

**GENETIC VARIATION AND INTERRELATIONSHIPS AMONG  
YIELD AND YIELD CONTRIBUTING TRAITS OF WHEAT**

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**JUNE, 2020**

**GENETIC VARIATION AND INTERRELATIONSHIPS AMONG  
YIELD AND YIELD CONTRIBUTING TRAITS OF WHEAT**

**By**

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A Thesis  
submitted to the Department of Genetics and Plant Breeding,  
Sher-e-Bangla Agricultural University, Dhaka  
in partial fulfillment of the requirements  
for the degree of

**MASTER OF SCIENCE (MS)  
IN  
GENETICS AND PLANT BREEDING**

**Semester: January-June, 2020**

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## **CERTIFICATE**

*This is to certify that the thesis entitled “GENETIC VARIATION AND INTERRELATIONSHIPS AMONG YIELD AND YIELD CONTRIBUTING TRAITS OF WHEAT” 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 (MS) in Genetics and Plant Breeding, embodies the results of a piece of bona fide research work carried out by BONNY AMIN, bearing Registration No. 12-04904 under my supervision and guidance. No part of this thesis has been submitted for any other degree or diploma in any other institution.*

*I further certify that any help or sources of information received during the course of this investigation has duly been acknowledged.*

*Dated: June, 2020*

*Dhaka, Bangladesh*

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*Dedicated To My  
Beloved Parents,  
Brothers and Teachers*

## ACKNOWLEDGEMENTS

Firstly, I am expressing my gratitude to the “**Almighty Allah**” (SWT) who has made me able to perform this research work and to submit the thesis successfully for the degree of Master of Science (M.S.) in **Genetics and Plant Breeding**. My deepest respect and love form the core of my heart is for “**Prophet Muhammad**” (SM) who is forever a torch of knowledge and guidance for humanity.

It is my great pleasure to express gratitude to my respected Supervisor, **Dr. Firoz Mahmud**, Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, for his continuous direction, scholastic supervision, constructive criticism, encouragement and valuable suggestions in carrying out the research work and preparation of this thesis. I was able to gather a lot of pleasant experience and enjoyed an independent working environment under his supervision.

I am conveying my earnest reverence, appraisal and enormous indebtedness to my respected Co-supervisor, **Dr. Md. Sarowar Hossain**, Professor, Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka, Bangladesh, for his sincere guidance, constructive suggestion, encouragement and amiable behavior during the whole period of the research.

I am also extremely grateful to **Prof. Dr. Kazi Md. Kamrul Huda**, Chairman, as well as to **Dr. Md. Shahidur Rashid Bhuiyan**, **Dr. Naheed Zeba**, **Dr. Jamilur Rahman**, **Dr. Mohammad Saiful Islam**, **Dr. Md. Asaduzzaman Siddiquee** and **Dr. Md. Abdur Rahim**, respected teachers of the Department of Genetics and Plant Breeding, Sher-e-Bangla Agricultural University, Dhaka for their valuable advices, and countless encouragement.

I am thankful to Bangladesh Agriculture Research Institute (Wheat Research Center), Gazipur and Bangladesh Agricultural Development Corporation, Seed Testing Laboratory and Training Center, Dhaka, to provide the seed and research support.

Special thanks went to my fellow mates and friends **Md. Abdullah Al Zaber**, **Shifullah Mahmud**, **Md. Shafiqur Rahman** and **Md. Azaharul Islam Arif**. They all supported me a lot during the period of experiment and without their co-operation the whole journey might be very difficult.

I also want to acknowledge the co-operation of our lab attendants, computer operator and all other staffs of the department as well as all staffs of Sher-e-Bangla Agricultural University, Dhaka, for their cordial support all time.

Finally, I recall indebtedness to my beloved parents and the family members along with relatives and well-wishers for their boundless affection prayers, encouragement, constant inspiration and moral support for my higher study. May Almighty bless and protect them all.

June, 2020  
SAU, Dhaka

The Author

## LIST OF CONTENTS

<b>CHAPTER</b>	<b>TITLE</b>	<b>PAGE NO.</b>
	<b>ACKNOWLEDGEMENTS</b>	<b>I</b>
	<b>LIST OF CONTENTS</b>	<b>II-V</b>
	<b>LIST OF TABLES</b>	<b>VI</b>
	<b>LIST OF PLATES</b>	<b>VII</b>
	<b>LIST OF APPENDICES</b>	<b>VIII</b>
	<b>ABBREVIATIONS AND SYMBOLS</b>	<b>IX</b>
	<b>ABSTRACT</b>	<b>X</b>
<b>I</b>	<b>INTRODUCTION</b>	<b>1-3</b>
<b>II</b>	<b>REVIEW OF LITERATURE</b>	<b>4-13</b>
	2.1 <b>Genetic Variability, Heritability and Genetic Advance</b>	4
	2.2 <b>Correlation Analysis</b>	8
	2.3 <b>Path Coefficient Analysis</b>	10
<b>III</b>	<b>MATERIALS AND METHODS</b>	<b>14-28</b>
	<b>3.1 Site Description</b>	<b>14</b>
	3.1.1 Location	14
	3.1.2 Soil and climate	14
	<b>3.2 Experimental Details</b>	<b>14</b>
	3.2.1 Plant materials	14
	3.2.2 Design and layout	15
	<b>3.3 Production Technology of Wheat</b>	<b>15</b>
	3.3.1 Land and Soil	15
	3.3.2 Seed rate	15
	3.3.3 Seed treatment	15
	3.3.4 Time of sowing	17
	3.3.5 Land preparation	17

<b>CHAPTER</b>	<b>TITLE</b>	<b>PAGE NO.</b>
3.3.6	Fertilizer application	17
3.3.7	Seed Treatment	19
3.3.8	Sowing method	19
3.3.9	Irrigation	19
3.3.10	Intercultural Operation	19
<b>3.4</b>	<b>Description of Data Collected</b>	<b>21</b>
3.4.1	Days to maturity	21
3.4.2	Plant height at maturity (cm)	21
3.4.3	Number of productive tillers per plant	21
3.4.4	Spike length (cm)	21
3.4.5	Peduncle length (cm)	21
3.4.6	Number of spikelets per spike	21
3.4.7	Number of grains per spike	22
3.4.8	Biological yield per plant (g)	22
3.4.9	Biomass/plot (g)	22
3.4.10	Harvest index (%)	22
3.4.11	1000 grain weight (g)	22
3.4.12	Grain yield per plant (g)	22
<b>3.5</b>	<b>Statistical Analysis</b>	<b>24</b>
3.5.1	Estimation of genetic parameters	25
3.5.2	Estimation of genotypic coefficient variation and phenotypic coefficient of variation	25
3.5.3	Estimation of heritability	26
3.5.4	Estimation of genetic advance	26
3.5.5	Estimation of genetic advance percent mean GA (%)	27
3.5.6	Estimation of correlation	27
3.5.7	Path co-efficient analysis	28

<b>CHAPTER</b>	<b>TITLE</b>	<b>PAGE NO.</b>
<b>IV</b>	<b>RESULTS AND DISCUSSION</b>	<b>29-49</b>
<b>4.1</b>	<b>Genetic Parameters</b>	<b>29</b>
<b>4.2</b>	<b>Genetic Variability, Heritability And Genetic Advance</b>	<b>29</b>
4.2.1	Days to maturity	29
4.2.2	Plant height at maturity, (cm)	30
4.2.3	Number of productive tillers per plant	32
4.2.4	Spike length (cm)	32
4.2.5	Peduncle length (cm)	33
4.2.6	Number of spikelets per spike	33
4.2.7	Number of grains per spike	35
4.2.8	Biological yield per plant (g)	35
4.2.9	Biomass/plot (g)	36
4.2.10	Harvest index (%)	36
4.2.11	1000 grain weight (g)	38
4.2.12	Grain yield per plant (g)	38
<b>4.3</b>	<b>Correlation Analysis</b>	<b>39</b>
4.3.1	Days to maturity	39
4.3.2	Plant height	41
4.3.3	Number of productive tillers per plant	41
4.3.4	Spike length	42
4.3.5	Peduncle length	42
4.3.6	Number of spikelets per spike	42
4.3.7	Number of grains per spike	43
4.3.8	Biological yield per plant	43
4.3.9	Biomass/plot	43
4.3.10	Harvest index	43
4.3.11	1000 grain weight	43
<b>4.4</b>	<b>Path Coefficient Analysis</b>	<b>44</b>
4.4.1	Days to maturity	44
4.4.2	Plant height	45



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<b>CHAPTER</b>	<b>TITLE</b>	<b>PAGE NO.</b>	
	4.4.3	Number of productive tillers per plant	45
	4.4.4	Spike length	45
	4.4.5	Peduncle length	46
	4.4.6	Number of spikelets per spike	46
	4.4.7	Number of grains per spike	48
	4.4.8	Biological yield per plant	48
	4.4.9	Biomass/plot	48
	4.4.10	Harvest index	49
	4.4.11	1000 grain weight	49
	4.4.12	Residual Effects	49
<b>V</b>	<b>SUMMARY AND CONCLUSION</b>	<b>50-51</b>	
	<b>REFERENCES</b>	<b>52-59</b>	
	<b>APPENDICES</b>	<b>60-62</b>	

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## LIST OF TABLES

TABLE NO.	TITLE	PAGE NO.
1	List of 10 wheat varieties along with their sources	16
2	Analysis of variance for twelve characters in wheat varieties	31
3	Mean analysis of yield contributing parameters	34
4	Estimation of genetic parameters in twelve characters of ten genotypes in wheat	37
5	Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of wheat	40
6	Path coefficient analysis showing direct (bold) and indirect effects of different characters on yield of Wheat	47

## LIST OF PLATES

PLATE NO.	TITLE	PAGE NO.
1	Research field after sowing	18
2	Crown Root Initiation stage	18
3	Irrigation at 18 DAS	18
4	Fertilizer application	18
5	Flowering stage of wheat	20
6	Field at the ripening stage	20
7	Researcher in the field	20
8	Harvesting stage of wheat	20
9	1000 seed weight of different wheat varieties (V1R2, V2R2, V3R1 and V9R3)	23

## LIST OF APPENDICES

PLATE NO.	TITLE	PAGE NO.
I	Map showing the experimental site under the study	60
II	Morphological, physical and chemical characteristics of initial soil (0-15 cm depth) of the experimental site	61-62

## LIST OF ABBREVIATIONS AND SYMBOLS

Abbreviation/ Symbol	Full Word
%	Percentage
&	And
Agric.	Agriculture
Agril.	Agricultural
BARI	Bangladesh Agricultural Research Institute
BADC	Bangladesh Agricultural Development Corporation
Breed.	Breeding
Cm	Centimeter
CV (%)	Coefficient of Variation
SD	Standard Variation
DAS	Days After Sowing
<i>et al.</i>	And Others
g	Gram
GA	Genetic Advance
GCV	Genotypic Coefficient of Variation
i.e.	That is
J.	Journal
L	Litre
mm	Millimeter
MT	Metric Ton
°	Degree Centigrade
PCV	Phenotypic Coefficient of Variation
SAU	Sher-E-Bangla Agricultural University
T	Ton
viz.	Namely

# **GENETIC VARIATION AND INTERRELATIONSHIPS AMONG YIELD AND YIELD CONTRIBUTING TRAITS OF WHEAT**

**BY  
BONNY AMIN**

## **ABSTRACT**

An experiment was carried out at the Research Field of Sher-e-Bangla Agricultural University, Dhaka, Bangladesh with 10 wheat varieties, sown in RCBD with 3 replications during November 2018 to March 2019. The purpose of this field experiment was to select the best varieties crossing for further research program. Analysis of variance showed significant differences among the varieties for all the traits. Days to maturity (0.84), plant height at maturity, (cm) (1.96), peduncle length (cm) (2.37), number of spikelet per spike (5.65), number of grains per spike (1.05) and grain yield per plant (g) (3.68) showed minimum difference between genotypic and phenotypic variance. Biomass/plot (g) showed high heritability (65.54) coupled with high genetic advance (370.17) and very high genetic advance (28.11) in percentage of mean. Correlation revealed that grain yield per plant had positive genotypic and phenotypic association with days to maturity ( $G = 0.996$  and  $P = 0.832$ ), number of productive tillers per plant ( $G = 0.444$  and  $P = 0.336$ ) and spike length (cm) ( $G = 0.761$  and  $P = 0.111$ ). Path analysis revealed that days to maturity (0.859), number of productive tillers per plant (0.078) and number of grains per spike (0.217) had positive direct effect on grain yield.

# CHAPTER I

## INTRODUCTION

Wheat (*Triticum aestivum L.*) is the world's most cultivated food crop under the family of Poaceae. The cereal crop is the second most-produced cereal after maize. It is known as the king of all cereal crops as it is widely grown than any other staple food crop, ecologically suitable and an essential source of carbohydrates. It has a high protein content of about 13% and a rich source of multiple nutrients and dietary fiber, which is relatively high compared to other major cereals.

In 2019, global wheat production 762.2M tonnes, growing by 3.9% compared with the previous year. The highest wheat-producing countries in 2019 were China (134M tonnes), India (102M tonnes) and Russia (75M tonnes), which combines a 41% contribution to global production, Global Wheat Exports (2020). Whereas, in 2019, wheat production for Bangladesh was only 1,200 thousand tonnes. Though wheat production of Bangladesh increased from 107 thousand tonnes in 1970 to 1,200 thousand tonnes in 2019 grew at an average annual rate of 7.12% (Bangladesh-Wheat production quantity, 2019). It is far too low production, comparing it to the national demand and highest wheat-producing countries globally.

It is estimated that in 2020 wheat production in Bangladesh will be 1250 (1000 MT), with an increase of 4.17 % than the previous year's national wheat production. However, in the 2020-21 marketing year, wheat imports will be 6.4 million tonnes (Bangladesh Grain Output, 2020).

So, it becomes mandatory to enhance wheat yield to satisfy the market demand by implementing a wheat hybridization program.

Yield is a complex trait, which results from the interaction between several inherent potentialities and the environment. It is an excellent choice to select the desirable genotypes under a planned breeding program to increase wheat yield. With the knowledge of yield contributing traits existing in available wheat genotypes, it becomes easier to select plant breeding materials and associate the desired characters.

Genotypic variation, heritability and genetic advance were measured for different yield contributing characters in wheat by many researchers (Kheiralla *et al.* 1993, Subhani and Khaliq 1994, Gupta and Verma 2000, Jedynski 2001). They disclosed that desirable character selection was useful to get high-yielding varieties by a population that showed broad genetic variability and high heritability. Several researchers found the components of variance, the correlation among yield contributing characters, and direct and indirect positive effects on yield (Tamam *et al.* 2000, Ismail *et al.* 2001, Kumar and Sukla 2002, Satyavart *et al.* 2002).

Continued wheat breeding programs with the selection of new germplasm materials as a donor of adapted genes are essential for developing new wheat cultivars (Fu, 2015 and Cobb *et al.* 2018) as the parents selected from wide genetic distance show present hybrid vigor with high yield performance. Therefore, evaluating genetic variation, pattern, and degree of genetic diversity helps breeders select diverse parents to be crossed in wheat hybridization programs (Ahmadi *et al.* 2012, Sajjad *et al.* 2018).

The phenotypic coefficients variation (PCV) and genotypic coefficients variation (GCV), heritability, and genetic advance for yield and yield contributing traits are significant concerns for wheat plant breeders (Rahman *et al.* 2016 and Rajput 2019). Simultaneously, the direction and correlation between grain yield and contributing characters determine the efficiency of breeding programs.

Besides, each trait's relative importance increased grain yield production (Naik *et al.* 2015, Rahman *et al.* 2016, Shamuyarira *et al.* 2019). Selection for grain yield considering other related characters as indirect selection criteria is an alternative breeding approach.

Likewise, genotypic and phenotypic correlations among traits could help in the breeding program through indirect selection for yield contributing characters by identifying the least essential characteristics that are easier to measure (Anil *et al.* 2012 and Jassim, 2019). Consequently, path analysis is an excellent statistical way to break down the correlations of yield contributing characters with grain yield into their direct and indirect effects (Anand *et al.* 2016, Meles *et al.* 2017, Rajput, 2019).



### **Objectives of this research**

- (i) Evaluate genetic variation as per quantitative traits of wheat genotypes
- (ii) Determine the interrelationships among yield and yield contributing traits
- (iii) Estimate the direct and indirect effect of correlated yield contributing characters

## **CHAPTER II**

### **REVIEW OF LITERATURE**

Wheat (*Triticum aestivum* L.) is the second most important staple food crop in Bangladesh. Its importance as a food and nutrition security crop has increased since independence. The country spent a considerable amount of foreign currency to import wheat, which could be reduced through enhancing and developing the existing germplasms. For this purpose, the genetic variability and diversity of the current germplasm should be evaluated and reviewed. Extensive research on wheat breeding has been performed in many countries to improve yield and yield contributing characters. Many literary works are available on genetic variability, correlation and path analysis of yield and yield contributing characters of wheat grown under a particular environment. An attempt has been made here to summarize the overall previous research findings relevant to the present experiment. Much research is found in journals, online, and books related to genetic heritability, correlation analysis, path correlation analysis, and genetic diversity analysis. Brief details of the previous research works are illustrated below, such as –

- ❖ Genetic variability, heritability and genetic advance
- ❖ Correlation analysis
- ❖ Path coefficient analysis

#### **2.1 Genetic Variability, Heritability and Genetic Advance**

Chaturvedi and Gupta (1995) carried out the genetic analysis for 12 grain and quality characters in 44 strains of spring wheat, using Raj 3077 and K78 as controls. Highly significant differences occurred in most of the characters studied. Generally, phenotypic variation was higher than the genotypic variation. Heritability estimates were high for protein content, spike length and plant height, moderate for seed hardness, flowering time, time to maturity, 1000-grain weight and grain weight/spike and low for the other traits.

Shoran (1995) researched to analyze phenotypic coefficients of variation (PCV) and genotypic coefficients of variation (GCV), Genetic advance (GA), heritability, and path coefficients for 12 characters. It was estimated in 50 genotypes of winter wheat (*Triticum aestivum*). High estimates of PCV, GCV, heritability and GA indicated scope for improvement through simple selection for grain weight/spike, grain yield/plant, grains/spike, 1000-grain weight, biological yield/plant, harvest index, tillers/plant, spikes/plant, and plant height. However, there was little variability and scope for selecting the material for days to flowering and maturity and spikelets/spike. Path analysis further indicated the importance of biological yield/plant, harvest index and grain weight/spike, as these characters showed the highest direct effects on grain yield.

Moghaddam *et al.* (1998) investigated moderate genetic variation observed for the number of spikes/plant, the number of grains spike<sup>-1</sup>, and grain weight in the wheat genotypes. They estimated 43 to 97% heritability for different traits. Genetic advance means percentage was around 20% for the number of spikes/plant, the number of grains spike<sup>-1</sup> and 1000-grain weight.

Based on the results experimented by Leilah and Al-Khateeb (2005) it is reasonable to assume that a high yield of wheat plants under drought conditions could be obtained by selecting breeding materials with high spikes/m<sup>2</sup>, 1000-grain weight, weight of grains/spike and biological yield.

Singh *et al.* (2006) experiment was carried out during 2002-04 for the purpose of studying genetic variability, heritability, genetic advance and interrelationships. It was estimated for ten yield contributing characters in wheat (*Triticum aestivum* L.) under waterlogged reclaimed soils. High values of phenotypic coefficient of variability, genotypic coefficient of variability, heritability and genetic advance indicated improvement scope in biomass/m<sup>2</sup>, grain yield/m<sup>2</sup>, tillers/ m<sup>2</sup>, plant height and grains/ear through selection.

Ali *et al.* (2008) investigated moderate heritability for the number of productive tillers per plant. High heritability was estimated for plant height, number of spikelets/spike, spike length, number of grains/spike, grain yield/plant and 1000 grain weight. Also, these traits indicated high genetic advance.

Ajmal *et al.* (2009) experimented with broad sense heritability, genetic advance and correlation coefficients for yield contributing characters in six wheat varieties. Also, their 12 F<sub>2</sub> progenies were investigated. The genotypes were highly different for plant height, number of tillers/plant, number of spikelets/spike, grains/spike and grain yield/plant.

The magnitude of broad sense heritability of plant height, tillers per plant, grains per spike and grain yield was high with values 0.94, 0.98, 0.92 and 0.91, respectively, and was low in number of spikelets per spike (0.24). The values of genetic advance ranged from 0.044 in 1000 grain weight to 25.289 in plant height investigated by Ajmal *et al.* (2009). Relatively high estimates of heritability and genetic advance for plant height, number of tillers, and grains per spike suggested that selection for these traits could be practiced more effectively.

Kotal *et al.* (2010) revealed the genetic advance as a percent over mean was formed high in the number of spikelets per panicle, days to maturity, grain yield per plant, harvest index and number of effective tillers per plant. GCV alone is not sufficient to determine the extent of variation perpetuated from one generation to the next. Also, they tested the genetic advance as a percent over mean was formed days to maturity, high in the number of spikelets per panicle, harvest index, grain yield per plant, and number of productive tillers/plant.

Gelalcha and Hanchinal (2013) had revealed that the residual effect in the present study was 0.065, showing that the component factors explained 93.5% of the variability in grain yield. This further concluded that the choice of yield attributing traits in the study was quite perfect. From the result of this experiment, it can be concluded that the genotypic and phenotypic correlations were consistent. Hence, there was little intervention of environmental effects in the expression of the characters.

An experiment carried by Kumar *et al.* (2014) observed that GCV and PCV were the highest estimates for grain yield per plant. Followed by biological yield and harvest index (GCV 22.87 and PCV 23.03) showed the highest GCV and PCV. Whereas, heritability analysis revealed that biological yield per plant was the highest heritability. Genetic advance showed that it was high for plant height,

biological yield per plant, and moderately related to harvest index and test weight; and the low genetic advance was observed for spike length. The research concluded that plant height, 1000 seed weight, and harvest index should be the most priority to select traits for breeding in wheat as these characters showed high heritability and high genetic advance. Moreover, analysis of variance revealed that most of the studied characteristics were highly significant among the selected genotypes.

Amin *et al.* (2015) The experiment was carried out with 50 wheat lines to study their genotypic variability, heritability, GCV, PCV, genetic advance, and CV percent considering 14 morphological characters at the experimental field of Regional Wheat Research Centre (RWRC), Bangladesh Agricultural Research Institute (BARI), Gazipur during November 2010 to March 2010. A significant variation was observed among the genotypes for all characters studied. High GCV and PCV values were observed for grain filling duration, grain filling rate, and seed yield. High heritability and higher genetic advance were observed for spikelets/spike and yield kg/ha.

Tripathi *et al.* (2015) experimented with genetic variability in wheat's 30 diverse genotypes during the Rabi season of 2007-2008 in Allahabad. The research revealed that there is a highly significant difference present among all the characters studied. It indicates the presence of substantial genetic variability among all the selected genotypes. The phenotypic and genotypic coefficient of variation (PCV and GCV) were moderate-high for the number of tillers per plant, later on, grain yield per plant and biological yield per plant. Whereas the heritability was the highest for plant height, followed by yield per plant, number of grains/spike, and grain yield per plant. It was observed that plant height and harvest index indicate substantial variability due to high heritability and high genetic advance.

Gharib *et al.* (2019) researched 35 wheat genotypes selected to clarify the interrelationships between yield and the yield contributing traits in Egypt during the 2015-2016 and 2016- 2017 growing seasons. The experiment showed that heritability in broad sense ( $h^2_b$ ) values were high for plant height (90.63 and 97.81 %), the number of grains/spike (95.33 and 84.66 %), 1000-grain weight (76.42

and 84.03 %), and days to maturity (86.18 and 66.56 %) during the first and second seasons, respectively. Also, there were positive genotypic and phenotypic correlations among the selected traits.

A field experiment by Mullualem *et al.* (2020) was designed with six blocks, and a total of 60 accessions and four checks were studied. This research revealed that the phenotypic coefficient of variation was higher than the genotypic coefficient of variation for all traits *viz.* the number of tillers/plant, plant height at maturity, biomass, and the number of spikelets/spike, which reveals that there was an environmental effect on these characters. The results also showed a highly significant difference among the samples for most of the traits studied. High heritability was also found for the number of tillers/plant, plant height at maturity, biomass, and the number of spikelets/spike at both experiment fields. This study revealed that the selection of these characters is highly potential in improving grain yield.

## **2.2 Correlation Analysis**

Comparison of high height with low height, it was experimented by Law *et al.* (1978). Their research revealed that grain yield was reduced for the plant's low height. Correlating height with the other yield contributing characters described that medium height would tend to have a positive correlated effect for increased yield. In different words, not too short would have correlated adverse effects on yield, and not too tall could create lodging.

García Del Moral *et al.* (2003) investigated wheat genotype selections based on simple correlation coefficients without regard to interactions among yield and yield components that may mislead the breeders to reach their primary breeding purposes.

Through an experiment, Okuyama *et al.* (2004) revealed direct effects on the yield of the number of spikes and the number of grains/spike, and both are positively correlated. Also, it showed high magnitude, and the total correlation coefficients of grain yield are intermediate with the number of spike  $m^{-2}$  and the number of

grains per spike. Therefore, the natural selection of these traits would be enough to increase grain yield. Likewise, the same result shows in the present research that the number of spikes  $m^{-2}$ , the number of grains per spike, and biomass of the yield should be considered particular traits for wheat yield increase.

Singh *et al.* (2006) experiment showed a significant correlation between grain yield and days to maturity, plant height, ear length, spikelets/ear, tillers/ $m^2$ , grain/ear and biomass/ $m^2$  under normal and with spikelets/ear, tillers/ $m^2$  and biomass/ $m^2$  under the waterlogged indicated scope for improving grain yield through simultaneous selection.

Ali *et al.* (2008) showed that grain yield per plant showed a highly significant positive correlation with the number of productive tillers per plant, the number of spikelets per spike and the number of grains per spike, and a significant positive correlation spike length.

Ajmal *et al.* (2009) experiment revealed that plant height significantly correlated with tillers' number at phenotypic and genotypic coefficients. Tillers per plant displayed a negative relationship with spikelets per spike and 1000 grain weight and the number of grains per spike.

Chhibber and Jain (2014) concluded that grain yield has a positive correlation with stem length, number of tillers, dry matter weight, and biological yield. Simultaneously, the plant's vegetative weight and reproductive dry matter content are positively correlated with the number of tillers, grain yield, and biological yield. As there is a positive correlation between biological yield and grain yield, grain yield can be improved by increasing biological yield. The increased biological yield would help aggregate more photosynthetic elements in developing grain.

Experiments by Ahmad *et al.* (2018) revealed that grain yield per plant has a highly significant positive inter-relationship with biological yield per plant (0.787 and 0.606), spike length (0.320 and 0.297), number of tillers per plant (0.500 and 0.383), and number of spikelets per spike (0.565 and 0.358). These results showed at both the genotypic and phenotypic levels. Whereas biological yield per plant (1.125) showed the highest positive direct association on grain yield later on

harvest index (0.678), days to maturity (0.100), the number of spikelets per spike (0.109), and spike length (0.060). Finally concluded, these characters can serve as the most significant selection criterion for wheat's increased grain yield.

### **2.3 Path Coefficient Analysis**

Law *et al.* (1978) has revealed that F3, F4 and F5 lines showed that both yields per plant and final plant height were positively correlated. This correlation occurred irrespective of plant spacing. Selection for height was found to be more effective at improving yield than direct selection for yield. The positive correlation between height and yield was observed among a set of inter-varietal chromosome substitution lines. At least one chromosome from each homologous group was shown to participate in this correlation, suggesting that all the chromosomes of wheat carry genes affecting this relationship.

Ehdaie and Waines (1989) observed that days to maturity, plant height. The number of spikes plant<sup>-1</sup>, number of grains spike<sup>-1</sup>, 1000-grain weight, and harvest index each had a positive direct effect on grain yield. The first two characters exhibited the highest and lowest direct effects, respectively. Effects of days to maturity, plant height, and the number of spikes plant<sup>-1</sup> were wholly or partially counter-balanced by their strong adverse indirect effects through the number of grains spike<sup>-1</sup>. 1000 grain weight and harvest index.

Reynolds *et al.* (1994) investigated sixteen spring wheat genotypes grown under hot, irrigated and low latitude locations during winter cropping cycles in 1990-1991 and 1991-1992 in Mexico, Egypt, India and Sudan. In 1990 and 1991, winter cycles in Brazil. The morphological traits such as above-ground biomass at maturity, grains m<sup>-2</sup>, days to anthesis and days to maturity. It was measured on both sowing dates in Mexico showed generally significant correlations with yields measured at the other sites.



Singh *et al.* (2006) experiment revealed path analysis further supported and highlighted the importance of biomass/m, plant height, spikelets/ear, days to heading and days to maturity under drained conditions and biomass/m, spikelets/ear and days to maturity under waterlogging conditions.

Ali *et al.* (2008) path coefficient analysis revealed that the number of productive tillers/plant and the number of grains/spike had the highest direct effect on grain yield/plant. Each must be given preference in selection along with optimum plant height to select superior wheat genotypes.

Ajmal *et al.* (2009) research showed that grain yield was positively and significantly correlated with the number of grains/spike and 1000 grain weight. Hence the traits are emphasized in the selection of wheat genotypes for improving productivity.

Iftikhar *et al.* (2012) revealed inter-relationship among yield and different yield-related traits were investigated by correlation and path coefficient analysis through sowing wheat varieties/lines under moisture stress conditions using randomized complete block design with three replications. The obtained results indicated that grain yield had a positive correlation with spike length, peduncle length, 1000-grain weight and grains per spike, whereas negative correlation with days to heading, plant height and tillers per plant.

Mohammadi *et al.* (2012) investigated the influence of 1000 kernel weight on grain yield in both environments because grain yield in wheat is frequently the sink limited. For this reason, the 1000 seed weight has been reported as a good trait for increasing grain yield in wheat under different conditions. The nearly equal value of correlation and path coefficients of plant height and grain yield showed plant height had a positive and direct effect on grain yield in both conditions and suggesting a criteria trait for improving grain yield. The results showed that genotype 12 is a high yielding potential genotype in limited moisture conditions.

Gelalcha and Hanchinal (2013) had revealed that traits such as number of tillers per plant, number of spikes/square meter, number of grains per spike, biomass and harvest index, which showed highly significant correlation with grain yield, can be used as selection indices in grain yield improvement. Except for days to flowering and plant height, all the traits affected grain yield indirectly, mainly through total biomass production. Therefore, selection for biomass will possibly improve other component characters, thereby improving grain yield

Chhibber and Jain (2014) research showed that the number of spikes/m<sup>2</sup>, the weight of grains/spike, biological yield, and 1000-grain weight were the highest potential yield contributing characters in influencing grain yield.

Nasri *et al.* (2014) investigated thousand-grain weight, the number of grains/spike, and the height plant showed significant positive correlations. In this research, the harvest index also showed a positive indirect effect ( $P = 0.51$ ) on grain yield. The highest negative direct effect was revealed for grain yield was found for the number of fertile spikes ( $P = - 0.449$ ) and the highest negative indirect effect for harvest index ( $P = - 0.35$ ). Finally, the number of fertile spikes was showed the highest impact on grain yield.

Ayer *et al.* (2017) investigated direct effects on grain yield. The highest (0.30-0.99) positive direct effect on grain yield was exhibited by biological yield (0.737) followed by harvest index (0.555). The positive direct effect on grain yield was also exhibited by 1000 grain weight (0.072) followed by days to flag leaf emergence (0.063), days to maturity (0.054), days to booting (0.043), days to heading (0.032), flag leaf area (0.018) and grains per spike (0.010). While days to anthesis followed by AUSRC at anthesis, days to flag leaf senescence, plant height, spike length and peduncle length negatively affected the grain yield, respectively -0.072, -0.044, -0.037, -0.028, -0.006 and -0.006.

Genotypic path analysis assessed by Rajput (2019) revealed that the weight of grains/spike exhibited a positive and robust association with grain yield and the highest positive direct effects on grain yield. Therefore, the weight of grains/spike should be preferred for a quick increase in grain yield.

Gharib *et al.* (2019) path analysis revealed direct effects on wheat grain yield for all traits and positively correlated in both seasons except days to maturity and plant height in the second season.

## **CHAPTER III**

### **MATERIALS AND METHODS**

The study was conducted in the research field of Sher-e-Bangla Agricultural University (SAU), Sher-e-Bangla Nagar, Dhaka-1207. The sowing date was 16 November 2018 for all the varieties. The materials and methods which were used for the research experiments are briefly described under the following headings:

#### **3.1 Site Description**

##### **3.1.1 Location**

The experimental field was located at 90° 33.5. E longitude and 23° 77.4' N latitude at an altitude of 9 meters above the sea level. The field experiment was set up on the medium high land of the experimental farm.

##### **3.1.2 Soil and climate**

The experiment site's soil was a medium high land, clay loam in texture and pH 5.47-5.63. The land was located in the Agro-ecological Zone of 'Madhupur Tract' (AEZ No. 28). The climate of the experimental site is sub-tropical, characterized by heavy rainfall from April to July. Also, sporadic rain occurs during the rest of the year.

#### **3.2 Experimental Details**

##### **3.2.1 Plant materials**

The experimental materials of the study were comprised of 10 wheat varieties (Table 1). The seed will be collected from **1.** Regional Wheat Research Centre, Bangladesh Agricultural Research Institute (BARI), Joydebpur, Gazipur-1701. **2.** Seed Testing Laboratory and Training Centre, Bangladesh Agricultural Development Corporation (BADDC), Majar road, Gabtoli, Dhaka-1216.

### **3.2.2 Design and layout**

The total area of the research area was 275 m<sup>2</sup>, which was subdivided into 30 plots. Each subplot length was 2.5 m and width 2 m, consisting of the whole subplot 5 m<sup>2</sup>. Plot to plot distance east to west and north to south was 75 cm and 50 cm, respectively. In each plot, 10 rows were maintained to sow the wheat seeds.

The experiment was conducted in Randomized Complete Block Design (RCBD) with three replications. The genotypes were randomly distributed within the replication. The experiment was established on one planting date on 16 November 2018.

## **3.3 Production Technology of Wheat**

### **3.3.1 Land and soil**

Wheat can be cultivated in high land and medium high land. Also, it may be grown in medium low land where water is not logged from November. Land and soil should be well-drained. Generally, loam, sandy loam and clay loam soils are suitable for wheat. For rainfed wheat cultivation or cultivation with residual moisture, clay soil is desirable.

### **3.3.2 Seed rate**

Considering the seed germination rate, more than 80%, 120 kg wheat seed/hectare was sown. For the large-sized wheat variety (BARI Gom 24), 15-20 kg more seed per hectare was sown to maintain plant spacing uniformity.

### **3.3.3 Seed treatment**

Seed treatment was done with Provax-200 @ 3g per kg of seed before sowing. It increased the plant population by 20-25% and grain yield by about 10-12%.

**Table 1. List of 10 wheat varieties along with their sources**

Sl.	Indicating	Varieties	Scientific Name	Source Name
1	G1	BARI Gom 21 (Shatabdi)	<i>Triticum aestivum L.</i>	WRC, BARI
2	G2	BARI Gom 23 (Bijoy)	<i>Triticum aestivum L.</i>	WRC, BARI
3	G3	BARI Gom 24 (Prodip)	<i>Triticum aestivum L.</i>	STL, BADC
4	G4	BARI Gom 25	<i>Triticum aestivum L.</i>	STL, BADC
5	G5	BARI Gom 27	<i>Triticum aestivum L.</i>	STL, BADC
6	G6	BARI Gom 28	<i>Triticum aestivum L.</i>	STL, BADC
7	G7	BARI Gom 29	<i>Triticum aestivum L.</i>	WRC, BARI
8	G8	BARI Gom 30	<i>Triticum aestivum L.</i>	STL, BADC
9	G9	BARI Gom 31	<i>Triticum aestivum L.</i>	WRC, BARI
10	G10	BARI Gom 32	<i>Triticum aestivum L.</i>	WRC, BARI

WRC = Wheat Research Centre, Wheat Research Centre, Bangladesh Agricultural Research Institute (BARI)

STL = Seed Testing Laboratory and Training Centre, Bangladesh Agricultural Development Corporation (BADC)

### **3.3.4 Time of sowing**

The optimum sowing time for wheat is 15-30 November. Since the winter is prolonged to some extent in the northern region, seeds could be sown up to the first week of December for optimum yield. If seeds are sown beyond this time, yield may be decreased by 1.3% for each day delay. However, varieties like BARI Gom 23, BARI Gom 24, BARI Gom 25, BARI Gom 26, and BARI Gom 28 possess an adequate level of heat tolerance sown up to mid-December with a moderate yield Islam (2014). In this research, wheat was sown on 16 November 2018.

### **3.3.5 Land preparation**

The experiment was prepared by Power Tiller (2-Wheel Tractor) to maintain land at optimum “Zoe” (appropriate moisture level) condition. PT performs three functions, *i.e.* ploughing, seeding in rows and laddering, simultaneously. Excess ploughing may reduce soil moisture, which may affect seed germination.

There was a shortage of moisture in the soil. Therefore, irrigation was given before plough. Also, there was a shortage of moisture in the soil, and there was not enough time to allow the soil to reach the “Zoe” (appropriate moisture level) condition after the pre-sowing irrigation. Light irrigation was applied after sowing seeds for proper germination.

### **3.3.6 Fertilizer application**

Urea, TSP, MP, Gypsum and Boric acid were applied at 220, 150, 100, 100, 6-7 kg per hectare. Two-thirds ( $2/3$ ) of urea and all other fertilizers were applied at the final land preparation as a basal dose. The rest  $1/3$  urea was top-dressed at first irrigation (18 days after sowing).

In this research, Urea 4 kg, TSP 4 kg, MOP 2.5 kg, Gypsum 2.7 kg, Boric Acid 150 g, and  $ZoSo_4$  300 g were applied as a basal dose.

Lime (Dolomite) was applied @ 1.0 ton/ha once in 3 years cycle. Lime was mixed with the soil by ploughing 1-2 weeks before seeding.



**Plate 1. Research field after sowing**



**Plate 2. Crown Root Initiation stage**



**Plate 3. Irrigation at 18 DAS**



**Plate 4. Fertilizer application**



### **3.3.7 Seed treatment**

Before sowing, seeds were treated with Autostin 15 g and Sevin 1 packet.

### **3.3.8 Sowing method**

Seeds were sown 20 cm apart, maintaining row to row distance, and seed to seed to distance was 15 cm for better germination and intercultural practices.

### **3.3.9 Irrigation**

Two or three irrigations are essential, depending on the soil moisture condition. First, irrigation was applied at the 3-leaves stage, *i.e.* 18 DAS at Crown Root Initiation stage. If the soil was too dry, irrigation was given as early as 15 DAS. The first irrigation was very light, and excess water was drained out immediately. If there was enough moisture in the soil, irrigation was delayed for some days. The second and third irrigations were applied at the maximum tillering stage (57 DAS) and the early stage of grain filling (75 DAS). Additional irrigation before or after sowing was essential if there was not enough soil moisture for seed germination. Before starting irrigation, the weather condition was observed. If there was a possibility of rain, irrigation was delayed. Third irrigation was light to avoid lodging.

### **3.3.10 Intercultural operation**

First, weeding was done at 28 DAS for a good yield. Weeds were controlled by hand pulling method after the first irrigation. No herbicides were applied in this experiment during the wheat cultivation season.



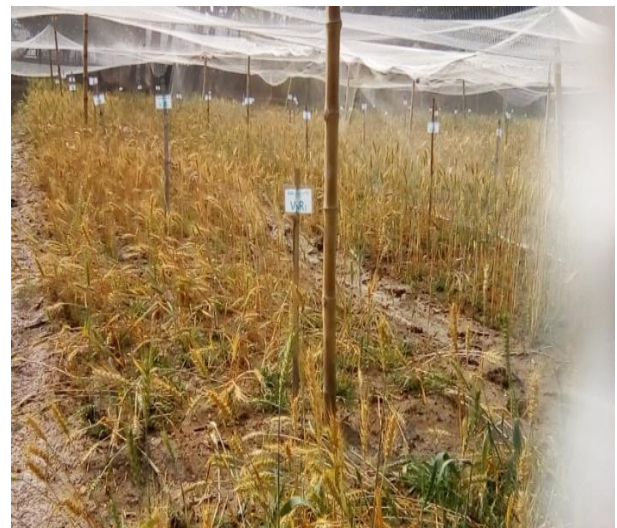
**Plate 5. Flowering stage of Wheat**



**Plate 6. Field at the ripening stage**



**Plate 7. Researcher at the field**



**Plate 8. Harvesting stage of Wheat**

### **3.4 Description of Data Collected**

The following attributes were collected in this research, selecting five plants randomly from each plot per replication.

The following attributes were collected based on the central four rows in each plot per replication.

#### **3.4.1 Days to maturity**

The total number of days from seed sowing to harvesting while the crop was in the field.

#### **3.4.2 Plant height at maturity (cm)**

The average height of five randomly taken plants at the maturity time from each plot of the replication was measured from the root ground level to the spike's top, including the awn.

#### **3.4.3 Number of productive tillers per plant**

The numbers of tillers per plant bearing productive heads were counted at harvest, and the average was recorded for the five randomly taken plants.

#### **3.4.4 Spike length (cm)**

The average spike length of five randomly taken plants from the central spike base to the top of the last spikelets, including awns, was recorded for each plot.

#### **3.4.5 Peduncle length (cm)**

Length from flag leaf to the base of the spike.

#### **3.4.6 Number of spikelets per spike**

The total number of spikelets on each plot's five plants' central spike was counted at maturity and the average was recorded.

#### **3.4.7 Number of grains per spike**

The total number of grains in the central spike was counted at harvest from five randomly taken plants.

#### **3.4.8 Biological yield per plant (g)**

Biological weight of each five randomly selected plants and the average was recorded.

#### **3.4.9 Biomass/plot (g)**

It was recorded by weighing the total above-ground yield harvested from each experimental plot at harvest time.

#### **3.4.10 Harvest index (%)**

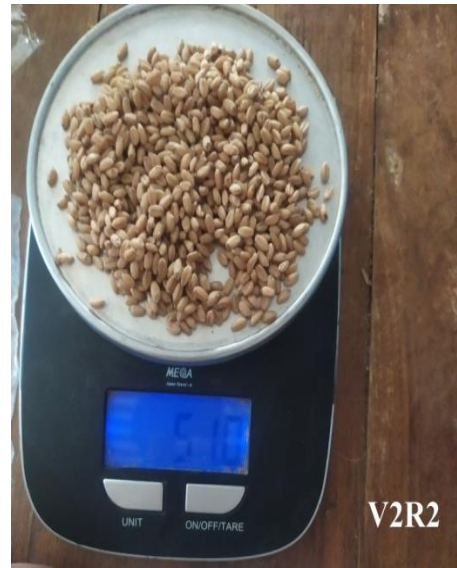
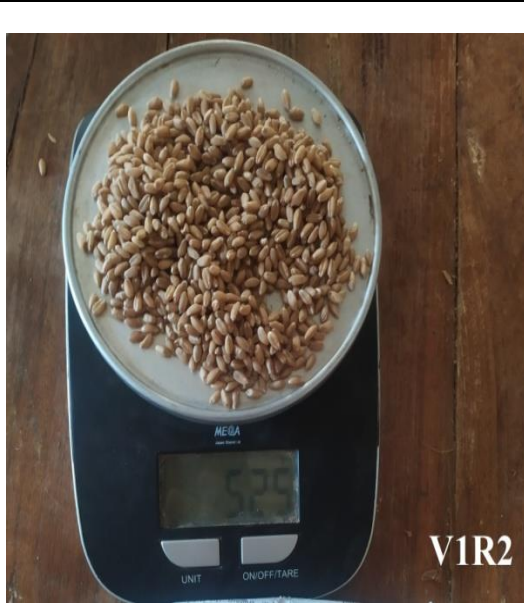
It was estimated by dividing grain yield per plot by biological yield per plot.

#### **3.4.11 1000 grain weight (g)**

Weight of 1000 grain from randomly sampled seeds per plot measured by sensitive balance.

#### **3.4.12 Grain yield per plant (g)**

The grain yield per plant of five randomly selected plants was measured using a sensitive balance after the seed's moisture is adjusted to 12.5% and average recorded.



**Plate 9. 1000 seed weight of different wheat varieties (V1R2, V2R2, V3R1 and V9R3)**

### 3.5 Statistical Analysis

The obtained data were statistically analyzed, and differences among wheat genotypes means were tested using a revised LSD test at the 0.05 level, according to Steel *et al.* (1997).

Genotypic and phenotypic correlation coefficients were computed among the studied traits, according to Kwon and Torrie (1964). Path analysis of the above-listed traits on grain yield was also performed according to Dewey and Lu (1959). Microsoft Excel program, SPSS and SAS 9.1 Computer program for Windows were used for the statistical analysis. Variance components included phenotypic ( $\sigma^2P$ ), and genotypic ( $\sigma^2G$ ) components were estimated according to Kwon and Torrie (1964) for the two growing seasons. The phenotypic and genotypic coefficients of variation were calculated according to the method suggested by Burton and DeVane (1953).

Genetic diversity was estimated following Mahalanobis's (1936) generalized distance ( $D^2$ ). Parents' selection in a hybridization program based on Mahalanobis's  $D^2$  statistic is more reliable as parents' requisite knowledge regarding a mass of characteristics is available before crossing. Rao (1977) reported that the quantification of genetic diversity through biometrical procedures had made it possible to choose genetically diverse parents for a successful hybridization program. Statistical analyses, such as Mahalanobis  $D^2$  and Canonical Variate Analysis (CVA), which quantify the differences among several quantitative traits, are efficient methods of evaluating genetic diversity. Mean data of each quantitative character were subjected to both univariate and multivariate analyses. For univariate analysis of variance, the analysis was done individually, and F-Test did the least of significance. Mean, range, coefficient of variation (CV) and correlation were estimated using the MSTAT computer program.

### 3.5.1 Estimation of genetic parameters

Estimation of phenotypic ( $\sigma^2p$ ), genotypic ( $\sigma^2g$ ) and environmental ( $\sigma^2e$ ) variance were calculated by the following formula Johnson *et al.* (1955).

$$\text{Genotypic variance } (\delta^2g) = \frac{MSG - MSE}{r}$$

Where,

$MSG$  = Mean Square due to Genotypes.

$MSE$  = Mean Square Error

$r$  = Number of replications

$$\text{Phenotypic variance } (\sigma^2p) = \sigma^2g + \sigma^2e$$

Where,

$\sigma^2g$  = Genotypic variance

$\sigma^2e$  = Environmental variance = MSE

### 3.5.2 Estimation of genotypic coefficient of variation and phenotypic coefficient of variation

Genotypic and phenotypic coefficients of variation were estimated according to the formula given by Burton (1952) and Singh and Chaudhary (1985).

$$\text{Genotypic Co-efficient of Variation (GCV \%)} = \frac{\sqrt{\sigma^2g}}{\bar{X}} \times 100$$

Where,

$\sigma^2g$  = Genotypic variance

$\bar{X}$  = Population mean

$$\text{Phenotypic Co-efficient of Variation (PCV \%)} = \frac{\sqrt{\sigma^2 p}}{\bar{X}} \times 100$$

Where,

$\sigma^2 p$  = Phenotypic variance

$\bar{x}$  = Population mean

### 3.5.3 Estimation of heritability

Heritability in a broad sense was estimated using the given formula suggested by Johnson *et al.* (1955),

$$\text{Heritability, } h^2 b = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$  = Genotypic variance

$\sigma^2 p$  = Phenotypic variance

### 3.5.4 Estimation of genetic advance

Expected genetic advance under selection was estimated using the formula suggested by Johnson *et al.* (1955).

$$\text{Genetic advanced (GA)} = \frac{\sigma^2 g}{\sigma^2 p} \times K \times \sigma p$$

Where,

$\sigma^2 g$  = Genotypic variance

$\sigma^2 p$  = Phenotypic variance

$\sigma p$  = Phenotypic standard deviation

$K$  = Selection intensity the value of which is 2.06 at 5% selection intensity



### 3.5.5 Estimation of genetic advance in percent of mean GA (%)

The estimate by the following formula is suggested by Comstock and Robinson (1952).

$$\text{Genetic advance in percent of mean GA (\%)} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Expected Genetic Advance

$\bar{X}$  = Population mean

### 3.5.6 Estimation of correlation

The genotypic and phenotypic correlation is estimated by the formula suggested by Miller *et al.* (1958).

$$\text{Genotypic correlation } r_{gxy} = \frac{\text{Cov}_{gxy}}{\sqrt{(\sigma^2_{gx} \times \sigma^2_{gy})}}$$

Where,

$\text{Cov}_{gxy}$  = Genotypic covariance between the trait x and trait y

$\sigma^2_{gx}$  = Genotypic variance of the trait x

$\sigma^2_{gy}$  = Genotypic variance of the trait y

Similarly,

$$\text{Phenotypic correlation } r_{pxy} = \frac{\text{Cov}_{pxy}}{\sqrt{(\sigma^2_{px} \times \sigma^2_{py})}}$$

Where,

$\text{Cov}_{pxy}$  = Phenotypic covariance between the trait x and y

$\sigma^2_{px}$  = Phenotypic variance of the trait x

$\sigma^2_{py}$  = Phenotypic variance of the trait y

### 3.5.7 Path co-efficient analysis

Path coefficient analysis was done according to the procedure employed by Dewey and Lu (1959), also quoted by Singh and Chaudhary (1985), using simple correlation values. The correlation coefficient is partitioned into direct and indirect independent variables on the dependent variable in path analysis. In order to estimate the direct and indirect effect of the correlated characters, say  $x_1$ ,  $x_2$  and  $x_3$  yield  $y$ , a set of simultaneous equations (three equations in this example) is required to be formulated as shown below:

$$r_{yx1} = P_{yx1} + P_{yx2}r_{x1x2} + P_{yx3}r_{x1x3}$$

$$r_{yx2} = P_{yx1}r_{x1x2} + P_{yx2} + P_{yx3}r_{x2x3}$$

$$r_{yx3} = P_{yx1}r_{x1x3} + P_{yx2}r_{x2x3} + P_{yx3}$$

Where  $r$ 's denote simple correlation coefficient, and  $P$ 's denote path co-efficient (Unknown).  $P$ 's in the above equations may be conveniently solved by arranging them in a matrix.

Total correlation, say between  $x_1$  and  $y$ , is thus partitioned as follows:

$$P_{yx1} = \text{direct effect of } x_1 \text{ on } y.$$

$$P_{yx2}r_{x1x2} = \text{indirect effect of } x_1 \text{ via } x_2 \text{ on } y.$$

$$P_{yx3}r_{x1x3} = \text{indirect effect of } x_1 \text{ via } x_3 \text{ on } y.$$

After calculating the direct and indirect effect of the characters, the residual effect ( $R$ ) was calculated by using the formula given below Singh and Chaudhary, (1985)

$$P^2_{RY} = 1 - \sum P_{iy}.r_{iy}$$

Where,

$$P^2_{RY} = (R^2); \text{ and hence residual effect, } R = (P^2_{RY})^{1/2}$$

$$P_{iy} = \text{Direct effect of the character on yield}$$

$$r_{iy} = \text{correlation of the character with yield.}$$

## **CHAPTER IV**

### **RESULTS AND DISCUSSION**

#### **4.1 Genetic Parameters**

The analysis of variance indicated a significantly higher amount of variability present among the genotypes for all the characters studied viz., days to maturity, plant height at maturity, (cm), peduncle length (cm), number of grains per spike, biological yield per plant (g), biomass/plot (g), harvest index (%), 1000 grain weight (g) and grain yield per plant (g) (Table 2). The results indicated that there exists high variability for yield and yield components among the genotypes studied. Therefore, there is much scope for selection for the majority of the traits in the genotypes. The mean sum of squares of all 12 characters is presented in (Table 3).

#### **4.2 Genetic Variability, Heritability and Genetic Advance**

##### **4.2.1 Days to maturity**

Highly significant variation was observed among all the genotypes (37.55) studied for this character (Table 2). The mean value of days to maturity was observed significantly, the lowest in G6 (104 days) (Table 3), suggesting that it matures earlier than others.

The highest days took to mature was found in G10 (113.33 days). The genotypic and phenotypic variance of days to maturity was observed 10.30 and 16.95, respectively, with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and genotypic values coefficient of variation and phenotypic coefficient of variation were 2.98% and 3.82%, respectively which indicated that the genotypes have relatively less variation (Table 4).

Days to maturity showed high heritability (60.79%), also found in the research of Chaturvedi and Gupta (1995), with low genetic advance (5.15) and genetic advance in percentage of mean (4.78%) (Figure 2), suggesting that the character is governed by non-additive gene action and improvement through selection can be influential.

#### **4.2.2 Plant height at maturity (cm)**

Significant variation was observed among all the genotypes (26.955) studied for this character (Table 2). The mean value of plant height at maturity (cm) was observed significantly the lowest in G8 (73.80 cm) (Table 3).

The highest plant height at maturity was found in G1 (84.25 cm), which gave a high grain yield per plant (5.00). Genotypic and phenotypic variance of plant height at maturity was observed 5.69 and 15.58, respectively, with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and genotypic coefficient values of variation and phenotypic coefficient of variation were 3.00% and 4.96%, respectively which indicated that the genotypes have relatively less variation (Table 4).

Plant height at maturity showed moderate heritability (36.53%), also investigated by Singh *et al.* (2006), with low genetic advance (2.97) and genetic advance in the percentage of mean (3.73%), indicating the presence of non-additive gene action and improvement through selection can be effective.

**Table 2. Analysis of variance for twelve characters in wheat varieties**

Characters	Mean sum of square		
	Replication (r-1) = 2	Genotype (g-1) = 9	Error (r-1)(g-1) = 18
Days to maturity	6.533	37.556**	6.644
Plant height at maturity, (cm)	10.941	26.955*	9.885
Number of productive tillers per plant	1.233	0.385 <sup>ns</sup>	0.196
Spike length (cm)	0.846	1.784 <sup>ns</sup>	1.459
Peduncle length (cm)	2.929	12.025**	1.265
Number of spikelets s per spike	0.233	2.015 <sup>ns</sup>	1.493
Number of grains per spike	0.700	61.663**	4.330
Biological yield per plant (g)	3.437	10.065*	3.404
Biomass/plot (g)	10532	173724**	25910
Harvest index (%)	4.900	163.589**	10.122
1000 grain weight (g)	2.721	140.514**	15.468
Grain yield per plant (g)	0.285	4.646**	0.312

\*\* = significant at 1% level

\* = significant at 5% level

ns = non-significant

### **4.2.3 Number of productive tillers per plant**

Non-significant variation was observed among all the genotypes (0.385) studied for this character (Table 2). The mean value of number of productive tillers per plant was observed lowest in G8 (2.00) (Table 3).

The highest number of productive tillers per plant was found in G1 (3.33), which gave a high grain yield per plant (5.00). Genotypic and phenotypic variance of number of productive tillers per plant was observed at 0.06 and 0.26, respectively, with a low difference between them, indicating that they were less responsive to environmental factors for their phenotypic expression. Values of genotypic coefficient of variation and phenotypic coefficient of variation were 9.91% and 20.10%, which indicated that the genotypes have relatively less variation (Table 4). The number of productive tillers per plant showed low heritability (24.29%) with low genetic advance (0.25) and genetic advance in percentage of mean (10.06%), suggesting slow progress of the trait through selection.

### **4.2.4 Spike length (cm)**

Non-significant variation was observed among all the genotypes (1.784) studied for this character (Table 2). The mean value of spike length (cm) was observed lowest in G5 (14.40) (Table 3).

The highest spike length (cm) was found in G9 (16.80). Genotypic and phenotypic variance of Spike length (cm) was observed 0.11 and 1.57, respectively, with low differences between them indicating that they were less responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 2.07% and 7.88%.

It indicated that the genotypes have relatively high variation (Table 4). Spike length (cm) showed low heritability (6.91%) with low genetic advance (0.18) and genetic advance in percentage of mean (1.12%), suggesting slow progress of the trait through selection.

#### **4.2.5 Peduncle length (cm)**

Highly significant variation was observed among all the genotypes (12.025) studied for this character (Table 2). The mean value of peduncle length (cm) was observed significantly lowest in G1 (10.63) (Table 3).

The highest peduncle length (cm) was found in G8 (17.13). Genotypic and phenotypic variance of peduncle length (cm) was observed at 3.59 and 4.85, respectively, with low differences between them indicating that they were less responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 14.56% and 16.93%.

Respectively which indicated that the genotypes have relatively low variation (Table 4). Peduncle length (cm) showed high heritability (73.94%) with low genetic advance (3.35) and genetic advance in percentage of mean (25.79%), indicating that the character is governed by non-additive gene action and improvement through selection can be effective.

#### **4.2.6 Number of spikelets per spike**

Non-significant variation was observed among all the genotypes (2.015) studied for this character (Table 2). The mean value of number of spikelets per spike was observed lowest in G8 (14) (Table 3).

The highest number of spikelets per spike was found in G4 (16.67). Genotypic and phenotypic variance of number of spikelets per spike was observed 0.17 and 1.67, respectively with low differences between them indicating that they were less responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 2.70% and 8.35%, respectively which indicated that the genotypes have relatively high variation (Table 4). The number of spikelets per spike showed low heritability (10.44%) with low genetic advance (0.28) and genetic advance in percentage of mean (1.80%), suggesting slow progress of the trait through selection.

**Table 3. Mean analysis of yield contributing parameters**

<b>Gen</b>	<b>DM</b>	<b>PH</b>	<b>NTPP</b>	<b>SL</b>	<b>PL</b>	<b>NSPS</b>	<b>NGPS</b>	<b>BYPP</b>	<b>BP</b>	<b>HI</b>	<b>TSW</b>	<b>GYPP</b>
G1	111.33	84.25	3.33	15.39	10.63	16.00	48.67	12.07	1805.30	25.67	51.32	5.00
G2	107.67	78.93	2.33	16.47	12.54	16.00	37.00	10.74	1055.30	30.33	53.65	3.62
G3	106.00	78.87	2.33	16.23	11.49	16.00	40.00	7.73	1352.30	39.00	70.65	2.55
G4	105.67	77.17	2.33	15.03	15.07	16.67	39.00	11.67	1455.70	34.67	58.38	2.76
G5	105.33	82.37	2.67	14.40	12.87	15.67	46.33	10.77	1568.30	49.33	56.90	1.63
G6	104.67	77.63	2.67	15.82	11.17	15.67	48.67	7.30	1256.00	44.67	64.06	2.47
G7	105.67	81.20	2.67	16.54	11.60	15.33	49.67	9.20	1248.70	44.33	67.80	2.57
G8	104.00	73.80	2.00	16.53	17.13	14.00	48.00	8.30	1284.00	42.33	52.88	2.90
G9	113.00	80.77	2.33	16.80	13.90	15.00	44.00	8.80	1095.00	45.33	53.55	4.73
G10	113.33	81.40	2.67	15.73	13.70	14.33	45.67	12.18	1049.00	41.33	53.67	5.27
<b>Min</b>	104.00	73.80	2.00	14.40	10.63	14.00	37.00	7.30	1049.00	25.67	51.32	1.63
<b>Max</b>	113.33	84.25	3.33	16.80	17.13	16.67	49.67	12.18	1805.30	49.33	70.65	5.27
<b>Mean</b>	107.67	79.64	2.53	15.90	13.01	15.47	44.70	9.88	1316.96	39.70	58.28	3.35
<b>CV (%)</b>	2.39	3.95	17.49	7.6	8.64	7.9	4.65	18.68	12.22	8.01	6.75	16.68
<b>SD</b>	3.54	3.00	0.36	0.77	2.00	0.82	4.53	1.83	240.63	7.38	6.84	1.24

DM= Days to maturity, PH= Plant height, NTPP= Number of tiller per plant, SL=Spike length, NSPS=Number of spikelets per plant, NGPS= Number of grains per spike, BYPP= Biological yield per plant, BP= Biomass per plot, HI=Harvest index, TSW= 1000-seed weight, GYPP= Grain yield per plant, CV (%) = coefficient of variation, SD = Standard deviation



#### **4.2.7 Number of grains per spike**

Highly significant variation was observed among all the genotypes (61.663) studied for this character (Table 2). The mean value of number of grains per spike was observed significantly the lowest in G2 (37) (Table 3).

The highest number of grains per spike was found in G7 (49.67). Genotypic and phenotypic variance of number of grains per spike was observed 19.11 and 23.44, respectively with moderate differences between them indicating that they were moderately responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 9.78% and 10.83%, respectively which indicated that the genotypes have relatively less variation (Table 4). The number of grains per spike showed high heritability (81.53%) with low genetic advance (8.13) and genetic advance in percentage of mean (18.19%), indicating that the character is governed by non-additive gene action and improvement through selection can be effective. This was also found in the research carried out by Shoran (1995).

#### **4.2.8 Biological yield per plant (g)**

Significant variation was observed among all the genotypes (10.065) studied for this character (Table 2). The mean value of biological yield per plant (g) was observed significantly the lowest in G6 (7.30) (Table 3).

The highest biological yield per plant (g) was found in G10 (12.18). Genotypic and phenotypic variance of biological yield per plant (g) was observed 2.22 and 5.62, respectively, with moderate difference between them indicating that they were moderately responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 15.09% and 24.01%, respectively which indicated that the genotypes have relatively high variation (Table 4). Biological yield per plant (g) showed moderate heritability (39.48%) with low genetic advance (1.93) and genetic advance in percentage of mean (19.53%). It indicated the presence of non-additive gene action and selection might be ineffective for the character indicating that the character is

governed by non-additive gene action, and improvement through selection cannot be effective.

#### **4.2.9 Biomass/plot (g)**

Highly significant variation was observed among all the genotypes (173724) studied for this character (Table 2). The mean value of biomass/plot (g) was observed significantly the lowest in G10 (1049.00) (Table 3).

The highest biomass/plot (g) was found in G1 (1805.30). Genotypic and phenotypic variance of biomass/plot (g) was observed 49271.33 and 75181.33, respectively, with high differences between them indicating that they were more responsive to environmental factors for the phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient variation were 16.85% and 20.82%, respectively which indicated that the genotypes have relatively moderate variation (Table 4). Biomass/plot (g) showed high heritability (65.54%) with high genetic advance (370.17) and genetic advance in percentage of mean (28.11%), suggesting additive gene effect is present and selection can be useful for the trait.

#### **4.2.10 Harvest index (%)**

Highly significant variation was observed among all the genotypes (163.589\*\*) studied for this character (Table 2). The mean value of harvest index (%) was observed significantly the lowest in G1 (25.67) (Table 3).

The highest harvest index (%) was found in G5 (49.33). Genotypic and phenotypic variance of harvest index (%) was observed 51.16 and 61.28, respectively, with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 18.02% and 19.72%, respectively, indicated that the genotypes have relatively less variation (Table 4).

Harvest index (%) showed high heritability (83.48%) with moderate genetic advance (13.46) and genetic advance in percentage of mean (33.91%), indicating the limited chance for the improvement of the character through selection, which was also suggested by Kumar *et al.* (2014).

**Table 4. Estimation of genetic parameters in twelve characters of ten genotypes in wheat**

Parameters	Mean	$\sigma^2_p$	$\sigma^2_g$	$\sigma^2_e$	PCV	GCV	ECV	Heritability	Genetic Advance (5%)	Genetic Advance (% of mean)
Days to maturity	107.67	16.95	10.30	6.64	3.82	2.98	0.84	60.80	5.16	4.79
Plant height at maturity, (cm)	79.64	15.58	5.69	9.89	4.96	3.00	1.96	36.53	2.97	3.73
Number of productive tillers per plant	2.53	0.26	0.06	0.20	20.10	9.91	10.19	24.29	0.25	10.06
Spike length (cm)	15.90	1.57	0.11	1.46	7.88	2.07	5.81	6.91	0.18	1.12
Peduncle length (cm)	13.01	4.85	3.59	1.26	16.93	14.56	2.37	73.94	3.35	25.79
Number of spikelets per spike	15.47	1.67	0.17	1.49	8.35	2.70	5.65	10.44	0.28	1.80
Number of grains per spike	44.70	23.44	19.11	4.33	10.83	9.78	1.05	81.53	8.13	18.19
Biological yield per plant (g)	9.88	5.62	2.22	3.40	24.01	15.09	8.92	39.48	1.93	19.53
Biomass/plot (g)	1317.00	75181.33	49271.33	25910.00	20.82	16.85	3.97	65.54	370.17	28.11
Harvest index (%)	39.70	61.28	51.16	10.12	19.72	18.02	1.7	83.48	13.46	33.91
1000 grain weight (g)	58.29	57.15	41.68	15.47	12.97	11.08	1.89	72.93	11.36	19.49
Grain yield per plant (g)	3.35	1.76	1.44	0.31	39.57	35.89	3.68	82.24	2.25	67.04

$\sigma^2_p$ : Phenotypic variance

$\sigma^2_g$ : Genotypic variance

$\sigma^2_e$ : Environmental variance

PCV: Phenotypic coefficient of variation

GCV: Genotypic coefficient of variation

ECV: Environmental coefficient of variation

GA (5%): Genetic advance

GAM: Genetic advance (% of mean)

#### **4.2.11 1000 grain weight (g)**

Highly significant variation was observed among all the genotypes (140.514) studied for this character (Table 2). The mean value of 1000 grain weight (g) was observed significantly the lowest in G1 (51.32) (Table 3).

The highest 1000 grain weight (g) was found in G3 (70.65). Genotypic and phenotypic variance of 1000 grain weight (g) was observed 41.68 and 57.15, respectively with high differences between them indicating that they were more responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 11.08% and 12.97%, respectively which indicated that the genotypes have relatively less variation (Table 4).

1000 grain weight (g) showed high heritability (72.93%) with moderate genetic advance (11.36) and genetic advance in percentage of mean (19.49%), indicating the limited chance for the improvement of the character through selection, this was found in the research of Moghaddam *et al.* (1998).

#### **4.2.12 Grain yield per plant (g)**

Highly significant variation was observed among all the genotypes (4.646) studied for this character (Table 2). The mean value of grain yield per plant (g) was observed significantly the lowest in G5 (1.63) (Table 3).

The highest grain yield per plant (g) was found in G10 (5.27). Genotypic and phenotypic variance of grain yield per plant (g) was observed 1.44 and 1.76, respectively with low differences between them indicating that they were less responsive to environmental factors for their phenotypic expression and values of genotypic coefficient of variation and phenotypic coefficient of variation were 35.89% and 39.57%, respectively which indicated that the genotypes have relatively moderate variation (Table 4). Grain yield per plant (g) showed high heritability (82.24%) with low genetic advance (2.25) and genetic advance in percentage of mean (67.04%), indicating that the character is governed by non-additive gene action, which was revealed by Kotal *et al.* (2010) and improvement through selection can be effective.

### 4.3 Correlation Analysis

Improvement of a particular character in all the breeding programs can be achieved by indirect selection via different characters. This requires a good understanding of various characters' association with the target character and among the different characters themselves. It is necessary to estimate the correlation of yield with different characters by visual assessment of the genotype.

The makeup and constitution correlation revealed the extent of association between completely different characters. It helped base choice procedure to a needed balance; once two opposite fascinating characters moved, the principal characters were selected. A positive correlation happens because of the coupling section of linkage and correlation arises because of repulsion section of linkage of genes dominant completely different traits. No correlation indicates that genes involved are situated so much apart on identical chromosomes or are situated on completely different bodies.

Yield being a cumulative character and an outsized range of genes governs it. The influence of every character on yield might be well-known through correlation studies to see the extent and nature of interrelationships among yield and yield attributing characters (Okuyama *et al.* 2004, Singh *et al.* 2006, Ali *et al.* 2008, Ahmad *et al.* 2018). The constitution and phenotypic correlation coefficient values for twelve characters in wheat genotypes studied are given (Table 5).

#### 4.3.1 Days to maturity

Days to maturity showed in the (Table 5) highly significant and positive correlation with plant height ( $G = 0.523$ ,  $P = 0.678$ ), number of productive tillers per plant ( $G = 0.93$ ), biological yield per plant ( $G = 0.694$ ) and grain yield per plant ( $G = 0.996$ ,  $P = 0.832$ ). It was also observed a highly significant but negative correlation with the number of spikelets per spike ( $G = -0.633$ ) and the 1000 grain weight ( $G = -0.619$ ,  $P = -0.364$ ). Non-significant and positive correlation with number of productive tillers per plant ( $P = 0.233$ ), spike length ( $G = 0.358$ ,  $P = 0.068$ ), number of grains per spike ( $P = 0.072$ ) and biological yield per plant ( $P = 0.280$ ) and non-significant but negative correlation peduncle length ( $G = -0.182$ ,  $P = -0.058$ ), number of spikelets per spike ( $P = -0.072$ ), number of grains per spike ( $G = -0.078$ ,  $P = -0.078$ ), biomass/plot ( $G = -0.262$ ,  $P = -0.200$ ).

**Table 5. Genotypic and phenotypic correlation coefficients among different pairs of yield and yield contributing characters for different genotype of wheat**

		DM	PH	NPTP	SL	PL	NSPS	NGPS	BYPH	BP	HI	TSW
PH	G	0.523**										
	P	0.678**										
NPTP	G	0.593**	0.991**									
	P	0.233 <sup>NS</sup>	0.560**									
SL	G	0.358 <sup>NS</sup>	-0.810**	-0.995**								
	P	0.068 <sup>NS</sup>	-0.199 <sup>NS</sup>	-0.159 <sup>NS</sup>								
PL	G	-0.182 <sup>NS</sup>	-0.928**	-0.917**	0.234 <sup>NS</sup>							
	P	-0.053 <sup>NS</sup>	-0.389*	-0.606**	0.064 <sup>NS</sup>							
NSPS	G	-0.633**	0.638**	0.884**	-2.509**	-0.843**						
	P	-0.036 <sup>NS</sup>	0.057 <sup>NS</sup>	0.090 <sup>NS</sup>	-0.066 <sup>NS</sup>	-0.389*						
NGPS	G	-0.078 <sup>NS</sup>	0.198 <sup>NS</sup>	0.716**	-0.032 <sup>NS</sup>	-0.179 <sup>NS</sup>	-0.991**					
	P	0.072 <sup>NS</sup>	0.261 <sup>NS</sup>	0.270 <sup>NS</sup>	-0.059 <sup>NS</sup>	-0.076 <sup>NS</sup>	-0.301 <sup>NS</sup>					
BYPH	G	0.694**	0.793**	0.954**	-0.992**	0.028 <sup>NS</sup>	0.991**	-0.211 <sup>NS</sup>				
	P	0.280 <sup>NS</sup>	0.299 <sup>NS</sup>	0.154 <sup>NS</sup>	-0.391*	0.036 <sup>NS</sup>	-0.161 <sup>NS</sup>	-0.121 <sup>NS</sup>				
BP	G	-0.262 <sup>NS</sup>	0.445*	.990**	-0.996**	-0.320 <sup>NS</sup>	0.997**	0.252 <sup>NS</sup>	0.319 <sup>NS</sup>			
	P	-0.080 <sup>NS</sup>	0.254 <sup>NS</sup>	0.278 <sup>NS</sup>	-0.356 <sup>NS</sup>	-0.190 <sup>NS</sup>	0.235 <sup>NS</sup>	0.288 <sup>NS</sup>	0.248 <sup>NS</sup>			
HI	G	-0.275 <sup>NS</sup>	-0.169 <sup>NS</sup>	-0.462*	0.260 <sup>NS</sup>	0.222 <sup>NS</sup>	-0.830**	0.427*	-0.652**	-0.356 <sup>NS</sup>		
	P	-0.200 <sup>NS</sup>	-0.112 <sup>NS</sup>	-0.249 <sup>NS</sup>	-0.109 <sup>NS</sup>	0.199 <sup>NS</sup>	-0.332 <sup>NS</sup>	0.291 <sup>NS</sup>	-0.332 <sup>NS</sup>	-0.264 <sup>NS</sup>		
TSW	G	-0.619**	-0.211 <sup>NS</sup>	-0.250 <sup>NS</sup>	0.205 <sup>NS</sup>	-0.493**	0.669**	0.023 <sup>NS</sup>	-0.734**	-0.049 <sup>NS</sup>	0.330 <sup>NS</sup>	
	P	-0.364*	-0.018 <sup>NS</sup>	0.031 <sup>NS</sup>	0.109 <sup>NS</sup>	-0.345 <sup>NS</sup>	0.160 <sup>NS</sup>	-0.051 <sup>NS</sup>	-0.424*	-0.032 <sup>NS</sup>	0.290 <sup>NS</sup>	
GYPP	G	0.996**	0.444*	0.488**	0.761**	0.003 <sup>NS</sup>	-0.711**	0.011 <sup>NS</sup>	0.574**	-0.224 <sup>NS</sup>	-0.497**	-0.669**
	P	0.832**	0.336 <sup>NS</sup>	0.211 <sup>NS</sup>	0.111 <sup>NS</sup>	-0.047 <sup>NS</sup>	-0.107 <sup>NS</sup>	0.023 <sup>NS</sup>	0.344 <sup>NS</sup>	-0.136 <sup>NS</sup>	-0.366*	-0.488**

DM= Days to maturity, PH= Plant height, NTPP= Number of tiller per plant, SL=Spike length, NSPS=Number of spikelets per plant, NGPS= Number of grains per spike, BYPP= Biological yield per plant, BP= Biomass per plot, HI=Harvest index, TSW= 1000-seed weight, GYPP= Grain yield per plant, NS = non-significant, \* = significant at 5% level, \*\* = significant at 1% level

### **4.3.2 Plant height**

Plant height showed a highly significant and positive correlation with number of productive tillers per plant ( $G = 0.991$ ,  $P = 0.560$ ), number of spikelets per spike ( $G = 0.698$ ), biological yield per plant ( $G = 0.793$ ), biomass/plot ( $G = 0.445$ ) and grain yield per plant ( $G = 0.444$ ). It was observed from (Table 5) that highly significant but negative correlation with spike length ( $G = -0.633$ ), 1000 grain weight ( $G = -0.810$ ) and peduncle length ( $G = -0.928$ ,  $P = -0.389$ ).

Non-significant and positive correlation with number of spikelets per spike ( $P = 0.057$ ), number of grains per spike ( $G = 0.198$ ,  $P = 0.261$ ), biological yield per plant ( $P = 0.299$ ), biomass/plot ( $P = 0.254$ ) and grain yield per plant ( $P = 0.444$ ) and non-significant but negative correlation spike length ( $P = -0.199$ ), harvest index ( $G = -0.169$ ,  $P = -0.112$ ), and 1000 grain weight ( $G = -0.211$ ,  $P = -0.018$ ).

### **4.3.3 Number of productive tillers per plant**

In the (Table 5) number of productive tillers per plant showed highly significant and positive correlation with number of spikelets per spike ( $G = 0.884$ ), number of grains per spike ( $G = 0.716$ ), biological yield per plant ( $G = 0.954$ ), biomass/plot ( $G = 0.990$ ) and grain yield per plant ( $G = 0.488$ ). It also observed that highly significant but negative correlation with spike length ( $G = -0.995$ ), peduncle length ( $G = -0.917$ ,  $P = -0.606$ ) and harvest index ( $G = -0.462$ ).

Non-significant and positive correlation with number of spikelets per spike ( $P = 0.090$ ), number of grains per spike ( $P = 0.270$ ), biological yield per plant ( $P = 0.154$ ), biomass/plot ( $P = 0.278$ ), 1000 grain weight ( $P = -0.031$ ) and grain yield per plant ( $P = -0.211$ ) and non-significant but negative correlation spike length ( $P = -0.159$ ), harvest index ( $P = -0.249$ ) and 1000 grain weight ( $G = -0.250$ ), also revealed by Ajmal *et al.* (2009).

#### **4.3.4 Spike length**

Spike length showed highly significant and positive correlation with grain yield per plant ( $G = 0.761$ ), also revealed by Ahmad et al. (2018). It was also showed in (Table 5) that highly significant but negative correlation with number of spikelets per spike ( $G = -2.509$ ), biological yield per plant ( $G = -0.992$ ,  $P = -0.391$ ), and biomass/plot ( $P = -0.996$ ). Non-significant and positive correlation with peduncle length ( $G = 0.234$ ,  $P = 0.064$ ), harvest index ( $G = 0.260$ ) 1000 grain weight ( $G = 0.205$ ,  $P = 0.109$ ) and grain yield per plant ( $P = 0.111$ ) and non-significant but negative correlation number of spikelets per spike ( $G = -0.066$ ), number of grains per spike ( $G = -0.032$ ,  $P = -0.059$ ), biomass/plot ( $P = -0.356$ ) and harvest index ( $P = -0.109$ ).

#### **4.3.5 Peduncle length**

Peduncle length showed in (Table 5) highly significant and negative correlation with number of spikelets per spike ( $G = -0.843$ ,  $P = -0.389$ ) and 1000 grain weight ( $G = -0.493$ ). Non-significant and positive correlation with biological yield per plant ( $G = 0.028$ ,  $P = 0.036$ ), harvest index ( $G = 0.222$ ,  $P = 0.199$ ) and grain yield per plant ( $G = 0.003$ ) and non-significant but negative correlation number of grains per spike ( $G = -0.179$ ,  $P = -0.076$ ), biomass/plot ( $G = -0.320$ ,  $P = -0.190$ ) 1000 grain weight ( $P = -0.345$ ) and grain yield per plant ( $P = -0.047$ ).

#### **4.3.6 Number of spikelets per spike**

Number of spikelets per spike showed highly significant and positive correlation with biological yield per plant ( $G = 0.991$ ), biomass/plot ( $G = 0.997$ ) and 1000 grain weight ( $G = 0.669$ ). It also observed in (Table 5) that highly significant but negative correlation with number of grains per spike ( $G = -0.991$ ), harvest index ( $G = -0.830$ ), and grain yield per plant ( $P = -0.711$ ). Non-significant and positive correlation with biomass/plot ( $P = 0.325$ ) and 1000 grain weight ( $P = 0.160$ ) and non-significant but negative correlation number of grains per spike ( $P = -0.301$ ), biological yield per plant ( $P = -0.161$ ), harvest index ( $P = -0.332$ ) and grain yield per plant ( $P = -0.047$ ).



#### **4.3.7 Number of grains per spike**

Number of grains per spike showed highly significant and positive correlation with harvest index ( $G = 0.427$ ). Non-significant and positive correlation with biomass/plot ( $G = 0.252$ ,  $P = 0.325$ ), harvest index ( $P = 0.291$ ), 1000 grain weight ( $G = 0.023$ ), and grain yield per plant ( $G = 0.011$ ,  $P = 0.023$ ) and non-significant in (Table 5) but negative correlation biological yield per plant ( $G = -0.211$ ,  $P = -0.121$ ) and 1000 grain weight ( $P = -0.051$ ).

#### **4.3.8 Biological yield per plant**

Biological yield per plant showed a highly significant and positive correlation with grain yield per plant ( $G = 0.548$ ), also investigated by Chhibber and Jain (2014). It also observed in (Table 5) that highly significant but negative correlation with harvest index ( $G = -0.652$ ) and 1000 grain weight ( $G = -0.734$ ,  $P = -0.424$ ). Non-significant and positive correlation with biomass/plot ( $G = 0.319$ ,  $P = 0.248$ ) and grain yield per plant ( $P = 0.344$ ) and non-significant but the negative correlation of the harvest index ( $P = -0.332$ ).

#### **4.3.9 Biomass/plot**

Biomass/plot showed in (Table 5) non-significant but negative correlation harvest index ( $G = -0.356$ ,  $P = -0.264$ ), 1000 grain weight ( $G = -0.049$ ,  $P = -0.032$ ), grain yield per plant ( $G = -0.224$ ,  $P = -0.136$ ).

#### **4.3.10 Harvest index**

Harvest index showed highly significant but negative correlation with grain yield per plant ( $G = -0.497$ ,  $P = -0.366$ ). Non-significant and positive correlation with 1000 grain weight ( $G = 0.330$ ,  $P = 0.290$ ) (Table 5).

#### **4.3.11 1000 grain weight**

1000 grain weight showed in (Table 5) highly significant but negative correlation with grain yield per plant ( $G = -0.669$ ,  $P = -0.488$ ).

#### 4.4 Path Coefficient Analysis

Though correlation analysis indicates the association pattern of component traits with yield, they merely represent the influence of a selected character on grain yield production despite providing cause and impact interrelationship. The path coefficient analysis technique was developed by Niles (1922) and demonstrated by Dewey and Lu (1959), facilitates the portioning of correlation coefficients into the direct and indirect contribution of various characters on yield.

It is a standardized partial parametric statistical analysis. As such, it measures direct influence of one variable upon others. Such calculated data would be highly expected. This research experiment showed that good value enabled the breeder to determine the necessary yield components and utilize the genetic stock for improvement in a planned process. The direct and indirect effects of the yield-conforming characters on yield were found out by using path analysis. Here grain yield per plant was considered as an effect (dependent variable) and days to maturity, plant height at maturity, (cm), number of productive tillers per plant, spike length (cm), peduncle length (cm), number of spikelets per spike, number of grains per spike, biological yield per plant (g), biomass/plot (g), harvest index (%), 1000 grain weight (g) and grain yield per plant (g) were treated as independent variables (Singh *et al.* 2006, Ajmal *et al.* 2009 and Nasri *et al.* 2014). Path coefficient analysis was showed the direct and indirect effects of different characters on wheat yield (Table 6).

##### 4.4.1 Days to maturity

Path coefficient analysis revealed that days to maturity had a positive direct effect (0.859) on grain yield per plant, which was also revealed by Ehdaie and Waines (1989). Days to maturity had a positive indirect effect on days to number of productive tillers per plant (0.046), peduncle length (0.063), number of spikelets per spike (0.028), biological yield per plant (0.003), biomass/plot (0.054), harvest index (0.092) and 1000 grain weight (0.159) while negative indirect effect on plant height (-0.269), spike length (-0.022) and number of grains per spike (-0.017). It showed in (Table 6) highly significant positive genotypic correlation (0.996) with grain yield per plant.

#### **4.4.2 Plant height**

Path coefficient analysis revealed that plant height negatively affected the (-0.514) grain yield per plant in (Table 6). Plant height had a positive indirect effect on days to maturity (0.450), number of productive tillers per plant (0.098), spike length (0.050), peduncle length (0.323), number of grains per spike (0.043), biological yield per plant (0.004), harvest index (0.054) and 1000 grain weight (0.054).

The negative indirect effect on the number of spikelets/spike (-0.028) and the biomass/plot (-0.092). Correlation positive significance (0.444) showed a significant positive genotypic correlation (0.444) with grain yield per plant.

#### **4.4.3 Number of productive tillers per plant**

Path coefficient analysis revealed in (Table 6) that the number of productive tillers per plant had a positive direct effect (0.078) on grain yield per plant. Number of productive tillers per plant had a positive indirect effect on days to maturity (0.514), spike length (0.097), peduncle length (0.319), number of grains per spike (0.156), biological yield per plant (0.004), harvest index (0.054) and 1000 grain weight (0.062).

While negative indirect effect on plant height (-0.509), number of spikelets per spike (-0.039) and biomass/plot (-0.206). Correlation was positive, highly significant (0.488), showed a highly significant positive genotypic correlation (0.488) with grain yield per plant.

#### **4.4.4 Spike length**

Path coefficient analysis revealed that Spike length had a negative direct effect (-0.062) on grain yield per plant. Spike length had a positive indirect effect on days to maturity (0.307), plant height (0.416). Number of spikelets per spike (0.110) and biomass/plot (0.344). While negative indirect effect showed in (Table 6) on number of productive tillers per plant (-0.078), peduncle length (-0.081), number of grains per spike (-0.007), biological yield per plant (-0.005), harvest index (-0.087), 1000 grain weight (-0.052). Correlation is positive, highly significant (0.761), showed a highly significant positive genotypic correlation (0.761) with grain yield per plant.

#### **4.4.5 Peduncle length**

Path coefficient analysis revealed in (Table 6) that peduncle length had a negative direct effect (-0.347) on grain yield per plant.

Peduncle length had a positive indirect effect on days to plant height (0.477), the number of spikelets per spike (0.037), biological yield per plant (0.001), biomass/plot (0.066) and 1000 grain weight (0.126).

While the negative indirect effect on days to maturity (-0.156), number of productive tillers per plant (-0.071), spike length (-0.014), number of grains per spike (-0.039) and harvest index (-0.074).

Correlation positive non-significant (0.003), showed a non-significant positive genotypic correlation (0.003) with grain yield per plant.

#### **4.4.6 Number of spikelets per spike**

Path coefficient analysis revealed that the number of spikelets per spike had a negative direct effect (-0.044) on grain yield per plant. The number of spikelets per spike had a positive indirect effect on days to number of productive tillers per plant (0.069), spike length (0.155), peduncle length (0.293), biological yield per plant (0.005) and harvest index (0.278) showed in (Table 6). While negative indirect effect on days to maturity (-0.544), plant height (-0.328), number of grains per spike (-0.215), biomass/plot (-0.208) and 1000 grain weight (-0.171). Correlation negative, highly significant (-0.711), showed a highly significant negative genotypic correlation (-0.711) with grain yield per plant.

**Table 6. Path coefficient analysis showing direct (bold) and indirect effects of different characters on yield of wheat**

<b>Direct Effects</b>	<b>DM</b>	<b>PH</b>	<b>NTPP</b>	<b>SL</b>	<b>PL</b>	<b>NSPS</b>	<b>NGPS</b>	<b>BYPH</b>	<b>BP</b>	<b>HI</b>	<b>TSW</b>	<b>GYPP</b>
<b>DM</b>	<b>0.859</b>	-0.269	0.046	-0.022	0.063	0.028	-0.017	0.003	0.054	0.092	0.159	0.996**
<b>PH</b>	0.450	<b>-0.514</b>	0.098	0.050	0.323	-0.028	0.043	0.004	-0.092	0.057	0.054	0.444*
<b>NTPP</b>	0.510	-0.509	<b>0.078</b>	0.097	0.319	-0.039	0.156	0.004	-0.206	0.154	0.064	0.488**
<b>SL</b>	0.307	0.416	-0.078	<b>-0.062</b>	-0.081	0.110	-0.007	-0.005	0.344	-0.087	-0.052	0.761**
<b>PL</b>	-0.156	0.477	-0.071	-0.014	<b>-0.347</b>	0.037	-0.039	0.0001	0.066	-0.074	0.126	0.003 <sup>NS</sup>
<b>NSPS</b>	-0.544	-0.328	0.069	0.155	0.293	<b>-0.044</b>	-0.215	0.005	-0.208	0.278	-0.171	-0.711**
<b>NGPS</b>	-0.067	-0.102	0.056	0.002	0.062	0.043	<b>0.217</b>	-0.001	-0.052	-0.143	-0.006	0.011 <sup>NS</sup>
<b>BYPH</b>	0.596	-0.408	0.074	0.061	-0.010	-0.043	-0.046	<b>0.005</b>	-0.066	0.218	0.188	0.574**
<b>BP</b>	-0.225	-0.229	0.078	0.062	0.111	-0.044	0.055	0.001	<b>-0.206</b>	0.119	0.013	-0.224 <sup>NS</sup>
<b>HI</b>	-0.236	0.087	-0.036	-0.016	-0.077	0.036	0.093	-0.003	0.073	<b>-0.334</b>	-0.085	-0.497**
<b>TSW</b>	-0.532	0.108	-0.019	-0.013	0.171	-0.029	0.005	-0.003	0.010	-0.110	<b>-0.256</b>	-0.669**
<b>Residual effects: 0.037</b>												

DM= Days to maturity, PH= Plant height, NTPP= Number of tiller per plant, SL=Spike length, NSPS=Number of spikelets per plant, NGPS= Number of grains per spike, BYPP= Biological yield per plant, BP= Biomass per plot, HI=Harvest index, TSW= 1000-seed weight, GYPP= Grain yield per plant, NS = non-significant, \* = significant at 5% level, \*\* = significant at 1% level.

#### **4.4.7 Number of grains per spike**

Path coefficient analysis revealed that number of grains per spike had a positive direct effect (0.217) on grain yield per plant, which was also experimented by Iftikhar *et al.* (2012). The number of grains per spike had a positive indirect effect showed in (Table 6) on days to number of productive tillers per plant (0.056), spike length (0.002), peduncle length (0.062) and number of spikelets per spike (0.043).

While negative indirect effect on days to maturity (-0.067), plant height (-0.102), biological yield per plant (-0.001), biomass/plot (-0.052), harvest index (-0.143) and 1000 grain weight (-0.006). Correlation positive non-significant (0.011). It showed a non-significant positive genotypic correlation (0.011) with grain yield per plant.

#### **4.4.8 Biological yield per plant**

Path coefficient analysis revealed in (Table 6) that biological yield per plant had a positive direct effect (0.005) on grain yield per plant. Biological yield per plant had a positive indirect effect on days to maturity (0.596), number of productive tillers per plant (0.074), spike length (0.061), harvest index (0.218) and 1000 grain weight (0.188).

While negative indirect effect on plant height (-0.408), peduncle length (-0.010), number of spikelets per spike (-0.043), number of grains per spike (-0.046) and biomass/plot (-0.066). Correlation is positive, highly significant (0.574). It showed a highly significant positive genotypic correlation (0.574) with grain yield per plant.

#### **4.4.9 Biomass/plot**

Path coefficient analysis revealed that biomass/plot had a negative direct effect (-0.206) on grain yield per plant. Biomass/plot had a positive indirect effect on days to number of productive tillers per plant (0.078), spike length (0.062), peduncle length (0.111), number of grains per spike (0.055), biological yield per plant (0.001), harvest index (0.119) and 1000 grain weight (0.013).

While negative indirect effect on days to maturity (-0.225), plant height (-0.229) and number of spikelets per spike (-0.044) in (Table 6). Correlation negative non-significant (-0.224), showed a non-significant negative genotypic correlation (-0.224) with grain yield per plant.

#### **4.4.10 Harvest index**

Path coefficient analysis revealed that the harvest index had a negative direct effect (-0.334) on grain yield per plant, which was also investigated by Nasri *et al.* (2014). Harvest index had a positive indirect effect on days to plant height (0.087), number of spikelets per spike (0.036), number of grains per spike (0.093) and biomass/plot (0.073).

While the negative indirect effect on days to maturity (-0.236), number of productive tillers per plant (-0.036), spike length (-0.016), peduncle length (-0.077), biological yield per plant (-0.003) and 1000 grain weight (-0.085). Correlation is negative, highly significant (-0.497), showed in (Table 5) a highly significant negative genotypic correlation (-0.497) with grain yield per plant.

#### **4.4.11 1000 grain weight**

Path coefficient analysis revealed that 1000 grain weight had a negative direct effect (-0.256) on grain yield per plant. 1000 grain weight had a positive indirect effect on days to plant height (0.108), peduncle length (0.171), number of grains per spike (0.005), also revealed by Ayer *et al.* (2017) and biomass/plot (0.010).

While negative indirect effect on days to maturity (-0.532), number of the productive tillers per plant (-0.019), spike length (-0.013), number of spikelets per spike (-0.029), biological yield per plant (-0.003) and harvest index (-0.110) showed in (Table 6). Correlation negative, highly significant (-0.669), showed a highly significant negative genotypic correlation (-0.669) with grain yield per plant.

#### **4.4.12 Residual Effects**

The residual effect (R) of path co-efficient analysis was 0.037, which reported that the traits under study contributed 96.3% of the seed yield/plant. It is said that some other factors that contributed 3.7 % to the seed yield/plant that is not included in the present study could have a significant effect on seed yield.

## **CHAPTER V**

### **SUMMARY AND CONCLUSION**

The present investigation was shown on 10 Wheat varieties on the title “Genetic Variation and Interrelationships among Yield and Yield Contributing Traits of Wheat.” The purpose of this experiment was to select the best varieties for the further research program.

The genetic variability, heritability, correlation, path analysis and genetic diversity were estimated for ten varieties. The wide genetic variability that exists in the available genotypes provides enormous scope for further improvement. The analysis of variance showed significant differences among the genotypes for all the traits viz. days to maturity, plant height at maturity (cm), peduncle length (cm), number of grains per spike, biological yield per plant (g), biomass/plot (g), harvest index (%), 1000 grain weight (g), grain yield per plant (g).

The highest days used to mature were found in G10 (113.33 days) and the lowest in G6 (104 days). The highest plant height at maturity (cm) was found in G1 (84.25 cm), and the lowest plant height at maturity (cm) was found in G1 G8 (73.80 cm). The highest number of productive tillers per plant was found in G1 (3.33) and the lowest number of productive tillers per plant was found in G8 (2.00). The highest spike length (cm) was found in G9 (16.80), and the lowest number of productive tillers per plant was found in G5 (14.40). The highest peduncle length (cm) was found in G8 (17.13), and the lowest peduncle length (cm) was found in G1 (10.63).

The highest number of spikelets per spike was found in G4 (16.67), whereas the lowest number of spikelets per spike was found in G8 (14). The highest number of grains per spike was found in G7 (49.67) and the lowest number of grains per spike was found in G2 (37). The highest biological yield per plant (g) was found in G10 (12.18) and the lowest biological yield per plant (g) was found in G6 (7.30).



The highest biomass/plot (g) was found in G1 (1805.30), whereas the lowest biomass/plot (g) was found in G10 (1049.00). The highest harvest index (%) was found in G5 (49.33) and the lowest harvest index (%) was found in G1 (25.67). The highest 1000 grain weight (g) was found in G3 (70.65), whereas the lowest 1000 grain weight (g) was found in G1 (51.32). The highest grain yield per plant (g) was found in G10 (5.27) and the lowest grain yield per plant (g) was found in G5 (1.63).

The phenotypic variance for all the characters was considerably higher than the genotypic variance. Days to maturity, peduncle length (cm), number of spikelets per spike, number of grains per spike, biological yield per plant (g) and grain yield per plant (g) showed the minimum difference between genotypic and phenotypic variance, which indicated low environmental influence on this character which might be due to their genetic control.

Biomass/plot (g) showed high heritability coupled with high genetic advance and a very high genetic advance in the mean percentage. In contrast, harvest index (%), 1000 grain weight (g) showed high heritability with moderate genetic advance and genetic advance in percentage of mean that revealed the possibility of the predominance of additive gene action in the inheritance of this character; therefore, the characters could be improved through a selection process.

Correlation revealed that grain yield per plant had a positive association with days to maturity, plant height at maturity (cm), number of productive tillers per plant, spike length (cm), number of grains per spike and biological yield per plant (g). Path analysis revealed that days to maturity, number of productive tillers per plant, number of grains per spike, and biological yield per plant (g) had a positive direct effect on the plant's grain yield, indicating these were the main contributors to the plant yield.

### **Recommendations**

1. Increased number of varieties will ensure more accurate analysis to get profound knowledge of genetic variation and interrelationship of yield contributing traits.
2. Further experiment in multi-location to evaluate the environmental effect on yield.
3. Early sowing should be preferable to get the maximum yield.

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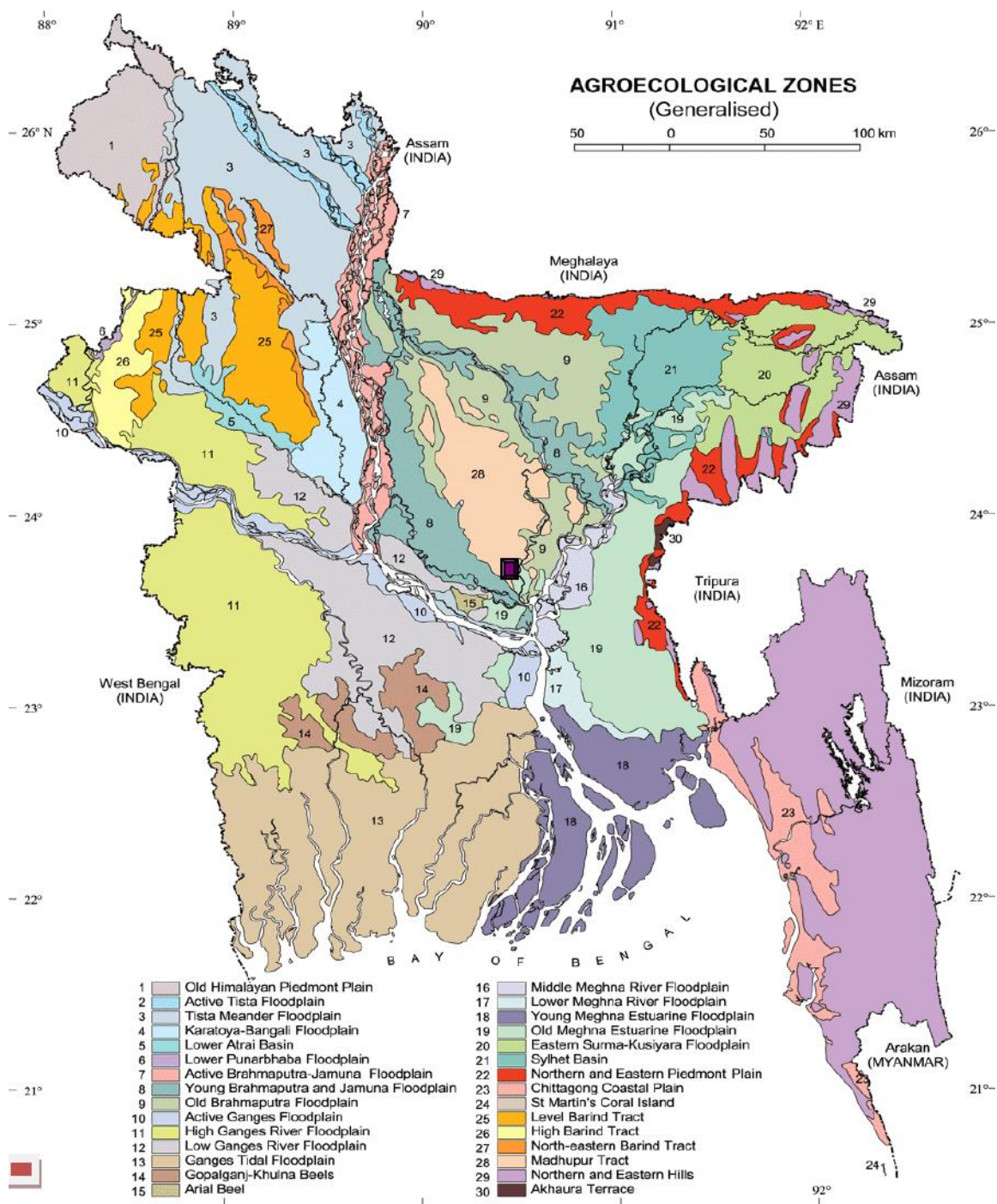
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# APPENDICES

Appendix I. Map showing the experimental site under the study



The experimental site of the research study

**Appendix II: Morphological, physical and chemical characteristics of initial soil  
(0-15 cm depth) of the experimental site**

**A. Morphological Characteristics of the Experimental Field**

<b>Morphological features</b>	<b>Characteristics</b>
Location	Agronomy Farm, SAU, Dhaka
AEZ	Madhupur Tract (28)
General Soil Type	Shallow red-brown terrace soil
Land type	High land
Soil series	Tejgaon
Topography	Fairly leveled
Flood level	Above flood level
Drainage	Well-drained

**B. Physical Composition of the Soil**

<b>Soil separates</b>	<b>%</b>	<b>Methods employed</b>
Sand	36.90	Hydrometer method (Day, 1915)
Silt	26.40	Do
Clay	36.66	Do
Texture class	Clay loam	Do

### C. Chemical Composition of Soil

Sl. No.	Soil characteristics	Analytical data	Methods employed
1	Organic carbon (%)	0.82	Walkley and Black, 1947
2	Total N (kg/ha)	1790.00	Bremner and Mulvaney, 1965
3	Total S (ppm)	225.00	Bardsley and Lanester, 1965
4	Total P (ppm)	840.00	Olsen and Sommers, 1982
5	Available N (kg/ha)	54.00	Bremner, 1965
6	Available P (kg/ha)	69.00	Olsen and Dean, 1965
7	Exchangeable K (kg/ha)	89.50	Pratt, 1965
8	Available S (ppm)	16.00	Hunter, 1984
9	pH (1:2.5 soil to water)	5.55	Jackson, 1958
10	CEC	11.23	Chapman, 1965