients of variation. They also noticed high heritability with moderate genetic advance for spike length in common wheat. It suggested that additive gene was controlling this trait and it was heritable in nature.

2.2.4. Grains/spike

Joshi *et al.* (1982) conducted an experiment with 30 elite and diverse varieties (including landraces) of common wheat from south western Iran. In that study, they noticed a wide range of variation for grains/spike. They also reported high genotypic and phenotypic coefficients of variation. Ehdaie and Waines (1989) reported higher genotypic and phenotypic coefficients of variation for grains/spike in bread wheat. They also observed high heritability with moderate genetic advance for this trait in bread wheat also. Maloo (1984) observed high genotypic coefficient of variation in bread wheat. High heritability accompanied with high genetic advance was also observed for this trait. On the contrary, Singh *et al.* (1978) reported low genotypic and phenotypic coefficient of variation. Low heritability and low genetic advance was also observed. They opined that it was influenced by environment under which the genotypes were grown.

2.2.5. Thousand grain weight

Nessa *et al.* (1994) reported high genotypic and phenotypic coefficients of variation for thousand grain weight in bread wheat. They estimated high genotypic advance accompanied by high heritability suggesting effects of additive gene for this character. Amin *et al.* (1992) reported low genotypic and phenotypic coefficients of variation for this trait. High heritability with low genetic advance was also observed. It was interesting to observe that some of the characters in spite of having high heritability estimate did not reveal equally high genetic advance which is cheaply due to the additive gene effect but if the heritability is mainly due to dominance and epistasis, the genetic advance would be low. Singh and Tewari (1990) observed low genotypic and phenotypic coefficients of variation. They also reported low heritability with low genetic advance. They suggested that the trait was influenced by environment under which the genotypes were grown. Pawar *et al.* (1988) observed moderate genotypic and phenotypic coefficients of variation for thousand grain weight. They also reported high heritability with high genetic advance for this trait. Trehan *et al.* (1970) estimated high heritability value in broad sense and high value of genetic advance which indicated at the scope for further improvement of this character by selection.

2.2.6. Harvest index

Progress in breeding higher yielding cultivars has been associated with an increase in harvest index in small grains such as wheat (Austin *et al.*, 1980); oats (Wych and Stuthan, 1983); rice (Vergara and Visperas, 1977) and barley (Wych and Stuthan, 1983). Harvest index had been measured the partitioning of photosynthates to economic yield and was considered as one of the most important physiological yield component (Donald and Hamblin, 1976). In most of the cases, the increase in harvest index had been considered to be an indirect result of breeding for higher grain yield, shorter straw and earliness. We were aware of very few small breeding programs that had routinely selected for harvest index to improve grain yield (Vergara and Visperas, 1977). To increase the probability of selecting genotypes with high grain yielding capacity, Donald and Hamblin (1976) suggested the use of harvest index and biomass as early generation selection criteria in addition to grain yield. Several studies have indicated that harvest index would be effective selection criteria for increasing grain yield in segregating generations of oats and spring wheat (Bhatt, 1977; Fischer and Kertesz, 1976; Rosielle and Frey, 1975; Nass, 1973 and Syme, 1972). It indicated that increasing grain yield via indirect selection for higher harvest index in F_2 generation of spring wheat was better than direct selection for grain yield.

Amin *et al.* (1992) reported wide range of variation for harvest index. They observed high genotypic and phenotypic coefficients of variation for this trait in bread wheat. High heritability accompanied by high genetic advance was also observed for harvest index. Ehdaie and Waines (1989) observed low genotypic and phenotypic coefficients of variation. High heritability associated with low genetic advance was also observed.

The poor genetic advance as they observed was due to low coefficient of variation. Singh *et al.* (1980) observed moderately high genotypic and phenotypic coefficients of variation. They also reported low heritability with low genetic advance. It might be due to influence of environment upon the expression of the character.

2.2.7. Vegetative period

Nessa *et al.* (1994) observed moderate genotypic and phenotypic coefficients of variation for this character. There was very little difference between genotypic and phenotypic coefficients of variation which suggested that environmental influence on this trait was very small. They also reported high heritability with high genetic advance for this trait. Sharma and Kaul (1986) reported low genotypic and phenotypic coefficients of variation. High heritability accompanied by low genetic advance was also observed. They explained such genetic advance as they noticed as the cause of presence of dominance and epistasis in the population. Similar results were observed by Amin *et al.* (1992), Pawar *et al.* (1988) and Singh *et al.* (1978). Tripathi *et al.* (1973) reported wide range of variation and high genotypic coefficients of variation for vegetative period in wheat. They also observed high heritability with moderate genetic advance for this character.

2.2.8. Grain filling period

Plant breeders and physiologists were interested in the possibility of identifying an optimum grain filling period for improving grain yield (Debra *et al.*, 1984). Several studies have dealt with the relationship between grain filling duration and grain yield in various crop species. There was considerable evidence suggesting that grain filling period had been important in determining yield in corn (*Zea mays*). Yagbasanlar (1987) reported that the length of the grain filling period was one of the important factors to increase the yield in wheat and critical factor under Mediterranean climatic condition. But Nass and Reiser (1975) and Metzger *et al.* (1984) reported that the length of grain filling period was not an important factor in determining yield in wheat and barley.

Miah (1997) reported low genotypic and phenotypic coefficients of variation or grain filling period in bread wheat. High heritability but low genetic advance was also observed for this trait. Yagbasanlar *et al.* (1995) reported that coefficient of variation for grain filling period was lower than other traits. Amin *et al.* (1992) observed low genotypic and phenotypic coefficients of variation for grain filling period in bread wheat. They also reported low heritability and low genetic advance. However, Samarria *et al.* (1987) suggested that grain filling period could be increased by selection.

2.2.9. Days to maturity

Variation, heritability and genetic advance for days to maturity were usually studied for developing early maturing varieties. Nessa *et al.* (1994) reported low genotypic and phenotypic coefficients of variation for days to maturity in wheat. The difference between them was very small indicating at less influence of environment on this trait. They observed high heritability and moderate genetic advance for this trait. Sharma and Kaul (1986) carried out an experiment with wheat and observed high genotypic and phenotypic coefficients of variation for this trait. High heritability and moderate genetic advance for this character was also reported. Tripathi *et al.* (1973) conducted an experiment with 16 varieties of wheat and reported moderate genotypic and phenotypic coefficients of variation. But they also observed low genotypic and phenotypic coefficient of variation along with high heritability with moderate genetic advance for this character.

2.2.10. Grain yield/plant

Inheritance of grain yield in bread wheat is a complex one. Grain yield in cereals is determined by some yield components. Grafious (1964) suggested that these yield components had expressed their genetic and environmental effects through grain yield.

Nessa *et al.* (1994) reported high genotypic and phenotypic coefficients of variation for grain yield/plant. High heritability and high genetic advance for grain yield/plant in bread wheat was also noticed. Sharma and Kaul (1986) reported high genotypic and phenotypic coefficients of variation with high heritability and high genetic advance. Pathak and Nema (1985) also observed high genotypic and phenotypic coefficients of variation with high heritability and high genetic advance for grain yield in bread wheat. Tripathi *et al.* (1973) observed high genotypic and phenotypic coefficients of variation in bread wheat for grain yield/plant. High heritability and moderate genetic advance was also noticed for this trait. High genetic advance for grain yield as observed in these studies was probably the root cause of high coefficient of variation and high heritability for grain yield in wheat.

2.3. Correlations between yield and yield component traits

The genetic improvement in dependant trait could be achieved by applying strong selection to a character which is genetically correlated with the dependant character. Correlation coefficient had been a statistical measure of degree (strength) and direction for the relationship between two or more variables. The value was ranged from ‘-1’ to ‘+1’. A positive value has been described as changes of two variables towards ‘same direction’ and negative value as ‘opposite direction’. If correlation coefficient was zero (0), it meant there was no correlation. There were four types of correlation coefficient *viz.* Simple linear correlation, multiple correlation, partial correlation and spurious correlation. A positive correlation had been favorable to the plant breeder because of its simultaneous help in improvement of both the characters. In Cereal crops, the yield components had been identified as number of spikes/plant, number of grains/spike and average grain weight (Engledow and Wadham, 1923).

Singh *et al.* (1978) estimated genotypic and phenotypic correlation in forty genotypes of bread wheat. They observed that grain yield/plant had highly significant and positive correlation with grains/spike, 1000-grain weight, vegetative period, spikes/plant and plant height. They also noticed that the genotypic correlation coefficient were higher than their corresponding phenotypic ones for most of the characters in general.

Miah (1997) observed non-significant negative correlation for vegetative period and spikes/m^2 associated with yield and test weight in soft red winter wheat whereas non-significant positive correlation for grains/spike, 1000-grain weight and grain filling period. Yagbasanlar *et al.* (1995) observed positively significant correlation for plant height, days to maturity, grain filling period and harvest index associated with grain yield/plant. Nessa *et al.* (1994) reported positively significant correlation for grain yield/plant associated with plant height, spikes/plant and vegetative period but non-significant negative correlation with days to maturity and 1000-grain weight in wheat. Dawari and Luthra (1991) reported highly significant and positive correlation for harvest index, spikes/plant and 1000-grain weight associated with grain yield/plant in bread wheat. Ehdaie and Waines (1989) observed non-significant negative correlation for vegetative period, spikes/plant and plant height associated with grain yield/plant whereas positively significant correlation for days to maturity and 1000-grain weight in wheat. Shamsuddin and Ali (1989) reported significantly positive correlation for plant height, spikes/plant, grains/spike, 1000-grain weight and days to maturity along with grain yield/plant but non-significant negative correlation for vegetative period.

Srivastave *et al.* (1985-86) observed non-significant positive correlation for grain yield/plant with 1000-grain weight but non-significant negative correlation with grain filling period, plant height, vegetative period and days to maturity. Rahman *et al.* (1983) in simple correlation studies reported significant and positive correlation of grain yield/plant associated with tillers/plant and kernels/spike but negative correlation with plant height and 1000-grain weight. Jaimini *et al.* (1974) estimated correlation and path coefficient analysis in bread wheat and observed that grain yield/plant was significant and positively correlated with spikes/plant, spikelets/spike and 1000-grain weight but non-significant and negatively correlated with vegetative period.

2.4. Direct and Indirect effects of correlated traits

The inability of correlation coefficient analysis to define a complete picture for the causal basis relationship of the study had lead path coefficient analysis to partition the components of correlation into direct and indirect effects.

In statistics, there were three types of regression coefficient *i.e.* Simple, Partial and Multiple regression coefficients. A path coefficient was simply a standardized partial regression coefficient that measures the direct and indirect influence of one variable upon another and permits separation of correlation coefficients into components of direct and indirect effects. Path coefficient had no physical unit but direction. It could be either positive or negative. Its value could be greater or less than unity.

Several scientists had observed positive direct effect on grain yield/plant via yield component characters in bread wheat. Das (1972) studied path analysis and reported that the highest direct effect was obtained for number of spikes/plant on grain yield. Shamsuddin (1987) studied path analysis and observed that spikes/plant, grains/spike and 1000-grain weight had direct effects on yield/plant. Shamsuddin and Ali (1989) studied genotypic and phenotypic correlation and path analysis in spring wheat and reported that grains/spike displayed considerable amount of direct effects on grain yield followed by spike length and 1000-grain weight. Paroda and Joshi (1970) observed that grains/spike and 1000-grain weight had positive direct effects on yield. Das and Mondal (1984) observed that number of grains/spike had a moderate direct effect on grain yield. They identified that number of grains/spike was one of the major component of yield in bread wheat. Shelembi and Wright (1991) reported that number of grains/spike had direct and strong effect on grain yield.

Many researchers had also observed negative direct effect on grain yield/plant via plant height (Barma *et al.*, 1991), vegetative period (Rahman *et al.*, 1983) and grain filling period (Razzaque *et al.*, 1981) in bread wheat.

Bhular *et al.* (1985) suggested from path analysis that 1000-grain weight was one of the most important yield components in durum wheat. Amin *et al.* (1990) observed that 1000-grain weight contributed maximum positive and direct effect to grain yield. Khan *et al.* (1994) found that 1000-grain weight exhibited positive association and high direct effect on grain yield and suggested hybridization program should include genotypes with greater number of grains/spike, high grain weight and high grain yield to obtain further improvement grain yield in bread wheat.

2.5. Genetic divergence of bread wheat genotypes

Study of genetic divergence was essential to meet the diversified goals of plant breeding such as breeding cultivars for increasing yield, wider adaption, desirable quality, pest and disease resistance (Joshi and Dhawan, 1966). In addition, genetic divergence was studied to identify specific parents for heterosis and recombination in breeding programs (Aditya, 1995).

Literatures concerning genetic divergence were presented here.

2.5.1 Multivariate techniques

Genetic diversity analysis involved several steps *i.e.* estimation of distance between the varieties, clustering and analysis of inter-cluster distance. Therefore, more than one multivariate technique was required to represent the results more clearly and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001; Juned *et at.*, 1988 and Ario, 1987).

Several statistical methods were usually used for discriminating among the genotypes *viz.* Mahalanobis' generalized distance (Mahalanobis, 1936), the algorithm method of Williams and Lambert (1960), Cooper's statistical classification with quadratic forms (Cooper, 1963) and Principal component analysis. The principal component analysis (PCA) resulted in the reduction of enormous variables to three independent linear combination principal component variables.

Balasch *et al.* (1984) reported that in classifying a number of tomato varieties/lines, different multivariate techniques were used and Principal Component Analysis (PCA), as a simple multivariate technique, was compared with factorial analysis and Mahalanobis' D^2 distance. It was marked that three methods gave similar results. But factorial discriminate and Mahalanobis' D^2 distance methods required collecting data plant by plant, while the PCA method required taking data by plots.

Principal Component Analysis was performed in soybean (Chowdhury, 1994) and in pea (Mian *et al.*, 1991) in order to assess genetic diversity among the germplasms of these crops.

Joshi and Kohli (2003) assessed the nature and magnitude of genetic divergence using non-hierarchical Euclidean cluster analysis in 73 tomatoes for different quantitative and qualitative traits.

Canonical Variate Analysis was performed to compute the inter-cluster Mahalanobis' values. Statistical distances represented the index of genetic diversity among the clusters.

2.5.2 Existence of genetic divergence in wheat

Chaturvedi and Gupta (1995) studied 12 yield components in 44 genotypes of wheat for genetic divergence was clustered in 13 diverse groups. Redhu *et al.* (1995) grouped 121 genotypes of wheat into 27 clusters. Sinha and Sharma (1979) conducted an experiment using five clusters of 35 genetic stocks for common wheat by means of

Mahalanobis' D^2-statistics. Srivastave *et al.* (1985-86) also studied genetic divergence for 40 and 30 wheat varieties (selected) from two separate screening nurseries could be grouped into 7 and 10 clusters, respectively.

Islam *et al.* (1995) observed that inter cluster distances were higher than the intra cluster distances which indicated broader genetic diversity among the genotypes of different groups in a multivariate analysis.

Jagadev *et al*. (1991) reported that the character contributing maximum to the divergence were given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization.

Yadav and Murty (1981) showed the maximum range of cluster mean for plant height. They also reported most divergence at both intra and inter cluster levels contributed by calm length and 100 grain weight in wheat.

CHAPTER III

MATERIALS AND METHODS

The study was carried out convincingly with twenty genotypes of wheat (*Triticum aestivum* L.) at experimental field of Sher-e-Bangla Agricultural University. Materials used and methodology followed for conducting the research along with data recording and analyzing procedure were described briefly as follows.

3.1. Experimental site

The research was conducted at the experimental field (Plot-43) of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh. Satellite view of the experimental site was shown in Plate 1, followed by an overview of the research plot in Plate 2.

3.2. Geographical location

Geographical location of the experimental site was described as 23° 74' N latitude and 90° 35' E longitude at an altitude of 8.6 meter above the sea level belonging to AEZ-28 (Modhupur Tract). The experimental site was shown in the AEZ map of Bangladesh (Appendix I).

3.3. Planting materials

Twenty genotypes of wheat (*Triticum aestivum* L.) were used for the present research work. The purity and germination percentage were leveled around 100% and 80%, respectively. The genetically pure and physically healthy seeds of these genotypes were collected from Wheat Research Centre (WRC) of Bangladesh Agricultural Research Institute (BARI), Gazipur. The name and origin of these genotypes were presented in Table 1.

3.4. Climate and Soil

Experimental site belonged to the subtropical climate with scanty rainfall associated with low to moderately low temperature. The records of air temperature, humidity and

Plate 1. Satellite view of the experimental site marked with red quadrilateral

Plate 2. An overview of the research plot

Table 1. List of twenty wheat genotypes along with their sources

Entry no.	Indicating Symbol of Genotype	Germplasm	Source
1	G_1	Kanchan	BARI
2	G_2	Protiva	BARI
3	G_3	Kallyansona	BARI
4	G_4	Sonalika	BARI
5	G_5	Durum	BARI
6	G_6	Akbar	BARI
7	G_7	Sourov	BARI
8	G_8	Gourob	BARI
9	G_9	Aghrani	BARI
10	G_{10}	BARI Gom 20	BARI
11	G_{11}	BARI Gom 21	BARI
12	G_{12}	BARI Gom 22	BARI
13	G_{13}	BARI Gom 23	BARI
14	G_{14}	BARI Gom 24	BARI
15	G_{15}	BARI Gom 25	BARI
16	G_{16}	BARI Gom 26	BARI
17	G_{17}	BARI Gom 27	BARI
18	G_{18}	BARI Gom 28	BARI
19	G_{19}	BARI Gom 29	BARI
20	G_{20}	BARI Gom 30	BARI

rainfall during the period of experiment were noted from the Bangladesh Meteorological Department, Agargaon, Dhaka (Appendix II). Soil of the experimental site belonged to shallow red brown terrace soils under Tejgaon series. Top soils were silty-clay in texture. Soil pH ranged from 5.47 to 5.63, organic matter was 0.82%. Experimental area was flat having available irrigation and drainage system. Physicochemical properties of the soil were presented in (Appendix III).

3.5. Design and layout of the experiment

A piece of land measuring 180 m^2 (25 m X 12 m) was given by SAU farm authority. The experiment was followed Randomized Complete Block Design (RCBD) with three replications. The twenty genotypes of the experiment were line sown at random into each replication. Border and Bed distance was maintained by 50 cm. The layout of the experiment was shown in Figure 1.

3.6. Methods

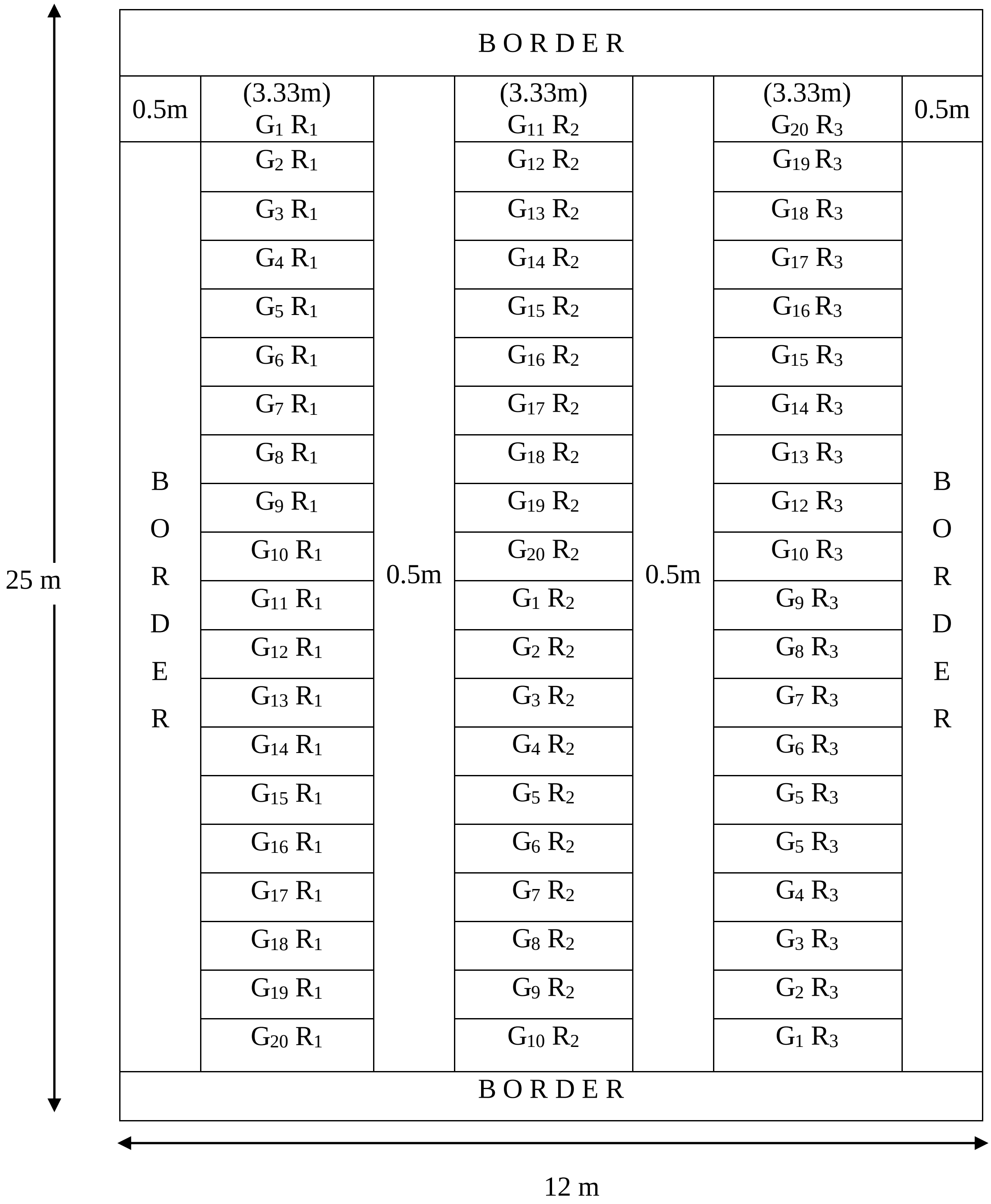
The experiment was conducted during November, 2015 to February, 2016. Production technology for wheat cultivation included land preparation, seed sowing, manuring and fertilization as recommended, irrigation, harvesting, threshing and drying. A brief depiction of them was given below.

3.6.1. Land preparation and fertilization

The land was prepared by ploughing with power tiller (Plate 3) followed by harrowing and laddering. All the stubbles and weeds were removed from the field. In the following day Cowdung was applied 126 kg. According to recommended fertilizer doses TSP, MP and Gypsum was applied 3 kg, ½ kg and 1 kg respectively. 1 kg Urea was also applied during final land preparation and rest 2 kg was split applied at tillering and panicle initiation stage.

3.6.2. Sowing of seeds

200 g seeds of each genotype comprising 4.0 kg of total seeds were line sown at 4-5 cm depth of soil. Row to row distance is 20 cm and distance between each variety is 25 cm. The sowing of seeds was carried out nicely in presence of my supervisor (Plate 4).



BORDER						
0.5m	(3.33m) G_1 R_1	0.5m	(3.33m) G_{11} R_2	0.5m	(3.33m) G_{20} R_3	0.5m
BORDER	G_2 R_1		G_{12} R_2		G_{19} R_3	BORDER
	G_3 R_1		G_{13} R_2		G_{18} R_3	
	G_4 R_1		G_{14} R_2		G_{17} R_3	
	G_5 R_1		G_{15} R_2		G_{16} R_3	
	G_6 R_1		G_{16} R_2		G_{15} R_3	
	G_7 R_1		G_{17} R_2		G_{14} R_3	
	G_8 R_1		G_{18} R_2		G_{13} R_3	
	G_9 R_1		G_{19} R_2		G_{12} R_3	
	G_{10} R_1		G_{20} R_2		G_{10} R_3	
	G_{11} R_1		G_1 R_2		G_9 R_3	
	G_{12} R_1		G_2 R_2		G_8 R_3	
	G_{13} R_1		G_3 R_2		G_7 R_3	
	G_{14} R_1		G_4 R_2		G_6 R_3	
	G_{15} R_1		G_5 R_2		G_5 R_3	
	G_{16} R_1		G_6 R_2		G_5 R_3	
	G_{17} R_1		G_7 R_2		G_4 R_3	
	G_{18} R_1		G_8 R_2		G_3 R_3	
	G_{19} R_1		G_9 R_2		G_2 R_3	
	G_{20} R_1		G_{10} R_2		G_1 R_3	
BORDER						

G = Genotype, R = Replication

Figure 1. Layout of the experimental field

Plate 3. Land preparation using power tiller

Plate 4. Sowing seeds of twenty wheat genotypes

3.6.3. Drainage and Irrigation

Drainage was made for suitable irrigation channel. At crown initiation stage, irrigation was a must. Otherwise, yield would be drastically low. So, after 18 days, 1st irrigation was given. 2nd irrigation was given after 58 days at panicle initiation stage and 3rd irrigation was given after 75 days at grain filling period (Plate 5 and Plate 6).

3.6.4. Thinning and Weeding

Weak and densely grown plants were discarded. Various weeds like bathua, nunia, bonno masur etc. was weeded out through raker and nirani (Plate 7).

3.6.5. Harvesting

Owing to individual life cycle, maturity period of each genotype would also be individual. Some were early ripening and some were late. Maturity of grain was investigated along with my supervisor for harvesting (Plate 8 and Plate 9).

3.6.6. Threshing and Drying

Threshing and drying was done carefully. Grains were solar dried (Plate 10) for 4 to 5 consecutive days and packed for submission to germplasm centre of Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka.

3.6.7. Plant Protection

75 g of Autostin fungicide was sprayed with 40 L water due to fungal attack. The attack was not severe and was mitigated efficiently.

3.6.8. Data Collection

Data on ten characters were collected from the ten plants which were randomly selected from the central row. These ten plants were harvested by uprooting.

Plant height (cm): Height of the main culm from the base to the top of the panicle excluding awn was measured in cm as plant height.

Spikes/plant (no.): Number of spikes was counted from each of the sample plants and was averaged over per plant.

Plate 5. Drainage making

Plate 6. Providing irrigation

Plate 7. Thinning and Weeding

Plate 8. Data collection of wheat genotype

Plate 9. Investigating maturity of grains for harvesting

Plate 10. Solar drying of wheat grain along with protective measure

Spike length (cm): Spike length was counted from each of the sample plants and was averaged over per plant.

Grains/spike (no.): Grains from ten main spikes of the sample plants were counted and were averaged.

1000-grain weight (g): One thousand clean sun dried grains were randomly counted from each plot and weighed in gram.

Harvest Index (%): The ratio of grain yield to the biological yield as per plot basis was measured through,

$$\text{Harvest index, HI (\%)} = \frac{Grain\ yield}{Biological\ yield} \times 100$$

Vegetative period (days): Days required from germination to 50% flowering were counted as vegetative period.

Grain filling period (days): Days required from 50% flowering to 50% physiological maturity were counted as grain filling period.

Days to maturity (days): Days required from 50% physiological maturity to 100 % physiological maturity were counted as days to maturity.

Grain yield/plant (g): Weight of the total grains of individual plant in gram was taken as grain yield/plant. It was economically the most important character.

Data collection were being started through uprooting plants (Plate 11) and ended at estimation of grain weight. Estimation of grain weight were done at laboratory of genetics and plant breeding in the central laboratory (Plate 12).

3.7. Data Analysis

Ten characters selected for study in wheat were quantitative characters. Variation for these traits was continuous and could not be grouped into discrete class. Univariate analysis of the individual character for genotypes was done for all the characters under study using the mean values (Singh and Chaudhary, 1985) and was estimated using MSTAT-C computer program.

Plate 11. Uprooting plants for data collection

Plate 12. Data collection in Laboratory of Genetics and Plant Breeding

Duncan’s Multiple Range Test (DMRT) was performed for all the characters to test the differences between the means of the genotypes. Mean, range and co-efficient of variation (CV %) were also estimated using MSTAT-C. Multivariate analysis was done using GENSTAT and Microsoft Excel through Principal Component Analysis (PCA), Cluster Analysis (CA) and Canonical Variate Analysis (CVA).

3.7.1. Measures of genetic variability

According to formula given by Johnson *et al.* (1955).

Genotypic Variance (σ_g^2),

$$\sigma_g^2 = \frac{GMS-EMS}{r}$$

Where,

GMS = Genotypic mean sum of square
EMS = Error mean sum of square
r = No. of replication

Phenotypic Variance (σ_{ph}^2),

$$\sigma_{ph}^2 = \sigma_g^2 + \text{EMS}$$

Where,

σ_g^2 = Genotypic Variance
EMS = Error mean sum of square

Environmental Variance (σ_e^2),

$$\sigma_e^2 = \sigma_{ph}^2 - \sigma_g^2 - \sigma_{ge}^2$$

Where,

σ_e^2 = Environmental Variance
σ_{ph}^2 = Phenotypic variance
σ_g^2 = Genotypic Variance
σ_{ge}^2 = Interaction between genotype and environment

Genotypic Coefficient of Variation,

$$\text{GCV} = \frac{\sqrt{\sigma_g^2}}{\overline{x}} \times 100$$

Where,

σ_g^2 = Genotypic Variance
$\overline{x}$ = Population mean

Phenotypic Coefficient of Variation,

$$\text{PCV} = \frac{\sqrt{\sigma_{ph}^2}}{\overline{x}} \times 100$$

Where,

σ_{ph}^2 = Phenotypic variance
$\overline{x}$ = Population mean

Environmental Coefficient of Variation,

$$\text{ECV} = \frac{\sqrt{\sigma_e^2}}{\overline{x}} \times 100$$

Where,

σ_e^2 = Environmental Variance

$\overline{x}$ = Population mean

Heritability in broad sense,

$$h_b^2 = \frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$$

Where,

σ_g^2 = Genotypic Variance

σ_{ph}^2 = Phenotypic variance

Genetic advance,

$$\text{GA} = h_b^2 \cdot \text{K} \cdot \sigma_{ph}$$

Where,

h_b^2 = heritability in broad sense

K = Selection differential, value is 2.06 at 5% selection intensity

σ_{ph} = Phenotypic standard deviation

Genetic advance in percent of mean,

$$\text{GA (\%)} = \frac{GA}{\overline{x}} \times 100$$

Where,

GA = Genetic advance

$\overline{x}$ = Population mean

3.7.2. Estimation of correlation coefficients

According to formula given by Miller *et al.* (1958) and Johnson *et al.* (1955).

Genotypic correlation,

$$r_{g_{1.2}} = \frac{Cov.g_{1.2}}{\sqrt{\sigma_{g_1}^2 \times \sigma_{g_2}^2}}$$

Where,

$Cov.g_{1.2}$ = genotypic covariance between the trait x_1 and trait x_2

$\sigma_{g_1}^2$ = genotypic variance of the trait x_1

$\sigma_{g_2}^2$ = genotypic variance of the trait x_2

Phenotypic correlation,

$$r_{ph_{1.2}} = \frac{Cov.ph_{1.2}}{\sqrt{\sigma_{ph_1}^2 \times \sigma_{ph_2}^2}}$$

Where,

$Cov.ph_{1.2}$ = Phenotypic covariance between the trait x_1 and trait x_2

$\sigma_{ph_1}^2$ = Phenotypic variance of the trait x_1

$\sigma_{ph_2}^2$ = Phenotypic variance of the trait x_2

3.7.3. Estimation of path coefficients

According to formula of Dewey and Lu (1959) quoted in Singh and Chaudhary (1985).

Assuming eight independent variable = x_1, x_2……..and x_8 (yield components)
One dependant variable = x_9 (grain yield/plant)

The relationship between them can be represented as follows.

$P_{19} + r_{12}P_{29} + r_{13}P_{39} + r_{14}P_{49} + r_{15}P_{59} + r_{16}P_{69} + r_{17}P_{79} + r_{18}P_{89} = r_{19}$

$r_{12} P_{19} + P_{29} + r_{23}P_{39} + r_{24}P_{49} + r_{25}P_{59} + r_{26}P_{69} + r_{27}P_{79} + r_{28}P_{89} = r_{29}$

$r_{13} P_{19} + r_{23}P_{29} + P_{39} + r_{34}P_{49} + r_{35}P_{59} + r_{36}P_{69} + r_{37}P_{79} + r_{38}P_{89} = r_{39}$

$r_{14} P_{19} + r_{24}P_{29} + r_{43}P_{39} + P_{49} + r_{45}P_{59} + r_{46}P_{69} + r_{47}P_{79} + r_{48}P_{89} = r_{49}$

$r_{15} P_{19} + r_{25}P_{29} + r_{53}P_{39} + r_{54}P_{49} + P_{59} + r_{56}P_{69} + r_{57}P_{79} + r_{58}P_{89} = r_{59}$

$r_{16} P_{19} + r_{26}P_{29} + r_{63}P_{39} + r_{64}P_{49} + r_{65}P_{59} + P_{69} + r_{67}P_{79} + r_{68}P_{89} = r_{69}$

$r_{17} P_{19} + r_{27}P_{29} + r_{73}P_{39} + r_{74}P_{49} + r_{75}P_{59} + r_{76}P_{69} + P_{79} + r_{78}P_{89} = r_{79}$

$r_{18} P_{19} + r_{28}P_{29} + r_{83}P_{39} + r_{84}P_{49} + r_{85}P_{59} + r_{86}P_{69} + r_{87}P_{79} + P_{89} = r_{89}$

Where,

P_{19}, P_{29}…..P_{89} = Path coefficient of the variables x_1, x_2……x_8 on variable x_9, respectively.

r_{19}, r_{29}……..r_{89} = correlation coefficient of the variables x_1, x_2……x_8 on variable x_9, respectively.

The residual effect was estimated as follows:

Residual effect, R = $\sqrt{1 - (r_{19}P_{19} + r_{29}P_{29} + \cdots\cdots\cdots\cdots\cdots + r_{89}P_{89})}$

3.7.4. Multivariate analysis

Genetic divergence among genotypes was assessed by different multivariate analysis. Rao (1952) suggested that the quantification of genetic diversity through biometrical procedure had made it possible to choose genetically diverse parents for hybridization program.

3.7.4.1. Principal Component Analysis (PCA)

PCA could be computed by Correlation matrix and genotype scores obtained from the first components (accounted for maximum variance) and succeeding components with latent roots greater than unity. Linear combination of a set of variate could be found from it. It was being used to investigate the interrelationships among several characters with yield and could be done from the sum of squares and product matrix for the character. Contribution of different morphological characters towards divergence was discussed from the latent vectors of the first two principal components.

3.7.4.2. Cluster Analysis (CA)

Cluster analysis was used to divide the genotypes of a data set into some number of mutually exclusive groups. Clustering was done using non-hierarchical classification. In GENSTAT, the algorithm was used to search for optimal values of chosen criterion proceeds as follows. Starting from some initial classification of the genotypes into required number of groups, the algorithm repeatedly transferred genotypes from one group to another so long as such transfer improved the value of the criterion. When no further transfer could be found to improve the criterion, the algorithm had switched to a second stage, which examined the effect of swooping on two genotypes of different classes and so on.

3.7.4.3. Canonical Vector Analysis (CVA)

Canonical vector analysis (CVA) was used to find linear combination of original variabilities that maximize the ratio of ‘between group’ to ‘within group’ variation, thereby giving functions of the original variables that could be used to discriminate between the groups. Thus, in this analysis a series of orthogonal transformations sequentially maximizing of the ratio of ‘among groups’ to ‘the within group’ variations. The canonical vector are based upon the roots and vectors of ‘WB’, where ‘W’ is the pooled within groups covariance matrix and ‘B’ is the among groups covariance matrix.

3.7.4.4. Calculation of D^2 values

The Mahalanobls's distance (D^2) values were calculated from transformed uncorrelated means of characters according to Rao (1952) and Singh and Chaudhary (1985).

$$\mathbf{D^2} = \sum_{1}^{x} \left(Y_i^j - Y_j^k\right)^2 \quad (j \neq k)$$

Where,
Y = Uncorrelated variable (i=1,2….to x)
x = No. of characters

3.7.4.5. Computation of cluster distances

Intra cluster distance = $\frac{\sum D_i^2}{n}$

Where,
$\sum D_i^2$ = Sum of distances between all possible combinations (n) of genotypes included in a cluster
n = All possible combinations

and

Inter cluster distance = $\frac{\sum D_{ij}^2}{n_i \times n_j}$

Where,
$\sum D_{ij}^2$ = Sum of distances between all possible combinations (n) of the populations in cluster i and j
n_i = No. of population in cluster i
n_j = No. of population in cluster j

3.8. Selection of genotypes for future breeding purpose

According to Singh and Chaudhary (1985), following points should be considered while selecting genotypes for hybridization program.

- Choice of cluster from which genotype(s) would be selected for use as parent(s)
- Selection of particular genotype(s) from the selected cluster(s)
- Relative contribution of the characters to the total divergence
- Other important traits from the genotype performance

CHAPTER IV

RESULTS AND DISCUSSION

The experiment was conducted to investigate the variation, correlation, path coefficient and genetic divergence for ten characters of twenty wheat (*Triticum aestivum* L.) genotypes. The data pertaining to ten characters were statistically analyzed with possible interpretations and diagrams. They were discussed under following headings.

4.1. Genetic variability

The range, mean, mean sum of square, variance components, coefficient of variance components, heritability and genetic advance (% mean) were considered as measurement for analyzing genetic variability. Analysis of variance (ANOVA) for ten characters of twenty wheat (*Triticum aestivum* L.) genotypes was presented in Appendix IV and Mean performance for those characters with least significant difference (LSD) and CV percentage was presented in Appendix V.

4.1.1. Performance and variation

Analysis of variance showed that there was significant variation for spikes/plant (0.754*) and strongly significant variation for nine characters *viz.* harvest index (245.228**), plant height (224.417**), grains/spike (119.104**), 1000-grain weight (109.350**), days to maturity (14.206**), spike length (7.523**), vegetative period (6.628**), grain filling period (6.536**) and grain yield/plant (4.090**) (Table 2). Miah and Shamsuddin (2002) also observed significant variation among the cultivars for all traits except for single character.

Different genotypes of wheat performed differently for ten characters. It was observed that G_6 (Akbar) performed maximum for plant height (95 cm), grains/spike (66) and days to maturity (110 days) (Appendix V). G_{12} (BARI Gom 22) performed better for harvest index (49.33%) and spike length (12.33 cm). G_{15} (BARI Gom 25) performed better for 1000-grain weight (56 g) and grain yield/plant (6.60 g). G_{20} (BARI Gom 30)

Table 2. Estimation of range, mean, mean sum of square, variance components and coefficient of variance components for ten characters of twenty genotypes in wheat (*Triticum aestivum* L.)

Characters	Range		Mean	GMSS	σ^2_{ph}	σ^2_g	σ^2_e	PCV	GCV	ECV
	Max.	Min.								
Plant height (cm)	95.00	63.00	74.08	224.417**	76.33	74.05	2.28	11.79	11.62	2.04
Spikes /plant (no.)	5.00	3.33	3.85	0.754*	0.53	0.11	0.41	18.83	8.77	16.66
Spike length (cm)	12.33	6.00	8.87	7.523**	2.92	2.30	0.63	19.29	17.10	8.92
Grains /spike (no.)	66.00	34.33	44.15	119.104**	44.63	37.24	7.39	15.13	13.82	6.16
1000-grain weight (g)	56.00	35.67	44.35	109.350**	37.92	35.72	2.20	13.88	13.48	3.35
Harvest index (%)	49.33	15.33	29.33	245.228**	82.94	81.14	1.80	31.05	30.71	4.57
Vegetative period (days)	67.67	62.33	64.70	6.628**	2.64	1.99	0.65	2.51	2.18	1.24
Grain filling period (days)	45.67	39.33	41.45	6.536**	2.55	1.99	0.55	3.85	3.41	1.79
Days to maturity (days)	110.00	101.00	106.58	14.206**	4.81	4.70	0.11	2.06	2.03	0.31
Grain yield /plant (g)	6.60	2.40	4.02	4.090**	1.37	1.36	0.01	29.14	29.00	2.93

* and ** denote significance at 5% and 1% level of probability, respectively.

Max. = maximum, Min. = minimum, GMSS = genotypic mean sum of square, σ^2_{ph} = phenotypic variance, σ^2_g = genotypic variance, σ^2_e = environmental variance, PCV = phenotypic coefficient of variation, GCV = genotypic coefficient of variation, ECV = environmental coefficient of variation, G = Genotype.

acted as early maturing variety (101 days) (Appendix V). Minimum number of spikes/plant (3.33) was shown by 7 genotypes *viz.* G_1 (Kanchan), G_2 (Protiva), G_5 (Durum), G_6 (Akbar), G_{10} (BARI Gom 20), G_{13} (BARI Gom 23) and G_{18} (BARI Gom 28) (Appendix V). This could be due to environmental influence. Mean values obtained for different characters resembles with G_7 (Sourov), G_8 (Gourob), G_9 (Aghrani), G_{10} (BARI Gom 20) and G_{12} (BARI Gom 22) (Appendix V). Sharma *et al.* (2007) also observed differential performance for 21 wheat varieties.

4.1.1.1. Plant height (cm)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the highest plant height (95 cm) was recorded in G_6 (Akbar) and the minimum plant height (63 cm) was recorded in G_3 (Kallyansona) and G_{20} (BARI Gom 30) with mean value of 74.08 cm (Table 2). Randhawa *et al.* (1975) also observed wide range of variation for plant height in bread wheat. Mean sum of square of plant height was found highly significant (224.417**) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 76.33 and 74.05, respectively. The phenotypic variance appeared to be slightly higher than the genotypic variance which suggested considerable influence of environmental variance (2.28) on the expression of the genes controlling this trait. It indicated at additive gene effect. Saha and Foridi (1987) also observed little environmental effect on plant height in bread wheat. The estimates of phenotypic coefficient of variation (11.79) and genotypic coefficient of variation (11.62) also indicated presence of variability among the genotypes for this trait (Table 2). Maloo (1984) reported moderate genotypic coefficient of variation. Pathak and Nema (1985) reported medium phenotypic and genotypic coefficient of variation for plant height in bread wheat.

4.1.1.2. Spikes/plant (no.)

In this study out of 20 genotypes of wheat (Triticum aestivum L.), the highest no. of spikes/plant (5.00) was recorded in G16 (BARI Gom 26) and the minimum no. of spikes/plant (3.33) was recorded in G1 (Kanchan), G2 (Protiva), G5 (Durum), G6 (Akbar), G10 (BARI Gom 20), G13 (BARI Gom 23) and G18 (BARI Gom 28) with mean value of 3.85 (Table 2). Mean sum of square of spikes/plant was found significant (0.754*) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 0.53 and 0.11, respectively. The phenotypic variance appeared to be higher than the genotypic variance which suggested considerable influence of environment on the expression of the genes controlling this trait. The estimates of phenotypic coefficient of variation (18.83) and genotypic coefficient of variation (8.77) also indicated presence of variability among the genotypes for this trait (Table 2). Singh and Tewari (1990) observed low genotypic coefficient of variation and high phenotypic coefficient of variation in Triticale. However, considerable amount of environmental coefficient of variation was observed over spikes/plant. ECV value (16.66) of this trait was much higher than GCV value (8.77) which suggested that selection of this trait would be ineffective.

4.1.1.3. Spike length (cm)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the longest spike length (12.33 cm) was recorded in G_{12} (BARI Gom 22) and the shortest spike length (6.00 cm) was recorded in G_3 (Kallyansona) and G_4 (Sonalika) with mean value of 8.87 cm (Table 2). Mean sum of square of spike length was found highly significant (7.523**) which indicated considerable amount of variation present in this character (Table 2). Biju and Malik (2007) and Bhutta *et al.* (2005) also observed significant variation for spike length in wheat. Phenotypic variance and genotypic variance were observed as 2.92 and 2.30, respectively. The phenotypic variance appeared to be slightly higher than the genotypic variance which suggested least influence of environment on the expression of the genes controlling this trait. It indicated at additive gene effect. The estimates of phenotypic coefficient of variation (19.29) and genotypic coefficient of variation (17.10) also indicated presence of variability among the genotypes for this trait (Table 2). However, moderate environmental coefficient of variation was observed over spike length (8.92) which suggested that selection of this trait would be reasonably rewarding for future hybridization.

4.1.1.4. Grains/spike (no.)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the highest no. of grains/spike (66.00) was recorded in G_6 (Akbar) and the minimum no. of grains/spike

(34.33) was recorded in G_{13} (BARI Gom 23) with mean value of 44.15 (Table 2). Joshi *et al.* (1982) noticed a wide range of variation for grains/spike in 30 diverse varieties of common wheat. Mean sum of square of grains/spike was found highly significant (119.104**) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 44.63 and 37.24, respectively. The phenotypic variance appeared to be higher than the genotypic variance which suggested considerable influence of environment on the expression of the genes controlling this trait. Higher environmental variance was observed for grains/spike (7.39). The estimates of phenotypic coefficient of variation (15.13) and genotypic coefficient of variation (13.82) also indicated presence of variability among the genotypes for this trait (Table 2). Singh *et al.* (1978) also observed low genotypic coefficient of variation and high phenotypic coefficient of variation. However, considerable amount of environmental coefficient of variation was observed for grains/spike (6.16). Therefore, selection of this trait would be moderately effective for future breeding purpose.

4.1.1.5. Thousand grain weight (g)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the highest amount of 1000-grain weight (56.00 g) was recorded in G_{15} (BARI Gom 25) and the minimum 1000-grain weight (35.67 g) was recorded in G_2 (Protiva) with mean value of 44.35 g (Table 2). Mean sum of square of 1000-grain weight was found highly significant (109.350**) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 37.92 and 35.72, respectively. The phenotypic variance appeared to be higher than the genetic variance which suggested considerable influence of environmental variance (2.20) on the expression of the genes controlling this trait. The estimates of phenotypic coefficient of variation (13.88) and genotypic coefficient of variation (13.48) also indicated presence of variability among the genotypes for this trait (Table 2). Pawar *et al.* (1988) observed moderate genotypic and phenotypic coefficient of variation for 1000-grain weight. Singh and Tewari (1990) and Amin *et al.* (1992) reported low genotypic and phenotypic coefficient of variation for 1000-grain weight. Therefore, selection of this trait would be moderately effective.

4.1.1.6. Harvest index (%)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the highest harvest index (49.33%) was recorded in G_{12} (BARI Gom 22) and the minimum harvest index (15.33%) was recorded in G_1 (Kanchan) with mean value of 29.33% (Table 2). Amin *et al.* (1992) also reported wide range of variation for harvest index. Mean sum of square of harvest index was found highly significant (245.228**) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 82.94 and 81.14, respectively. The phenotypic variance appeared to be higher than the genotypic variance which suggested considerable influence of environmental variance (1.80) on the expression of the genes controlling this trait. The estimates of phenotypic coefficient of variation (31.05) and genotypic coefficient of variation (30.71) also indicated presence of variability among the genotypes for this trait (Table 2). Singh *et al.* (1980) observed moderately high genotypic and phenotypic coefficient of variation. However, considerable amount of environmental coefficient of variation was observed for harvest index (4.57). Therefore, selection of this trait would be rewarding for future breeding purpose.

4.1.1.7. Vegetative period (days)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the maximun vegetative period (67.67 days) was recorded in G_5 (Durum) and the minimum vegetative period (62.33 days) was recorded in G_4 (Sonalika) with mean value of 64.70 days (Table 2). Tripathi *et al.* (1973) also reported wide range of variation for vegetative period in wheat. Mean sum of square of vegetative period was found highly significant (6.628**) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 2.64 and 1.99, respectively. The phenotypic variance appeared to be slightly higher than the genotypic variance which suggested least influence of environment on the expression of the genes controlling this trait. It indicated at additive gene effect. The estimates of phenotypic coefficient of variation (2.51) and genotypic coefficient of variation (2.18) also indicated presence of variability among the genotypes for this trait (Table 2). Sharma and Kaul (1986) reported low genotypic and phenotypic coefficients of variation. Similar results were observed by Amin *et al.* (1992), Pawar *et al.* (1988) and Singh *et al.* (1978).

4.1.1.8. Grain filling period (days)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the maximum grain filling period (45.67 days) was recorded in G_3 (Kallyansona) and the minimum grain filling period (39.33 days) was recorded in G_7 (Sourov), G_{10} (BARI Gom 20) with mean value of 41.45 days (Table 2). Mean sum of square of grain filling period was found highly significant (6.536**) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 2.55 and 1.99, respectively. The phenotypic variance appeared to be slightly higher than the genotypic variance which suggested least influence of environment on the expression of the genes controlling this trait. It indicated at additive gene effect. The estimates of phenotypic coefficient of variation (3.85) and genotypic coefficient of variation (3.41) also indicated presence of variability among the genotypes for this trait (Table 2). Miah (1997) and Amin *et al.* (1992) reported low genotypic and phenotypic coefficient of variation for grain filling period in bread wheat.

4.1.1.9. Days to maturity (days)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the maximum days to maturity (110.00 days) was recorded in G_6 (Akbar) and the minimum days to maturity (101.00 days) was recorded in G_{20} (BARI Gom 30) with mean value of 106.58 days (Table 2). Mean sum of square of days to maturity was found highly significant (14.206**) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 4.81 and 4.70, respectively. The phenotypic variance appeared to be slightly higher than the genotypic variance which suggested least influence of environment on the expression of the genes controlling this trait. It indicated at additive gene effect. The estimates of phenotypic coefficient of variation (2.06) and genotypic coefficient of variation (2.03) also indicated presence of variability among the genotypes for this trait (Table 2). Nessa *et al.* (1994) reported low genotypic and phenotypic coefficient of variation for days to maturity in bread wheat. The difference between them was very small indicating at less influence of environment on this trait.

4.1.1.10. Grain yield/plant (g)

In this study out of 20 genotypes of wheat (*Triticum aestivum* L.), the maximum amount of grain yield/plant (6.60 g) was recorded in G_{15} (BARI Gom 25) and the minimum grain yield/plant (2.40 g) was recorded in G_{16} (BARI Gom 26) with mean value of 4.02 g (Table 2). Mean sum of square of grain yield/plant was found highly significant (4.090**) which indicated considerable amount of variation present in this character (Table 2). Phenotypic variance and genotypic variance were observed as 1.37 and 1.36, respectively. The phenotypic variance appeared to be slightly higher than the genotypic variance which suggested least influence of environment on the expression of the genes controlling this trait. It indicated at additive gene effect. The estimates of phenotypic coefficient of variation (29.14) and genotypic coefficient of variation (29.00) also indicated presence of variability among the genotypes for this trait (Table 2). Tripathi *et al.* (1973) reported high genotypic and phenotypic coefficient of variation for grain yield/plant in bread wheat. Similar result was observed by Pathak and Nema (1985), Sharma and Kaul (1986) and Nessa *et al.* (1994) for grain yield/plant in bread wheat. Therefore, selection of this trait would be rewarding for future breeding purpose.

4.1.2. Heritability and genetic advance

The heritability in broad sense, genetic advance at 5% selection intensity and genetic advance in percent of mean for ten characters of twenty wheat genotypes were presented in Table 3.

4.1.2.1. Plant height (cm)

Plant height showed very high heritability (97.01%) with moderate genetic advance in percent of mean (23.57%) which indicated that this trait was controlled by additive gene (Table 3). Both Maloo (1984) and Pathak and Nema (1985) reported high estimates of heritability for plant height in bread wheat. Randhawa *et al.* (1975) reported high heritability associated with high genetic advance for plant height in bread wheat. Selection of this trait would be reasonable for breeding purpose.

Table 3. Estimation of heritability and genetic advance for ten characters of 20 (twenty) genotypes in wheat (*Triticum aestivum* L.)

Characters	Heritability, h_b^2 (%)	Genetic advance, GA (5%)	Genetic advance, GA (% mean)
Plant height (cm)	97.01	17.46	23.57
Spikes/plant (no.)	21.70	0.32	8.42
Spike length (cm)	78.61	2.77	31.23
Grains/spike (no.)	83.43	11.48	26.01
1000-grain weight (g)	94.19	11.95	26.94
Harvest index (%)	97.83	18.35	62.57
Vegetative period (days)	75.51	2.53	3.91
Grain filling period (days)	78.33	2.58	6.21
Days to maturity (days)	97.68	4.41	4.14
Grain yield/plant (g)	98.99	2.39	59.43

h_b^2 = Heritability in broad sense,
GA (5%) = Genetic advance at 5% selection intensity
GA (% mean) = Genetic advance in percent of mean

4.1.2.2. Spikes/plant (no.)

Spikes/plant showed low heritability (21.70%) with low genetic advance in percent of mean (8.42%) which indicated that this trait was controlled by non-additive gene (Table 3). Maloo (1984), Pawar *et al.* (1988) and Mahmood and Shahid (1993) reported high heritability with high genetic advance for spikes/plant. Present findings were a disagreement to usual report. It may be due to significant influence of environment on this trait (Singh and Tewari, 1990 and Tripathi *et al.,* 1973).

4.1.2.3. Spike length (cm)

Spike length showed moderately high heritability (78.61%) with moderate genetic advance in percent of mean (31.23%) which indicated that this trait was controlled by additive gene (Table 3). Moderate heritability would be due to favorable environmental influence but selection of such trait would be effective owing to its high genetic advance.

4.1.2.4. Grains/spike (no.)

Grains/spike showed moderately high heritability (83.43%) with moderate genetic advance in percent of mean (26.01%) which indicated that this trait was controlled by additive gene (Table 3). Ehdaie and Waines (1989) also observed high heritability with moderate genetic advance for grains/spike in bread wheat. Maloo (1984) reported high heritability with high genetic advance for this trait. Selection of this trait would be rewarding for yield improvement.

4.1.2.5. Thousand grain weight (g)

Thousand grain weight showed very high heritability (94.19%) with moderate genetic advance in percent of mean (26.94%) which indicated that this trait was controlled by additive gene (Table 3). It was interesting to observe that this character did not reveal equally high genetic advance inspite of having very high heritability. Mostly it could be due to additive gene effect whereas if the heritability is mainly due to dominance and epistasis, the genetic advance would be low. Amin *et al.* (1992) reported high heritability with low genetic advance for 1000-grain weight in bread wheat.

4.1.2.6. Harvest index (%)

Harvest index showed high heritability (97.83%) with high genetic advance in percent of mean (62.57%) which indicated that this trait was controlled by additive gene (Table 3). Amin *et al.* (1992) also reported high heritability accompanied by high genetic advance for harvest index in bread wheat. Selection of this trait would be rewarding for future breeding program.

4.1.2.7. Vegetative period (days)

Vegetative period showed moderately high heritability (75.51%) with low genetic advance in percent of mean (3.91%) which indicated that this trait was controlled by non-additive gene (Table 3). Sharma and Kaul (1986) explained such genetic advance since presence of dominance and epistasis in the population. Similar results were observed by Amin *et al.* (1992), Pawar *et al.* (1988) and Singh *et al.* (1978).

4.1.2.8. Grain filling period (days)

Grain filling period showed moderate heritability (78.33%) with low genetic advance in percent of mean (6.21%) which indicated that this trait was controlled by non-additive gene (Table 3). Miah (1997) reported high heritability and low genetic advance for grain filling period in bread wheat.

4.1.2.9. Days to maturity (days)

Days to maturity showed high heritability (97.68%) with low genetic advance in percent of mean (4.14%) which indicated that this trait was controlled by non-additive gene (Table 3). Tripathi *et al.* (1973), Sharma and Kaul (1986) and Nessa *et al.* (1994) observed high heritability and moderate genetic advance for days to maturity in bread wheat. Selection of this trait would be misleading due to environmental effect.

4.1.2.10. Grain yield/plant (g)

Grain yield/plant showed very high heritability (98.99%) with high genetic advance in percent of mean (59.43%) which indicated that this trait was controlled by additive gene (Table 3). High genetic advance for this trait was probably due to high coefficient of variation and high heritability for grain yield/plant in wheat. Nessa *et al.* (1994), Sharma and Kaul (1986) and Pathak and Nema (1985) observed high heritability with high genetic advance whereas Tripathi *et al.* (1973) observed moderate genetic advance for this trait. Selection of this trait would be rewarding for future breeding program.

4.2. Correlation coefficient analysis

Yield being a complex character was influenced by several inter-dependable quantitative traits. Selection for this trait would not be effective unless the influence of other yield components were taken into consideration. Selection pressure for improvement of any character highly associated with yield would affect other correlated characters simultaneously. Therefore knowledge regarding association of yield and yield components provides guideline to select the character for improvement with a clear understanding. In this regard, phenotypic and genotypic correlation coefficient among different pair of yield and yield contributing characters for twenty wheat genotypes were shown in Table 4. Correlation coefficient analysis had shown that genotypic correlation coefficient was slightly higher than the corresponding phenotypic correlation coefficient for most of the characters. It revealed that, phenotypic expression was modified due to the strong inherent association and environmental effect by reducing their phenotypic correlation value.

4.2.1. Plant height (cm)

Plant height had shown highly significant and positive correlation with grains/spike (0.725** & 0.661**), harvest index (0.591** & 0.572**), spike length (0.448** & 0.388**), 1000-grain weight (0.416** & 0.400**) and days to maturity (0.341** & 0.332**) at both genotypic and phenotypic level, respectively (Table 4 and Figure 4) which indicated that if plant height was increased, then grains/spike, harvest index, spike length, 1000-grain weight and days to maturity would also be increased. It had shown significant positive correlation with grain yield/plant (0.316* & 0.308*) at both level (Table 4) which indicated that if plant height was increased then grain yield/plant would also be increased. Shamsuddin and Ali (1989), Nessa *et al.* (1994) and Yagbasanlar (1995) also observed significantly positive correlation for plant height with garin yield/plant. It had shown non-significant positive correlation

Table 4. Estimation of genotypic and phenotypic correlation coefficients for yield and yield contributing characters in twenty wheat (*Triticum aestivum* L.) genotypes

Characters	Level	Plant height (cm)	Spikes/plant (no.)	Spike length (cm)	Grains/spike (no.)	Thousand grain weight (g)	Harvest index (%)	Vegetative period (days)	Grain filling period (days)	Days to maturity (days)
Spike/plant	G	- 0.169	-							
	P	- 0.091	-							
Spike length	G	0.448**	0.081	-						
	P	0.388**	0.023	-						
Grains/spike	G	0.725**	- 0.070	0.521**	-					
	P	0.661**	- 0.056	0.427**	-					
Thousand grain weight	G	0.416**	0.431**	0.771**	0.310*	-				
	P	0.400**	0.198	0.657**	0.272*	-				
Harvest index	G	0.591**	0.026	0.597**	0.474**	0.750**	-			
	P	0.572**	0.021	0.495**	0.425**	0.722**	-			
Vegetative period	G	0.231	- 0.049	- 0.281*	- 0.342**	- 0.071	0.012	-		
	P	0.185	0.038	- 0.211	- 0.292*	- 0.075	0.032	-		
Grain filling period	G	- 0.078	0.639**	- 0.071	0.033	0.042	0.011	- 0.102	-	
	P	- 0.075	0.249	- 0.077	0.039	0.022	0.022	- 0.018	-	
Days to maturity	G	0.341**	- 0.231	- 0.150	0.266*	0.092	0.280*	0.331**	0.403**	-
	P	0.332**	- 0.066	- 0.126	0.231	0.080	0.277*	0.310*	0.376**	-
Grain yield /plant	G	0.316*	- 0.068	0.563**	0.487**	0.551**	0.783**	- 0.190	- 0.022	0.038
	P	0.308*	- 0.029	0.501**	0.441**	0.534**	0.773**	- 0.163	- 0.035	0.036

** denotes significance at 1%, * denotes significance at 5%

G: genotypic correlation coefficient, P: Phenotypic correlation coefficient for vegetative period (0.231 & 0.185) and non-significant negative correlation with spikes/plant (-0.169 & -0.091) and grain filling period (-0.078 & -0.075) at both level (Table 4). Association between these traits was largely influenced by environmental factors.

4.2.2. Spikes/plant (no.)

Spikes/plant had shown highly significant and positive correlation with grain filling period (0.639**) and 1000-grain weight (0.431**) at genotypic level (Table 4) which indicated that if spikes/plant was increased, then grain filling period and 1000-grain weight would also be increased. It had shown non-significant positive correlation with 1000-grain weight (0.249), grain filling period (0.198) and vegetative period (0.038) at phenotypic level but with spike length (0.081 & 0.023) and harvest index (0.026 & 0.021) at both genotypic and phenotypic level, respectively (Table 4). It had shown non-significant negative correlation with vegetative period (-0.049) at genotypic level but with days to maturity (-0.231 & -0.066), grains/spike (-0.070 & -0.056) and grain yield/plant (-0.068 & -0.029) at both genotypic and phenotypic level, respectively (Table 4 and Figure 4). Ehdaie and Waines (1989) also observed non-significant negative correlation for spikes/plant with grain yield/plant. Miah (1997) observed non-significant negative correlation for spikes/m^2 with grain yield. Association between these traits was largely influenced by environmental factors.

4.2.3. Spike length (cm)

Spike length had shown highly significant and positive correlation with 1000-grain weight (0.771** & 0.657**), harvest index (0.597** & 0.495**), grain yield/plant (0.563** & 0.501**) and grains/spike (0.521** & 0.427**) at both genotypic and phenotypic level, respectively (Table 4 and Figure 4) which indicated that if spike length was increased then 1000-grain weight, harvest index, grain yield/plant and grains/spike would also be increased. It had shown significantly negative correlation with vegetative period (-0.281*) at genotypic level which indicated that if spike length was increased then vegetative period would be decreased.

It had shown non-significant negative correlation with vegetative period (-0.211) at phenotypic level but with days to maturity (-0.150 & -0.126) and grain filling period

(-0.071 & -0.077) at both genotypic and phenotypic level, respectively (Table 4). Association between these traits was largely influenced by environmental factors.

4.2.4. Grains/spike (no.)

Grains/spike had shown highly significant and positive correlation with grain yield/plant (0.487** & 0.441**) and harvest index (0.474** & 0.425**) at both genotypic and phenotypic level, respectively (Table 4 and Figure 4) which indicated that if grains/spike was increased then grain yield/plant and harvest index would also be increased. Singh *et al.* (1978) and Dawari and Luthra (1991) also reported highly significant and positive correlation for grain yield/plant with grains/spike. It had shown highly significant and negative correlation with vegetative period (-0.342**) at genotypic level which indicated that if grains/spike was increased then vegetative period would be decreased. It had shown significant positive correlation with days to maturity (0.266*) at genotypic level but with 1000-grain weight (0.310* & 0.272*) at both genotypic and phenotypic level, respectively (Table 4) which indicated that if grains/spike was increased then days to maturity and 1000-grain weight would also be increased. It had shown significant negative correlation with vegetative period (-0.292*) at phenotypic level which indicated that if grains/spike was increased then vegetative period would be decreased. It had shown non-significant positive correlation with days to maturity (0.231) at phenotypic level but with grain filling period (0.033 & 0.039) at both genotypic and phenotypic level, respectively. Genotypic correlation coefficient (0.033) of grain filling period is lower than its corresponding phenotypic correlation coefficient (0.039) which suggested that both environmental and genotypic correlation act in the same direction and maximized their expression at phenotypic level. Association between these traits was largely influenced by environmental factors.

4.2.5. Thousand grain weight (g)

1000-grain weight had shown highly significant and positive correlation with harvest index (0.750** & 0.722**) and grain yield/plant (0.551** & 0.534**) at both genotypic and phenotypic level, respectively (Table 4) which indicated that if 1000-grain weight was increased then harvest index and grain yield/plant would also be increased. Singh *et al.* (1978) and Dawari and Luthra (1991) reported that 1000-grain weight were highly significant and positively associated with grain yield/plant. It had shown non-significant positive correlation with days to maturity (0.092 & 0.080) and grain filling period (0.042 & 0.022) at both genotypic and phenotypic level, respectively (Table 4). It had shown non-significant negative correlation with vegetative period (-0.071 & -0.075) at both level. Association between these traits was largely influenced by environmental factors.

4.2.6. Harvest index (%)

Harvest index had shown highly significant and positive correlation with grain yield/plant (0.783** & 0.773**) at genotypic and phenotypic level, respectively (Table 4 and Figure 4) which indicated that if harvest index was increased then grain yield/plant would also be increased. Dawari and Luthra (1991) reported that harvest index were highly significant and positively associated with grain yield/plant. It had shown significant and positive correlation with days to maturity (0.280* & 0.277*) at both level (Table 4) which indicated that if harvest index was increased then days to maturity would also be lengthen. It had shown non-significant positive correlation with vegetative period (0.012 & 0.032) and grain filling period (0.011 & 0.022) at both levels. Genotypic correlation coefficient of vegetative period (0.012) and grain filling period (0.011) is lower than its corresponding phenotypic correlation coefficient (0.032 and 0.022, respectively) which suggested that both environmental and genotypic correlation act in the same direction and maximized their expression at phenotypic level. Association between these traits was largely influenced by environmental factors.

4.2.7. Vegetative period (days)

Vegetative period had shown highly significant and positive correlation with days to maturity (0.331**) at genotypic level (Table 4 and Figure 4) which indicated that if vegetative period was lengthen then days to maturity would also be lengthen. It had shown significant positive correlation with days to maturity (0.310*) at phenotypic level which indicated that if vegetative period was lengthen then days to maturity would also be lengthen. It had shown non-significant negative correlation with grain yield/plant (-0.190 & -0.163) and grain filling period (-0.102 & -0.018) (Table 4). Shamsuddin and Ali (1989), Ehdaie and Waines (1989), Miah (1997) and Jaimini *et* *al.* (1974) observed non-significant negative correlation for grain yield/plant and vegetative period. Association between these traits was largely influenced by environmental factors.

4.2.8. Grain filling period (days)

Grain filling period had shown highly significant and positive correlation with days to maturity (0.403** & 0.376**) at genotypic and phenotypic level, respectively (Table 4) which indicated that if grain filling period was lengthen then days to maturity would also be lengthen. It had shown non-significant negative correlation with grain yield/plant (-0.022 & -0.035) at both level (Table 4). Association between these traits was largely influenced by environmental factors. Srivastave *et al.* (1985-86) also observed non-significant negative correlation for grain yield/plant with grain filling period.

4.2.9. Days to maturity (days)

Days to maturity had shown non-significant positive correlation with grain yield/plant (0.038 & 0.036) (Table 4). Association between these traits was largely influenced by environmental factors. It was interesting to observe that this character did not reveal equally high genetic advance inspite of having very high heritability mostly it could be due to additive gene effect whereas if the heritability is mainly due to dominance and epistasis, the genetic advance would be low Amin *et al.* (1992).

4.3. Path coefficient analysis

The direct and indirect effects of yield contributing characters on yield were worked out by using path analysis. Yield per plant was considered as dependant variable and plant height, spikes/plant, grains/spike, spike length, 1000-grain weight, harvest index, vegetative period, grain filling period and days to maturity were treated as independent variables. Direct and indirect effect of different characters via path analysis was shown in Table 5. The residual effect was 0.52, indicated that contribution of component characters on grain yield/plant was 48% by the nine characters studied in path analysis, the rest 52% was the contribution of other factors such as characters not studied and sampling error.

Table 5. Partitioning of genotypic correlations into direct (bold) and indirect effects for different characters of twenty genotypes in wheat (*Triticum aestivum* L.)

Characters	Effects via									Genotypic correlation with grain yield/plant
	PH	SPP	SL	GPS	TGW	HI	VP	GFP	DM	
Plant Height (cm)	**-0.486**	-0.068	0.248	0.169	-0.332	0.687	0.001	0.03	0.07	0.316*
Spikes/plant (no.)	0.082	**0.405**	0.045	-0.016	-0.344	0.030	0.000	-0.22	-0.05	-0.068
Spike length (cm)	-0.218	0.033	**0.554**	0.121	-0.615	0.694	-0.001	0.02	-0.03	0.563**
Grains/spike (no.)	-0.352	-0.028	0.289	**0.233**	-0.247	0.551	-0.001	-0.01	0.05	0.487**
Thousand grain weight (gm)	-0.202	0.175	0.427	0.072	**-0.798**	0.872	0.000	-0.01	0.02	0.551**
Harvest index (%)	-0.287	0.011	0.331	0.110	-0.599	**1.163**	0.000	0.00	0.06	0.783**
Vegetative period (days)	-0.112	-0.020	-0.156	-0.080	0.057	0.014	**0.004**	0.04	0.07	-0.190
Grain filling period (days)	0.04	0.26	-0.04	0.01	-0.03	0.01	0.00	**-0.35**	0.08	-0.022
Days to maturity (days)	-0.17	-0.09	-0.08	0.06	-0.07	0.33	0.00	-0.14	**0.21**	0.038

Residual effect = 0.520 ** = Significance at 1% * = Significance at 5%

PH: Plant height (cm), SPP: Spikes/plant (no.), SL: Spike length (cm), GPS: Grains/spike (no.), TGW: 1000-grain weight (gm), HI: Harvest Index (%), VP: Vegetative Period (days), GFP: Grain filling period (days), DM: Days To Maturity (days) and GYP: Grain yield/plant (gm)

4.3.1. Plant height (cm)

Path coefficient analysis had shown that, plant height had negative direct effect (-0.486) on grain yield/plant. Barma *et al.* (1991) observed negative direct effect of plant height on grain yield/plant. Direct selection based on this trait would be ineffective. It had positive indirect effect via spike length (0.248), grains/spike (0.169), harvest index (0.687), vegetative period (0.001), grain filling period (0.03) and days to maturity (0.07) (Table 5). On the other hand, it had negative indirect effect on spikes/plant (-0.068) and 1000-grain weight (-0.332) (Table 5). Plant height finally made significantly positive correlation with grain yield/plant (0.316*) (Table 5). These results indicated that if plant height was increased then grain yield/plant would be increased mostly through the positive indirect effect of plant height with other characters.

4.3.2. Spikes/plant (no.)

Path coefficient analysis had exhibited that, spikes/plant had positive direct effect (0.405) on grain yield/plant. Such result indicated that direct selection based on this trait would be effective for yield improvement. Das (1972) reported highest direct effect of spikes/plant on grain yield/plant. Shamsuddin (1987) also observed that spikes/plant had direct effect on grain yield/plant. It had positive indirect effect on plant height (0.082), spike length (0.045) and harvest index (0.03) (Table 5). On the other hand, it had negative indirect effect on grains/spike (-0.016), 1000-grain weight (-0.344), grain filling period (-0.22) and days to maturity (-0.05) (Table 5). Spikes/plant finally made non-significant negative correlation with grain yield/plant (-0.068) (Table 5).

4.3.3. Spike length (cm)

Path coefficient analysis had demonstrated that, spike length had positive direct effect (0.554) on grain yield/plant. Such result indicated that direct selection based on this trait would be effective for yield improvement. Shamsuddin and Ali (1989) reported that length of spike had considerable amount of direct effect on grain yield/plant. It had positive indirect effect on spikes/plant (0.033), grains/spike (0.121), harvest index (0.694) and grain filling period (0.02) (Table 5). On the other hand, it had negative indirect effect on plant height (-0.218), 1000-grain weight (-0.615), vegetative period (-0.001) and days to maturity (-0.03) (Table 5). Spike length showed the highest negative indirect effect (-0.615) on grain yield/plant via 1000-grain weight. Spike length finally made highly significant positive correlation with grain yield/plant (0.563**) (Table 5). These results indicated that if spike length was increased then grain yield/plant would be increased mostly through the positive indirect effect of spike length with other characters.

4.3.4. Grains/spike (no.)

Path coefficient analysis had revealed that, grains/spike had positive direct effect (0.233) on grain yield/plant. Such result indicated that direct selection based on this trait would be effective for yield improvement. Paroda and Joshi (1970), Das and Mondal (1984) and Shamsuddin and Ali (1989) had observed positive direct effect of grains/spike on grain yield/plant in bread wheat. Shelembi and Wright (1991) also reported that no. of grains/spike had direct and strong effect on grain yield/plant. It had positive indirect effect on spike length (0.289), harvest index (0.551) and days to maturity (0.05) (Table 5). On the other hand, it had negative indirect effect on plant height (-0.352), spikes/plant (-0.028), 1000-grain weight (-0.247), vegetative period (-0.001) and grain filling period (-0.01) (Table 5). Grains/spike finally made highly significant positive correlation with grain yield/plant (0.487**) (Table 5). These results indicated that if grains/spike was increased then grain yield/plant would be increased mostly through the positive indirect effect of grains/spike with other characters.

4.3.5. Thousand grain weight (g)

Path coefficient analysis had shown that, 1000-grain weight had negative direct effect (-0.798) on grain yield/plant. Direct selection based on this trait would be ineffective. Present findings were disagreement to the usual report. It could be due to environmental influence. Bhular *et al.* (1985) suggested that 1000-grain weight was one of the most important yield components in durum wheat. It had positive indirect effect on spikes/plant (0.175), spike length (0.427), grains/spike (0.072), harvest index (0.872) and days to maturity (0.02) (Table 5). 1000-grain weight had shown highest positive indirect effect (0.872) on grain yield/plant via harvest index. On the other hand, it had negative indirect effect on plant height (-0.202) and grain filling period (-0.01) (Table 5). 1000-grain weight finally made highly significant positive correlation with grain yield/plant (0.551**) (Table 5). These results indicated that if 1000-grain weight was increased then grain yield/plant would be increased mostly through the positive indirect effect of 1000-grain weight with other characters.

4.3.6. Harvest index (%)

Path coefficient analysis had revealed that, harvest index had positive direct effect (1.163) on grain yield/plant. Such result indicated that direct selection based on this trait would be effective for yield improvement. It had positive indirect effect on spikes/plant (0.011), spike length (0.331), grains/spike (0.110) and days to maturity (0.06) (Table 5). On the other hand, it had negative indirect effect on plant height (-0.287) and 1000-grain weight (-0.599) (Table 5). Harvest index finally made highly significant positive correlation with grain yield/plant (0.783**) (Table 5). These results indicated that if harvest index was increased then grain yield/plant would be increased mostly through the positive indirect effect of harvest index with other characters.

4.3.7. Vegetative period (days)

Path coefficient analysis had exhibited that, vegetative period had positive direct effect (0.004) on grain yield/plant. But Rahman *et al.* (1983) observed negative direct effect of vegetative period on grain yield/plant in bread wheat. It had positive indirect effect on 1000-grain weight (0.057), harvest index (0.014), grain filling period (0.04) and days to maturity (0.07) (Table 5). On the other hand, it had negative indirect effect on plant height (-0.112), spikes/plant (-0.020), spike length (-0.156) and grains/spike (-0.080) (Table 5). Vegetative period finally made non-significant negative correlation with grain yield/plant (-0.190) (Table 5).

4.3.8. Grain filling period (days)

Path coefficient analysis had shown that, grain filling period had negative direct effect (-0.35) on grain yield/plant. Direct selection based on this trait would be ineffective. Razzaque *et al.* (1981) had also reported negative direct effect of grain filling period on grain yield/plant in bread wheat. It had positive indirect effect on plant height (0.04), spikes/plant (0.26), grains/spike (0.01), harvest index (0.01) and days to maturity (0.08) (Table 5). On the other hand, it had negative indirect effect on spike length (-0.04) and 1000-grain weight (-0.03) (Table 5). Vegetative period finally made non-significant negative correlation with grain yield/plant (-0.022) (Table 5).

4.3.9. Days to maturity (days)

Path coefficient analysis had revealed that, days to maturity had positive direct effect (0.21) on grain yield/plant. Such result indicated that direct selection based on this trait would be effective for yield improvement. It had positive indirect effect on grains/spike (0.06) and harvest index (0.33) (Table 5). On the other hand, it had negative indirect effect on plant height (-0.17), spikes/plant (-0.09), spike length (-0.08), 1000-grain weight (-0.07) and grain filling period (-0.14) (Table 5). Days to maturity finally made non-significant positive correlation with grain yield/plant (0.038) (Table 5).

4.4. Diversity analysis

Genetic divergence among twenty genotypes of wheat (*Triticum aestivum* L.) was studied through Principal Component Analysis (PCA), Non hierarchical cluster analysis and Canonical Variate Analysis (CVA) using GENSTAT computer program. Contribution of characters towards divergence was also analyzed from latent vectors obtained from principal component analysis (PCA). Genotypic score obtained through PCA were presented in Appendix VI. Balasch *et al.* (1984) also marked that three methods gave similar result but required different scheme for collecting data.

4.4.1. Principal Component Analysis (PCA)

Principal components for ten characters were computed from the correlation matrix and genotypic scores. The PCA yielded Eigen value and percent variance accounted for each principal component axes along with cumulative percent. Eigen values above unity covered 80.68% of total variation whereas percent variance above unity covered 98.66% of total variation. The first two principal component axes were accounted for 37.56% and 16.82%, respectively (Table 6) of total variation.

Based on principal component axes I and II, a two dimensional scattered diagram of the cultivars were obtained which revealed that all the genotypes were apparently distributed into five clusters (Figure 5).

Soybean (Chowdhury, 1994) and pea (Mian *et al.*, 1991) were also assessed for genetic diversity analysis among the germplasms of those crops through Principal Component Analysis.

4.4.2. Non-hierarchical Clustering

The computation from co-variance matrix gave non-hierarchical clustering. Joshi and Kohli (2003) also followed non-hierarchical Euclidean cluster analysis for assessing genetic divergence in tomato.

Non-hierarchical clustering had grouped the twenty genotypes of wheat into 5 different clusters. There were 8 genotypes in cluster I, 5 genotypes in cluster V, 4 genotypes in cluster IV, 2 genotypes in cluster III and single genotype in cluster II (Table 7).

Cluster I comprised of G_1 (Kanchan), G_2 (Protiva), G_3 (Kallyansona), G_9 (Aghrani), G_{13} (BARI Gom 23), G_{16} (BARI Gom 26), G_{19} (BARI Gom 29) and G_{20} (BARI Gom 30); cluster II consisted of G_6 (Akbar); cluster III consisted of G_{12} (BARI Gom 22) and G_{15} (BARI Gom 25); cluster IV consisted of G_4 (Sonalika), G_7 (Sourov), G_{17} (BARI Gom 27) and G_{18} (BARI Gom 28) and cluster V included G_5 (Durum), G_8 (Gourob), G_{10} (BARI Gom 20), G_{11} (BARI Gom 21) and G_{14} (BARI Gom 24).

Table 6. Eigen value, % variance accounted for each principal component axes and cumulative percent of total variation for ten characters of 20 wheat (*Triticum aestivum* L.) genotypes

Principal component axes	Eigen values	% Variance	Cumulative percent
I	3.7564	37.56	27.56
II	1.6818	16.82	54.38
III	1.5125	15.13	69.51
IV	1.1166	11.17	80.68
V	0.7643	7.64	88.32
VI	0.4804	4.80	93.12
VII	0.3369	3.37	96.49
VIII	0.2167	2.17	98.66
IX	0.0899	0.90	99.56
X	0.0444	0.44	100.00

Table 7. Distribution of twenty wheat genotypes in different clusters

Cluster	Number of genotypes	Genotypes
I	8	G_1, G_2, G_3, G_9, G_{13}, G_{16}, G_{19} and G_{20}
II	1	G_6
III	2	G_{12} and G_{15}
IV	4	G_4, G_7, G_{17} and G_{18}
V	5	G_5, G_8, G_{10}, G_{11} and G_{14}

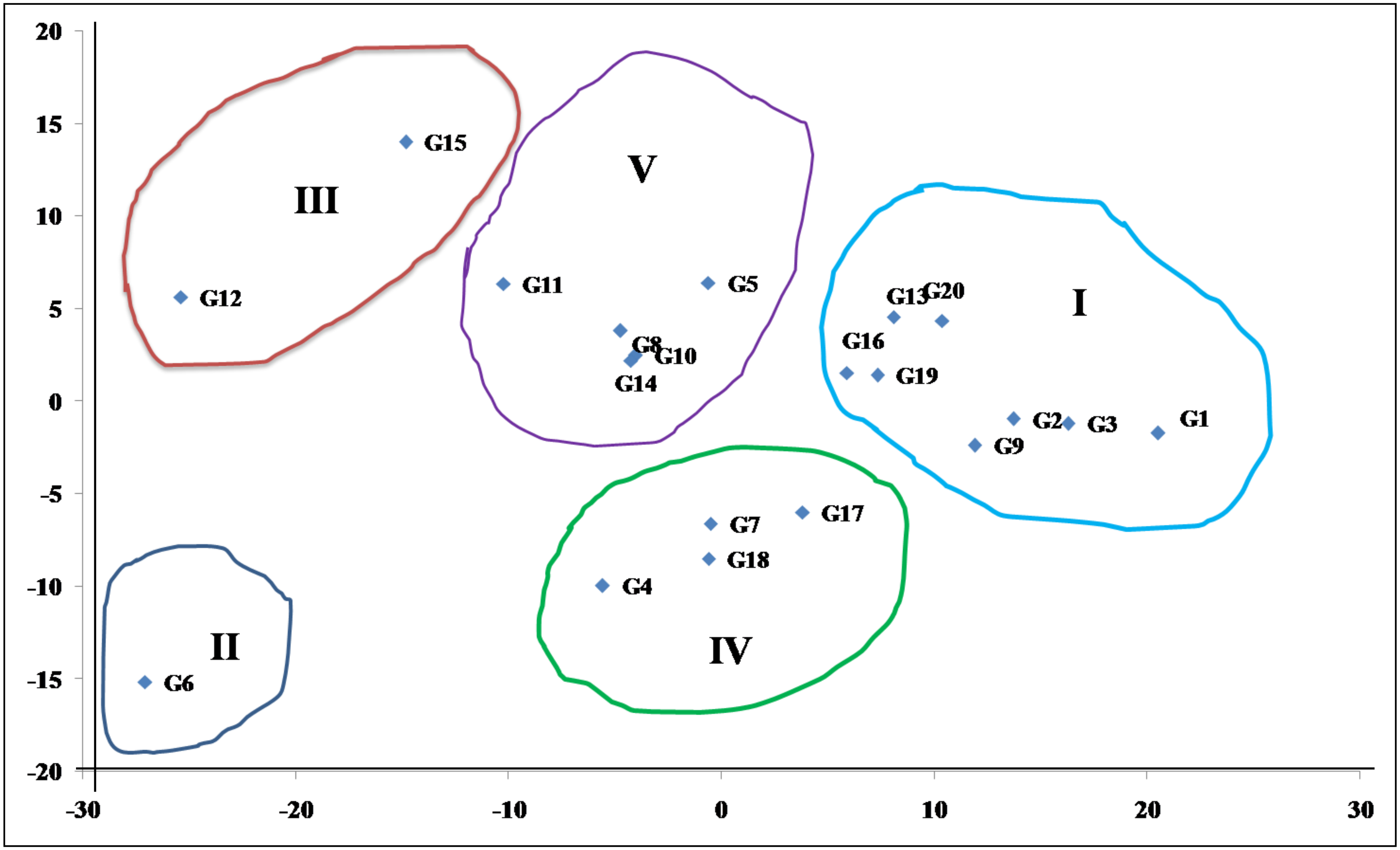


Figure 5. Scatter diagram of twenty wheat genotypes based on principal component score superimposed with clustering

These results confirmed the clustering pattern of the genotypes obtained through principal component analysis. Chaturvedi and Gupta (1995) studied 12 yield components in 44 genotypes of wheat for genetic divergence and it was clustered into 13 diverse groups. Sinha and Sharma (1979) conducted an experiment using five clusters of 35 genetic stocks for common wheat by means of Mahalanobis' D^2-statistics. Srivastave *et al.* (1985-86) also studied genetic divergence for 40 and 30 wheat varieties (selected) from two separate screening nurseries that grouped them into 7 and 10 clusters, respectively. Redhu *et al.* (1995) also grouped 121 genotypes of wheat into 27 clusters.

Cluster mean value for ten characters of wheat genotypes were presented in Table 8.

It was observed that cluster I produced lowest mean value for plant height (66.37 cm), spike length (8.29 cm), grains/spike (40.58), harvest index (21.54%), days to maturity (105.88 days) and grain yield/plant (3.35 g). It indicated that the genotypes included in this cluster were semi dwarf and produced lower amount of grains/spike, shorter spike length, low yielding and early maturing varieties.

Cluster II produced highest mean value for plant height (95 cm), grains/spike (66) and days to maturity (110 days). It produced lowest mean value for vegetative period (62.67 days) and spikes/plant (3.33) and Intermediate mean value for other characters. This suggested that this cluster produced tall plant with lower amount of spikes per plant, higher amount of grains/spike, medium seed size and late maturing varieties. Yadav and Murty (1981) also found the maximum range of cluster mean for plant height.

Cluster III produced maximum mean value for spikes/plant (4), spike length (11.5 cm), 1000-grain weight (55 g), harvest index (47.67%), vegetative period (65.17 days), grain filling period (42.5 days) and grain yield/plant (5.98 g). It indicated that produced plants were moderately tall with higher amount of spike/plant, longer spike length, higher amount of 1000-grain weight, medium number of grains/spike and grain yield/plant with medium duration.

Table 8. Cluster mean for ten characters of 20 wheat (*Triticum aestivum* L.) genotypes

Characters	I	II	III	IV	V
Plant height (cm)	66.37 (L)	95 (H)	79.33	80.17	75.27
Spikes/plant (no.)	3.96	3.33 (L)	4 (H)	3.75	3.8
Spike length (cm)	8.29 (L)	11	11.5 (H)	8.42	8.67
Grains/spike (no.)	40.58 (L)	66 (H)	48	45.83	42.6
1000-grain weight (g)	41.67	49.67	55 (H)	39.67 (L)	47.07
Harvest index (%)	21.54 (L)	37	47.67 (H)	26.58	35.13
Vegetative period (days)	64.25	62.67 (L)	65.17 (H)	65.75 (H)	64.8
Grain filling period (days)	41.92	41.67	42.5 (H)	40.83	40.73 (L)
Days to maturity (days)	105.88 (L)	110 (H)	107.67	106.25	106.87
Grain yield/plant (g)	3.35 (L)	5.4	5.98 (H)	3.65	4.32

H: High value
L: Low value

Cluster IV produced highest vegetative period (65.75 days) and lowest 1000-grain weight (39.67 g). Rest was intermediate values for other characters. This indicated that produced plants were semi dwarf with medium amount of spikes/plant, grains/spike, medium size seed, moderate amount of grain yield/plant and medium duration plant.

Cluster V produced lowest mean value for grain filling period (40.73 days) and intermediate values for other characters. It indicated that produced plants were semi dwarf with medium amount of spikes/plant, grains/spike, medium size seed and moderate amount of grain yield/plant and medium duration plant.

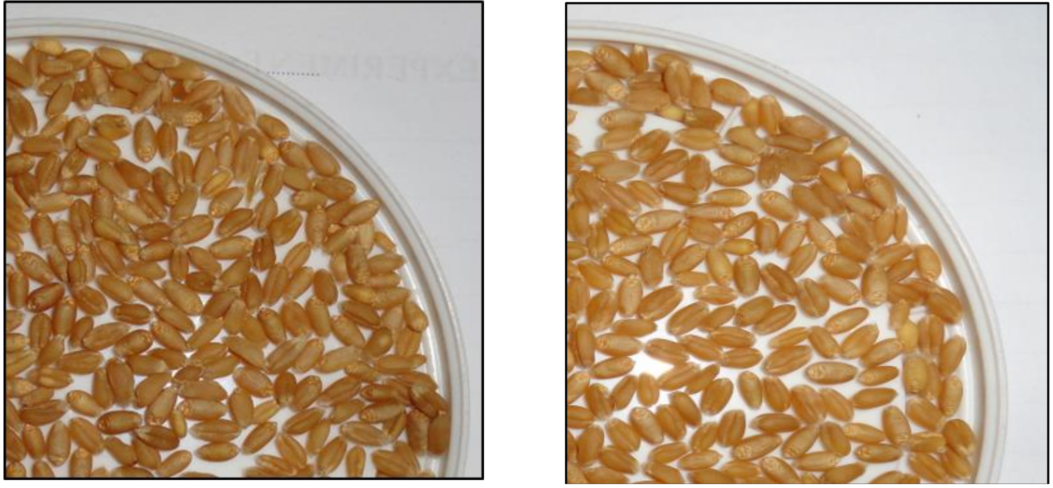
In a nutshell, it was observed that spikes/plant, vegetative period, grain filling period and days to maturity were more or less similar for all the five clusters. Maximum range of variability was observed for plant height (66.37 cm to 95 cm) among all the characters in five clusters. Cluster I and II included most of the diverse characters including plant height, spike length, grains/spike and grain yield/plant.

Grain Types of G_{19} from cluster I, G_6 from cluster II, G_{12} from cluster III, G_{17} from cluster IV and G_{10} from cluster V were presented in Plate 13

G$_{19}$ from cluster I
(BARI Gom 29)

G$_{6}$ from cluster II
(Akbar)

G$_{12}$ from cluster III
(BARI Gom 22)



G$_{17}$ from cluster IV
(BARI Gom 27)

G$_{10}$ from cluster V
(BARI Gom 20)

Plate 13. Different types of seed grain from cluster I to cluster V

4.4.3. Canonical Variate Analysis (CVA)

Canonical variate analysis was done to compute the inter cluster distances. The average intra and inter cluster distances (D^2) were presented in Table 9 and list of five nearer and furtherer inter cluster distances from each cluster were shown in Table 10 for comparison. From Table 9, it was observed that inter cluster distances were higher than the intra cluster distances which indicated broader genetic diversity among the genotypes of different groups. Islam *et al.* (1995) also observed greater inter cluster distance than intra cluster distance in a multivariate analysis.

The highest inter cluster distance was noticed between the clusters I & II (22.607) and was followed by the distances between clusters III & II (20.961), V & II (19.904) and IV & II (17.759) (Table 10) which indicated that genotypes from cluster I & II, if involved in hybridization might produce a wide spectrum of segregating population.

On the other hand, the maximum intra cluster distance was found in cluster I (3.45) (Table 9) comprising eight genotypes which indicated that most diverse material would be found in cluster I while minimum was found in cluster V (1.43) (Table 9) comprising five genotypes which indicated least diversity. Moreover, cluster II and cluster III had exhibited zero (0.0) intra cluster distance due to insufficient number of genotypes per cluster.

The different multivariate analysis *viz.* principal component analysis (PCA), non-hierarchical cluster analysis and canonical variate analysis were superimposed in Figure 5, from which it could be concluded that different multivariate techniques supplemented and confirmed one another and it was obvious from the results of many researchers (Bashar, 2002; Uddin, 2001; Juned *et at.*, 1988 and Ario, 1987).

4.4.4. Contribution of characters towards divergence

Characters contributing maximum towards divergence were given greater emphasis for deciding on the cluster for the purpose of further selection and choice of parents for hybridization (Jagadev *et al*., 1991). For this reason, latent vectors were obtained from principal component analysis (PCA) (Table 11).

Table 9. Average intra and inter cluster distances (D^2 values) for twenty wheat (*Triticum aestivum* L.) genotypes

Cluster	I	II	III	IV	V
I	**3.45**	22.607	16.538	6.095	7.002
II		**0.00**	20.961	17.759	19.904
III			**0.00**	16.242	10.213
IV				**2.52**	7.391
V					**1.43**

* Bold figure denotes intra cluster distance

Table 10. List of five nearer and furtherer clusters from each cluster for comparing the divergence among wheat (*Triticum aestivum* L.) genotypes

Sl No.	Cluster	Nearest Cluster with D^2 values	Farthest Cluster with D^2 values
1	I	IV (6.095)	II (22.607)
2	II	IV (17.759)	I (22.607)
3	III	V (10.213)	II (20.961)
4	IV	I (6.095)	II (17.759)
5	V	I (7.002)	II (19.904)

Table 11. **Latent vectors for ten characters of twenty genotypes of wheat (*Triticum aestivum* L.)**

Characters	**Vector-1**	**Vector-2**
Plant height (cm)	-0.1244	-0.5464
Spikes/plant (no.)	-2.9489	-0.8257
Spike length (cm)	0.0549	0.2978
Grains/spike (no.)	0.5223	-0.0698
1000-grain weight (g)	0.3040	0.0796
Harvest index (%)	0.3062	0.6864
Vegetative period (days)	0.7283	1.0863
Grain filling period (days)	0.2674	0.5864
Days to maturity (days)	0.1579	-0.6459
Grain yield/plant (g)	-0.1874	-2.1261

In vector-I, spike length (0.0549), grains/spike (0.5223), 1000-grain weight (0.3040), harvest index (0.3062), vegetative period (0.7283), grain filling period (0.2674) and days to maturity (0.1579) (Table 11) showed positive result. It indicated that these characters exhibited significant contribution towards divergence for first principal component axis.

In vector-II, spike length (0.2978), 1000-grain weight (0.0796), harvest index (0.6864), vegetative period (1.0863) and grain filling period (0.5864) (Table 11) showed positive result. It indicated that these characters exhibited significant contribution towards divergence for second principal component axis.

The role of spike length, 1000-grain weight, harvest index, vegetative period and grain filling period was significant towards genetic divergence in both the vectors and could be considered for future hybridization.

4.4.5. Selection of parents for future hybridization

To identify specific parents for heterosis, genetic divergence and mean performance was studied (Aditya, 1995). Therefore, the genotype G_{12} (BARI Gom 22) for longest spike length and highest percentage of harvest index from cluster III, G_{15} (BARI Gom 25) for maximum 1000-grain weight from cluster III, G_6 (Akbar) for shorter vegetative period from cluster II and G_{10} (BARI Gom 20) for shorter grain filling period from cluster V could be selected for future hybridization program.

CHAPTER V

SUMMARY AND CONCLUSION

Current research was taken up with twenty genotypes of wheat (*Triticum aestivum* L.) at the field laboratory of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh during November, 2015 to April, 2016. The trial was conducted following Randomized Complete Block Design (RCBD) with three replications. Data on ten yield attributing characters *viz.* plant height, spikes per plant, spike length, grains/spike, 1000-grain weight, harvest index, vegetative period, grain filling period, days to maturity and grain yield/plant were recorded for statistical analysis.

From ANOVA, it was observed that out of ten characters, nine characters had shown highly significant variation where harvest index (245.228**), plant height (224.417**), grains/spike (119.104**) and 1000-grain weight (109.350**) showed the greater values. Besides, one character *i.e.* spikes/plant had shown significant variation (0.754*).

Mean agronomic performance in this study revealed that the tallest plant was G_6 (Akbar) achieving 95 cm height. Highest no. of spikes/plant (5.00) had obtained by G_{16} (BARI Gom 26), longest spike length (12.33 cm) by G_{12} (BARI Gom 22), highest no. of grains/spike (66.00) by G_6 (Akbar), maximum 1000-grain weight (56 g) by G_{15} (BARI Gom 25), highest percentage of harvest index (49.33%) by G_{12} (BARI Gom 22), shortest vegetative period (62.33 days) by G_4 (Sonalika), shortest grain filling period (39.33 days) by G_7 (Sourov) and G_{10} (BARI Gom 20), minimum days to maturity (101 days) by G_{20} (BARI Gom 30) and highest amount of grain yield/plant (6.60 g) had obtained by G_{15} (BARI Gom 25). It indicated that different genotypes performed better for different characters.

Moreover, it was observed that phenotypic variance for most of the characters were slightly higher than corresponding genotypic variance. It had indicated that there was less environmental influence along with additive gene effect. However, moderate environmental influence was observed over plant height (2.28), 1000-grain weight (2.20) and harvest index (1.80). Higher environmental influence was observed over grains/spike

(7.39). Again, phenotypic coefficient of variation (PCV) was also noticed slightly greater than genotypic coefficient of variation (GCV) which indicated towards least environmental influence. However, considerable amount of environmental variation was observed over spikes/plant (16.66), spike length (8.92), grains/spike (6.16) and harvest index (4.57). But GCV value (8.77) of spikes/plant was appeared much lower than ECV value (16.66) which suggested that selection of this trait would be ineffective. Therefore, Selection for grains/spike and harvest index would be rewarding for breeding purpose.

Estimation of heritability and genetic advance specified high heritability with high genetic advance for harvest index (H=97.83, GA=62.57) and grain yield/plant (H=98.99, GA=59.43). Plant height (H=97.01, GA=23.57), 1000-grain weight (H=94.19, GA=26.94) and grains/spike (H=83.43, GA=26.01) had shown high heritability associated with moderate genetic advance. These results indicated at the additive gene action and selection of these traits would be effective. Spike length had shown moderate heritability with moderate genetic advance (H=78.61, GA=31.23) which indicated at the additive gene action and selection of such trait would be reasonable. Although days to maturity (H=97.68, GA=4.14) had high heritability, selection would be misleading due to its lower genetic advance (4.14). Such result revealed that genes controlling this trait were non-additive gene but high heritability was due to favorable environmental influence. Vegetative period (H=75.51, GA=3.91) and grain filling period (H=78.33, GA=6.21) had shown moderate heritability but low genetic advance. Selection of this trait would be ineffective. However, spikes/plant (H=21.70, GA=8.42) had shown low heritability associated with low genetic advance which suggested that it was controlled by non-additive gene. Selection should be discarded in this case. Therefore, grain yield/plant and harvest index would give good response for yield improvement program.

Correlation coefficient analysis had shown that genotypic correlation co-efficient was slightly higher than the corresponding phenotypic correlation co-efficient for most of the characters. It revealed that phenotypic expression was modified due to the strong inherent association and environmental influence by reducing their phenotypic correlation values. In few cases, phenotypic correlation co-efficient was higher than their corresponding genotypic correlation co-efficient which suggested that both environmental and genotypic correlation, in these cases, act in the same direction and maximized their expression at phenotypic level. Grain yield/plant had shown highly significant and positive correlation with harvest index (G=0.783**, P=0.773**), spike length (G=0.563**, P=0.501**), 1000-grain weight (G=0.551**, P=0.534**) and grains/spike (G=0.487**, P=0.441**). It was indicated that if grain yield/plant was increased then harvest index, spike length, 1000-grain weight and grains/spike would also be increased. It had significant and positive correlation with plant height (G=0.316*, P=0.308*) which indicated that if grain yield/plant was increased then plant height would also be increased. Again, it had non-significant positive correlation with days to maturity (G=0.038, P=0.036) and non-significant negative correlation with grain filling period (G= -0.022, P= -0.035), spikes/plant (G= -0.068, P= -0.029) and vegetative period (G= -0.190, P= -0.163). Non-significant association of these traits indicated that the association between these traits was largely influenced by environmental factors.

Path coefficient analysis revealed that harvest index had highest positive direct effect (1.163) on grain yield/plant followed by spike length (0.554), spikes/plant (0.405), grains/spike (0.233), days to maturity (0.21) and vegetative period (0.004). Such results indicated that direct selection based on these characters would be effective for yield improvement in wheat (*Triticum aestivum* L.). On the other hand, negative direct effect on grain yield/plant was observed over plant height (-0.486), 1000-grain weight (-0.798) and grain filling period (-0.35). So direct selection based on these characters would be ineffective. 1000-grain weight had shown highest positive indirect effect (0.872) on grain yield/plant via harvest index whereas spike length showed the highest negative indirect effect (-0.615) via 1000-grain weight. Therefore, correlation and path coefficient studies discovered that harvest index, spike length, 1000-grain weight, grains/spike and spikes/plant and days to maturity were the most important yield contributing characters to grain yield/plant which could be taken under consideration for future hybridization program.

Genetic diversity analysis among twenty wheat (*Tritivum aestivum* L.) genotypes was performed through Principal Component Analysis (PCA), non-hierarchical cluster analysis and Canonical Variate Analysis (CVA) using GENSTAT computer program. From PCA it was observed that first two principal component axes were accounted for 54.38% of total variation among genotypes. According to the scatter diagram based on first two principal component axes, the genotypes were grouped into five divergent clusters. Among five clusters, cluster I contained maximum number of genotypes (8) followed by 5 genotypes in cluster V, 4 genotypes in cluster IV, 2 genotypes in cluster III and single genotype in cluster II. Non-hierarchical clustering confirmed this cluster pattern. Mean cluster value showed that spikes/plant, vegetative period, grain filling period and days to maturity were more or less similar for all the five clusters. Maximum range of variability was observed for plant height (66.37 cm to 95 cm) among all the characters in five clusters. Cluster I and II included most of the diverse characters including plant height, spike length, grains/spike and grain yield/plant which indicated that for developing high yielding varieties, genotypes of these groups could be selected in hybridization program.

Canonical variate analysis was done to compute the intra and inter cluster distances. The farthest inter-cluster distance was observed between clusters I and II (22.607) which indicated that distinct diversity was present there. On the other hand, the intra cluster distance was ranged between 1.43 and 3.45 where the maximum intra-cluster distance was found in cluster I (3.45) comprising eight genotypes which indicated that most diverse material would be found there. Cluster II and cluster III had exhibited zero (0.0) intra cluster distance due to insufficient number of genotypes per cluster.

The different multivariate analysis *viz.* principal component analysis, non-hierarchical cluster analysis and canonical variate analysis gave similar result showing confirmation for one another. However, contribution of characters towards divergence was determined by comparing the latent vectors. Out of ten, only five characters *viz.* spike length, 1000 grain weight, harvest index vegetative period and grain filling period were found to play significant role to contribute towards divergence.

Therefore, the genotype G_{12} (BARI Gom 22) for longest spike length and highest percentage of harvest index from cluster III, G_{15} (BARI Gom 25) for maximum 1000-grain weight from cluster III, G_6 (Akbar) for shorter vegetative period from cluster II and G_{10} (BARI Gom 20) for shorter grain filling period from cluster V could be selected for future hybridization program.

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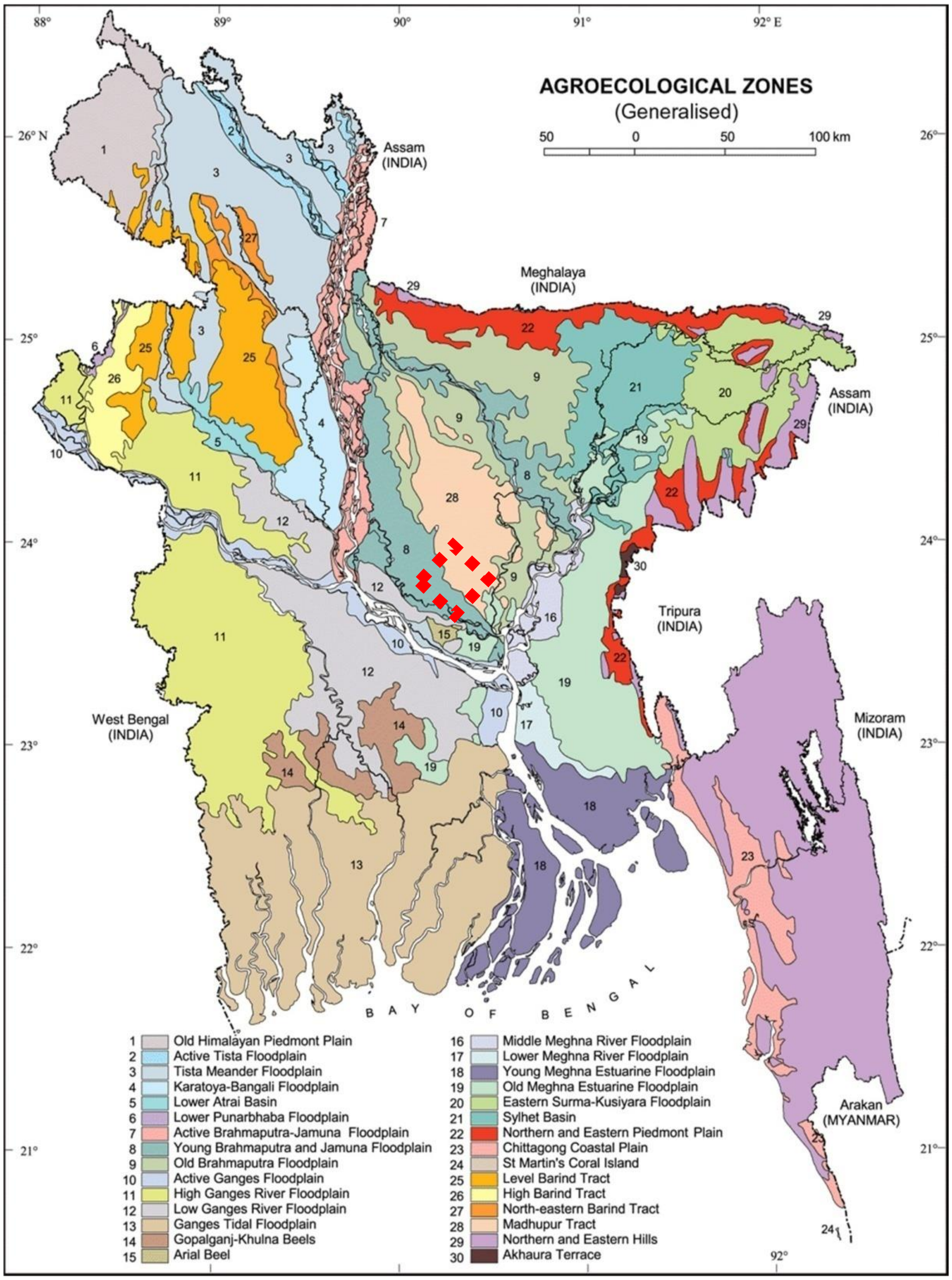
APPENDICES

Appendix I. Map showing the experimental site under the study



◆ The experimental site under study

Appendix II. Monthly records of air temperature, relative humidity and rainfall during the period from November, 2015 to April, 2016.

Month	Air temperature (ºC)*		Relative humidity (%)*	Rainfall (mm)
	Maximum	Minimum		
November, 2015	26.82	16.05	77	00
December, 2015	21.4	13.5	75	00
January, 2015	25.5	12.7	67	00
February, 2015	28.1	16.2	65	25
March, 2015	31.4	19.4	53	12

*Monthly average

* Source: Bangladesh Meteorological Department (Climate and weather division), Agargaon, Dhaka.

Appendix III. Soil properties of experimental field analyzed by Soil Resource Development Institute (SRDI), Khamarbari, Farmgate, Dhaka.

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Research Field, SAU, Dhaka
AEZ	Madhupur Tract (AEZ 28)
General Soil Type	Shallow red brown terrace soil
Land Type	High land
Soil Series	Tejgaon
Topography	Fairly leveled

B. Physical and chemical properties of the soil before experiment

Characteristics	Values
% Sand	28
% Silt	40
% Clay	32
Texture	Loamy
pH	5.6
Organic matter (%)	0.82
Total N (%)	0.05
Available P (ppm)	20.01
Exchangeable K (me/100g Soil)	0.11
Available S (ppm)	43

Appendix IV. Analysis of variance (ANOVA) for ten characters of twenty wheat (*Triticum aestivum* L.) genotypes

Source of Variation		**Replication**	**Genotype**	**Error**
Degrees of freedom (d.f.)		**r-1=(3-1)=2**	**g-1=(19-1)=19**	**(r-1)(g-1)=38**
Mean sum of square (MSS)	Plant height (cm)	6.254	224.417**	2.280
	Spikes/plant (no.)	7.850	0.754*	0.411
	Spike Length (cm)	0.117	7.523**	0.625
	Grains/spike (no.)	1.850	119.104**	7.394
	1000-grain weight (g)	3.150	109.350**	2.203
	Harvest Index (%)	9.867	245.228**	1.796
	Vegetative Period (days)	1.050	6.628**	0.646
	Grain filling period (days)	5.850	6.536**	0.552
	Days To Maturity (days)	1.217	14.206**	0.111
	Grain yield/plant (g)	0.056	4.090**	0.014

* denotes 5% level of probability

** denotes 1% level of probability

Appendix V. Mean performance of twenty wheat (*Triticum aestivum* L.) genotypes for different characters

Genotypes	Plant height (cm)	Spikes /plant (no.)	Spike length (cm)	Grains /spike (no.)	Thousand grain weight (g)	Harvest index (%)	Vegetative period (days)	Grain filling period (days)	Days to maturity (days)	Grain yield/plant (g)
Kanchan	63.33j	3.333c	6.667gh	37.00gh	36.67h	15.33n	66.33ab	40.67ef	108.0c	2.600jk
Protiva	65.00ij	3.333c	7.333fgh	41.33efg	35.67h	22.67jkl	64.33cde	40.33ef	104.7f	4.333e
Kallyansona	63.00j	4.000abc	6.000h	41.67defg	37.33h	19.33m	63.67def	45.67a	109.0b	2.733j
Sonalika	85.00b	4.333abc	6.000h	46.67bcd	38.00h	30.33g	67.67a	41.67cde	109.0b	2.967i
Durum	70.00fg	3.333c	8.333def	41.67defg	43.33fg	36.00d	62.33f	41.00de	107.0d	4.267ef
Akbar	95.00a	3.333c	11.00b	66.00a	49.67bc	37.00d	62.67f	41.67cde	110.0a	5.400c
Sourov	80.00cd	3.667bc	8.667def	45.00bcdef	41.67g	26.00hi	64.33cde	39.33 f	104.0g	3.400h
Gourob	74.00e	4.000abc	9.000de	45.00bcdef	47.00de	35.00de	64.33cde	39.43f	106.0e	4.067g
Aghrani	69.00gh	3.667bc	8.667def	40.00fg	38.33h	21.00lm	64.67cd	42.33bcd	106.7d	2.600jk
BARI Gom 20	74.00e	3.333c	9.000de	46.00bcde	47.00cde	33.33ef	64.33cde	39.33f	106.0e	4.067fg
BARI Gom 21	79.67d	4.000abc	7.667efg	40.00fg	49.00bcd	40.00c	65.67bc	42.33bcd	107.7c	5.700b
BARI Gom 22	86.00b	4.000abc	12.33a	50.00b	54.00a	49.33a	64.67cd	43.23b	106.7d	5.367c
BARI Gom 23	70.67fg	3.333c	9.333cd	34.33h	46.67de	24.00ijk	65.67bc	40.67ef	106.7d	3.067i
BARI Gom 24	78.67d	4.333abc	9.333cd	40.33fg	49.00bcd	31.33fg	67.33a	41.67cde	107.7c	3.500h
BARI Gom 25	72.67ef	4.000abc	10.67bc	46.00bcde	56.00a	46.00b	65.67bc	41.67cde	108.7b	6.600a
BARI Gom 26	70.00g	5.000a	9.333cd	42.67cdef	50.00b	21.67kl	63.67def	42.67bc	107.0d	2.400k
BARI Gom 27	73.33e	3.667bc	9.333cd	47.00bc	36.00h	26.67h	65.33bc	41.67cde	108.0c	4.800d
BARI Gom 28	82.33c	3.333c	9.667bcd	44.67cdef	43.00fg	23.33jkl	65.67bc	40.67ef	104.0g	3.433h
BARI Gom 29	67.00hi	4.333abc	9.667bcd	44.33cdef	43.67fg	24.67hij	62.67f	41.33cde	104.0g	4.400e
BARI Gom 30	63.00j	4.667ab	9.333cd	43.33cdef	45.00ef	23.67ijk	63.00ef	41.67cde	101.0h	4.700d
LSD	2.496	1.060	1.307	4.495	2.453	2.215	1.329	1.228	0.5507	0.1956
% CV	2.04	2.04	2.04	2.04	2.04	2.04	2.04	2.04	2.04	2.04
S_d	1.51	0.64	0.79	2.72	1.48	1.34	0.80	0.74	0.33	0.12
S.E.	0.57	0.24	0.30	1.03	0.56	0.51	0.30	0.28	0.13	0.04

LSD = Least significant difference, % CV = coefficient of variation in percent, S_d = Standard deviation, S.E. = Standard error, Values with same letter(s) are statistically identical at 5% level of probability.

Appendix VI. Principal component score I and II

Sl no.	PCA 1	PCA 2
1	20.510	-1.723
2	13.712	-0.969
3	16.281	-1.220
4	-5.574	-9.971
5	-0.617	6.382
6	-27.077	-15.181
7	-0.520	-6.621
8	-4.743	3.808
9	11.891	-2.395
10	-4.037	2.485
11	-10.227	6.328
12	-25.394	5.616
13	8.082	4.549
14	-4.254	2.184
15	-14.829	14.002
16	5.886	1.520
17	3.814	-6.010
18	-0.603	-8.523
19	7.328	1.402
20	10.372	4.336