

**GENOTYPE-ENVIRONMENT INTERACTION IN YIELD OF
HILL COTTON GENOTYPES**

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**GENOTYPE-ENVIRONMENT INTERACTION IN YIELD OF
HILL COTTON GENOTYPES**

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CERTIFICATE

This is to certify that the thesis entitled ‘**Genotype-Environment Interaction in Yield of Hill Cotton Genotypes**’ submitted to the Faculty of Agriculture, Sher-e-Bangla Agricultural University, Dhaka, in partial fulfillment of the requirements for the degree of **MASTER OF SCIENCE in GENETICS AND PLANT BREEDING**, embodies the result of a piece of bonafide research work carried out by **Kiran Moy Dewan**, Registration number: **14-06315** under my supervision and guidance. No part of the thesis has been submitted for any other degree or diploma.

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

Dated: December, 2014
Dhaka, Bangladesh

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DEDICATED

TO

MY BELOVED PARENTS

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TABLE OF CONTENTS

CHAPTER	TITLE	PAGE
	ACKNOWLEDGEMENTS	i
	LIST OF CONTENTS	ii
	LIST OF TABLES	v
	LIST OF APPENDICES	vii
	LIST OF ABBREVIATED TERMS	viii
	ABSTRACT	ix
I.	INTRODUCTION	01
II.	REVIEW OF LITERATURE	05
	2.1 Genotypes and environment	05
	2.2 Stability with environment	07
	2.3 Genotype selection	11
	2.4 Yield components and yields	14
	2.5 Earliness	17
	2.6 Flower and boll formation	18
	2.7 Fiber quality and environment	18
	2.8 Genotype and fibre quality	19
III.	MATERIALS AND METHODS	21
	3.1 Location of the experimental site	21
	3.2 Climatic condition	21
	3.3 Characteristics of soil	21
	3.4 Experimental details	22
	3.4.1 Treatment of the experiment	22
	3.4.2 DesiHCG and layout of the experiment	22

CHAPTER	TITLE	PAGE
	3.4.3 Land preparation	23
	3.4.4 Application of manure and fertilizers	23
	3.4.5 Sowing of seeds in the field	24
	3.4.6 Intercultural operations	24
	3.5 Crop sampling and data collection	24
	3.6 Data collection	24
	3.7 Statistical analysis	26
	3.8 Eberhart and Russell's method of stability analysis	27
	3.9 Estimation of variability	28
IV.	RESULTS AND DISCUSSION	31
	4.1 Analysis of mean by genotypes, environment and their interaction	31
	4.1.1 Days to 1 st flowering	33
	4.1.2 Days to 1 st boll split	33
	4.1.3 Plant height (cm)	36
	4.1.4 Vegetative branches per plant	36
	4.1.5 Fruiting branches per plant	39
	4.1.6 Boll per plant	39
	4.1.7 Single boll weight (g)	42
	4.1.8 Seed cotton yield per hectare	42
	4.1.9 Lint yield per hectare	45
	4.1.10 Ginning out turn-GOT	45
	4.1.11 Seed index	48
	4.1.12 Lint index	48
	4.2 Variability study for 12 traits of cotton	51

CHAPTER	TITLE	PAGE
	4.2.1 Days to 1 st flowering	51
	4.2.2 Days to 1 st boll split	51
	4.2.3 Plant height (cm)	53
	4.2.4 Vegetative branches per plant	53
	4.2.5 Fruiting branches per plant	53
	4.2.6 Boll per plant	54
	4.2.7 Single boll weight (g)	54
	4.2.8 Seed cotton yield per hectare	55
	4.2.9 Lint yield per hectare	55
	4.2.10 Ginning out turn-GOT	55
	4.2.11 Seed index	56
	4.2.12 Lint index	56
V.	SUMMARY AND CONCLUSION	57
	REFERENCES	61
	APPENDIX	73

LIST OF TABLES

Table No.	TITLE	PAGE
1.	Fertilizers and manure applied for the experimental field	23
2.	Pooled analysis of variance (ANOVA) for different traits of cotton genotypes in a genotype-environment interaction study	32
3.	Average days to 1 st flowering, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	34
4.	Average days to 1 st boll split, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	35
5.	Average plant height, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	37
6.	Average vegetative branches per plant, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	38
7.	Average fruiting branches per plant, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	40
8.	Average boll per plant, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	41
9.	Average single boll weight (g), coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	43
10.	Average seed cotton yield per hectare, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	44

Table No.	TITLE	PAGE
11.	Average lint yield per hectare, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	46
12.	Average ginning out turn-GOT, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	47
13.	Average seed index, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	49
14.	Average lint index, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model	50
15.	Variability of different traits of cotton genotypes	52

LIST OF APPENDICES

Appendix No.	TITLE	PAGE
I.	Monthly average of air temperature, relative humidity and total rainfall of the experimental site during the period from May to September, 2014	73
II.	Physical characteristics of field soil analyzed in Soil Resources Development Institute (SRDI) laboratory, Khamarbari, Farmgate, Dhaka	73
III.	Photograph showing the experimental plot	74
IV.	Photograph showing the leaves of different cotton genotypes	75
V.	Photograph showing the boll of different cotton genotypes	75

LIST OF ABBREVIATED TERMS

ABBREVIATION	FULL NAME
AEZ	Agro-Ecological Zone
<i>et al.</i>	and others
BBS	Bangladesh Bureau of Statistics
cm	Centimeter
⁰ C	Degree Celsius
DAS	Date After Seeding
etc	Etcetera
FAO	Food and Agriculture Organization
GOT	Ginning out turn
MP	Muriate of Potash
RCBD	Randomized Complete Block Design
m ²	Square meter
TSP	Triple Super Phosphate
UNDP	United Nations Development Program
SAU	Sher-e-Bangla Agricultural University

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ABSTRACT

The experiment was conducted at the Chittagong Hill Tracts (CHT) areas of Bangladesh i.e. Bandarban, Rangamati and Khagrachari during May to September 2014 to study the genotype environment interaction effect on yield of some selected hill cotton genotypes. The experiment consisted of two factors: Factor A: Location (3 locations) - L₁: Bandarban; L₂: Rangamati and L₃: Khagrachari; Factor B: Different cotton genotypes- G₁: HCG-4; G₂: HCG-13, G₃: HCG-15, G₄: HCG-21, G₅: HCG-26, G₆: HCG-42, G₇: HCG-51 and V₈: HC-1 (Check). The two factors experiment was laid out in split-plot design with three replications where location factor was assigned in main plot (Bandarban, Rangamati and Khagrachari) and cotton genotypes in sub-plot. In case of location environment, the maximum boll per plant was recorded from Bandarban (19.13) whereas the minimum boll per plant from Rangamati (16.23). The highest single boll weight was recorded from Bandarban (4.65 g) whereas the lowest from Rangamati (3.92 g). The highest seed cotton yield per hectare was recorded from Bandarban (1825 kg), whereas the lowest seed cotton yield per hectare from Rangamati (1691 kg). The highest lint yield per hectare was recorded from Khagrachari (809 kg), whereas the lowest lint yield per hectare from Rangamati (681 kg). For genotypes, maximum boll per plant (24.61), single boll weight (5.18 g), seed cotton yield per hectare (2170 kg) and lint yield per hectare (927 kg) was observed in HCG-13 and lowest value was observed in check variety HC-1 for all the cases. In case of interaction of environments and genotypes, highest boll per plant (27.03), single ball weight (5.29 g), seed cotton yield per hectare (2170 kg), lint yield per hectare (981 kg) was observed in HCG-13 at Bandarban than the Rangamati and Khagrachari. In all the environments check HC-1 gave the lowest value. Genotype HCG-13 was found highest yielder than the other genotypes and showed better performance at Bandarban than the Rangamati and Khagrachari.

CHAPTER I

INTRODUCTION

Cotton (*Gossypium hirsutum* L.) is an important fibre yielding crop of global importance and important industrial raw materials belonging to the family Malvaceae. It is grown in tropical and subtropical regions of more than 80 countries of the world. Among these countries, China, USA, Russia, India, Brazil, Pakistan, Turkey, Egypt, Mexico and Sudan are accounted for 85-90% of the total cotton production (Zeng *et al.*, 2014). Cotton refers to those species of the genus *Gossypium* which bear spinnable seed coat fibres.

There are about 42 species of the genus *Gossypium* out of these only four species, viz. *Gossypium arboreum*, *G. herbaceum*, *G. hirsutum* and *G. barbadense* are cultivated and the rest are wild. The first two species are diploid ($2n = 2x = 26$) and are native of Old world. Diploid cultivated species are also known as Desi cottons or Asiatic cottons because they are cultivated in Asian region. The last two of the above mentioned cultivated species are tetraploid ($2n = 4x = 52$) and are referred to as New world cottons. The *G. hirsutum* is known as American cotton or upland cotton and *G. barbadense* is also referred to as Sea Island cotton or Egyptian cotton or Tanguish cotton. The *G. hirsutum* is the predominant species, which alone contributes about 90% to the global production.

Cotton is the major textile fibre used by man in the world and it plays a key role in economic and social welfare (Munro, 1994). Although it is grown primarily as a fibre crop, but after the lint, the long twisted unicellular hairs are removed by ginning, the seed can be crushed to extract vegetable oil and protein rich animal food (Mathews, 1989). Cottonseed cake, an industrial byproduct of cotton, is a valuable source of protein for ruminant cattle. In Bangladesh, cotton provides raw materials to domestic cotton industry containing 363 spinning mills, 1623 weaving mills, more than 3 lacs of handlooms, 2,822 knitting and 4,500 garment industries (BTMA, 2002). Current domestic requirement of cotton is about 4.3 m

bales against production of 128,365 bales which accounts only 3% of the yearly cotton requirement (Anon., 2008). Therefore, cotton industries of Bangladesh predominantly depend upon import where nearly 98% of the requirement is fulfilled by importing raw cotton from different foreign countries. In this context, it is imperative to increase cotton production in Bangladesh to feed the cotton industry, to save the hard earned foreign exchange and to attain self sufficiency in raw cotton. Cotton production in Bangladesh may be increased either by horizontally or vertically or by both the ways. But in fact, it is almost impossible to increase cotton production horizontally because of severe competition to other crops in limited land. Yield enhancement of cotton by alternate may be possible because the productivity of cotton in Bangladesh is only 450 kg lint ha⁻¹ against world average yield of 556 kg lint ha⁻¹. Higher yield of cotton may be achieved by selecting appropriate variety specifically suited to local ecological condition.

Cotton (*Gossypium arboreum*) is an important crop for hill farming. It has been cultivated since the prehistoric time in hill districts of Bangladesh. Cotton is important to tribal people not only for their source of income but also in their religious rites. The hill people make their clothing with the hill cotton. Blankets are also produced with this hill cotton. The hill cotton is exported to different countries. Hill cotton is a long duration crop and generally hilly farmers grow cotton in Jhum system i.e. they cultivate cotton with other crops like rice, maize, chilies, sesame, okra, marpha, pigeon pea etc. in the same pit at a time in hill slope. As a result every crop has to compete to each other for nutrient, moisture, sunshine, air and other growth factors. For intra and inter species competition the yield of cotton, rice and other component crops is low and unstable. On the other hand, in Jhum cultivation environmental pollution and soil erosion is very high. Some indigenous varieties of cotton are being cultivated for a long time in Jhum cultivation. The bolls of the varieties are of different shape and size: big, medium or small. Fibre colour is white or khaki. Two released varieties are now being cultivated named HC-1(white) and HC-2(khaki).

Cotton yield is a polygenic complex character, depends on several contributing characters coupled with varying environmental condition (Larik *et al.*, 1997; Khan, 2003, Khan *et al.*, 2009). It also has been stagnant for the last two decades and very low as compared to other cotton growing countries of the World (Khan and Hassan, 2011). Hill cotton is generally grown in Jhum system. It has to compete for nutrients, moisture, sunlight and air with other crops; as a result the yield of cotton is very poor. Factors responsible for the low cotton production include, excessive rains at the time of sowing, high temperature and its fluctuations at flowering stage, late wheat harvesting resulting in decline of area under cotton, incidence of cotton leaf curl virus (CLCuV) and lack of resistant cultivars, pest attack and improper production technology in the major cotton growing areas (Khan *et al.*, 2009). In any crop improvement program, knowledge on nature of gene action and inheritance of traits is essential so as to choose a suitable breeding methodology in crop improvement (Vineela *et al.*, 2013).

Development of an effective breeding program depends on the existence of genetic variability for various economic characters in the gene pool. Selection is effective only when there is enough magnitude of variability in the breeding population. An understanding of precise magnitude of variability present in a population is important in formulating the most appropriate breeding technique for improvement of various characters. Crop performance depends on genotype, the environment in which the crop is grown, and the interaction between the genotype and environment (Gomez and Gomez, 1984). Genotype is defined as an individual's genetic make-up and the phenotypic expression of a genotype depends on environments that may be defined as the sum total of circumstances surrounding or affecting an organism or a group of organisms. Cultivars of a crop as genotypes, when grown under a wide range of environmental conditions (exposed to different soil types, fertility levels, moisture contents, temperatures, photoperiods, biotic and abiotic stresses and cultural practices) also perform differently for various morphological and yield traits.

The variability among different genotypes arises either due to geographical separation or due to genetic barriers to the crossability. Genetic variability plays an important role in plant breeding because hybrids between lines of diverse origin generally display a great heterosis than those between closely related strains (Singh, 1983) which permits to select the genetically divergent parents to obtain the desirable recombination of the segregating generations. The choice of the most suitable breeding method for the rational improvement of yield and its components in any crop largely depends upon the genetic variability, correlations and association between qualitative and quantitative characters, heritability estimates, and adaptability parameters in different environments. The behavior of yield characters may be cross over or cross over nature depending upon the ranking order of genotypic performance under different environments (Ali *et al.*, 2005; Ahamd *et al.*, 2006). The G×E interactions may change the response and performance of a crop, and hence, the extent of the environmental effects on a trait determines the importance of testing over years and locations.

Eberhart and Russell (1966) defined stability as the ability to show a minimum interaction with the environment. Hence, the stability of genotype performance is directly to the effect of G×E. Breeding for genotypes stability is accomplished with respective field testing, trait evaluation and selection of genotypic that rank at or near the top of a series of individual field trials conducted across a range of environments and years. In the hill tracts wide range of cotton genotypes were existed but the suitable genotypes for hilly areas are not defined. As a result cultivation of hill cotton is decreasing day by day due to the lack of high yielding variety. Under the above mentioned situation, the present piece of work was undertaken with the following objectives-

- To evaluate the influence of G×E on lint yield and (ginning out turn) GOT of selected hill cotton genotypes;
- To identify the genotypes suitable for specific locations of hill tracts; and
- To identify the stable genotype(s) suitable for the three hill tracts.

CHAPTER II

REVIEW OF LITERATURE

Cotton is one of the important fiber crops our country and it plays a vital and effective role in the economy of Bangladesh. Very few research reports are available on the improvement of this crop have been done in various part of the world including Bangladesh and the work so far done in Bangladesh is not adequate and conclusive. Research effort on genetic variability, character association and environmental influence seems to be also inadequate and not conclusive. Nevertheless, some of the important and informative works and research findings so far been done at home and abroad on this aspect have been reviewed in this chapter under the following headings:

2.1 Genotypes and environment

Gul *et al.* (2014) reported that legacy of seed cotton yield and other quantitative traits are highly persuaded by environmental aspects. Therefore, phenotypic response of a genotype is ascertained by genetic and environmental factors upon it, although occurrence of a third effect, of no less importance i.e. genotype by environmental interaction (GEI). Significant mean squares for genotypes, environments and G×E interactions revealed genetic variability among cotton genotypes as well as environments inconsistency. They also reported that the environment accounts for 61.86%, 26.99% and 18.64% of total variation for bolls plant⁻¹, seed cotton yield and sympodia plant⁻¹, respectively, considering the larger effects of environment in combination with genotypes on plant growth and morphology.

Zeng *et al.* (2014) analysis of genotype (G) by environment (E) interactions and their influence on performance of cotton (*Gossypium hirsutum* L.) cultivars can help cotton breeders improve performance stability of cultivars across environments. Data from multi-location trials of the Regional High Quality Tests conducted as part of the USDA-ARS National Cotton Variety Tests to analyze

G×E and relationships among test locations for mega environments. The trials were located in the Western, Plains, Central, Delta, and Eastern regions of the U.S. Cotton Belt. Effects of G×location for lint yield were either larger or comparable to the effects of G×year. The relationships among test locations were analyzed in GGE biplot and no clear mega environments were identified among test locations across years. Nevertheless, the locations of Las Cruces, NM in the Western and Lubbock, TX in the Plains test regions were identified as distinct from the test locations in the other areas. It was hypothesized that the environments in the U.S. Cotton Belt belonged to one mega environment with the areas in the Western and Plains as a subregion.

Root and shoot growth of the cotton genotypes also significantly affected by soil type (Suresh *et al.*, 2005). Cotton prefers moderate rainfall but highly susceptible to water logging conditions especially at the seedling stage (20 days after sowing) than at flowering (80 days after sowing) or at later stages (Hebbar, 2003).

The performance of a cotton genotype is dependent on the genetic capacity and the environment where it is grown, and the interaction between the genotype and the environment (Yan, 2001; Yan and Hunt, 2001; Kerby *et al.*, 2000) and genotype environment independently (Yan and Hunt, 2001).

The cotton production is very much depended on the total temperature. The optimum temperature required for cotton cultivation is 30⁰C-33⁰C. Temperature bellow 10⁰C retards boll development and maturity. Temperature responses of different varieties for time to first squares, squaring to flowering, main stem and fruiting branch node formation and duration of leaf and internodes expansion were positive and linear. Johanson (1997) conducted a study to compare fruiting and maturity pattern of six cotton varieties and found that fruiting and growth pattern were inconsistent across environment.

Many environmental factors (temperature, wind, precipitation, light, heat, cold, drought, soil type) affect cotton performance. Cotton canopy architecture, plant

height, branch formation, fruiting and boll development can be affected by temperature (Hodges *et al.*, 1993 Reddy *et al.*, 1990), growth regulator application (Reddy *et al.*, 1990), light intensity (Sassenrath-Cole, 1995), and herbivore by insect and other animals (Rosenthal and Kotanen, 1994; Terry, 1992).

2.2 Stability with environment

Moiana *et al.* (2014) conducted an experiment to determine the productivity, genotypic adaptability and genotypic stability of nine cotton cultivars (*Gossypium hirsutum*) in Mozambique. The genotypic stability and genotypic adaptability were assessed by Residual Maximum Likelihood (REML) and predict breeding values using Best Linear Unbiased Prediction (BLUP) methodology. The cultivars ISA 205, STAM 42 and REMU 40 showed superior productivity when they were selected by the Harmonic Mean of Genotypic Values (HMGV) criterion in relation to others. In turn, the cultivars CA 222, STAM 42 and ISA-205 were superior when selected by the Relative Performance of Genotypic Values (RPGV) and Harmonic Mean of the Relative Performance of Genotypic Values (HMRPGV). The cultivars CA 324 had the lower values for all criteria above. The cultivars CA 222 and STAM 42 will be the most recommended for farmers in cotton-growing regions and for the Cotton Breeding Program of Mozambique.

Silva *et al.* (2014) evaluated the performance of doubled haploid (DH) genotypes as compared to their parents in three diverse environments in Minas Gerais state to determine possible genotype-by-environment (G×E) interactions, and to estimate stability parameters when pertinent. A set of eight cotton genotypes which included DH) obtained through semigamy and their respective progenitors, all developed by EPAMIG breeding program were planted in field trials, at three representative locations of the regions: Triangulo Mineiro (Uberaba), Alto Paranaíba (Patos de Minas) and North (Nova Porteirinha). No significant G×E interactions were found for the great majority of the characters evaluated. The double-haploids were, in general, more stable than the parental genotypes from which they were derived, which demonstrated that the semigamy method is efficient and promising for the development of new genotypes. It was not

confirmed the hypothesis that the high levels of expected homozygosity of the DH genotypes could imply lesser stability over different environments. In the location of Uberaba, the DH genotypes in general presented smaller variation than their respective parents for the traits evaluated and presented improved values for the characters, thus confirming the efficiency of the method. The DH-EPAMIG-4 was more variable than its parental genotype and the other DH genotypes.

Multi-location trials of the Regional High Quality Tests conducted by Zeng *et al.* (2014) as part of the USDA-ARS National Cotton Variety Tests were used to analyze $G \times E$ and relationships among test locations for mega environments. They reported that the daily minimum temperature was significantly correlated to environment scores of the first principal component axis with r values -0.41 and -0.30 for the early and late growing seasons, respectively. This result suggests that genetic improvement of cotton cultivars for tolerance to low temperature during the early and late growing season could increase yield stability.

Comparative studies on stability parameters and sustainability index for selecting stable genotypes in Asiatic cotton (*Gossypium arboreum* L.) was carried out by Verma *et al.* (2013) according to Eberhart and Russell model with sustainability index model. Stability analysis was carried out on seven *Gossypium arboreum* genotypes for seed cotton yield, seed index, lint index, number of bolls per plant, boll weight, GOT, 2.5% staple length, micronaire and bundle strength on three years data, viz. 2004, 2005 and 2006. Based on the linear component (bi), non-linear response (S^2di) and high mean performance (\bar{x}), the genotypes LD 861 and CISA 614 were found stable for seed cotton yield while based on sustainability index and best performance, the only genotype CISA 614 was found to be stable. For other traits like seed index, lint index, GOT, no. of bolls per plant, boll weight and micronaire, the deviation from regression was non-significant and on the basis of sustainability index, the variety CISA 614 was found stable having sustainability index more than 80%. For seed index, GOT, micronaire, 2.5% staple length, bundle strength, the entire genotypes recorded very high sustainability index, which indicated that these characters are least influenced by

the environmental factors, however, the genotype CISA 614 has high sustainability index for 2.5% span length whereas very high sustainability index was expected.

Three field experiments were carried out by Dewdar (2013) at the Faculty of Agriculture, El-Fayoum University, Fayoum, Egypt, to study the magnitude and nature of G×E interaction and determine of stability of yield potentiality for five Egyptian cotton varieties. Significant differences were observed among cotton varieties for seed cotton yield per plant, lint yield per plant, number of open bolls, boll weight, lint % and lint index. Combined analysis showed highly significant between the genotypes, between environments and for G×E interaction of all traits under study. These results showed that genotypes of Giza 90 and Giza 80 were more stable varieties. This implies that the genotypes had low contribution to the genotypic by environment interaction. These results showed that high yielding genotypes can differ in yield stability, and suggest that yield stability and high mean yield are not mutually exclusive. Therefore, the genotypes Giza 90 and Giza 80 could be used as breeding stock that could be incorporated in crosses with the objectives of improving the previously mentioned traits.

Twelve cotton cultivars were evaluated by Arega-Gashaw (2013) for cottonseed yield, lint qualities and other agronomic traits. Fiber quality parameters (staple length, fiber strength, lint fineness and short fiber index) were also examined. ANOVA revealed significant variations among cultivars for all agronomic and lint quality traits, except for fiber strength. Of the cultivars examined, Delcero consistently out-smarted in lint quality in moisture-stressed environments of northeastern Ethiopia. Farmers are encouraged to grow genetically superior cultivars to meet the lint quality standards of local textile industries and international markets. Moreover, Delcero could be utilized as elite parents for future lint quality breeding. Lint yield was strongly and positively associated with lint quality traits, implying the possibility of simultaneous improvement for both lint yield and lint quality traits under moisture-stressed environments. Stability analysis using AMMI model showed that Deltapine-90 was relatively stable

across diverse environments for cottonseed yield. Growing Deltapine-90 in the moisture-stressed environments of northeastern Ethiopia could help to minimize yield shock and ensures farmers to have reasonable harvest under unpredictable and fluctuating environments.

The study was conducted by Riaz *et al.* (2013) to determine the yield stability, adaptability and to analyze the G×E interaction of 9 cotton genotypes at six locations in Punjab, Pakistan during the growing season of 2010 and 2011 (twelve environments). Additive main effects and multiplicative interactions (AMMI) analysis revealed that the major contributions to treatment sum of squares were environments (38.51%), G×E (35.27%) and genotypes (26.22%), respectively, suggesting that the seed cotton yield of genotypes were under the major environmental effects of GE interactions. The first two principal component axes (PCA 1 and 2) cumulatively contributed to 64.34% of the total G×E interaction and were significant ($p \leq 0.01$). The biplot technique was used to identify appropriate genotype to special locations/environments. Results showed that genotypes BH-172, MNH-814 and NIAB-2009 with the lowest interaction, and genotypes FH-4243, FH-113, CIM-496, CIM-573, VH-289 and MNH-886 with the highest interaction were the most stable and unstable genotypes, respectively. Moreover, genotypes NIAB-2009, MNH-814, VH-289, MNH-886, CIM-573 and BH-172 were more suitable for Sahiwal, Vehari and Bahawalpur conditions while genotypes FH-4243, FH-113 and CIM-496 were better suited for Faisalabad conditions.

Lint yield, lint percent, fiber length, fiber strength, fiber micronaire, and uniformity index were evaluated by Snider *et al.* (2013) for seven commercially available cotton cultivars across 33 environments in on-farm trials throughout Georgia. The following were quantified: the percentage of variability in each response variable accounted for by genotype and environment, trait stability for each cultivar across all yield environments, and genotypic and environmental correlations between all parameters of interest. Environment was the dominant factor governing lint yield (96.1% environment, 1.2% genotype), fiber length

(80.6% environment, 5.1% genotype), strength (47% environment, 27.7% genotype), micronaire (63.8% environment, 9.9% genotype), and uniformity (69.8% environment, 6.5% genotype). In contrast, lint percentage was impacted more by genotype (51.5%) than by environment (38.8%). 'PHY 565 WRF' was identified as the most stable cultivar across all yield environments for all agronomic and fiber quality traits examined. Environmental correlations showed that fiber length, strength, and uniformity were all positively correlated with yield. These findings suggest that any improvements in the yield environment brought about through improved production practices or favorable environmental conditions will be conducive to improving fiber quality in cotton.

Comparative studies on stability parameters and sustainability index for selecting stable genotypes in Asiatic cotton (*Gossypium arboreum* L.) was carried out by Verma *et al.* (2013) according to Eberhart and Russell model with sustainability index model and observed that for many characters the results were found in conformity based on Eberhart and Russell model and hence the sustainability index model may be used for selecting the stable genotypes, however for 2.5% staple length it was found contrary.

2.3 Genotype selection

Gul *et al.* (2014) reported that legacy of seed cotton yield and other quantitative traits are highly persuaded by environmental aspects. Therefore, phenotypic response of a genotype is ascertained by genetic and environmental factors upon it, although occurrence of a third effect, of no less importance i.e. genotype by environment interaction (GEI). The GEI was characterized using eight upland cotton cultivars viz., SLH-284, CIM-446, CIM-473, CIM-496, CIM-499, CIM-506, CIM-544 and CIM-707. Based on two-year studies, CIM-496 exhibited the best performance followed by CIM-554 and SLH-284 for improvement in seed cotton and lint yields.

Dhivya *et al.* (2014) recorded the highest phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) by seed index, plant height,

lint index and boll weight. Genotypic co-efficient of variation had a similar trend as PCV. High heritability along with high genetic advance was observed in traits viz., number of sympodia per plant, single plant yields, seed index and micronaire value. The combinations of high heritability with high genetic advance will provide a clear base on the reliability of that particular character in selection of variable entries. Based on *per se* performance, the accessions MCU5, TCH1715, TCH1716 and G16 were identified as potential donors for single plant yield (g) and number of bolls per plant.

A study was carried out by Dhamayanathi *et al.* (2010) with twenty five *Gossypium barbadense* L. genotypes to obtain information on genetic variability, heritability and genetic advance for seed cotton yield and its yield attributes. Significant differences were observed for characters among genotypes. High genetic differences were recorded for nodes per plant, sympodia, bolls as well as fruiting points per plant, seed cotton yield, lint index indicating ample scope for genetic improvement of these characters through selection. Results also revealed high heritability coupled with high genetic advance for yield and most of the yield components as well as fibre quality traits. Sympodia per plant, fruiting point per plant, number of nodes per plant, number of bolls per plant, and lint index were positively correlated with seed cotton yield per plant and appeared to be interrelated with each other.

Genotype selection is a key management component in any cropping system. The yield and fiber quality potential of cotton at harvest begin with selection of genotype. Tuteja *et al.* (2006) reported wide differences existed in productivity potential and plant type of cotton. Generally, high yield potential is a predominant consideration but maturity, plant size and fiber properties and also important factors for genotype selection. Less vigorous genotypes are more susceptible to stresses caused by inadequate moisture, cool or high temperature, thrips feeding, seedling diseases, nematodes and other pests.

Kudachikar and Janagoudar (2001) reported that high-yielding genotypes were characterized by low leaf area, high total dry matter content, leaf efficiency, harvest index, and boll number.

Cotton producers are currently faced with rising cost of production and static declining return for their commodity (Jost and Cothren, 2000). To combat these challenges, producers are continually searching for new alternatives to optimize their profit. Selection of *Bt* transgenic cotton varieties may be a favourable choice for them. Because *Bt* cotton provides a fairly high degree of resistance to lepidopterous pest (Gore *et al.*, 2000; Perlak *et al.*, 2001) and is thus widely adopted in both developed and developing countries (Qaim and Zilberman, 2003). Sarker *et al.* (2001) reported that 50% of the total production was damaged by the lepidopterous (Bollworm) insect. A series of studies conducted in the USA and South Africa which indicated that the yield of *Bt* cotton was significantly higher than local non *Bt* cotton varieties, and contributed to nearly 60% reduction in pesticides (Traxler and Falck-Zepeda, 1999; Qaim and Zilberman, 2003).

Hybrid cotton varieties may be another choice because it is more tolerant to stress factors than non-hybrid cotton. Some authors indicated that yield advantage of hybrid cotton is partly because of its high photosynthetic rate (P_n) and photosynthate allocation (Bhardwaj and Weaver, 1984; Wells and Meredith, 1986; Chen *et al.*, 1998). The relative high P_n without mid-day depression probably contributed to enhanced yield of hybrid cotton, compared with non-hybrid. Mid-day depression of P_n may be attributed to photoinhibition (Powels, 1984), carbohydrate feedback inhibition (Peet and Kramer), 1980), high temperature (Perry *et al.*, 1983), water stress and stomatal closure due to increase vapour pressure deficit (Pettigrew *et al.*, 1990).

Most of the cotton cultivars which were grown commercially possess the normal leaf type. Leaf shapes of okra-leaf cultivars can greatly alter canopy structure and light interception characteristics (Wells *et al.*, 1986). Okra leaf cultivars are characterized by moderately cleft leaves and relatively small leaf area. They

typically have less vegetative growth, early maturity, greater flower production ability, and less boll rot than normal leaf cotton (Wells and Meredith, 1986; Jones, 1982). But a major disadvantage of okra leaf cotton is lower leaf area index in the early stages of development (Wells and Meredith, 1986).

In cotton shorter plant height, higher number of bolls per plant and boll weight, lower number of days to flowering and boll split are desirable (Alam *et al.*, 1996). Adarsha *et al.* (2004) suggested that cotton genotypes should possess the following morpho-physiological characters for getting higher yield: medium duration (160-170 days), (ii) medium number of monopodial branches (1.27) and higher number of sympodial branches (at least 21.0) and (iii) higher number of bolls per plants, boll weight and harvest index.

2.4 Yield components and yields

Sixty eight diverse genotypes of American cotton *Gossypium hirsutum* L. were evaluated by Pujer *et al.* (2014) for 13 quantitative and fibre quality traits. The variability studies indicated that high PCV and GCV was observed in case of seed cotton yield per plant and number of bolls per plant while moderate PCV and GCV was observed in case of days to first flower, plant height and boll weight. Seed cotton yield per plant, days to first flower, plant height, number of bolls per plant and boll weight showed high heritability with high genetic advance over mean. The correlation study revealed that seed cotton yield was found to be positively and significantly correlated with traits like days to first flower, plant height, number of monopodial branches, number of bolls per plant, seed index, lint index, ginning out turn, and uniformity ratio, whereas it had negative association with boll weight, 2.5% span length, fibre fineness, and bundle strength. Path analysis revealed that days to first flower, number of monopodial branches, number of bolls/plant, boll weight, seed index, lint index, ginning out turn and uniformity ratio showed positive direct effect on seed cotton yield. Hence selection for these traits would be quite effective to improve the seed cotton yield in upland cotton.

Vinodhana *et al.* (2013) estimated variability, correlation and path coefficient analysis by using eight lines and seven testers and their 56 F₁s made with the parents of *G. hirsutum* and *G. barbadense* genotypes of diverse origin. High heritability coupled with high genetic advance was noticed for the characters seed yield per plant, number of bolls per plant indicating the presence of additive gene action in the expression of these traits. Correlation studies revealed that seed cotton yield had positive significant correlation with number of bolls per plant and fibre length. The value of genotypic correlation coefficient was higher than phenotypic correlation coefficient, which denoted that there was strong association between these two characters genetically, but the phenotypic value was lessened by the significant interaction of environment. Number of bolls per plant had significant positive association with plant height and fibre length. The positive significant correlation was observed for seed index, lint index and micronaire value with boll weight at genotypic and phenotypic level. Thus for increasing seed cotton yield in cotton due emphasis should be given to number of bolls per plant, boll weight (g), seed index, lint index and fibre length (mm) characters.

Khan *et al.* (2009) mentioned that genetic variances were found almost greater than the environmental variances and correlation of seed cotton yield with other different traits was found significantly positive for majority traits. Plant height, sympodia per plant, staple length, and staple strength exhibited high narrow sense heritability due to the presence of additive gene action (Basal and Turgut, 2005; Ali and Khan, 2007), whereas, monopodia per plant, number of bolls, lint percentage and seed cotton yield possesses low narrow sense heritability which was due to presence of dominant gene effects (Ahmad *et al.*, 2003; Haq and Azhar, 2004).

Meena *et al.* (2007) evaluated different upland cotton cultivars for yield and other economic traits and observed significant variations. This genetic analysis suggested that plant height, sympodia per plant, staple length and fibre strength could be improved through individual plant selection, while exploitation of

heterosis would be necessary to attain the genetic advancement in monopodia per plant, number of bolls, lint percentage and seed cotton yield.

Plant height of cotton cultivars differed significantly. It was positively correlated with bolls and seed cotton yield (Khan, 2003; Khan *et al.*, 2009; Batool *et al.*, 2010; Taohua and Haipeng, 2006). Khan *et al.* (2009) reported that the genetic variability for plant height among different upland cotton cultivars was present and mentioned that plant height was positively correlated with bolls and seed cotton yield if lodging did not occur. Some scientist (Murthy, 1999; Batool *et al.*, 2010) also reported that positive correlation between plant height and yield and noted that plant height contributed 70% of the total variability for seed cotton yield.

Among the yield components bolls per plant is the key independent component and play prime role in managing seed cotton yield. Number of open boll had the highest direct effect on lint yield per plant (Zeina *et al.*, 1998). Other authors (Abouzaid *et al.*, 1997; Ganapathy *et al.*, 2006 and Khan *et al.*, 2009) also reported variable number of bolls per plant in upland cotton genotypes and exhibited very high positive correlation with seed cotton yield.

Boll weight is second major yield component after bolls per plant and have a greater contribution in enhancement of yield. A significant positive correlation was observed between the average number of bolls per plant, mean boll weight and seed cotton yield per plant (Zende *et al.*, 2003). Similarly, several scientists (Ivanova and Stoyanova, 1996; Terziv *et al.* 1996; Abouzaid *et al.*, 1997; Khan *et al.*, 2009) obtained the similar result for boll weight and seed cotton yield in different cotton genotypes. Others (Afiah and Ghoneim, 2000; Badr, 2003; Khan, 2003; Soomro *et al.*, 2008) also observed significant variations for boll weight and revealed highly positive effect on yield.

Seeds per locule were significant and positively associated with seed cotton yield and contributed 70% of the total variability for cotton yield (Khan *et al.*, 2010;

Iqbal *et al.*, 2003). Murthy (1999) and Wang *et al.* (2004) derived information on genetic variability and observed positive yield correlation with seeds per locule and other yield traits. Genetic variability and positive correlation between seeds per bolls and seed cotton yield was derived in *Hirsutum* and reported by many authors (Iqbal *et al.*, 2003; Wang *et al.*, 2004). Likewise, other authors (Khan *et al.*, 2010) also found high genetic variability for seeds per boll and seed cotton yield.

Cotton plants grow with monopodial vegetative, main stem and lateral monopodial and sympodial fruiting branches. Short duration genotypes were characterized by minimum spreading of their vegetative branches. Reduced number of lateral monopodial branches that were formed before sympodial fruiting branches that resulting in an earlier onset of flowering (Kohel *et al.*, 1987). Number of sympod per plant is one of the important factors of yield contributing characters of cotton. Higher number of sympodial branches per plant and boll weight had the highest positive direct effect on yield. On the other hand, number of monopodial branches per plant and ginning out turn had a negative effect on yield (Muhammad *et al.*, 2003).

Variability in yield and yield attributes among genotypes are common in cotton. Seed cotton yield per unit area is the function of yield of individual plant and population densities. Lint yield of upland cotton is determined by a number of individual components (Worley *et al.*, 1976). Yield components such as the plant height, number of sympodia per plant, node of first fruiting branch, days to first flowering, number of bolls per plant, boll weight, days to 50% boll split, and seed index differed significantly in the cotton genotypes.

2.5 Earliness

Earliness of the crop maturity is important in the avoidance of frost damage, insect and disease buildup, soil moisture depletion and weathering of the open cotton. Moreover, early maturity helps to fit the crop into cropping pattern, allowing rotation with a winter crop. Number of nodes to the first fruiting branch,

plants height, date to first square, date to first flower and date of first open boll can be used for efficient selection of early genotypes.

Node number of first fruiting branch is an important characteristics which affecting the earliness of the crop. Lower the NFB sooner the first flower appears of cotton. Two preliminary indicators (main stem node number of first sympodial branch and days taken to open first flower) are reliable and efficient for predicting the earliness of cotton genotype (Saira *et al.*, 2002). Saced and Kausar (2005) reported that earliness was measured in terms of flowering time of cotton.

2.6 Flower and boll formation

Cotton genotypes differed significantly for flower and boll production, and earliness in crop maturity (Cook and EL-Zik, 1993). Although it is an inherent character of the genotype, but sometimes it also depends on other factors. Like evaporation, humidity, light and temperature are the principal climatic factors that governed cotton flower and boll production (Sawan *et al.*, 1999). Similar study revealed that modern cultivars developed squares faster than 20-30 years older ones, when grown at the same temperature (Reddy *et al.*, 1993). Fan *et al.* (1989) found that boll size; boll weight and fiber properties were positively correlated with flowering date and boll retention.

2.7 Fiber quality and environment

Further, Yuan *et al.* (2002) observed that fibre properties are easily influenced by different environments. It was found that the fibre strength, length, micronaire and elongation were stable in different environments since they had higher broad-sense heritability. However, low broad-sense heritability was observed for fibre length uniformity which is so easily influenced by environments.

But these traits are highly influenced by the environment with special reference to the fineness (Percy *et al.*, 2006). Other authors (Bradow *et al.*, 1997) found that weather factors that affect carbon assimilation, such as temperature which influences on micronaire. Reddy *et al.*, (1999) showed that

micronaire increased linearly with the increase in temperature up to 26⁰C but decreased at 32⁰C. Recently, much variability in the performance of cotton cultivars has been attributed to differences in environment (Kerby *et al.*, 2000).

Cotton fiber is an extension of a seed epidermal cell, the most basic component of lint yield in cotton must be the number of fibers per seed, or more precisely, the number of spinnable fibers per unit seed surface area (Worley *et al.*, 1976). Cotton fiber quality is no longer an afterthought it is becoming an increasingly important issue in modern textile industry.

Fibre quality of a specific cotton genotype is a composite of various characteristics including staple length, fiber strength, fineness, maturity and fiber elongation. These traits have their individual importance in spinning, weaving and dyeing units (Munro, 1987). Yarn strength is the processing result greatest interest to yarn and textile manufacturers (Bradow *et al.*, 1999). In addition fiber uniformity is also of tremendous value in the textile industry. It is highly correlated with the spinning and weaving process which convert the fiber into fabrics.

Meredith and Bridge (1972) reported that within upland cotton genotypes, genes heavily influence fiber length, strength, and fineness. Other studies have suggested that the relative genetic and environmental influences on fibre strength are determined by a few major genes, rather by variation in the growth environment (May, 1999).

2.8 Genotype and fibre quality

Physiological and morphological differences were observed among cotton cultivars in relation to fibre quality. It was found that growing cotton under non-irrigated conditions resulted in the production of shorted and weaker fibre with reduced micronaire. They also mentioned that the fibre properties of cultivars were inconsistently affected by non-irrigated and irrigated conditions indicating variability inherent in cotton fibre (Meena *et al.*, 2007).

Fibre elongation and fibre dry weight were closely associated with species and varietal differences. The rate elongation was not uniform over the entire elongation period. The dry weight (secondary thickening) started only after elongation ceased and continued to increase until opened (Mishra *et al.*, 2005)

Murtaza *et al.* (2004) determined the genetic variation in 8 upland cotton cultivars for fibre strength and staple length. They revealed that the gene action governing fibre strength and staple length in cotton. Additive dominance effects controlled fibre strength, whereas epistatic effects controlled staple length in cotton. In other studied Segarra and Gannaway (1994) established that micronaire and fibre strength are to some extent as a function of cultivar difference.

Reddy *et al.* (2005) reported that genotypic and phenotypic ratio was high for 2.5% span length and bundle strength, indicating that these traits were not much influenced by the environment. Heritability estimates were high for ginning percentage, span length, bundle strength and seed cotton yield, indicating the amenability of these traits in the selection process. High heritability coupled with high genetic advance for ginning percentage, span length, bundle strength and seed cotton yield indicates the operation of additive gene action in the inheritance of these traits.

Iqbal *et al.* (2006) observed the traits ginning out turn percentage (GOT) and staple length had the direct negative effect on seed cotton yield.

It may be understood from the above reviews that different environment significantly influences the growth, development and yield of cotton. On the other hand, genotypes itself as an important factor for economical cotton production and different traits played a major role in the improvement of cotton yield.

CHAPTER III

MATERIALS AND METHODS

The experiment was conducted in three hilly districts of Bangladesh during May to September 2014. The materials and methods that were used for conducting the experiment have been presented in this chapter. It includes a short description of the location of experimental site, soil and climate condition of the experimental area, materials used for the experiment, design of the experiment, data collection and data analysis procedure.

3.1 Location of the experimental site

The experiment was conducted at the Chittagong Hill Tracts (CHT) areas of Bangladesh i.e. Bandarban, Rangamati and Khagrachari. It was located in 21.25⁰N to 23.45⁰N latitude and 91.54⁰N to 92.50⁰N longitude. The region is surrounded by Myanmar and Mizoram (India) in the east, Tripura (India) in the north and the districts of Chittagong and Cox's Bazar in the west and south, respectively. Jhum is the traditional farming system in these areas.

3.2 Climatic condition

Experimental area is situated in the sub-tropical climate zone, which is characterized by heavy rainfall during the months of April to September and scanty rainfall during the rest period of the year. Details of the meteorological data during the period of the experiment was collected from the Bangladesh Meteorological Department, Chittagong and presented in Appendix I.

3.3 Characteristics of soil

Experimental site belongs to the Chittagong Coastal Plain (UNDP, 1988) under AEZ No. 23 and the soil of the plot was medium high in nature with adequate irrigation facilities. The soil texture of the experiment was clay loam. The nutrient status of the farm soil as per the Soil Resource and Development Institute (SRDI), Dhaka under the experimental plot has been presented in Appendix II.

3.4 Experimental details

3.4.1 Treatment of the experiment

The experiment consisted of two factors:

Factor A: Location (3 locations)

- i. L₁: Bandarban
- ii. L₂: Rangamati and
- iii. L₃: Khagrachari

Factor B: Different cotton genotypes

- i. G₁: HCG-4
- ii. G₂: HCG-13
- iii. G₃: HCG-15
- iv. G₄: HCG-21
- v. G₅: HCG-26
- vi. G₆: HCG-42
- vii. G₇: HCG-51
- viii. V₈: HC-1 (Check)

There were 24 (3 × 8) treatments combination such as L₁G₁, L₁G₂, L₁G₃, L₁G₄, L₁G₅, L₁G₆, L₁G₇, L₁G₈, L₂G₁, L₂G₂, L₂G₃, L₂G₄, L₂G₅, L₂G₆, L₂G₇, L₂G₈, L₃G₁, L₃G₂, L₃G₃, L₃G₄, L₃G₅, L₃G₆, L₃G₇ and L₃G₈.

3.4.2 Design and layout of the experiment

The two factors experiment was laid out in split-plot design with three replications where location factor was assigned in main plot (Bandarban, Rangamati and Khagrachari) and cotton genotypes in sub-plot. Each area contains 24 plots where 8 genotypes were allotted at random in 3 times. There were 72 unit plot altogether in the experiment. The size of the each plot was 3 m × 2 m. The distance maintained between two blocks and two plots were 1.0 m and 0.5 m, respectively.

3.4.3 Land preparation

The plot selected for conducting the experiment was opened in the 1st week of May 2014 with a power tiller, and left exposed to the sun for a week. After one week the land was harrowed, ploughed and cross-ploughed several times followed by laddering to obtain until good tilth. Weeds and stubbles were removed, and finally obtained a desirable tilth of soil was obtained for sowing cotton seeds. The experimental plot was partitioned into unit blocks and blocks into unit plots in accordance with the design of the experiment. Cowdung and chemical fertilizers as indicated below in the section 3.4.4 were mixed with the soil of each unit plot.

3.4.4 Application of manure and fertilizers

The sources of N, P₂O₅, K₂O, S, Zn, Mg and B as urea, TSP, MP, zypsum, zinc sulphate, magnesium sulphate and borax respectively, were applied. The entire amount of fertilizer except urea and MP were applied during the final land preparation. Urea was applied in basal and three equal installments at 15, 45 and 75 days after transplanting, with the amount was as per the mentioned below. MP was applied in basal at 15 and 45 days after transplanting with the amount was as per the mentioned below. Well-rotten cowdung 10 t per ha also applied during final land preparation. The following amount of manures and fertilizers were used which shown in Table 1 as recommended by cotton development board.

Table 1. Fertilizers and manure applied for the experimental field

Manures and Fertilizers	Dose per ha	Application			
		Final land preparation	1 st installment	2 nd installment	3 rd installment
Cowdung	10 tons	10 ton	--	--	--
Urea	200 kg	200 kg	50 kg	50 kg	100 kg
TSP	175 kg	175 kg	--	--	--
MP	175 kg	175 kg	75 kg	100 kg	--
Zypsum	100 kg	100 kg	--	--	--
Zinc Sulphate	20 kg	20 kg	--	--	--
Magnesium Sulphate	20 kg	20 kg	--	--	--
Borax	20 kg	20 kg	--	--	--

3.4.5 Sowing of seeds in the field

The seeds of cotton were defuzzed and treated with Gaucho @ 5 g per kg seed and were sown 2-3 seeds per hill¹ on 12th May 2014 at Bandarban, 14th May 2014 at Khagrachari and 16th May 2014 at Rangamati in furrows maintaining the row to row spacing of 90 cm and plant to plant spacing 45 cm. Seeds were placed in pit to a depth of 4-5 cm and then covered with loose soil. The seedlings of different genotypes emerged between 6-8 days after sowing.

3.4.6 Intercultural operations

Thinning

Seeds started germination of 6 Days After Sowing (DAS). Thinning was done two times; first thinning was done at 8 DAS and second was done at 15 DAS to maintain optimum plant population in each plot.

Irrigation, drainage and weeding

Irrigation was provided before 15 and 30 DAS for optimizing the vegetative growth of cotton for the all experimental plots equally. Proper drain also made for drained out excess water from irrigation and also rainfall from the experimental plot. The crop field was weeded and herbicides were applied as per treatment of weed control methods.

Protection against insect and pest

At early stage of growth few worms (*Agrotis ipsilon*) infested the young plants and at later stage of growth pod borer (*Maruca testulalis*) attacked the plant. Ripcord 10 EC was sprayed at the rate of 1 mm with 1 litre water for two times at 15 days interval after seedlings germination to control the insects.

3.5 Crop sampling and data collection

Ten plants from each treatment were randomly selected and marked with sample card and data were recorded as per the objectives of the experiment.

3.6 Data collection

The following data were recorded at different stages:

3.6.1 Days to 1st flowering

Days required for sowing to 1st initiation of flower was counted from the date of sowing to the initiation of flowering and was recorded. Data were recorded as the average of 10 plants selected from the inner rows of each plot.

3.6.2 Days to 1st ball split

Days required for sowing to 1st split of cotton boll was counted from the date of sowing to the 1st split of cotton boll and was recorded. Data were recorded as the average of 10 plants selected from the inner rows of each plot.

3.6.3 Plant height (cm)

Plant height was measured from the ground level to the tip of the longest stem and mean value was calculated. Plant height was recorded during 1st flowering as the average of 10 plants to observe the growth rate of plants.

3.6.4 Vegetative branches per plant

The total number of vegetative branches per plant was counted from plant of each unit plot. Data were recorded as the average of 10 plants selected at random from the inner rows of each plot.

3.6.5 Fruiting branches per plant

The total number of fruiting branches per plant was counted from plant of each unit plot. Data were recorded as the average of 10 plants selected at random from the inner rows of each plot.

3.6.6 Boll per plant

The number of cotton boll per plant was counted from plant of each unit plot and the number of boll per plant was recorded. Data were recorded as the average of 10 plants selected at random from the inner rows of each plot.

3.6.7 Single boll weight (g)

The weight of individual cotton boll was recorded in gram (gm) by an electronic balance from 10 boll of selected 10 plants and converted individually.

3.6.8 Seed cotton yield per hectare

Yield of seed cotton per plot was recorded as the harvested whole cotton boll with seeds from per plot and converted in hectare and expressed in kilogram.

3.6.9 Lint yield per hectare

Lint per plot was recorded as the harvested whole cotton boll from per plot and converted in hectare and expressed in kilogram.

3.6.10 Ginning out turn (GOT)

Ginning out turn was calculated from seed cotton yield and lint yield of cotton by using the following formula and expressed in percentage.

$$\text{Ginning out turn (\% GOT)} = \frac{\text{Weight of lint (kg/ha)}}{\text{Weight of seed cotton (kg/ha)}} \times 100$$

3.6.11 Seed index

One hundred cleaned, dried seeds were counted randomly from each harvest sample and weighed by using a digital electric balance and weight was expressed in gram as seed index (g).

3.6.12 Lint index

Lint index was calculated from weight of lint and lint yield of cotton by using the following formula and expressed in percentage.

$$\text{Lint index} = \frac{\text{Weight of lint (kg/ha)}}{\text{Weight of seed (kg/ha)}} \times \text{Seed index}$$

3.7 Statistical analysis

The data obtained for different characters were statistically analyzed by using MSTAT-C computer package program. The mean values of all the recorded characters were evaluated and analysis of variance was performed by the 'F' (variance ratio) test. The significance of the difference among the treatment combinations of means was estimated by Duncan's Multiple Range Test (DMRT) at 5% level of probability (Gomez and Gomez, 1984). Moreover, recorded parameters were also subjected to stability analysis using Eberhart and Russell (1966) model. The salient aspect of Eberhart and Russell model is given below:

3.8 Eberhart and Russell's method of stability analysis

Eberhart and Russell (1966) used the following model to study the stability of genotypes under different environments:

$$Y_{ij} = \mu_i + b_i I_j + i_j \quad (I = 1, 2, \dots, n \text{ and } j = 1, 2, \dots, l)$$

Where,

Y_{ij} = mean of the i^{th} genotypes in the j^{th} environment

μ_i = mean of i^{th} genotypes over all the environment

$b_i I_j$ = regression coefficient that measures the response of the i^{th} genotype on the environmental index to varying environments

$$b_i = \frac{\sum_{j=1}^n Y_{ij} I_j}{\sum_{j=1}^n Y_j^2}$$

I_j is the environmental index which is defined as the deviation of mean of all genotypes at a given time from over all mean

$$\text{i.e. } I_j = \bar{Y}_{.j} - \bar{y}_{..}$$

Where

$\bar{Y}_{.j}$ = Mean at j^{th} environment

$\bar{y}_{..}$ = Over all mean

i_j = deviation from regression of the i^{th} genotype at the j^{th} environment

$$i_j = \left[\sum_{i=1}^t y_{ij}^2 - \frac{Y_i^2}{t} \right] - \frac{(\sum_{j=1}^l Y_{ij} I_j)^2}{\sum_{j=1}^l I_j^2}$$

Where t = Number of environment

The term phenotypic index has been introduced in the Eberhart and Russell (1966) model for easy interpretation and quick conclusion. The phenotypic index of a genotype may be considered as one of the stability parameters in place of overall genotypes mean and can be represented as $p_i = Y_i - \bar{y}_{..}$ i.e. deviation of genotype mean from grand mean.

With the restriction $\sum p_i = 0$, where p_i = phenotypic index for i th genotype; the Eberhart and Russell's model was slightly modified by substituting p_i for overall variety mean (μ_i) as follows:

$$Y_{ij} = (Y_{..} + P_i) + b_i I_j + e_{ij}$$

And another stability parameter, $S^2 d_i$ was calculated as

$$S^2 d_i = \left[\sum_j e_{ij}^2 / S^2 \right] - (Se^2 / r)$$

Where

S = No. of environments

Se^2 = MS for pooled error and

r = number of replications

The hypothesis that there is no response of genotype to location ($H_0: b = 0$) and there is no deviation from regression ($H_0: S^2 d_i = 0$) were tested approximately by the F-test. $H_0: b = 0$ where, $F = MS$ due to linear regression/error MS $H_0: S^2 d_i = 0$.

Where $F = MS$ due to deviation/pooled error MS. The individual variety response (Regression co-efficient) and their deviation from regression were tested by using appropriate t-test and F-test against the hypothesis that it did not differ significantly from unity and zero, respectively as-

$$t = \left| \frac{1 - b_i}{S_E(b)} \right|$$

$$\text{Where } S_E(b) = \frac{\overline{MS \text{ due to pooled deviation}}}{\sum_j I_j^2}$$

With $(n-1)$ df, n = number of genotypes and $F = \left[\sum_j e_{ij}^2 / S^2 \right]$ pooled error.

3.9 Estimation of variability

Genotypic and phenotypic coefficient of variation and heritability were estimated by using the following formulae:

3.9.1 Estimation of components of variance from individual environment

Genotypic and phenotypic variances were estimated with the help of the following formula suggested by Johnson *et al.* (1955). The genotypic variance (σ_g^2) was estimated by subtracting error mean square (σ_e^2) from the genotypic mean square and dividing it by the number of replication (r). This is estimated by using the following formula -

$$\text{Genotypic variance } (\sigma_g^2) = \frac{MS_V - MS_E}{r}$$

Where,

MS_V = genotype mean square

MS_E = error mean square

r = number of replication

The phenotypic variance (σ_p^2), was derived by adding genotypic variances with the error variance, as given by the following formula –

$$\text{Phenotypic variance } (\sigma_{ph}^2) = \sigma_g^2 + \sigma_e^2$$

Where,

σ_{ph}^2 = phenotypic variance

σ_g^2 = genotypic variance

σ_e^2 = error variance

3.9.2 Estimation of genotypic co-efficient of variation (GCV) and phenotypic co-efficient of variation (PCV)

Genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated following formula as suggested by Burton (1952):

$$\% \text{ Genotypic coefficient of variance} = \frac{\sigma_g}{\bar{x}} \times 100$$

Where,

σ_g = genotypic standard deviation

\bar{x} = population mean

$$\% \text{ Phenotypic coefficient of variance} = \frac{\sigma_{ph}}{\bar{x}} \times 100$$

Where,

σ_{ph} = phenotypic standard deviation

\bar{x} = population mean

3.9.3 Estimation of heritability

Heritability in broad sense was estimated following the formula as suggested by Johnson *et al.* (1955):

$$\text{Heritability (\%)} = \frac{\sigma_g^2}{\sigma_{ph}^2} \times 100$$

Where,

σ_g^2 = genotypic variance and σ_{ph}^2 = phenotypic variance

3.9.4 Estimation of genetic advance

The following formula was used to estimate the expected genetic advance for different characters under selection as suggested by Allard (1960):

$$GA = \frac{\sigma_g^2}{\sigma_p^2} \times K \cdot \sigma_{ph}$$

Where,

GA = Genetic advance

σ_g^2 = genotypic variance

σ_{ph}^2 = phenotypic variance

σ_{ph} = phenotypic standard deviation

K = Selection differential which is equal to 2.64 at 5% selection intensity

3.9.5 Estimation of genetic advance in percentage of mean

Genetic advance in percentage of mean was calculated by the following formula given by Comstock and Robinson (1952):

$$\text{Genetic Advance in percentage of mean} = \frac{\text{Genetic advance}}{\bar{x}} \times 100$$

CHAPTER IV

RESULTS AND DISCUSSION

The study was conducted to find out genotype and environmental (location) interaction for different genotypes of cotton. Results related to eight cotton genotypes under three locations in different environment of hilly areas of Bangladesh are discussed in the form of Eberhart and Russell's (1966) model of stability analysis. The findings obtained from the study are presented under the following heads:

4.1 Analysis of mean by genotypes, environment and their interaction

From the pooled analysis of variance, it was observed that genotypic effects were significant for all characters under the present study indicating the presence of variation among the genotypes for these characters. The environments (location of Bandarban, Rangamati and Khagrachari) were also significantly influenced all the characters. The genotype \times environment interaction showed significant variation significant for all the characters (Table 2). It was observed that high mean performances of different studied characters is not fixed for any particular genotype that means a genotype showing high mean for a character may or may not show high means for the other characters that were studied under the present study.

Genotype-environments interactions were also found significant for all the traits (Table 2) which suggested that the genotypes interacted significantly with the changes of environments and prediction for most of the genotypes appeared to be feasible for all the associated characters. Such interaction helps to select superior genotypes by changing their relative productiveness in different environmental condition.

Table 2. Pooled analysis of variance (ANOVA) for different traits of cotton genotypes in a genotype-environment interaction study

Characters	Replication (df:2)	Environments (df:2)	Genotypes (df:7)	Genotypes × Environments (df:14)	Error (df:42)
Days to 1 st flowering	0.269	172.226**	62.044**	23.144*	11.545
Days to 1 st boll split	0.154	293.002**	74.193**	20.176*	10.500
Plant height (cm)	22.976	582.891*	2528.304**	137.597**	44.860
Vegetative branches per plant (No.)	0.046	2.831**	4.219**	0.574**	0.044
Fruiting branches per plant (No.)	0.034	39.171**	46.733**	1.737**	0.540
Boll per plant (No.)	0.968	50.669**	150.453**	7.104**	1.951
Single boll weight (g)	0.027	3.368**	6.357**	0.274*	0.154
Seed cotton yield per hectare (kg)	2382.69	120476.07*	786022.39**	56166.15**	9563.05
Lint yield per hectare (kg)	9.347	105740.60**	184774.60**	4139.19**	779.478
Ginning out turn-GOT (%)	0.793	98.998*	25.282**	12.922**	5.186
Seed index (g)	0.014	0.566**	0.153*	0.132*	0.063
Lint index (g)	0.024	5.825*	1.455**	0.751**	0.241

*: Significant at 0.05 level of probability;

** : Significant at 0.01 level of probability

4.1.1 Days to 1st flowering

The mean performances of eight genotypes for days to 1st flowering of cotton in three environments are presented in Table 3. The average environmental effects summarized and found that the minimum days to 1st flowering was recorded from Bandarban (53.78) which was statistically similar to Khagrachari (54.08), whereas the maximum days from Rangamati (58.57). Genotypes taken for the study were significantly different from each other in terms of days to 1st flowering and the minimum days required for 1st flowering was found from HCG-13 (52.21) which was statistically similar to HCG-26 (52.44), again the maximum days was recorded from HC-1 (59.00). Due to the interaction of environments and genotypes, the minimum (49.73) days to 1st flowering was observed from environment of Bandarban with genotypes HCG-13, whereas the maximum days (65.07) from environment of Rangamati with genotype HCG-42. Among all the genotypes, genotype HCG-51 and HCG-21 had the highest and lowest ($P_i = 4.91$ and -2.95) phenotypic indices, respectively indicating their importance as desirable and undesirable genotypes in consideration of days to 1st flowering.

4.1.2 Days to 1st boll split

The mean performance of eight genotypes for days to 1st boll split of cotton in three environments presented in Table 4. It was found that the minimum days to 1st boll split was recorded from Khagrachari (114.61) which was statistically similar to Bandarban (115.59), whereas the maximum days was recorded from Rangamati (121.09). In case of genotypes for days to 1st boll split the minimum days required for 1st boll split (113.02) was found from HCG-26 which was statistically similar to HCG-13 (114.40), again the maximum days from HC-1 (121.71). Considering of interaction effects the minimum days to 1st boll split (109.60) was observed from Khagrachari with genotypes HCG-26, whereas the maximum days (127.07) from Rangamati with genotype HC-1. Genotype HCG-13 and HCG-42 were the desirable and undesirable genotypes for days to 1st boll split had the highest and the lowest phenotypic indices ($P_i = 5.67$ and -4.08), respectively.

Table 3. Average days to 1st flowering, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	59.07	55.53	57.09	57.23	5.45	-1.88	0.964**	-0.674
HCG-13	49.73	57.07	49.83	52.21	7.22	2.29	1.094**	-1.045
HCG-15	50.07	61.87	52.60	54.84	6.44	1.64	0.768**	-0.782
HCG-21	58.53	57.20	59.07	58.27	6.12	-2.95	1.123**	-1.742
HCG-26	50.40	55.87	51.04	52.44	5.23	-0.28	0.982**	-0.452
HCG-42	52.53	56.27	51.70	53.50	4.89	-1.69	0.742**	0.561
HCG-51	54.53	59.67	54.81	56.34	6.22	4.91	0.894**	-0.783
HC-1 (Check)	55.40	65.07	56.55	59.00	4.89	-0.99	1.006**	0.671
Environmental mean	53.78	58.57	54.08					
Environmental index	0.311	-0.781	0.451					

Table 4. Average days to 1st boll split, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	118.93	118.93	115.80	117.89	3.90	4.33	2.452**	-0.451
HCG-13	110.27	121.27	111.67	114.40	4.56	5.67	4.341**	1.568
HCG-15	113.40	124.47	111.13	116.33	5.89	-3.55	2.901**	-1.556
HCG-21	119.47	120.07	119.87	119.80	6.23	4.22	4.561**	-3.767
HCG-26	111.80	117.67	109.60	113.02	3.90	2.45	2.679**	-2.569
HCG-42	115.80	117.07	113.40	115.42	5.89	-4.08	3.745**	-2.789
HCG-51	116.47	122.20	115.93	118.20	4.77	-3.81	2.561**	3.093
HC-1 (Check)	118.60	127.07	119.47	121.71	4.03	1.78	1.006**	1.679
Environmental mean	115.59	121.09	114.61					
Environmental index	-0.439	1.231	2.091					

4.1.3 Plant height (cm)

The mean performances of eight genotypes for plant height of cotton in three environments are presented in Table 5. The average environmental effects summarized and found that the longest plant observed at Bandarban (130.24 cm), whereas the shortest plant observed at Rangamati (120.39 cm). Genotypes taken for the study were significantly different from each other in terms of plant height and the longest plant was found from HCG-4 (160.98 cm) followed by HC-1 (134.07 cm), again the shortest plant was recorded from HCG-13 (105.40 cm). Due to the interaction of environments and genotypes, the longest plant (165.15 cm) was observed from environment of Khagrachari with genotypes HCG-4, whereas the shortest plant (102.18 cm) from environment of Rangamati with genotype HCG-13. Among all the genotypes, genotype HCG-4 and HCG-13 had the highest and the lowest ($P_i = 8.12$ and -5.67) phenotypic indices, respectively. Thus indicating their importance as desirable and undesirable genotypes in consideration of plant height.

4.1.4 Vegetative branches per plant

The mean performances of eight genotypes for vegetative branches per plant in three environments are presented in Table 6. It was found that the maximum vegetative branches per plant was produced in Bandarban (3.01), whereas the minimum vegetative branches per plant from Rangamati (2.37). In case of genotypes for vegetative branches per plant the maximum vegetative branches per plant (3.49) was found from HC-1, again the minimum number from HCG-13 (1.64). Considering interaction effects the maximum vegetative branches per plant (4.23) was observed from Khagrachari with genotypes HCG-4, whereas the minimum number (1.53) from Bandarban with genotype HCG-13. Genotype HCG-4 and HCG-13 were the desirable and undesirable genotypes for vegetative branches per plant had the highest and lowest phenotypic indices ($P_i = 8.12$ and -5.67), respectively.

Table 5. Average plant height, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	163.59	154.21	165.15	160.98	6.22	8.12	7.786**	3.561
HCG-13	108.18	102.18	105.84	105.40	5.34	-5.67	3.789**	-4.098
HCG-15	140.35	116.38	127.62	128.12	4.89	1.64	5.896**	-5.901
HCG-21	126.68	119.46	105.31	117.15	5.90	-2.95	6.912**	-3.091
HCG-26	131.69	116.44	124.91	124.35	3.89	-0.28	1.671**	4.091
HCG-42	121.83	103.10	123.23	116.06	6.77	-1.69	2.891**	-0.087
HCG-51	113.65	116.69	122.34	117.56	3.55	4.91	5.678**	-3.671
HC-1 (Check)	135.92	134.68	131.59	134.07	5.09	-0.67	3.78**	2.117
Environmental mean	130.24	120.39	125.75					
Environmental index	-1.84	0.341	0.087					

Table 6. Average vegetative branches per plant, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	3.73	2.37	4.23	3.44	6.39	0.167	1.671**	1.781
HCG-13	1.53	1.77	1.63	1.64	8.33	1.901	0.891**	-0.781
HCG-15	2.17	1.97	2.27	2.13	7.05	-0.561	0.561**	1.561
HCG-21	3.93	2.80	3.40	3.38	8.67	1.891	0.912**	-0.561
HCG-26	2.43	2.60	2.33	2.46	9.33	-1.167	0.451**	1.781
HCG-42	2.60	2.27	2.60	2.49	5.77	0.891	0.341**	-0.781
HCG-51	3.93	2.30	2.97	3.07	8.90	3.891	0.589**	1.671
HC-1 (Check)	3.77	2.90	3.80	3.49	7.62	-1.561	0.671**	0.459
Environmental mean	3.01	2.37	2.90					
Environmental index	0.047	-0.452	0.193					

4.1.5 Fruiting branches per plant

The mean performances of eight genotypes for fruiting branches per plant of cotton in three environments are presented in Table 7. The average environmental effects summarized and found that the maximum fruiting branches per plant was recorded from Bandarban (12.33), whereas the minimum number from Rangamati (9.82). Genotypes taken for the study were significantly different from each other in terms of fruiting branches per plant and the maximum fruiting branches per plant was found from HCG-13 (14.71), again the minimum number was recorded from HC-1 (7.02). Due to the interaction of environments and genotypes, the maximum (15.43) fruiting branches per plant was observed from environment of Bandarban with genotypes HCG-13, whereas the minimum number (6.13) from environment of Rangamati with genotype HC-1. Among all the genotypes, genotype HCG-13 and HCG-42 had the highest and the lowest ($P_i = 2.782$ and -1.68) phenotypic indices, respectively indicating their importance as desirable and undesirable genotypes in consideration of fruiting branches per plant.

4.1.6 Boll per plant

The mean performances of eight genotypes for boll per plant of cotton in three environments are presented in Table 8. It was found that the maximum boll per plant was recorded from Bandarban (19.13), whereas the minimum boll per plant from Rangamati (16.23). In case of genotypes for boll per plant the maximum boll per plant was found from HCG-13 (24.61), again the minimum boll per plant from HC-1 (11.58). Considering of interaction effect the maximum boll per plant (27.03) was observed from Bandarban with genotypes HCG-13, whereas the minimum number (10.47) from Rangamati with genotype HC-1. Genotype HCG-13 and HCG-42 were the desirable and undesirable genotypes for boll per plant had the highest and the lowest phenotypic indices ($P_i = 2.181$ and -2.901), respectively.

Table 7. Average fruiting branches per plant, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	12.73	9.47	10.40	10.87	4.26	1.891	1.891**	0.781
HCG-13	15.43	14.03	14.67	14.71	5.99	2.782	0.891**	0.891
HCG-15	13.90	12.10	12.83	12.94	7.09	1.64	0.901**	-0.561
HCG-21	13.43	10.10	13.10	12.21	6.55	-1.67	1.123**	0.891
HCG-26	12.17	10.73	12.20	11.70	6.09	-0.451	1.895**	1.901
HCG-42	10.73	8.07	11.50	10.10	5.89	-1.68	0.901**	-0.861
HCG-51	11.73	7.97	11.00	10.23	6.77	1.891	1.451**	0.589
HC-1 (Check)	8.50	6.13	6.43	7.02	5.89	0.781	0.891**	1.781
Environmental mean	12.33	9.82	11.52					
Environmental index	-0.099	-0.561	0.341					

Table 8. Average boll per plant, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	16.43	13.53	14.43	14.80	7.89	0.781	2.901**	-1.566
HCG-13	27.03	21.73	25.07	24.61	8.90	2.181	1.091**	2.901
HCG-15	21.60	18.13	20.40	20.04	8.77	2.098	2.908**	-0.561
HCG-21	22.67	18.97	21.53	21.06	7.54	-1.891	3.891**	4.891
HCG-26	17.87	16.87	14.67	16.47	5.81	0.891	0.781**	-1.478
HCG-42	15.90	16.57	20.60	17.69	6.77	-2.901	2.190**	-0.981
HCG-51	17.80	13.57	14.97	15.44	7.89	0.891	1.671**	0.567
HC-1 (Check)	13.77	10.47	10.50	11.58	5.90	1.561	2.091**	1.091
Environmental mean	19.13	16.23	17.77					
Environmental index	0.217	0.671	-0.341					

4.1.7 Single boll weight (g)

The mean performances of eight genotypes for single boll weight of cotton in three environments are presented in Table 9. The average environmental effects were summarized and found that the highest single boll weight was recorded from Bandarban (4.65 g), whereas the lowest from Rangamati (3.92 g). Genotypes taken for the study were significantly different from each other in terms of single boll weight and the highest single boll weight was found from HCG-13 (5.18 g), again the lowest single boll weight was recorded from HC-1 (2.46 g). Due to the interaction of environments and genotypes, the highest (5.29 g) single boll weight was observed from environment of Bandarban with genotypes HCG-13, whereas the lowest (2.40 g) from environment of Rangamati with genotype HC-1. Among all the genotypes, genotype HCG-13 and HCG-15 had the highest and the lowest ($P_i = 1.091$ and -0.901) phenotypic indices, respectively indicating their importance as desirable and undesirable genotypes in consideration of single boll weight.

4.1.8 Seed cotton yield per hectare

The mean performances of eight genotypes for seed cotton yield per hectare of cotton in three environments are presented in Table 10. It was found that the highest seed cotton yield per hectare was recorded from Bandarban (1825 kg), whereas the lowest seed cotton yield per hectare from Rangamati (1691 kg). In case of genotypes for seed cotton yield per hectare the highest seed cotton yield per hectare (2071 kg) was found from HCG-13, again the lowest seed cotton yield per hectare from HC-1 (1171 kg). Considering of interaction effects the highest seed cotton yield per hectare (2170 kg) was observed from Bandarban with genotypes HCG-13, whereas the lowest yield (1107 kg) from Rangamati with genotype HC-1. Genotype HCG-13 and HCG-15 were the desirable and undesirable genotypes for seed cotton yield per hectare had the highest and the lowest phenotypic indices ($P_i = 10.15$ and -5.568), respectively.

Table 9. Average single boll weight (g), coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	4.25	3.61	4.07	3.98	8.90	0.891	0.371**	0.166
HCG-13	5.29	5.08	5.18	5.18	9.45	1.091	0.781**	0.671
HCG-15	5.02	4.36	4.45	4.61	6.78	-0.901	0.341**	0.009
HCG-21	5.01	3.74	4.38	4.37	9.16	0.091	0.891**	-0.891
HCG-26	4.84	4.52	5.03	4.80	8.34	1.001	0.271**	0.321
HCG-42	5.20	4.20	5.21	4.87	7.98	-0.091	0.461**	-0.455
HCG-51	5.04	3.43	4.63	4.37	6.89	0.914	0.222**	-0.571
HC-1 (Check)	2.56	2.40	2.41	2.46	9.98	-0.341	0.301**	0.089
Environmental mean	4.65	3.92	4.42					
Environmental index	-0.048	-0.781	0.451					

Table 10. Average seed cotton yield per hectare, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	1587	1232	1739	1519	6.78	8.561	17.781**	1.891
HCG-13	2170	2037	2007	2071	5.52	10.15	39.087**	3.897
HCG-15	2035	1890	1972	1965	4.56	-5.568	14.891**	4.673
HCG-21	1930	1907	1877	1905	3.78	6.091	7.903**	-5.902
HCG-26	1755	2009	1764	1843	5.78	8.901	5.897**	7.091
HCG-42	2022	1896	1965	1961	6.09	-3.901	8.904**	-5.902
HCG-51	1863	1451	1891	1735	3.78	6.091	6.893**	-2.561
HC-1 (Check)	1238	1107	1168	1171	4.89	-5.056	5.903**	1.981
Environmental mean	1825	1691	1798					
Environmental index	20.65	-23.78	4.89					

4.1.9 Lint yield per hectare

The mean performances of eight genotypes for lint yield per hectare of cotton in three environments are presented in Table 11. It was found that the highest lint yield per hectare was recorded from Bandarban (809 kg), whereas the lowest lint yield per hectare from Rangamati (681 kg). In case of genotypes for lint yield per hectare the highest lint yield per hectare (927 kg) was found from HCG-13, again the lowest lint yield per hectare from HC-1 (466 kg). Considering of interaction effects the highest lint yield per hectare (981 kg) was observed from Bandarban with genotypes HCG-13, whereas the lowest yield (406 kg) from Rangamati with genotype HC-1. Genotype HCG-13 and HC-1 were the desirable and undesirable genotypes for lint yield per hectare had the highest and the lowest phenotypic indices ($P_i = 13.43$ and -7.901), respectively. The genotype with higher mean yield, regression co-efficient (b_i) mean to unity and deviation from regression (S^2_{di}) value close to zero would be suitable for all environment (Islam *et al.*, 1981). But under the present trial no genotypes showed such type of findings.

4.1.10 Ginning out turn (GOT)

The mean performances of eight genotypes for ginning out turn (GOT) of cotton in three environments are presented in Table 12. It was found that the highest GOT was recorded from Bandarban (44.28%), whereas the lowest GOT from Rangamati (40.33%). In case of genotypes for GOT, the highest GOT (44.80%) was found from HCG-13, again the lowest GOT from HC-1 (39.63%). Considering of interaction effects the highest GOT (47.68%) was observed from Bandarban with genotypes HCG-21 whereas the lowest GOT (36.70%) from Rangamati with genotype HC-1. Genotype HCG-13 and HCG-15 were the desirable and undesirable genotypes for GOT had the highest and the lowest phenotypic indices ($P_i = 3.97$ and -3.09), respectively.

Table 11. Average lint yield per hectare, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	670	514	728	638	3.56	7.098	13.781**	-1.781
HCG-13	981	855	945	927	5.89	13.43	5.891**	2.189
HCG-15	846	755	835	812	6.08	-5.891	6.891**	0.901
HCG-21	920	785	823	843	3.78	9.081	9.781**	-2.901
HCG-26	801	753	807	787	4.58	3.901	3.781**	0.891
HCG-42	904	740	824	823	5.06	-4.891	3.891**	-0.901
HCG-51	810	641	803	751	4.55	5.901	5.981**	3.901
HC-1 (Check)	538	406	452	466	4.69	-7.901	3.891**	2.891
Environmental mean	809	681	777					
Environmental index	-11.26	-18.67	0.921					

Table 12. Average ginning out turn (GOT), coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	42.23	42.00	41.87	42.03	6.09	-2.45	2.701**	0.381
HCG-13	45.31	41.99	47.11	44.80	5.78	3.97	4.093**	1.341
HCG-15	41.60	39.96	42.33	41.30	5.35	-3.09	1.341**	-0.561
HCG-21	47.68	41.18	43.99	44.28	4.89	1.67	2.091**	-1.351
HCG-26	45.80	37.48	45.94	43.07	5.89	-1.89	0.671**	0.391
HCG-42	44.71	39.08	42.33	42.04	4.90	0.782	1.562**	-0.481
HCG-51	43.43	44.22	42.54	43.40	6.53	-1.90	2.091**	0.381
HC-1 (Check)	43.48	36.70	38.73	39.63	5.33	1.23	0.783**	1.097
Environmental mean	44.28	40.33	43.11					
Environmental index	0.765	-0.781	0.451					

4.1.11 Seed index

The mean performances of eight genotypes for seed index of cotton in three environments are presented in Table 13. It was found that the highest seed index was recorded from Bandarban (6.62 g), whereas the lowest seed index from Rangamati (6.35 g). In case of genotypes the highest seed index (6.58 g) was found from HCG-13, again the lowest seed index from HC-1 (6.16 g). Considering of interaction effects the highest seed index (6.91 g) was observed from Bandarban with genotypes HCG-21, whereas the lowest seed index (6.04 g) from Rangamati with genotype HCG-42. Genotype HCG-15 and HCG-26 were the desirable and undesirable genotypes for seed index had the highest and the lowest genotypic indices ($P_i = 1.54$ and -1.34), respectively.

4.1.12 Lint index

The mean performances of eight genotypes for lint index of cotton in three environments are presented in Table 14. It was found that the highest lint index was recorded from Bandarban (5.31 g), whereas the lowest lint index from Rangamati (4.32 g). In case of genotypes the highest lint index (5.35 g) was found from HCG-13, again the lowest lint index from HC-1 (4.08 g). Considering of interaction effects the highest lint index (6.32 g) was observed from Bandarban with genotypes HCG-21, whereas the lowest lint index (3.58 g) from Rangamati with genotype HC-1. Genotype HCG-13 and HCG-51 were the desirable and undesirable genotypes for seed index had the highest and the lowest phenotypic indices ($P_i = 1.091$ and -2.78), respectively.

Table 13. Average seed index, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	6.66	6.53	6.51	6.57	5.67	0.901	0.451**	1.061
HCG-13	6.71	6.57	6.45	6.58	4.89	1.51	0.561**	-0.891
HCG-15	6.30	6.61	6.41	6.44	3.81	1.54	0.281**	0.561
HCG-21	6.92	6.26	6.14	6.44	4.78	-0.89	0.391**	-0.781
HCG-26	6.77	6.25	6.44	6.49	3.75	-1.34	1.091**	1.891
HCG-42	6.89	6.04	6.33	6.42	6.33	1.12	0.595**	0.341
HCG-51	6.52	6.40	6.56	6.50	4.78	-1.09	0.234**	0.009
HC-1 (Check)	6.22	6.16	6.09	6.16	4.12	1.04	0.341**	0.321
Environmental mean	6.62	6.35	6.36					
Environmental index	-0.037	-0.561	0.451					

Table 14. Average lint index, coefficient of variation, response and stability parameters of eight cotton genotypes evaluated under three locations environment using Eberhart and Russell's model

Name of genotypes	Environments (Location)			Mean	CV(%)	Phenotypic index (Pi)	Regression coefficient (bi)	Deviation from regression (S _{2d})
	Env-1 (Bandarban)	Env-2 (Rangamati)	Env-3 (Khagrachari)					
HCG-4	4.88	4.75	4.69	4.77	9.22	0.781	0.341**	-0.098
HCG-13	5.58	4.75	5.72	5.35	7.78	1.091	0.098**	0.0341
HCG-15	4.49	4.40	4.70	4.53	11.08	0.561	0.341**	0.091
HCG-21	6.32	4.39	4.84	5.18	7.98	1.09	0.781**	-0.764
HCG-26	5.83	3.75	5.48	5.02	10.17	-1.90	0.343**	0.007
HCG-42	5.57	3.88	4.72	4.72	9.77	1.06	0.567**	-0.067
HCG-51	5.00	5.08	4.87	4.98	11.56	-2.78	0.289**	0.451
HC-1 (Check)	4.78	3.58	3.87	4.08	10.56	-1.78	0.453**	0.045
Environmental mean	5.31	4.32	4.86					
Environmental index	0.180	-0.671	-0.061					

4.2 Variability study for 12 traits of cotton

Genotypic and phenotypic variance, heritability, genetic advance and genetic advance in percentage of mean were estimated for 12 traits in 8 variety of cotton and presented in Table 15.

4.2.1 Days to 1st flowering

Days to 1st flowering refers to phenotypic variance (28.38) was higher than the genotypic variance (16.83) that indicating that high environmental influence on this characters which was supported by narrow difference between phenotypic (9.60%) and genotypic (7.40%) co-efficient of variation. The moderate difference for this parameter was also suggested a moderately significant influence of environment. Moderate heritability (59.32%) in days to 1st flowering attached with low genetic advance (8.34) and high genetic advance in percentage of mean (15.04). Moderate estimate of heritability and low genetic advance for days to 1st flowering suggested that this character was predominantly controlled by environment with complex gene interaction and this also indicated the importance of both additive and non additive genetic effects for the control of this character.

4.2.2 Days to 1st boll split

Data revealed that days to 1st boll split refers to phenotypic variance (31.73) was higher than the genotypic variance (21.23) that indicating that moderate environmental influence on this characters which was supported by narrow difference between phenotypic (4.81%) and genotypic (3.93%) co-efficient of variation. The moderate difference for this parameter was also suggested a considerable environmental influences in regards to this characters. Moderate heritability (66.91%) in days to 1st boll split attached with moderate genetic advance (9.95) and low genetic advance in percentage of mean (8.50). The moderate heritability along with low genetic advance in percentage of mean of this trait indicated that environmental control was predominant for this characters which was also governed by complex gene interaction.

Table 15. Variability of different traits of cotton genotypes

	Genotypic variance (σ^2_g)	Phenotypic variance (σ^2_p)	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability (%)	Genetic Advance (GA)	GA in percentage of mean
Days to 1 st flowering	16.83	28.38	7.40	9.60	59.32	8.34	15.04
Days to 1 st boll split	21.23	31.73	3.93	4.81	66.91	9.95	8.50
Plant height (cm)	827.81	872.67	22.93	23.55	94.86	73.98	58.97
Vegetative branches per plant (No.)	1.39	1.44	42.70	43.37	96.94	3.07	110.98
Fruiting branches per plant (No.)	15.40	15.94	34.96	35.57	96.61	10.182	90.72
Boll per plant (No.)	49.50	51.45	39.72	40.50	96.21	18.22	102.87
Single boll weight (g)	2.068	2.22	33.22	34.43	93.07	3.66	84.60
Seed cotton yield per hectare (kg)	258819.78	268382.83	28.72	29.25	96.44	1318.94	74.46
Lint yield per hectare (kg)	61331.71	62111.19	32.77	32.98	98.75	649.69	85.97
Ginning out turn-GOT (%)	6.70	11.89	6.08	8.10	56.36	5.13	12.05
Seed index (g)	0.03	0.09	2.69	4.73	32.26	0.26	4.03
Lint index (g)	0.40	0.65	13.17	16.63	62.67	1.33	27.52

4.2.3 Plant height (cm)

Phenotypic variance (872.67) was higher than the genotypic variance (827.81) in terms of plant height indicating that high environmental influence on this characters which was supported by low difference between phenotypic (23.55%) and genotypic (22.93%) co-efficient of variation. The low difference for this parameter was also suggested a minimum influence of environment and management practices greatly influences in regards to plant height. High heritability (94.86%) in plant height attached with high genetic advance (73.98) and high genetic advance in percentage of mean (58.97). The high heritability along with high genetic advance in percentage of mean of plant height indicated the possible scope for improvement through selection of the character and breeder may expect reasonable benefit in next generation in respect of this trait.

4.2.4 Vegetative branches per plant

Phenotypic variance (1.44) was higher than the genotypic variance (1.39) in consideration of vegetative branches per plant indicating that the environmental influence on this characters which was supported by low difference between phenotypic (43.37%) and genotypic (42.70%) co-efficient of variation. The low difference for this parameter was also suggested the minimum influence of environment. High heritability (96.94%) in vegetative branches per plant attached with low genetic advance (3.07) and very high genetic advance in percentage of mean (110.98%). The high heritability along with high genetic advance in percentage of mean of vegetative branches per plant indicated the minimum scope for improvement through selection of the character and breeder may not expect reasonable benefit in next generation in respect of this trait.

4.2.5 Fruiting branches per plant

Phenotypic variance (15.94) was higher than the genotypic variance (15.40) in consideration of fruiting branches per plant indicating that little environmental influence on this characters which was supported by low difference between phenotypic (35.57%) and genotypic (34.96%) co-efficient of variation. The low difference for this parameter was also suggested the minimum influence of

environment. High heritability (96.61%) in fruiting branches per plant attached with low genetic advance (10.18) and very high genetic advance in percentage of mean (90.72%). The high heritability along with high genetic advance in percentage of mean of fruiting branches per plant indicated the minimum scope for improvement through selection of the character and breeder may not expect reasonable benefit in next generation in respect of this trait.

4.2.6 Boll per plant

Phenotypic variance (51.45) was higher than the genotypic variance (49.50) in consideration of boll per plant indicating that environmental influence on this characters which was supported by low difference between phenotypic (40.50%) and genotypic (39.72%) co-efficient of variation. The low difference for this parameter was also suggested very minimum influence of environment. High heritability (96.21%) in boll per plant attached with low genetic advance (18.22) and very high genetic advance in percentage of mean (102.87%). The high heritability along with high genetic advance in percentage of mean of boll per plant indicated that breeder may not expect reasonable benefit in next generation in respect of this trait and also the minimum scope for improvement through selection of the character.

4.2.7 Single boll weight (g)

Phenotypic variance (2.22) was higher than the genotypic variance (2.068) in consideration of single boll weight indicating that environmental influence on this characters which was supported by low difference between phenotypic (34.43%) and genotypic (33.22%) co-efficient of variation. The low difference for this parameter was also suggested lowest influence of environment for this character. High heritability (93.07%) in single boll weight attached with low genetic advance (3.66) and very high genetic advance in percentage of mean (84.60%). The high heritability along with high genetic advance in percentage of mean of single boll weight indicated the minimum scope for improvement through selection of the character and breeder may not expect reasonable benefit in next generation in respect of this trait.

4.2.8 Seed cotton yield per hectare

Phenotypic variance (268382.83) was the highest than the genotypic variance (258819.78) in terms of seed cotton yield per hectare indicating that high environmental influence on this characters which was supported by low difference between phenotypic (29.25%) and genotypic (28.72%) co-efficient of variation. The low difference for this parameter was also suggested a minimum influence of environment. High heritability (96.44%) in seed cotton yield per hectare attached with high genetic advance (1318.94) and low genetic advance in percentage of mean (74.46). The high heritability along with low genetic advance in percentage of mean of seed cotton yield per hectare indicated the possible scope for improvement through selection of the character and breeder may expect reasonable benefit in next generation in respect of this trait.

4.2.9 Lint yield per hectare

Phenotypic variance (62111.19) was the highest than the genotypic variance (61331.71) in terms of lint yield per hectare indicating that less environmental influence on this characters which was supported by low difference between phenotypic (32.98%) and genotypic (32.77%) co-efficient of variation. The low difference for this parameter was also suggested the lowest influence of environment. High heritability (98.75%) in lint yield per hectare attached with high genetic advance (649.69) and low genetic advance in percentage of mean (85.97). The high heritability along with low genetic advance in percentage of mean of lint yield per hectare indicated the possible scope for improvement through selection of the character and breeder may expect reasonable benefit in next generation in respect of this trait.

4.2.10 Ginning out turn-GOT

Ginning out turn refers to phenotypic variance (11.89) was the highest than the genotypic variance (6.70) that indicating that high environmental influence on this characters which was supported by narrow difference between phenotypic (8.10%) and genotypic (6.08%) co-efficient of variation. The high difference for this parameter was also suggested highly significant influence of environment.

Moderate heritability (56.36%) in ginning out turn attached with low genetic advance (5.13) and high genetic advance in percentage of mean (12.05). Moderate estimate of heritability and high genetic advance in percentage of mean were registered for ginning out turn suggested that this character was predominantly controlled by environment with complex gene interaction and this also indicated the importance of both additive and non additive genetic effects for the control of this character.

4.2.11 Seed index

Data revealed that seed index refers to phenotypic variance (0,09) was higher than the genotypic variance (0.03) that indicating that moderate environmental influence on this characters which was supported by narrow difference between phenotypic (4.73%) and genotypic (2.69%) co-efficient of variation. The moderate difference for this parameter was also suggested a considerable environmental influences in regards to this characters. Low heritability (32.26%) in seed index attached with low genetic advance (0.26) and moderate genetic advance in percentage of mean (4.03). The low heritability along with moderate genetic advance in percentage of mean of this trait indicated that environment control was not predominant for this character.

4.2.12 Lint index

Lint index refers to phenotypic variance (0.65) was the highest than the genotypic variance (0.40) that indicating that high environmental influence on this characters which was supported by narrow difference between phenotypic (16.63%) and genotypic (13.17%) co-efficient of variation. The high difference for this parameter was also suggested highly significant influence of environment. Moderate heritability (62.67%) in lint index attached with low genetic advance (1.33) and high genetic advance in percentage of mean (27.52). Moderate estimate of heritability and high genetic advance in percentage of mean were registered for lint index suggested that this character was predominantly controlled by complex gene interaction and this also indicated the importance of both additive and non additive genetic effects for the control of this character.

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APPENDICES

Appendix I. Monthly average of air temperature, relative humidity and total rainfall of the experimental site during the period from May to September, 2014

Month (2014)	*Air temperature (°C)		*Relative humidity (%)	*Total rainfall (mm)
	Maximum	Minimum		
May	35.17	25.67	72	194
June	33.05	24.08	68	509
July	32.58	24.20	79	299
August	31.06	24.78	81	483
September	32.18	24.80	73	230

* Monthly average,

* Source: Bangladesh Meteorological Department (Climate & weather division), Chittagong

Appendix II. Physical characteristics of field soil analyzed in Soil Resources Development Institute (SRDI) laboratory, Khamarbari, Farmgate, Dhaka

A. Morphological characteristics of the experimental field

Morphological features	Characteristics
Location	Chittagong Hill Tracts
AEZ	Chittagong Coastal Plain (23)
Land type	High land
Topography	Hilli areas
Flood level	Above flood level
Drainage	Well drained

B. Physical and chemical properties of the initial soil

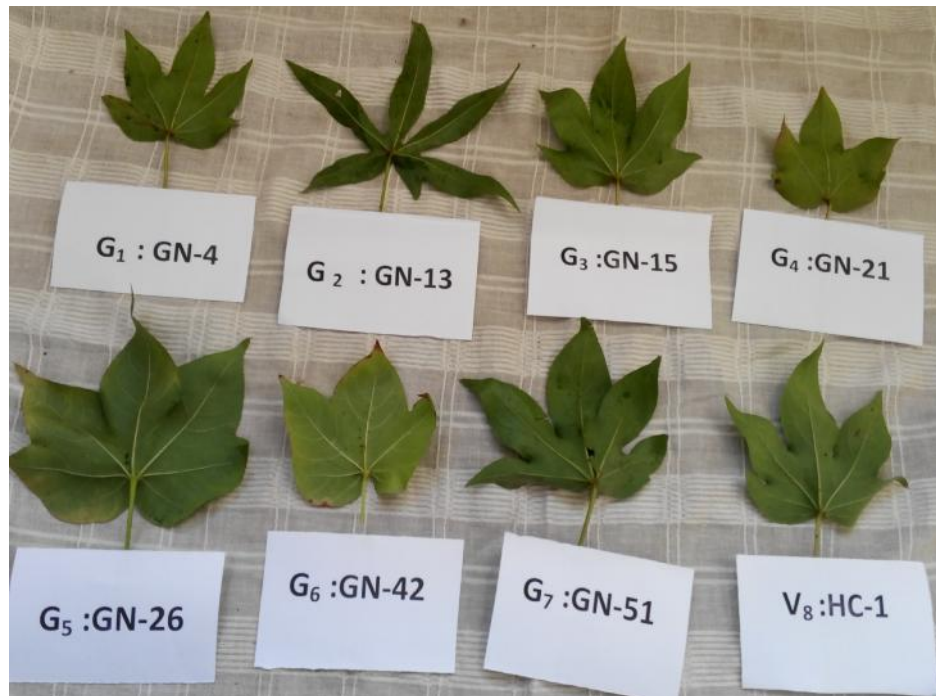
Characteristics	Value
% Sand	23
% Silt	48
% clay	29
Textural class	Silty-clay
pH	6.3
Organic matter (%)	1.21
Total N (%)	0.061
Available P (ppm)	3.90
Exchangeable K (me/100 g soil)	0.56
Available S (ppm)	17.7
Available B (ppm)	0.28
Available Zn (ppm)	4.36

Source: Soil Resources Development Institute (SRDI), Khamarbari, Farmgate, Dhaka

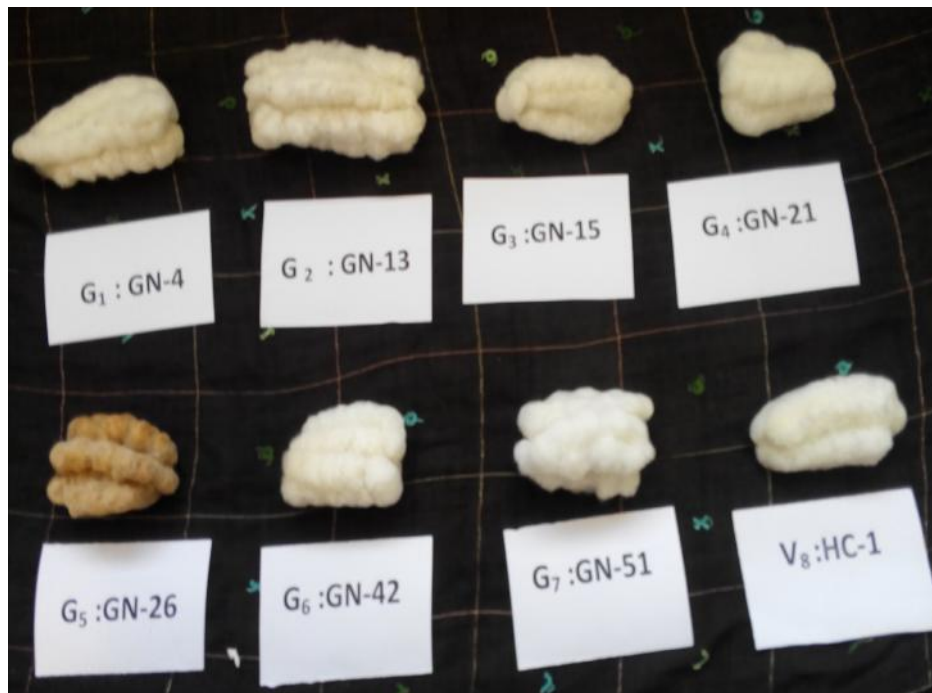
Appendix III. Photograph showing the experimental plot



Appendix IV. Photograph showing the leaves of different cotton genotypes



Appendix V. Photograph showing the boll of different cotton genotypes



CHAPTER V

SUMMARY AND CONCLUSION

The experiment was conducted at the Chittagong Hill Tracts (CHT) areas of Bangladesh i.e. Bandarban, Rangamati and Khagrachari during the period from May to September 2014 to study the genotype environment interaction effect of yield and yield parameters of some selected hill cotton genotypes. The experiment consisted of two factors: Factor A: Location (3 locations)- L₁: Bandarban; L₂: Rangamati and L₃: Khagrachari; Factor B: Different cotton genotypes- G₁: HCG-4; G₂: HCG-13, G₃: HCG-15, G₄: HCG-21, G₅: HCG-26, G₆: HCG-42, G₇: HCG-51 and V₈: HC-1 (Check). The two factors experiment was laid out in split-plot design with three replications where location factor was assigned in main plot (Bandarban, Rangamati and Khagrachari) and cotton genotypes in sub-plot.

From the pooled analysis, it was observed that genotypic effects were significant for all characters under the present study indicating the presence of variation among the genotypes for these characters. The environments (location of Bandarban, Rangamati and Khagrachari) also significantly influenced all the characters. The genotype × environment interaction was showed significant variation for all the characters.

In case of location environment, the minimum days to 1st flowering was recorded from Bandarban (53.78), whereas the maximum days from Rangamati (58.57). The minimum days to 1st boll split was recorded from Khagrachari (114.61), whereas the maximum days from Rangamati (121.09). The longest plant from Bandarban (130.24 cm), whereas the shortest plant from Rangamati (120.39 cm). The maximum vegetative branches per plant was produced in Bandarban (3.01), whereas the minimum vegetative branches per plant from Rangamati (2.37). The maximum fruiting branches per plant was recorded from Bandarban (12.33), whereas the minimum number from Rangamati (9.82). The maximum boll per plant was recorded from Bandarban (19.13), whereas the minimum boll per plant

from Rangamati (16.23). The highest single boll weight was recorded from Bandarban (4.65 g), whereas the lowest from Rangamati (3.92 g). The highest seed cotton yield per hectare was recorded from Bandarban (1825 kg), whereas the lowest seed cotton yield per hectare from Rangamati (1691 kg). The highest lint yield per hectare was recorded from Khagrachari (809 kg), whereas the lowest lint yield per hectare from Rangamati (681 kg). The highest GOT was recorded from Bandarban (44.28%), whereas the lowest GOT from Rangamati (40.33%). The highest seed index was recorded from Bandarban (6.62 g), whereas the lowest seed index from Rangamati (6.35 g). The highest lint index was recorded from Bandarban (5.31 g), whereas the lowest lint index from Rangamati (4.32 g).

For genotypes, the minimum days required for 1st flowering was found from HCG-13 (52.21), again the maximum days was recorded from HC-1 (59.00). The minimum days required for 1st boll split (113.02) was found from HCG-26, again the maximum days from HC-1 (121.71). The longest plant was found from HCG-4 (160.98 cm), again the shortest plant was recorded from HCG-13 (105.40 cm). The maximum vegetative branches per plant (3.49) was found from HC-1, again the minimum number from HCG-13 (1.64). The maximum fruiting branches per plant was found from HCG-13 (14.71) again the minimum number was recorded from HC-1 (7.02). The maximum boll per plant was found from HCG-13 (24.61), again the minimum boll per plant from HC-1 (11.58). The highest single boll weight was found from HCG-13 (5.18 g), again the lowest single boll weight was recorded from HC-1 (2.46 g). The highest seed cotton yield per hectare (2071 kg) was found from HCG-13, again the lowest seed cotton yield per hectare from HC-1 (1171 kg). The highest lint yield per hectare (927 kg) was found from HCG-13, again the lowest lint yield per hectare from HC-1 (466 kg). In case of genotypes for GOT the highest GOT (44.80%) was found from HCG-13, again the lowest GOT from HC-1 (39.63%). The highest seed index (6.58 g) was found from HCG-13, again the lowest seed index from HC-1 (6.16 g). In case of genotypes the highest lint index (5.35 g) was found from HCG-13, again the lowest lint index from HC-1 (4.08 g).

Due to the interaction of environments and genotypes, the minimum (49.73) days to 1st flowering was observed from location environment of Bandarban with genotypes HCG-13, whereas the maximum days (65.07) from location environment of Rangamati with genotype HC-1. The minimum days to 1st boll split (109.60) was observed from Khagrachari with genotypes HCG-26, whereas the maximum days (127.07) from Rangamati with genotype HC-1. The longest plant (163.59 cm) was observed from location environment of Bandarban with genotypes HCG-4, whereas the shortest plant (102.18 cm) from location environment of Rangamati with genotype HCG-13. The maximum vegetative branches per plant (4.23) was observed from Khagrachari with genotypes HCG-4, whereas the minimum number (1.53) from Bandarban with genotype HCG-13. The maximum (15.43) fruiting branches per plant was observed from location environment of Bandarban with genotypes HCG-13, whereas the minimum number (6.13) from location environment of Rangamati with genotype HC-1. The maximum boll per plant (27.03) was observed from Bandarban with genotypes HCG-13, whereas the minimum number (10.47) from Rangamati with genotype HC-1. The highest single boll weight (5.29 g) was observed from location environment of Bandarban with genotypes HCG-13, whereas the lowest (2.40 g) from location environment of Rangamati with genotype HC-1. The highest seed cotton yield per hectare (2170 kg) was observed from Bandarban with genotypes HCG-13, whereas the lowest yield (1107 kg) from Rangamati with genotype HC-1. The highest lint yield per hectare (981 kg) was observed from Bandarban with genotypes HCG-13, whereas the lowest yield (406 kg) from Rangamati with genotype HC-1. The highest GOT (47.68%) was observed from Bandarban with genotypes HCG-21, whereas the lowest GOT (36.70%) from Rangamati with genotype HC-1. The highest seed index (6.92 g) was observed from Bandarban with genotypes HCG-21, whereas the lowest seed index (6.04 g) from Rangamati with genotype HCG-42. The highest lint index (6.32 g) was observed from Bandarban with genotypes HCG-21, whereas the lowest lint index (3.58 g) from Rangamati with genotype HC-1.

In case of heritability and genetic advance, moderate heritability (59.32%) in days to 1st flowering attached with low genetic advance (8.34) was observed. Moderate heritability (66.91%) in days to 1st boll split attached with moderate genetic advance (9.95) was recorded. High heritability (94.86%) in plant height attached with high genetic advance (73.98) was observed. High heritability (96.94%) in vegetative branches per plant attached with low genetic advance (3.07) was found. High heritability (96.61%) in fruiting branches per plant attached with low genetic advance (10.18) was recorded. High heritability (96.21%) in boll per plant attached with low genetic advance (18.22) was found. High heritability (93.07%) in single boll weight attached with low genetic advance (3.66) was observed. High heritability (96.44%) in seed cotton yield per hectare attached with high genetic advance (1318.94) was found. High heritability (98.75%) in lint yield per hectare attached with high genetic advance (649.69) was recorded. Moderate heritability (56.36%) in ginning out turn attached with low genetic advance (5.13) was found. Low heritability (32.26%) in seed index attached with low genetic advance (0.26) was observed. Moderate heritability (62.67%) in lint index attached with low genetic advance (1.33) was found.

Conclusion:

Based on the performance of eight cotton genotypes HCG-13 followed by HCG-21 and HCG-42 was found to be highest yielder. Genotype HCG-13 was found better performance in environmental condition of Bandhaban than the other two locations.

Recommendations

Considering the above findings of the present experiment, the following recommendations and suggestions may be made:

1. Selected genotypes are needed in different agro-ecological zones (AEZ) of Bangladesh for regional adaptability and other performance.
2. More genotypes with different crosses with different environment may be included for further study.

