ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION ANALYSIS IN UPLAND COTTON (*Gossypium hirsutum* L.)

A PhD DISSERTATION

BY

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JUNE, 2017

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Certification

*This is to certify that the thesis entitled "***Additive main effects and multiplicative interaction analysis in upland cotton (Gossypium hirsutum L.)"*** a study on cotton, prepared by the examinee, bearing Registration No.: 1005133, Session: 2010, Department of Genetics and Plant Breeding, Hajee Mohammad Danesh Science and Technology University, Dinajpur, for the award of the degree of Doctor of Philosophy in Genetics and Plant Breeding, is a record of original research work carried out by him under my supervision. The work is an original and unique one and to the best of my knowledge, no part of the thesis has been produced elsewhere for any degree.*

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Declaration

I do hereby declare that the thesis entitled “**Additive main effects and multiplicative interaction analysis in upland cotton (*Gossypium hirsutum* L.)**” is a record of my research work, original and unique, and no part of this thesis has been presented elsewhere for any degree or diploma.

The Author
HSTU, Dinajpur

DEDICATED

TO MY

BELOVED MOTHER,

DEPARTED FATHER AND

ELDER BROTHER

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The Author
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Abbreviations

AEC	Average Environment Coordination
AFIS	Advanced Fiber Information System
AHP	Analytic Hierarchy Process
AMMI	Additive Main Effects and Multiplicative Interaction
ANOVA	Analysis Of Variance
ASV	AMMI Stability Value
ATC	Average Tester Coordinator
BG	Breeder-Geneticists
CDB	Cotton Development Board
CLCuV	Cotton Leaf Curl Virus
CV	Coefficient of Variation
FAF	Fibre Attachment Force
FQI	Fibre Quality Index
G x E	Genotype Environment Interaction
GAM	Genetic Advance as percent Mean
GCV	Genotypic Coefficient of Variation
GEI	Genotype Environment Interaction
GGE	Genotype main effects and Genotype × Environment interaction
GOT	Ginning Out Turn
GRAS	Generally Recognized As Safe
GSI	Genotype Stability Index
HVI	High Volume Instrumentation
HYV	High Yielding Variety
IPCA	Interaction Principal Component Analysis
MATLAB	Matrix Laboratory
MCDM	Multiple-Criteria Decision-Making
MET	Multi-environmental Trials
MEYT	Multi-environmental Yield Trials
MFQI	Modified Fibre Quality Index
MS	Mean Squares
NFB	Node number of first fruiting branches
PCA	Principle Component Analysis
PCV	Phenotypic Coefficient of Variation
PDI	Premium-Discount Index
PPB	Participatory Plant Breeding
PVS	Participatory Variety Selection
QCOTTON	Queensland Cotton
QTL	Quantitative Trait Loci
RCBD	Randomized Complete Block Design
RHQ	Regional High Quality
RIL	Recombinant Inbred Line
SCI	Spinning Consistency Index
SPAD	Single Photon Avalanche Diode
SVD	Singular Value Decomposition

ADDITIVE MAIN EFFECTS AND MULTIPLICATIVE INTERACTION ANALYSIS IN UPLAND COTTON (*Gossypium hirsutum* L.)

Abstract

Twenty genetically diverged genotypes of upland cotton (*Gossypium hirsutum* L.) received from Cotton Development Board, Dhaka were used to investigate their performances in three locations (Jessore, Rangpur and Dinajpur) over four consecutive years (2010-11, 2011-12, 2012-13 and 2013-14). At the beginning of investigation, the genotypes were characterized and evaluated on 12 morphophysiological characters including seed cotton yield (kg ha^{-1}). Days to 1st flowering was long and ranged from 47-56 days, suggested prolong crop duration in cotton. The unbrust bolls plant^{-1} was a detrimental character for reducing yield potential of the genotypes. The PCV(Phenotypic Coefficient of Variation) value was higher than corresponding GCV(Genotypic Coefficient of Variation) for all characters, suggested polygenic controlled of the characters and thus had environmental effects (locations and years) for the full expression of the characters. Among the twelve characters, plant height, bolls per plant, boll weight and seeds per boll exhibited higher than 90% heritabilities but plant height itself showed wider difference between PVC and GCV, indicated the strong effect of environment. Therefore, except plant height other three characters might into consideration in selection or hybridization program to improve the ultimate character seed cotton yield. High heritability (h^2b=90.36%) coupled with high genetic advanced (58.49%) was estimated for bolls plant^{-1} hence the character might improve through simple selection which ultimately improve yield potential in cotton. A total of 55 pairs of characters combinations were drawn both at genotypic (r_g) and phenotypic (r_p) levels to estimate correlation coefficients. Vegetative branches plant^{-1} and unbrust bolls plant^{-1} exhibited negative and significant association and six characters namely secondary fruiting branches plant^{-1}, main stem nodes plant^{-1}, days to 1st flowering, bolls plant^{-1}, boll weight and seeds boll^{-1} showed positive and significant association with seed cotton yield both at genotypic and phenotypic levels. But simultaneous consideration of genetic parameters, genotypic and phenotypic correlation coefficients and path analysis of genotypic correlation with seed cotton yield. Five characters might consider constructing selection indices for ultimate improve of seed cotton yield among the genotypes. The higher genotypic correlation coefficient in respect of related phenotypic correlation coefficient suggested inherent relationships of the characters either positive or negative directions with seed cotton yield.

Since genotypic associations little change with changing the locations and years the therefore, genotypic correlation coefficients of 11 characters with seed cotton yield were separated into direct and indirect effects through path coefficient analysis. The highest direct effect (1.982) was paid by seeds boll^{-1} followed by boll weight (1.568) and bolls plant^{-1}(1.5226). The cumulative indirect effect of the characters failed to change the directions of direct effects to develop genotypic associations with seed cotton yield. Five insect viz. thrips, cotton bug, bollwarm, aphid and whitefly were reported in the cotton field during cropping season. The bollwarm was not a major insect in our country but aphid was a major for transmitting virus. The genotype, JA-08/D showed complete resistant to insect attack. The genotypes, JA-08/0526 and BC-0303 were insect susceptible due to severe infestation by insects. The additive main effects of genotypes were estimated by subtracting environmental and multiplicative interaction effects. AMMI analysis revealed significant effects of genotypes, locations, years and their all possible interaction effects upon the expression of the selected characters. Five items like IPCA1, IPCA2, regression coefficient (bi), deviation from regression (s^2di), and average stability value (ASV) were taken into account of assessing response and stability of the genotypes over the locations and across the years. The environmental conditions of Jessore were more superior to Rangpur and Dinajpur for cultivation of cotton. The highest seed cotton yield (3430 kg ha^{-1}) was obtained from JA-08/D followed by JA-08/C (3329 kg ha^{-1}) and JA-08/E (3226 kg ha^{-1}). The highest ginning out turn (43.05%) was estimated from JA-08/D followed by JA-08/C (42.33%) and JA-08/B (42.00%). The highest lint index was calculated in BC-10 (7.37). Three genotypes JA-08/D, CB-10 and CB-11 showed the highest (8.00) fuzz grade. Simultaneous consideration of evaluation of morphophysiological and fiber quality characters, three genotypes such as JA-08/D, JA-08/C and JA-08/E might consider for developing high seed cotton yielding varieties through appropriate breeding programs.

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CHAPTER I

INTRODUCTION

Agriculture is extremely vulnerable to climate change. Higher temperatures eventually reduce yields of desirable crops while encouraging weed and pest proliferation. Changes in precipitation patterns increase the livelihood of short-run crop failures and long-run production declines. Although there will be gains in some crops in some regions of the world, the overall impacts of climate change on agriculture are expected to be negative, threatening global food security (IFPRI, 2009). Climate change will affect cotton production as a result of higher concentrations of CO_2 and increases in temperature. Both these changes will set off actions through water availability and the incidence of cotton pests and diseases that will have direct and indirect impacts on cotton production.

1.1 Evolutionary history of cotton

Northern Territory (Australia), whites and pale yellows (Mexico, Africa–Arabia) and even a deep sulphur-yellow (*G. tomentosum* from Hawaii). Seed coverings range from nearly glabrous to the naked eye (e.g., *G. klotzschianum* and *G. davidsonii*), to short stiff, dense, brown hairs that aid in wind-dispersal (*G. australe* and *G. nelsonii*), to long, fine white fibers that characterize highly improved forms of the four cultivated species. There are even seeds that produce fat bodies to facilitate ant-dispersal (section Grandicalyx cottons from NW Australia, Seelanan *et al.,* 1999). Much of this morphological diversity is described in detail by Fryxell (1979). The foregoing discussion suggested that the cotton genus has a history that extends back millions of years, so perhaps it is not surprising that the genus achieved worldwide distribution, with several primary centers of diversity in the arid or seasonally arid tropics and subtropics. Particularly species-rich regions include Australia, especially the Kimberley region in NW Australia, the Horn of Africa and southern Arabian Peninsula, and the western part of central and southern Mexico. Recognition of these groups of related species and their individual constituents reflects accumulated scientific understanding that has emerged from a long history of basic plant exploration and taxonomic and evolutionary study. The taxonomy of the genus has been summarized in several useful volumes (Fryxell, 1979, 1992 and Hutchinson *et al.,* 1947; Saunders, 1961 and Watt, 1907). The most recent and widely followed taxonomic treatments were those of Fryxell (1979 and 1992), in which species were grouped into four subgenera and eight sections. This classification system is primarily based on morphological and geographical evidence, although most infrageneric alignments are congruent with cytogenetic and molecular data sets as well, as will be discussed later. At present, *Gossypium* includes approximately 50 species (Fryxell, 1992), but remarkably, new species continue to be discovered (Fryxell, 1992). However, the evolutionary history of cotton is presented below-

Gossypium arboreum (Asiatic cotton) x *Gossypium thurberi* (American wild cotton)
$2n=26(A_2)$ ⇩ $2n=26(D_1)$
Gossypium hirsutum (Upland cotton)
$2n=4x=52(AD)_1$

Gossypium herbaceum x *Gossypium raimondii*
$2n=26(A_1)$ ⇩ $2n=26(D_5)$
Gossypium barbadense (Egyptian cotton)
$2n=4x=52(AD)_2$

Source: Singh (2010).

1.2 Cotton production in Bangladesh and in the world

Cotton is the second most important cash crop in Bangladesh after jute. Under normal conditions, it can only meet 3% of the country's demand for raw cotton that is used for yarn and textiles. It is planted in July, which coincides with the beginning of the monsoon and harvesting started in December. Bangladesh cotton production was 120,000 (480lb) bales in 2013-14, over 11% from previous year. Area harvested was 45,000 hectares in 2013 as compared to 40,000 hectares in 2012. The area increased 12.5% was attributed to implementation of Bangladesh Cotton Development Board. The goal is to gradually convert 20,000 hectares from tobacco to cotton cultivation and increasing cultivation of cotton in the saline prone coastal areas in the southern parts of Bangladesh. Cotton yields are forecasted to reach average levels assuming favorable growing weather. Cotton yields in Bangladesh do not strongly follow a trend and it production in Bangladesh is susceptible to excessive rainfall and flooding. In the last few years growing conditions have been favorable. Since 2009 the Bangladesh Cotton Development Board in conjunction with private seed companies has assisted farmers with introducing short duration and high yielding Chinese hybrid seeds.

Table: 1.1 Top ten cotton producing countries in the world

Rank	Country	Production (MT)
1.	China	6,870,000
2.	India	5,321,000
3.	America	3,598,000
4.	Pakistan	2,215,000
5.	Brazil	1,638,103
6.	Uzbekistan	1,052,000
7.	Australia	973,497
8.	Turkey	851,000
9.	Greece	367,000
10.	Mexico	220,000

Source: National Geographic World Maps (2014).

1.3 Different parameters of cotton fibre

1.3.1 Fibre length

The crucial index of fibre quality in cotton is determined by the spinning performance. Among the fibre properties which contribute most to spinning value are staple length, fibre fineness and strength. The staple length constitutes the basic norm for evaluating quality of cotton in the trade and by the consuming textile industry. Fibre length has been directly correlated with the spinning capacity. The worth of cotton is mainly determined based on the fibre length. Fibre length is generally measured by three ways, as halo length, mean length, and 2.5% span length. Halo length is the length of fibre with attached seed, and it can be measured with the help of halo disc. The mean halo length is the arithmetic mean of the length of all the fibres present within the sample. 2.5% span length is the distance from the clamp on fibre beard to a point up to which only 2.5% of the fibres extend. This is the fibre length representing the majority of the fibres and expressed in millimeter, and measured by the digital fibre graph. Five stable length categories were used for the classification of cotton in India proposed by Singh (2004).

1.3.2 Fibre strength

Of the fibre quality traits, fibre strength is the second most important property of cotton fibre and it determines the yarn strength. The fibre strength is essential for high speed spinning such as rotobar and jet spinning. Fibre strength is generally measured by stelometer. Fibre strength can be determined either on individual fibre or on a bundle fibre. Fibre strength is also known as tensile strength, and expressed as tenacity in gram pretax at 1/8" gauge.

1.3.3 Other fibre quality parameters

Fibre fineness is the relative measure of size, diameter and linear density of fibres, which denotes the fineness of fibres. It's also known as micronaire. The ratio between 50 and 2.5% span length is known as uniformity ratio, and it is expressed as percentage. Uniformity ratio denotes the percentage of longer fibres. Fibre elongation percentage is the percentage increase in jaw separation of instrument under load elongation of the fibre bundle. It is a measure of the percentage increase in jaw separation of instrument under load.

1.4 Quality of cotton fibre

A big diversity of cotton varieties and a variability of cotton fiber properties makes that a complex and precise assessment of basic fiber parameters and quality classification is a very important problem for traders and spinners as well as for agriculture people, who should tend to improve the cotton yield features. In the field of development of devices and methods for cotton parameter assessments a lot of work has already been done. The more relevant historical experience was the last 20 years, during which a transition from the human classing to instrumental classing began with introduction of the HVI line (Shofner and Shofner, 2000 and Shofner *et al.,* 2002). We are witnessed of a big progress in fiber quality measurement methods. A lot of efforts has been and still are undertaken to improve the existing measurement methods or to develop new ones for a better, more comprehensive and objective fiber assessment. The progress in the field of measuring systems and appropriate applications of gathered knowledge is still important due to the growing competition of cotton industry with the industry of man-made fibers, which features can be planned in the engineered way. We have entered the new millennium with many fully automized measurement systems like HVI Spectrum (Frydrych and Matusiak, 2002), AFIS (Zhang *et al.,* 2003), Fibre Lab (Mor, 2002 and Mor, 2003), thermo detectors (Lille, 2001), IsoTester (Kipp *et al.*, 2003), Premier ART (Automatic Rapid Tester) (Frydrych *et al.,* 2001) at our disposal enabling not only determination of particular parameters, but also their complex statistical analysis. Modern instruments allow measuring not only physical-mechanical parameters by the bundle or individual fiber methods, but also intrinsic parameters like maturity, stickiness, color and outer factors influencing the cotton quality depending on the cultivation harvesting and ginning conditions like trash content, seed coat fragment content and nep content. Very important for communication between the cotton people is the unification of fiber parameters describing the given properties. ITMF Cotton Committee on the Cotton Testing Methods to achieve this goal discusses every two year the problem of progress in measurement techniques and recommends the most precise and useful methods for application. In this way the world of people interested in cotton measurements became smaller, more acquainted and has more willing for a co-operation and positive competition (Foulk *et al.,* 2009) It is evident that a progress in cotton fiber quality testing systems follows the development of spinning technologies, which with the increase of technological speeds require fibers of the better and more precisely assessed quality. The advantages of the developments in measurement techniques should be used practically in the industrial reality. As we know from the practical point of view still very important and emerging in the spinning practice is a problem of SFC (Zhang *et al.,* 2003), stickiness (Mor, 2002) and neps (Mor, 2000). Many research works on these subjects have been recently done, for example, among the others Dr. Matusiak finished her Ph.D. thesis on predicting the yarn neppiness basing on cotton fibre characteristics (Frydrych *et al.* 2001, Frydrych and Matusiak, 2002 and Matusiak, 2002).

1.5 Genotype x environment interaction

Interaction of genotype by environment (G x E) is an important component in genetic variance analysis for quantitative traits in crops. Significant G x E component reduces correlations between genotype and phenotype values (Kang, 1998) and affects breeding for genetic improvement, especially for quantitative traits in crops. It was reported that 25 to 45% and 15 to 25% of the yield gain in barley (*Hordeum vulgar*e L.) and wheat (*Triticum aestivum* L.), respectively, were attributed to G x E in a study of grain yield in these two crops during 1976 to 1977 (Simmonds, 1981). Significant G x E component necessitates multiple locations for performance tests of genotypes in breeding programs, whereas the extent of genotypic effect relative to G x E component might reduce the number of environments necessary for performance tests.

In cotton, numerous studies regarding the genotypic and the G x E components have been conducted since the middle of the last century. In the analysis of four cultivars from National Cotton Variety Tests during 1960 and 1962, the ratio of G x location (L) component relative to genotypic component for lint yield was 2.3 (Abou-El-Fittough *et al*., 1969). The ratios of the component of G × E relative to genotypic component were less than 1.0 for fiber properties in the same study. In 12 location-year yield trials of cotton cultivars in South Carolina, the portion of sums of squares attributed to the total variation for E, G, and G x E were 90%, 2%, and 8%, respectively (Campbell and Jones, 2005). In a yield trial of 31 cotton varieties in three Mediterranean countries, the ratio of G x E component to genotypic component was 6.4 (Baxevanos *et al*., 2008). Most recently, Meredith *et al.,* (2012) reviewed six studies conducted worldwide between 1964 and 2011 for G x E effects on lint yield and fiber quality. The average attributes of E, G, and G x E to the total variation of lint yield was 86%, 5%, and 9%, respectively, in these studies. The average total variation of fiber strength was 44% and 16% due to G and G x E, respectively, and that for fiber length was 27% and 17% due to G and G × E, respectively. In summary of these previous studies, G x E effects were greater than genotype effects for lint yield, whereas the effects of G x E were usually small relative to genotypic effects for fiber properties. Although significant G x E interactions warrant multiple location trials for stability, i.e., agronomic performance across different environments, analysis of relationships among test locations might identify the unnecessarily repeated locations and reduce the number of test sites. Test locations can be grouped into a so-called mega environment based on their close relationships in terms of G x E interactions for crop performance so that the test locations within a mega environment are homogeneous, whereas the variation among the groups maximized (Yan and Kang, 2003). These types of groups of test locations can be visualized by their separation in graphs using GGE biplot. However, in most cases, the identification of mega environments was not simple due to either unpredictable G x E interactions or year (Y) x L interactions. In a test of 28 soybean (*Glycine max* L. Merr.) cultivars from 1997 to 1999 at three to four locations in Ontario, Canada, a complex mega environment was identified with unpredictable G x L xY interactions (Yan and Kang, 2003). In a study of sites for cotton trials of Delta and Pine in Spain during 1999 to 2006, Baxevanos *et al.* (2008) analyzed eight 1-yr yield data sets for G x L interactions and two multiyear yield data sets for G x L x Y interactions and revealed crossover G x L interactions, but not sufficient for mega environment differentiation. Bach *et al.,* (2012) examined eight potato (*Solanum tuberosum* L.) clones and four cultivars at three locations in

Ontario, Canada during 2009 and 2010 and found no significant mega environments for potato fiber component.

1.6 AMMI analysis

A detailed description and discussion of various aspects of G x E interaction analysis is available in numerous articles (Freeman,1973; Hill, 1975; Denis and Vivcourt,1982; Westcott,1986; Lin *et al.,* 1986; Beaker and Leon,1988; Crossa,1990; Romagosa *et al.,*1993; Cooper and Delacy,1994; Eeuwijk,1995; Kang and Gauch,1996; Cooper and Hammer, 1996; Hulme *et al*., 1997 and Kang, 2002). Finally G x E interaction through AMMI analysis approach proved more effective to assess performances of genotypes across the diversified environments.

Upland cotton (*Gossypium* spp.) is the primary source of natural fibre worldwide. In Bangladesh, it is an important cash crop and life line of the textile industry. Hundreds of farmers are directly associated with cultivation and harvesting of cotton crop and sale of lint. Many others are indirectly linked with cotton value chain. Cotton production in Bangladesh is very low when compared to many other cotton producing countries. The world cotton productivity is 759 kg lint/ha compared to Bangladesh's average of 550 kg lint/ha. Sustainable cotton production requires identification and cultivation of stable cultivars. Several methods of estimating phenotypic stability across environments by determining G x E interaction effects are available (Eberhart and Russel, 1966; Crossa, 1990; and Gauch, 1992). Cotton genotypes have been evaluated by many scientists for G x E interaction effects for seed cotton yield and insect resistance (Naveed *et al*., 2006, Naveed *et al*., 2007 a and b and Khan *et al*., 2008 a and b). Among the various statistical procedures developed for the study of G x E interaction, AMMI model has been revealed to be efficient because it captures a large portion of the G x E sum of squares and austerely separates main and interaction effects that present agricultural researchers with different kinds of opportunities, and this model often provides agronomically meaningful interpretation of the data (Ebdon and Gauch, 2002). The results of AMMI analysis are useful in supporting breeding program decisions such as specific adaptations to target (tolerances to disease, heat and drought, cold) and selection of environments or test site locations (Gauch and Zobel, 1997).

AMMI has been used successfully by researchers on crops such as barley (Gebremedhin *et al*., 2014), bread wheat (Purchase *et al*., 2000), coconut (Odewale *et al*., 2012) cotton

(Campbell and Jones, 2005), durum wheat (Mohammadi and Amri, 2011), field pea (Fikere *et al.*, 2010), lucern (Smith and Smith, 1992), maize (Ma'ali, 2008), potatoes (Steyn *et al.*, 1993) rice (Nassir and Ariyo, 2011) and tobacco (Sadeghi *et al.*, 2011). The graphical version of the cultivar means and the first interaction principle component analysis (PCA) scores eases interpretation and identification of high yielding cultivars. Principal component analysis is a variable reduction procedure and is the most frequently used multivariate method (Crossa, 1990 and Purchase, 1997). Its aim is to transform the data from one set of coordinate axes to another, which preserves, as much as possible, the original configuration of the set of points and concentrates most of the data structure in the first principal component axis.

Objectives:

The objectives of this study were-

1. Response of cotton genotypes at elevated climatic changes during growth and development stages
2. Study of adaptation and genotype x environment interaction in cotton genotypes grown at different environments in the country
3. Identification of cotton genotypes which have high seed cotton yield and stable performance across the different environments of our country
4. Study of relationships, similarities and dissimilarities of seed cotton yield with different stability parameters to quantify GxE interaction effect.
5. Identification of stable genotype/genotypes by determining G x E interaction effects obtained by AMMI analysis of seed cotton yield over the environments

CHAPTER II

REVIEW OF LITERATURE

2.1 Genetic variability in upland cotton

Neelima and Chenga (2008) studied fifty four genotypes of American cotton (*Gossypium hirsutum* L.) comprising of four lines and ten testers and their 40 hybrids produced in a line x tester fashion were evaluated for qualitative and quantitative traits. Results revealed that number of sympodia per plant, boll weight and seed cotton yield per plant showed moderate estimates of phenotypic and genotypic coefficient of variation. Moderate heritability coupled with moderate genetic advance was observed for number of sympodia per plant, number of bolls per plant, seed index, and seed cotton yield per plant indicating the operation of both additive and non-additive gene action in the inheritance of these traits. Low heritability coupled with low genetic advance was observed for days to 50% flowering, ginning percentage, 2.5% span length, micronaire, maturity coefficient and bundle strength indicating that these characters are controlled by non-additive genes and simple selection would be effective.

Wadeyar and Kajjidoni (2015) evaluated two hundred and two progenies at two locations *viz*., Agricultural Research Station, Annigeri and Main Agricultural Research Station, Dharwad to estimate genetic variability and to identify superior progenies for seed cotton yield, yield contributing and fibre quality traits. The analysis of variance revealed presence of sufficient variability in the material for seven traits at both locations. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for number of bolls per plant and seed cotton yield per plant, while, moderate variability estimate was recorded for plant height and low PCV and GCV were noticed for boll weight, ginning out turn, seed index and lint index traits at both the locations. High heritability was observed for seed index exhibited 97 percent with moderate genetic advance as percent mean (GAM) at both the locations. High GAM was observed for number of bolls per plant, seed cotton yield and plant height. Moderate GAM was noticed for boll weight and seed index traits at both locations. An attempt was made to identify superior progenies, maximum number of superior progenies were observed for seed cotton yield at Dharwad (33 progenies) followed by Annigeri (24 progenies).

The success of a good breeding programme usually depends upon the quantum of genetic variability present in the breeding materials. Thus, knowledge on genetic variability, heritability and genetic advance in tetraploid cotton is very essential for a breeder to choose good parents and to decide the correct breeding methodology for crop improvement. Alkuddsi *et al.* (2013) carried out an experiment during kharif 2008 in cotton (*G. hirsutum* L.) to determine variability, heritability and gentic advance for seed cotton yield and its components. Fourty eight hybrids produced through Line x Tester mating design using 6 *hirsutum* non Bt lines (RAH 318 (L1), RAH 243 (L2), RAH 128 (L3), RAH 146 (L4), RAH 97 (L5) and RAH 124 (L6)) and 8 *hirsutum* non Bt testers (SC 14 (T1), SC 18 (T2), SC 7 (T3), SC 68 (T4), RGR 32 (T5), RGR 24 (T6), RGR 58 (T7) and RGR 37 (T8)) to generate information on genetic parameters in respect of seed cotton yield and yield attributing characters (days to 50% flowering, plant height, number of bolls per plant, number of sympodia per plant, number of monopodia per plant, mean boll weight, ginning out turn, seed index, and lint index). The 48 F_1 hybrids were sown in a randomized complete block design (RCBD) with two replications at the Agricultural Research Station, Bavikere, UAS, Bangalore. The mean performance of 48 hybrids used in the present study indicated that the hybrid RAH 97 x SC18 was superior for 4 characters viz., plant height, mean boll weight, seed cotton yield per plant and seed index, while the hybrid RAH 146 x RGR37 was superior in respect of 2 characters, plant height and seed cotton yield per plant. The analysis of variance among 48 hybrids and checks tested in 2 replications indicated that mean sum of squares for hybrids was highly significant for all the characters except number of monopodia per plant, mean boll weight and seed index indicating presence of significant differences among the hybrids evaluated in respect of these traits. The mean sum of squares for hybrids vs checks was highly significant for plant height, number of sympodia per plant, number of bolls per plant, seed cotton yield per plant and ginning out turn revealing superiority of hybrids over checks and presence of heterosis in respect of these traits. High genotypic co-efficient of variability were obtained for seed cotton yield (16.69) and number of bolls per plant (14.15), while low for days to 50% flowering (1.15) and number of monopodia per plant (2.84). However, high phenotypic co-efficient of variability were obtained for seed cotton yield (25.24) and number of bolls per plant (26.54) and low for days to 50% flowering (3.15) and ginning out turn (11.13). Plant height (6.98), number of bolls per plant (3.62), seed cotton yield (2.58) and ginning out turn (1.83), showed high magnitude of genetic advance, whereas, number of bolls per plant (15.54) and seed cotton yield (22.74) exhibited high genetic advance expressed as a percentage of the mean.

Killi *et al.* (2005) studied five cotton genotypes from Azerbaijan and two standard cotton varieties for the region to determine genetic and environmental variability, broad sense heritability and correlation coefficients of seed cotton yield, yield component and lint quality traits. There were significant differences among the genotypes for most of the traits. Genotypic and phenotypic variances were highest for seed cotton yield followed by plant height, whereas the maximum genotypic and phenotypic coefficients of variability were found in number of monopodial branches, fiber strength, seed cotton yield and number of mature bolls. Broad sense heritability estimates ranged from very low to high. Heritability values were estimated maximum level for fiber strength (94.60%), fiber length (94.58%) and seed cotton weight (91.80%), while low level for 1000-seed weight (6.67%) and plant height (20.60%). High heritability for fiber strength, fiber length and seed cotton weight indicated that these characteristics were affected less than the others by the environmental conditions. Positive correlations between seed cotton yield and plant height, number of sympodial branches, number of mature bolls, seed cotton weight, 100-seed weight, fiber length, fiber uniformity were found. Successful selection can be made on these characteristics for seed cotton yield.

Irum *et al.* (2011) carried out a study to determine the genetic variability, broad sense heritability, genetic advance and correlation among the six seedling traits and their direct and indirect effects on cotton yield by using path coefficient analysis. Thirty cotton genotypes were studied in green house using randomized complete block design with 3 replications at Cotton Research Station Multan, Pakistan. The genotypes exhibited a wide range of variability for all the traits except shoot length. Moderate to high heritability estimates were found for all traits. All the seedling traits showed positive and significant correlation with cotton yield both at genotypic and phenotypic level. Path coefficient analysis showed that root length had the highest and positive direct effect on cotton yield. Positive direct effects were produced by shoot length, root length, shoot/root length ratio, shoot weight and root weight, while shoot/root weight ratio had negative direct effects. The information obtained from the current studies will be utilized in successful cotton breeding program.

Vineela *et al.* (2013) conducted an investigation to elicit information on extent of genetic variability, heritability and genetic advance for twenty-one characters in 84 intra *hirsutum* cotton hybrids (*Gossypium hirsutum* L.) plus two checks which were derived by involving twelve lines and seven testers in line X tester fashion. These lines were developed from new heterotic genepools. These 84 intra *hirsutum* cotton hybrids along with two checks were evaluated during kharif 2010-11. Wide variability was observed incase of number of sympodia, specific leaf weight, crop growth rate at peak flowering stage, crop growth rate at boll formation stage, crop growth rate at maturity stage. High heritability accompanied by high genetic advance was observed in case of plant height, number of monopodia, number of sympodia, relative water content, specific leaf weight, crop growth rate at peak flowering stage, crop growth rate at boll formation stage, crop growth rate at maturity stage, boll weight, seed index and lint index indicating the role of additive gene action in the inheritance of these traits and directional selection could be profitably applied on these traits in the genetically diverse material.

Ahmad *et al.* (2008) carried out an experiment to determine the genetic variability, correlation and regression coefficient of the seed cotton yield with various morphological and yield contributing traits in five upland cotton cultivars. The cultivars viz; CIM-473, CIM-496, CIM-499, CIM-506 and CIM-707 were sown in a randomized complete block (RCB) design with four replications at NWFP Agricultural University, Peshawar, Pakistan during May 2005. All the genotypes revealed highly significant differences (P_0.01) for monopodia and sympodia per plant, bolls per plant and seeds per boll, while the plant height, first internode length, boll weight and seed cotton yield per plant manifested significant variations among the cultivars. Boll per sympodia was having non-significant differences in mean values. All the parameters manifested positive correlation with seed cotton yield except monopodia per plant and first internode length. Cultivar CIM-499 performed well by having better boll set, early maturity and increased seed cotton yield, while other four cultivars were having statistically at par seed cotton yield. During future breeding programme the yield related traits may also be kept in mind during making selection as they were the major attributes of the seed cotton yield.

Khan *et al.* (2010) conducted an experiment during 2005 at NWFP Agricultural University Peshawar, Pakistan to study the genetic variability, heritability, genetic gain and correlation for cotton seed, fiber and cotton seed oil % in *Gossypium hirsutum* cultivars. Analysis of variance manifested highly significant differences among the genotypes for all the traits except seeds per locule. Genetic potential range of eight cotton cultivars for different parameters was recorded i.e. seeds locule-1 (6.33 to 6.60), seeds boll-1 (26.10 to 28.47), seed index (8.61 to 9.69 g), lint index (5.35 to 6.05 g), lint % (35.17 to 38.13 %), seed cotton yield

(1200 to 2450 kg ha/sup -1/) and cotton seed oil % (27.52 to 30.15%). Genetic variances were found almost greater than the environmental variances for all the traits except seeds locule-1 and seed index. High broad sense heritability and selection response were also formulated for seeds boll-1 (0.67, 0.84), seed index (0.77, 0.47 g), lint index (0.96, 0.33 g), lint % (0.96, 1.66 %), seed cotton yield (0.98, 643.16 kg) and cotton seed oil % (0.87, 1.28 %), respectively. Correlation of yield with other traits was found positive for majority of traits except seeds locule-1 and cotton seed oil %. Seed cotton yield is our ultimate goal in growing cotton besides lint %. Highest seed cotton yield was recorded in CIM-499 followed by CIM-473, CIM-496 and CIM-506 and were also found as the second and third top scoring genotypes for seeds per boll, seed index, lint % and cotton seed oil %. Cultivar SLH-279 performed better for lint index, lint % and oil %. This type of correlation is rarely found and ultra desirable by the cotton breeders and a little genetic gain in seed and lint traits and oil content is a great accomplishment.

Vinodhana *et al.* (2013) studied variability, correlation and path coefficient analysis using eight lines and seven testers and their 56 F_1s made with the parents of *G.hirsutum* and *G. barbadense* genotypes of diverse origin. The phenotypic coefficient of variation which measures the total variation was found to be greater than the genotypic coefficient of variation in majority of characters in the present study. The closer magnitude of GCV and PCV indicated that genotype had played greater role rather than environment. High heritability coupled with high genetic advance was noticed for the characters seed yield/plant, number of bolls/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/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/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/plant, boll weight (g), seed index, lint index and fibre length (mm) characters. Path coefficient analysis revealed that number of sympodia/plant, number of bolls/plant, boll weight (g), seed index and lint index directly influenced the seed cotton yield with high direct effects. It was concluded that these characters could be considered as significant selection criteria for seed cotton yield improvement in cotton.

Soomro *et al.* (2008) estimated ten F_2 intraspecific cross combinations derived from genetically diverse genotypes of *Gossypium hirsutum* for genetic selection parameters. All the F_2 populations along with their respective parents were laid out in three replications in a randomized complete block (RCB) design at Agriculture Research Institute, Tandojam Sindh, Pakistan in 2004. The mean values of all the genotypes differed significantly (P=0.01) for all the characters understudy viz; number of sympodial branches per plant, boll weight, number of bolls per plant and seed cotton yield per plant. The results indicated that the hybrid FH-901 x Cedix produced significantly higher seed cotton yield per plant with maximum number of bolls per plant and higher boll weight followed by NIAB-78 x Cedix. The progeny NIAB-78 x Cedix performed better for number of bolls per plant and seed cotton yield per plant. It concluded that a good prospects exised for selecting FH-901 x Cedix and NIAB-78 x Cedix hybrids for further synthesis and development of new cotton genotypes.

Srinivas and Bhadru (2015) estimated gene effects for 5 fiber quality traits from 6 upland cotton crosses through generation mean analysis from 6 generations (P_1, P_2, F_1, F_2, BC_1 and BC_2). Results revealed that dominant genes played major role for the traits 2.5% span length (CPD 420 × 4084 and NA 1325 × LK 861), uniformity ratio (NA 1325 × 4084), micronaire value (BC 68-2 × 4084) and bundle strength (CPD 420 × 4084 and BC 68-2 × 4084) whereas, additive gene effects [d] were found to be important for the traits 2.5% span length (NA 1325 × 4084 and BC 68-2 × 4084) and micronaire value (NA 1325 × LK 861). The traits, ginning percentage (CPD 420 × 4084), 2.5% span length (NA 1325 × LK 861 and NA 1325 × 4084), uniformity ratio (NA 1325 × 4084), micronaire value (CPD 420 × 4084, NA 1325 × LK 861, BC 68-2 × LK 861 and BC 68-2 × 4084) and bundle strength (CPD 420 × 4084) were possessing opposite sign of [h] and [l] indicating the role of duplicate gene action controlling the traits which will pose hindrance to a plant breeder while attempting selection in the long run. Therefore, heterosis breeding would be advantageous and none of the studied traits were found to be controlled by the complementary type of interaction. Epistatic gene interactions additive × additive (i), additive × dominance (j) and dominance × dominance (l) also showed significant role in inheritance of all fiber characters in one or other cross, whereas linkage or higher order interactions were observed for the inheritance of ginning percentage, micronaire value and bundle strength in cross CPD 420 × 4084 and ginning percentage in NA 1325 × 4084.

2.2 Genetic parameters in upland cotton

Khan *et al.* (2007) studied the performance of six cotton cultivars i.e. MNH-93, CIM-448, NIAB-78, CIM-446, CIM-1100 and Karishma was evaluated at the Faculty of Agriculture, Gomal University, D.I. Khan in 2004 in a Randomized Complete Block Design (RCBD) with three replications having net plot size of 2.7 x 5.5 m^2. Significant differences (P-0.05) among various cultivars were observed for all the traits. Results showed that the cultivar Karishma produced the maximum staple length (29.57mm), boll weight plant-1 (4.7 g), G.O.T % (36.47) and lint yield (798.9 kg ha-1). The cultivar CIM-446 produced maximum seed index (9.80 g).

Dhivya *et al.* (2014) studied the analysis of variance study indicated the presence of significant difference among all the traits in *Gossypium hirsutum* accessions. The highest phenotypic coefficient of variation (GCV) and genotypic coefficient of variation (GCV) were recorded 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 G cot 16 were identified as potential donors for single plant yield (g), number of bolls per plant, 2.5% span length (mm) and bundle strength (g/tex). So these accessions may be utilized for crossing programme to improve a particular character in crop improvement.

2.3 Correlation and Path analysis in cotton

Thiyagu *et al.* (2010) reported that plant height, number of sympodial branches per plant, number of bolls per plant along with 2.5 percent span length, bundle strength and elongation percentage showed significant positive association with seed cotton yield per plant at genotypic level indicating that these characters can be improve simultaneously. Correlation studies was made with parents, F_1's of 15 (lines) × 4 (testers) and one check hybrid (TCHB 213) in interspecific crosses of cotton (*Gossypium* spp). The direct and indirect effect of path analysis revealed that the number of bolls per plant, boll weight, number of sympodial branches per plant, plant height, 2.5 percent span length, bundle strength, elongation percentage, lint index and seed index are the major yield contributing traits in interspecific crosses and should be considered for improving yield under wide hybridization in cotton. The correlation and path co-efficient analysis revealed that simultaneous selection based on plant height, number of bolls per plant, number of sympodial branches per plant, 2.5 percent span length, bundle strength and elongation percentage may be promising in improving the seed cotton yield per plant.

Phenotypic correlation and path coefficient analysis have been worked out by Salahuddin *et al.* (2010) for some important characters in fifteen genotypes (six parents, nine crosses) of American upland cotton (*Gossypium hirsutum* L.). Sympodial branches, bolls per plant, boll weight, G.O.T (%) and lint index were found to be positively correlated with yield per plant in all the genotypes at 1.0 percent level of probability. Further partitioning of correlation coefficients into direct and indirect path ways of influences showed that the characters having most influence on seed cotton yield were bolls per plant and boll weight, which should be taken care of while selecting for higher yields in further breeding programme.

Farooq *et al.* (2014) studied to determine genotypic, phenotypic correlation coefficients and path analysis between seed cotton yield, earliness, fiber and yield contributing traits in 53 cotton cultivars. Heritability and genetic advance was computed to determine the selection procedure for the material studied. The maximum value of GCV% and PCV % was observed in CLCuV% and seed cotton yield. The maximum broad sense heritability was found in traits like FS (99%) followed by BW (98%) GOT% (97%) and FF (96%). Moderate estimates of heritability were found for nodes to 1st fruiting branch (35%), monopodia per plant (34%) and sympodia per plant (43%). Regarding correlation studies seed cotton yield have positive genotypic correlation with bolls per plant, plant height, boll weight, staple length and strength, earliness index and GOT%. Path coefficient analysis results revealed that the traits like earliness index% showed the maximum positive direct effect on yield (0.63) followed by days taken to 1st square (0.17), GOT% (0.16), plant height (0.15), boll weight (0.15) and sympodia per plant (0.11). The traits like EI% and boll weight showed positive correlation, higher heritability estimates and positive direct effect on yield thus may be used as selection criteria to increase yield.

Rauf *et al.* (2004) reported that path coefficients were computed to estimate the contribution of individual characters to yield in cotton. The calculated correlations indicate that boll number per plant, sympodial branches had positive and significant correlation with seed cotton yield at genotypic level. Internodal length had negative but significant genotypic correlation. Number of bolls per plant had the maximum positive direct effect on seed cotton yield per plant followed by boll weight; whereas, internodal length had the maximum negative direct effect on seed cotton yield.

Ahuja *et al.* (2006)) showed that improvement in fibre length is important for the textile industry in utilising high speed yarn spinning technology and in expanding the array of yarn products. High tensile strength fibre is needed for good spinning, especially with fast modern spinning machines. The usual practice of estimating correlation coefficients and the direct and indirect effects of component traits of seed cotton yield is without grouping the genetic material on the basis of fibre length and strength. Hence, the present investigation was carried out on these aspects by grouping the 20 F_1 hybrids into 3 sets on the basis of fibre length and strength, viz, (i) 10 hybrids of low fibre strength (≤20 g tex–1) and medium staple length (≤25.0 mm), (ii) 10 hybrids of high fibre strength (≥24 g tex–1) and longer fibre length (≥28 mm), and (iv) 20 hybrids, i.e. all the 10 hybrids of set 1 and set 2 of *Gossypium hirsutum* L. cotton for agronomic and fibre quality traits. Significant genotypic difference existed among the hybrids in all the sets for all the characters studied. The direction of association coefficient of the traits and direct effects on seed cotton yield differed for all the traits except for the number of bolls per plant, boll weight and fibre strength in set 1 and set 2. Set 1 gave the same direction of association with seed cotton yield as obtained in set 3 of usual practice except for the traits ginning out turn (GOT) and days to flowering, whereas set 2 gave similar information to the usual practice for the traits days to flowering, total bolls, boll weight and GOT, and differed for other traits. The present study, therefore, indicated that the hybrid population needs to be grouped on the basis of fibre length and fibre strength prior to estimation of correlation coefficients and direct and indirect effects of other traits on seed cotton yield.

Araujo *et al.* (2012) studied to evaluate the relative contribution of agronomic and technological components on the fiber yield in upland cotton cultivars. The experiment was carried out with 11 upland cotton cultivars in a completely randomized blocks design with three replications. Initially, we performed analysis of variance, with the F test at 5% probability for the effect of cultivar as fixed effects as well as block and environment effects as random. Then the values were ordered according to cluster test Scott-Knott, at 5% probability level. The significance of the null hypothesis that all possible canonical correlations are null was evaluated using the chi-square test. The correlations were estimated through the path analysis. By examining the canonical correlations there was dependence between the two groups of variables and therefore it is possible to promote changes in certain characteristics through the selection of others correlated. Plants of upland cotton with higher fiber yield were influenced by the decrease in average weight of the cotton boll. When there is a reduced fiber yield, there is also an increase in uniformity and strength thereof. The fiber resistance had negative indirect effects on the fiber uniformity and length.

Farooq *et al.* (2015) designed a research work to estimate genotypic and phenotypic correlation coefficients and path analysis at the genotypic level between seed cotton yield and yield contributing traits in 18 cotton cultivars. The material was sown on 15th of May to observe association among yield and its related traits. Heritability was estimated to determine the selection criteria under normal growing conditions. The values of phenotypic coefficient of variation (PCV%) were higher in magnitude than the genotypic coefficient of variation (GCV%) for all the traits. Heritability (broad sense) revealed higher estimates for all traits like plant height (98%), cotton leaf curl virus (CLCuV%) (96.8%), nodes to first fruiting branch (95%), bolls per plant (91.5%), sympodia per plant (88.8%), yield (88%) monopodia per plant (84.7%) and for boll weight (82.3%). The results of phenotypic and genotypic correlation showed that sympodia per plant showed positive significant correlation with boll per plant, boll weight and yield at both genotypic and phenotypic levels. Boll weight showed strong association with the yield at both levels. Path coefficient analysis revealed that all traits influenced directly and positively on yield except for bolls per plant. The traits showing strong association along with higher heritability may be considered for selection in future breeding endeavors.

Ekinci *et al.* (2010) carried out an experiment to determine direct and indirect effects of some characters (single leaf area, leaf SPAD value, number of nods, number of sympodial branches, number of monopodial branches, single boll weight, number of bolls) on seed cotton yield. The experiment was carried out with four cotton varieties, two of which okra-leaf (Adana 98, Siokra 1/4) and two of which normal-leaf (Teks and Stoneville 453) cotton (*Gossypium hirsutum* L.) and was conducted the randomized block design with 4 replications. In order to increase seed cotton yield in the studies of breeding program and selection orderly leaf SPAD value, number of sympodial branches, single boll weight, number of monopodial branches and number of bolls characters determined that must be high. Results showed that in order to increase seed cotton yield in the studies of breeding program and selection the highness of leaf SPAD value, number of sympodial branches, single boll weight, number of monopodial branches and number of bolls characters should be considered important.

Ramdan *et al.* (2014) conducted two cycles of direct selection were accompanied with two selection intensities, i.e., 5% and 10% were utilized to improve productivity with acceptable fiber quality characters of the cotton cross Giza 88 x Pima S6. Comparing mean performance of F2 with those of F3 and F4 generations revealed increase in mean values for all characters with advanced generations from F_2 to F_4, indicating an accumulation of favorable alleles. GCV and PCV were comparatively high for seed cotton yield / plant, lint yield/plant, micronaire reading and boll weight. F_2 generation showed high GCV and PCV values than those of the succeeding generation for all characters. The closer magnitude of GCV and PCV in F_3 and F_4 generations indicated that genotype had played greater role rather than environment for most characters. Heritability estimates in broad sense improved considerably for all characters from F_2 to advanced F_3 and F_4 generations. The undesirable negative relationship between seed cotton yield/plant or lint yield/plant with the other yield or fiber characters were converted to positive and desirable in F_4 generation. This was due to one cycle of direct selection. The predicted and realized advances were high for boll weight , lint yield / plant and lint index in F_2 generation , while the actual advance in F_3 generation at two selection intensities had higher values for lint yield/plant, seed cotton yield/plant, lint index and boll weight. There were close agreement between predicted and realized advances for lint yield/plant, lint index, lint percentage and seed index, which may be due to the predominance of additive genetic effect. The gains from selection for six selected characters were high in both F_3 and F_4 generations as compared with F2 generation due to high genetic variance relative to environmental variance. The selection intensity at 5 % achieved highly improvement in most selected characters in F_3 and F_4 generations for predicted and actual genetic advances. Improvement of fiber length was achieved by using direct selection for lint percentage and lint index at 5% selection intensity. The correlated response of fiber characters when selection was predicted for yield characters indicated that it might be more profitable to practice direct selection for lint percentage and lint index compared to selecting for the rest yield characters. Some families showed the best values for yield and fiber quality characters together and surpassed the better parent variety Giza 88 extra long stable. The breeder may utilize such families in breeding programs aiming to improve yield and fiber characters.

Rao and Gopinath (2013) carried out correlation and path coefficient analysis on 28 interspecific hybrids and 8 parents of cotton (*Gossypium hirsutum*). Genotypic correlation studies revealed that number of bolls per plant, boll weight, number of monopodia per plant, number of sympodia per plant, seed index, lint index and plant height have significant association with seed cotton yield per plant. Path coefficient analysis showed that number of bolls per plant exhibited the maximum direct effect on seed cotton yield per plant followed by boll weight, number of sympodia per plant and lint index. The maximum positive indirect effect on seed cotton yield per plant was observed through number of bolls per plant. Thus due emphasis should be given to number of bolls per plant, boll weight and lint index for improvement in seed cotton yield.

Thiyagu *et al.* (2010) studied correlation with parents, F_1's of 15 (lines) × 4 (testers) and one check hybrid (TCHB 213) in interspecific crosses of cotton *(Gossypium* spp) revealed that plant height, number of sympodial branches per plant, number of bolls per plant along with 2.5 percent span length, bundle strength and elongation percentage showed significant positive association with seed cotton yield per plant at genotypic level indicating that these characters can be improved simultaneously. The direct and indirect effect of path analysis revealed that the number of bolls per plant, boll weight, number of sympodial branches per plant, plant height, 2.5 per cent span length, bundle strength, elongation percentage, lint index and seed index are the major yield contributing traits in interspecific crosses and should be considered for improving yield under wide hybridization in cotton. The correlation and path co-efficient analysis revealed that simultaneous selection based on plant height, number of bolls per plant, number of sympodial branches per plant, 2.5 per cent span length, bundle strength and elongation percentage may be promising in improving the seed cotton yield per plant.

2.4 Selection index in cotton

Saleh (2013) investigated and aimed to evaluate five upland cotton (*Gossypium hirsutum* L.) (Aleppo118, Aleppo33/1, Aleppo90, Raqqa5, and Deir-Ezzor22) varieties based on physiological indices and genetic variation using AFLP marker. These varieties were evaluated under control and saline conditions (50, 100 & 200 mM NaCl) for 56 days. Various physiological indices were detected in this investigation. In this respect, Deir-Ezzor22 variety differed by showing high salt tolerance relative to the other tested varieties. Otherwise, PCR amplification with 7 AFLP PCs primer combinations revealed that Deir-Ezzor22 variety characterized by 15 unique positive markers compared to the other tested varieties. Based on physiological study and AFLP technique, it can be concluded that genetic variation detected by AFLP marker supported the physiological indices among the tested cotton varieties. These varieties present considerable interest for genetic studies and plant improvement.

Zhang *et al.* (2009) reported that crop seeds are important sources of protein, oil, and carbohydrates for food, animal feeds, and industrial products. Recently, much attention has been paid to quality and functional properties of crop seeds. However, seed traits possess some distinct genetic characteristics in comparison with plant traits, which increase the difficulty of genetically improving these traits. In this study, diallel analysis for seed models with genotype by environment interaction G x E effect was applied to estimate the variance-covariance components of seed traits. Mixed linear model approaches were used to estimate the genetic covariances between pair-wise seed and plant traits. The breeding values (BV) were divided into two categories for the seed models. The first category of BV was defined as the combination of direct additive, cytoplasmic and maternal additive effects which should be utilized for selecting stable cultivars over multi-environments. The three genetic effects, together with their GE interaction, were included in the second category of BV for selecting special lines to be grown in specific ecosystems. Accordingly, two types of selection indices for seed traits, i.e., general selection index and interaction selection index, were developed and constructed on the first and the second category BV, respectively. These proposed selection indices can be applied to solve the difficult task of simultaneously improving multiple seed traits in various environments. Data of crop seeds with regard to four seed traits and four yield traits based on the modified diallel crosses in Upland cotton (*Gossypium hirsutum* L.) were used as an example for demonstrating the proposed methodology.

Bertan *et al.* (2008) opined that selection of the appropriate parents to be used in artificial crosses is one of the main decisions faced by plant breeders that will facilitate the exploitation of the maximum genetic variability and production of superior recombinant genotypes. Several techniques have been used in aiding the identification of genotypes with promising and desirable agronomical traits for hybridization. In this way, the objective of the present review is to gather available information for the selection of parents based on different breeding designs and analytical tools showing their similarities and high lighting the main advantages and disadvantages of their use.

Abbas *et al.* (2011) conducted a research work and planned to screen a part of cotton germplasm to find out their salt tolerance potential at seedling stage measuring root length, shoot length, root fresh weight, root dry weight and shoot dry weight. A control and two levels of NaCl (10 & 20 dS m^{-1}) and 50 cotton genotypes in completely randomized design were used. Data indicated that there was significant reduction in all seedling traits. It was also observed that 24 genotypes could not show even emergence at 20 dS m^{-1} salinity level. Moderate to high genetic variability was observed in all traits at all levels of salinity except at relative salinity of 10 dS m^{-1}. High heritability and high genetic advance was also found for most of the traits. Some genotypes were ranked top on the basis of root length, while others performed well on the basis of shoot dry weight. Thus, to get rid of this complication, selection index was performed by giving an equal weight to all the seedling traits studied. As a result, top 6 genotypes (NIAB-999, CIM-707, NIAB-78, MNH-93, CIM-446 & CIM-443) performing well at 20 dS m^{-1} were declared salt tolerant.

Majumdar *et al.* (2004) studied on a method of selecting cotton bales to meet the specified ring yarn properties using artificial neural networks. Five yarn properties and yarn count were used as inputs, whereas the Spinning Consistency Index (SCI) and micronaire were the outputs to the neural network models. Bales were selected according to the predicted combinations of SCI and micronaire. The properties of yarns spun from selected bales show good association with the target yarn properties.

Ibrahim *et al.* (2012) evaluated set of sixteen guar genotypes under rain-fed conditions at Kazgeil, Northren Kordofan State, Sudan in 1998/99 season, using a four x four triple partially balanced lattice designs. Data recorded at were used for partitioning the genotypic correlations between seed yield and five of its components into direct and indirect effects. Moreover, different selection indices were constructed using different combinations of these characters. The path analysis showed that number of pods/plant had the highest positive direct effect (2.653) on seed yield/plant followed by number of seeds per pod. On the other hand number of fruiting nodes/main stem exerted the highest negative direct effect (-1.383) on seed yield/plant. The selection index involving single trait viz.1000 seed weight gave the minimum expected genetic advance (0.6) and relative efficiency (83.33%). However, the index involving all the six traits exhibited the highest expected genetic advance (2.03) and the maximum relative efficiency (281.94%). The two trait selection index of number of pods/plant and 1000-seed weight scored the relative efficiency of 138.89% which is equal to the relative efficiency of the individual trait index of number of reproductive branches/plant.

2.5 Genotype x Environment interaction in cotton

Genetically diverse ten genotypes were tested by Ali *et al.* (2009) under three different spacing which were S1 (90 cm x 45 cm), S2 (90 cm x 50 cm) and S3 (90 cm x 60 cm) at Cotton Research, Training and Seed Multiplication Farm, Sadarpur, Dinajpur during the growing season, 2006-2007. Analysis of variance revealed significant effect of the spacing over the characters studied. Phenotypic index, regression coefficient and deviation from regression coefficient were the fundamental clues of G x E interaction. After furnishing the results, the genotype D-1 found to be the suitable and the spacing 90 cm x 60 cm was the most favorable for the characters and the seed cotton yield along with yield of lint was high in D-1 (2.19 kg/plot) over three spacing.

Campbell *et al.* (2012) reported that Genotype × Environment (G × E) interactions and trait correlations significantly impact efforts to develop high-yield, high-quality, and environmentally stable upland cotton (*Gossypium hirsutum* L.) cultivars. Knowledge of both should be used to design optimal breeding programs and effective selection criteria. In this study, we examined the G × E interactions and trait correlations present in the 70 year Pee Dee cotton germplasm enhancement program. Since beginning in 1935, the Pee Dee program has employed a variety of unique germplasm and breeding methods to release >80 improved germplasm lines and cultivars. Results suggest that significant G × E interactions exist for several agronomic and fiber quality performance traits that are mostly due to changes in magnitude. Negative genotypic correlations still persist between lint percent/lint yield and fiber length/fiber strength. However, apparently the breeding methods and selection criteria used over 70 year have lessened the negative relationship between agronomic performance and fiber quality over time to some degree. The results provide cotton breeders a resource to select specific Pee Dee germplasm lines for increased environmental stability. Cotton breeders can also use the information herein to select specific Pee Dee germplasm lines that represent rare recombination events that combine high yield and fiber quality potential.

Dewdar (2013) stated that stability analysis helps in understanding the adaptability of genotypes over different environmental conditions and the identification of adaptable genotypes. Three field experiments were carried out at the Faculty of Agriculture, El-Fayoum University, Fayoum, Egypt to study the magnitude and nature of genotype × environment interaction and determine of stability of yield potentiality for five Egyptian cotton varieties. Significant differences were observed among cotton genotypes 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 Gene– environment interaction of all traits under study. These results showed that genotypes of Giza 90 and Giza 80 were more stable genotypes. This implies therefore that there genotypes are low contribution to the genotypic by environment interaction. Our results showed that high yield 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.

Machado *et al.* (2002) reported that seed cotton yield of *Gossypium hirsutum* L. data from the regional cotton variety trials of the EPAMIG breeding program from 1990 to 1999 were analyzed with the objectives of: estimating both the magnitude of genotype by environment interactions and the genotype adaptability and stability according to the methods proposed by Eberhart and Russell, Lin and Binns and Annicchiarico; and selecting advanced lines to compose the final trials of the program. Four groups of genotypes and environments were assembled and analyzed. For the first one, significant genotype x year and genotype x location x year interactions were detected. The most stable genotypes were MG-864492 and IAC 20. Significant second-order interactions were estimated for the three remaining groups studied. In the second group the most stable strains were MG-863192 (according to Eberhart and Russell method) and MG-863579 (according to Lin & Binn’s and Annicchiarico’ s methods). For the third genotype-environment group, the most stable genotype under all methods was MG-864133. The cultivar EPAMIG 5 Precoce-1, in the fourth group, presented stable performance also under the three methodologies tested.

Thomson and Cunningham (1979) found that Stoneville 7A and Deltapine Smooth Leaf, bred in the Mississippi delta, were the highest yielders among a small group of medium-staple United States cultivars compared over three seasons and three sites in the Ord River valley

(15° 39´S.), north-western Australia. Significant cultivar x year interactions existed for lint yield, lint percentage, boll weight, micronaire and Pressley strength, and significant cultivar x site x year interactions occurred for lint yield, lint percentage and staple length. Significant cultivar x site interactions occurred only for lint yield and pressley strength. From the expected standard errors of cultivar means an evaluation procedure involving sampling for seed cotton yield over 3 years at each of six sites and two replications, but sampling for other agronomic and fibre quality attributes only at one site, was suggested. This procedure should result in standard errors of 5% or less of the mean values for all attributes. Consistency and stability of cultivar behavior was assessed by simple rank methods, and Finlay and Wilkinson's joint regression method. The consistency of performance was such that a high probability of choosing the top yielders successfully would have attended early selection.

Rajakumar *et al.* (2012) evaluated twenty two Bt cotton hybrids at three locations at Main Agricultural Research Station Raichur, Agricultural Research Station Siruguppa and Agricultural Research Station Bheemarayanagudi and sown on 15 July during the *kharif* 2010. The objective of this study was to determine genotype × environment (G × E) interaction and stability of Bt cotton hybrids, and effect of different environments on seed cotton yield to understand its adaptation to varying environments. Hybrids were tested by two stability parameters as linear regression coefficient (bi) and deviations from regression (S^2di). Significant differences were observed for the mean yields in the three environments. Mean seed cotton yield ranged from 1478 to 2203 kg/ha. Genotypes showed significant interaction with environments. Regression coefficients ranged from 0.19 to 1.70 and deviations from regression were significant for all the hybrids except Tulasi-4BG-II, Tulasi-117 BG-II, Chirutha BG-II, ACH-155-2 BG-II, Rakhi-621 BG-II and RCH-2 BG-II. It was concluded that three high yielding cotton genotypes MRC-7347 BG-II, ACH-177-2 BG-II and MRC-7351 BG-II were found to be stable hybrids.

Laghari *et al.* (2003) stated that stability in yield of seed cotton over wide range of environments has long been desired by plant breeders. To determine the possible effects of environment and genotypic differences for yield, three advanced strains/genotypes of cotton viz. AEHM-4/4/89, AEH-2/90, AENB-10/87 along with two commercial checks viz., NIAB-78 and Rehmani were tested over different environments in Sindh. Genotypes, locations and genotype x environment (GxE) interactions were highly significant ($P \leq 0.01$) indicating genetic variability between genotypes by changing environments. Stability parameters calculated were regression coefficient (bi), S.E. and deviation from regression (S^2d). Genotypes, AENB-10/87, NIAB-78 and AEH-2/90 had the highest mean seed cotton yield, regression coefficient (bi) less than or close to unity (0.749, -0.295 and 0.215, respectively), the lowest deviation from regression (S^2d) (0.083, 0.025 and 0.071 respectively) suggesting above average stability and adaptability over environments. AEHM-4/4/89 and commercial check Rehmani produced low mean yields than the grand mean with the highest regression coefficient (bi) and the highest deviation from regression coefficient (S^2d) had below average stability and are specifically adapted to favorable environments.

Thirteen genotypes of cotton developed through hybridization and mutation breeding techniques were evaluated by Ali *et al.* (2012) during two consecutive years 2002-2003 and 2003-2004 on eight locations covering most of the area of Punjab province including Faisalabad, Toba Tek Singh and Jhang. The eight sets of experiments were conducted in the naturally highly saline sodic soils, EC ranges from 7.8-36.1 d/Sm, pH=8.1-8.8, SAR=10.1-40.5, Saturation percentage 31.3-40.8 and texture Sandy Clay loam and Clay loam. The seed yield data was collected at maturity and stability parameters were computed to know genotypic environment interaction and varietals performance. The combined analysis of variance showed highly significant variance in case of varieties, locations and varieties x environment (Lin) also showed highly significant differences. It means that genotypes exhibited different behavior in different locations/environments which is due to their different genetic make up. The behavior may be cross over (in which significant change in ranking order occurs from one environment to another) or cross over nature (in which case the ranking of genotypes remains constant across environments and the interaction is significant because of change in the magnitude of response) depending upon the ranking order of genotypes performance under different environments. In our study only S-12 behavior was of almost non cross over nature, while others had cross over type of interaction. Based on over all seed cotton yield, variety NIAB-999 and CIM-707 produced the highest seed cotton yield (3.2 t/ha, 3.17t/ha). The lowest seed cotton yield was noted in S-12 (1.86 t/ha). All the three parameters of stability i.e. overall mean seed cotton yield, regression coefficient and standard deviation to regression provided clear evidence that variety NIAB-999 and CIM-707 produced the maximum stable yield compared to S-12.

Killi and Harem (2006) conducted an experiment to determine genotype x environment (GE) interaction and stability of cotton genotypes, and effect of different environments on seed cotton yield to understand its adaptation to varying environments. Fourteen cotton genotypes were evaluated at four locations across Aegean region of Turkey in 1997 and 1998. Genotypes were tested by two stability parameters as linear regression coefficient (bi) and deviations from regression (S^2d). Significant differences were observed for the mean yields in the 8 environments. Mean seed cotton yield ranged from 4.58 to 5.80 t ha^{-1}. Genotypes showed significant interaction with environments. Regression coefficients ranged from 0.23 to 1.46, and deviations from regression were significant for only four genotypes. It was concluded that three high yielding cotton genotypes viz. SG-1001, SG-125 and DLP-5409 were found to be stable genotypes.

Meredith *et al.* (2012) showed the total variation for 26 traits into environment (E), genotype (G) and genotype x environment (GE) variance components for the 2001 through 2007 Regional High Quality (RHQ) tests with 98 genotypes. It evaluated 26 traits and 56 year-location environments. There were four yield traits, five yield components, six traditional breeder-geneticists (BG) fiber traits, seven High Volume Instrumentation (HVI) fiber traits, and four gossypol traits. Yield variance components for lint, seed, oil, and N were similar with an average of 87, 5, and 8% of the total variance due to E, G, and GE, respectively. Lint%, E, G, and GE were 57, 33, and 10%, respectively and were similar to oil% E, G, and GE which were 53, 37, and 10%, respectively. Length, strength, and micronaire's G components for BG fiber were 28, 52, and 16%, respectively. For the HVI samples, G was similar with 36, 48, and 18%, respectively. Average G for total gossypol and its two isomers, plus (+) and minus (-) was 36, 47, and 29%, respectively. The plus (+) percent of total gossypol was 17, 72, and 11% for E, G, and GE, respectively. This was the lowest E% and the highest G% of all the 26 traits. The results of this study suggested that during the last 50 yrs, little changed in E, G, and GE variance components occurred.

Zeng *et al.* (2014) reported that analysis of genotype (G)-by-environment (E) interactions and their influence on performance of cotton (*Gossypium hirsutum* L.) cultivars can help cotton breeders to 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 during 2003 and 2009 were used 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 sub region. 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.

Campbell and Jones (2005) stated that plant breeding programs involving a wide range of crop plants routinely practice selection (directly or indirectly) for genotypes that display stability for a given trait or set of traits across testing environments through the genotype evaluation process. Genotype stability for trait performance is a direct measure of the presence and effect of genotype × environment interactions, which result from the differential performance of a genotype or cultivar across environments. The genotype evaluation process also requires selection of the proper field trial locations that best represent the target environments the breeding program is directed toward. In this study, we assessed the extent to which genotype×environment interactions affected agronomic performance (lint yield, gining out turn) and fiber quality (fiber length, fiber strength, uniformity index, micronaire, fiber elongation) in a series of cotton (*Gossypium hirsutum* L.) performance trials in 12 location–year environments in South Carolina. Genotype × environment interactions affecting lint yield were larger in higher yielding environments, while interactions for fiber strength were greater for genotypes with lower mean fiber strength values. Two regions within the South Carolina cotton production areas were identified as proper testing locations for lint yield performance, while testing for fiber strength can be accomplished in any location within the statewide cotton production areas.

Pettigrew (2001) studied the fifer quality under sunlight and reported that inferior fibers produced compared with that produced in abundant sunlight environments. This response to low light suggests that insufficient photosynthetic assimilates are the cause of the fiber quality reductions. The primary objective of this research was to determine how fiber carbohydrates respond to varying levels of sunlight during development. A field study was conducted from 1995 to 1997 in which cotton was exposed to two light regimes during reproductive growth: (i) incident sunlight and (ii) 70% of incident sunlight achieved with shade cloth. Samples of fiber, ovules, and leaves subtending the boll were collected at 0, 14, 21, and 35 d post anthesis (DPA) and analyzed for starch, glucose, fructose, and sucrose. Fiber quality was determined at the end of the season. With some exceptions, the shade treatment reduced carbohydrates levels in the leaf and ovule tissue. At 14 DPA, starch was reduced 29% in fiber grown under shade. Sucrose level in shade fiber was reduced 31% at 21 DPA. The carbohydrate reductions at 14 and 21 DPA occurred during a period of fiber development when strength is determined. These carbohydrate reductions parallel the 3% fiber strength reductions seen with low light. The reduced sucrose levels at 21 DPA induced by the shade also occur during fiber secondary cell wall deposition and match the lower fiber micronaire produced under shade. These data present compelling evidence that adequate carbon assimilates are required to produce fiber quality approaching genetic maximums.

2.6 AMMI analysis in cotton

Gauch (2005) stated that the additive Main effects and Multiplicative Interaction (AMMI) model, Genotype main effects and Genotype × Environment interaction (GGE) model, and Principal Components Analysis (PCA) are singular value decomposition (SVD) based statistical analyses often applied to yield-trial data. This paper presents a systematic comparison, using both statistical theory and empirical investigations, while considering both current practices and best practices. Agricultural researchers using these analyses face two inevitable choices. First is the choice of a model for visualizing data. AMMI is decidedly superior, not for statistical reasons, but rather for agricultural reasons. AMMI partitions the overall variation into genotype main effects, environment main effects, and genotype × environment interactions. These three sources of variation were present agricultural researchers with different challenges and opportunities, so it is the best to handle them separately, while still considering all three in an integrated manner. Second is the choice of a member of a given model family for gaining predictive accuracy. AMMI, GGE, and other SVD-based model families are essentially equivalent, but the best practices require model diagnosis for each individual data set to determine which member is the most predictively accurate. Making these two choices well allows researchers to extract more usable information from their data, thereby increasing efficiency and accelerating progress.

Blanche Sr. (2005) conducted a study in 2001-2004 evaluating genotype by environment interactions in cotton (*Gossypium hirsutum* L.). Genotype by Environment interactions were characterized using GGE biplot for conventional cotton cultivars and their transgenic derivatives. Significant interactions existed for several non-target traits. Transgenic cultivars were taller, had greater height to node ratios, larger seed, and lower lint percentages. Transgenic cultivars containing the Bollgard gene yielded more than their conventional parents and STV4691B was the highest yielding, most stable cultivar. In 2002-2004, GGE Biplot was used to identify two levels (high/low) of discriminating locations for three distinct selection criteria. Crosses were made with parents recommended by a least squares means analysis for each population criteria and F_2 plants were planted in the high and low discriminating locations for each population. Gains by selection (h^2) were calculated by regressing is the F2:3 plants on their F2 parents. Genotypic variance was greater among $F_{2:3}$ progeny in discriminating environments compared to non-discriminating environments, regardless of population. Heritability was greater in the population containing fiber traits compared to yield. In 2004, GGE Biplot was compared to other widely-accepted stability analysis tools**.** Correlation coefficients between GGE biplot (stability evaluation) and the Cultivar Superiority Measure, Shukla's Stability Variance, the Eberhart-Russell regression model, Kang's yield stability statistic, and AMMI were 0.54, 0.91, 0.86, 0.63, and 0.55, respectively. Correlation coefficients in between GGE biplot (mean performance + stability evaluation) and the Cultivar. Superiority Measure, the Eberhart-Russell regression model, Kang's yield stability statistic, and AMMI were 0.95, 0.60, 0.85, and -0.33, respectively. Based on the results of this study and our experience using GGE Biplot, Model 3 with an entry-focused scaling is the most valuable analysis for breeders engaged in cultivar development. GGE Biplot was used with the 1993-2003 Louisiana Official Variety Trials to identify the most desirable (discriminating and representative) test locations in Louisiana for yield and fiber length. St. Joseph loam was ranked 1st for yield, Winnsboro irrigated was ranked 1st for fiber length, and St. Joseph loam was ranked 1st to simultaneously select for both traits. Winnsboro non-irrigated should not be used to select for yield or fiber length.

Calvalho (2016) stated that in cotton breeding programs, it is necessary to identify genotypes with predictable behavior on the length of fibers, and which are responsive to environmental variations, in specific or broad conditions. The aim of this study was to employ the methodology of mixed models for simultaneous selection of cotton genotypes with greater length of fibers, adaptability and stability. It was evaluated 36 lines in three trials located in

Apodi (2013 and 2014) and Santa Helena (2013,) in a randomized block design with two replications. Genetic parameters were estimated by the restricted maximum likelihood/best linear unbiased predictor method (REML/BLUP) and the selection was based on the method of harmonic mean of the relative performance of genetic values. The genotypes CNPA 2012-55, CNPA 2012-58, CNPA 2012-62 and CNPA 2012-64 can be grown in all tested environments, since they gather greater length of fibers, stability and adaptability.

Riaz *et al.* (2013) conducted an experiment to determine the yield stability, adaptability and to analyze the GE interaction of 9 cotton genotypes using a randomized complete block design (RCBD) with three replications 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%), GE (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 GE 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

Gashaw (2013) conducted a field experiments at moisture-stressed areas of Kobo and Mersa, Ethiopia from 2005-2007 cropping seasons. The experiment was laid-out using completely randomized block design with three replications. Twelve cotton cultivars were evaluated for cottonseed yield, lint qualities and other agronomic traits. Fiber quality parameters (staple length, fiber strength, lint fineness and short fiber index) were examined. Analysis of variance (ANOVA) for each location and pooled over locations and years, as well as correlations of lint yield with lint quality traits were analyzed using GenStat Discovery Edition-3 software. 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 seed cotton 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.

Wang *et al.* (2014a) stated that in general, the quality of fruits depends on local conditions experienced by the fruit during its development. In cotton, fruit quality, and more specifically the quality of the fibre in the fruit, depends on interactions between fruit position in the plant architecture, temperature and agronomic practices, such as sowing time, mulching with plastic film and topping of the plant's main stem and branches. To quantify this response of cotton fibre quality to environment and management, we developed a simulation model of cotton growth and development, CottonXL. Simulation of cotton fibre quality (strength, length and micronaire) was implemented at the level of each individual fruit, in relation to thermal time (represented by physiological age of the fruit) and prevailing temperature during development of each fruit. Field experiments were conducted in China in 2007 to determine model parameters, and independent data on cotton fibre quality in three cotton producing regions in China were used for model validation. Simulated values for fibre quality closely corresponded to experimental data. Scenario studies simulating a range of management practices predicted that delaying topping times can significantly decrease fibre quality, while sowing date and film mulching had no significant effect. We conclude that CottonXL may be used to explore options for optimizing cotton fibre quality by matching cotton management to the environment, taking into account responses at the level of individual fruits. The model may be used at plant, crop and regional levels to address climate and land-use change scenarios.

Ying (2004) reported that Henan regional trial data of cotton varieties in 2002 were analyzed by AMMI model and the interaction of genotype and environment (G x E) were discussed. The results showed that the data analyzed by AMMI model could explain the interaction of G × E effectively and strikingly increase the ability of tested varieties.

Pretorius *et al.* (2015) conducted a field trial to evaluate yield performance of different cotton cultivars under irrigation in South Africa by using the AMMI model. Five genotypes were evaluated over three seasons (2003 to 2006) at six locations. The additive main effects and multiplicative interaction (AMMI) statistical model was used to investigate the cultivar x environment interaction (GEI), yield stability and adaptation to environments. AMMI analysis indicated that cotton yield showed highly significant differences ($p<0.01$) affected by Environments (E), genotypes (G) and genotype x environment interaction (GEI). 84.0 % of the total sum of squares was attributed to environmental fluctuations showing that the environments were diverse, with large differences among environmental means accounting for most of the variation in cotton yield. Results showed that NuOPAL was the best performing cultivar in 15 out of 18 observations in fibre yields.

Sergio and Santos (2009) performed an experiment to evaluate the convenience of defining the number of multiplicative components of additive main effect and multiplicative interaction models (AMMI) in genotype x environment interaction experiments in cotton with imputed or unbalanced data. A simulation study was carried out based on a matrix of real seed-cotton productivity data obtained in trials with genotype x environment interaction carried out with 15 genotypes at 27 locations in Brazil. The simulation was made with random withdrawals of 10, 20 and 30% of the data. The optimal number of multiplicative components for the AMMI model was determined using the Cornelius test and the likelihood ratio test onto the matrix completed by imputation. A correction based on the data missing in the Cornelius procedure was proposed for testing the hypothesis when the analysis is made from averages and the repetitions are not available. For data imputation, the methods considered used robust sub models, alternating least squares and multiple imputations. For analysis of unbalanced experiments, it is advisable to choose the number of multiplicative components of the AMMI model only from the observed information and to make the classical estimation of parameters based on the matrices completed by imputation.

2.7 Different aspects of cotton

Ashokkumar *et al.* (2014) stated that the cultivated *Gossypium* spp. represents the most important, natural fibre crop in the world. India is the only country cultivating all the four cultivated species of cotton. Among the *Gossypium* spp., *Gossypium hirsutum* is the most cultivated species in many countries. Breeding for high cotton yield is still the primary goal of cotton breeding programs, but improving fibre quality has become increasingly important.

The enhancement of fibre quality traits like fibre length, strength, and fibre fineness is an essential requirement for the modern textile industry. *G. hirsutum* is characterized by its high lint yield while *Gossypium barbadense* has good fibre quality. Through a conventional breeding strategy, introgression of useful alleles for fibre quality from wild species and *G. barbadense* to *G. hirsutum* will be the effective way to improve the fibre quality traits. The identification of the stable quantitative trait loci (QTLs) affecting fiber traits across different generations will be very helpful in molecular marker-assisted selection to improve fiber quality of cotton cultivars. In this review, we present an overview of the genetics and conventional and molecular breeding techniques that have been used to increase the favorable fibre quality traits in cotton**.**

Majumdar *et al.* (2005) showed a comparative study of the methods used to determine the technological value or overall quality of cotton fibre. Three existing methods, namely the fibre quality index (FQI), the spinning consistency index (SCI) and the premium-discount index (PDI) have been considered, and a new method has been proposed based on a multiple-criteria decision-making (MCDM) technique. The efficacy of these methods was determined by conducting a rank correlation analysis between the technological values of cotton and yarn strength. It was found that the rank correlation differs widely for the three existing methods. The proposed method of MCDM (multiplicative AHP) could enhance the correlation between the technological value of cotton and yarn strength.

Dinakarana *et al.* (2012) conducted a field trial to assess the salt tolerance of 32 popular upland varieties released for general cultivation between 1980 and 2001 in India. The study was carried out in normal as well as saline-alkaline condition; in which salinity were created using bore well water irrigation and the average electrical conductivity level of bore well water is 3.10 ds/m. The 32 upland cotton genotypes under both salinity and normal conditions revealed high GCV and genetic gain for number of bolls per plant, boll weight, lint yield per plant, 2.5 per cent span length, leaf area index, Na-K ratio and seed cotton yield and these traits could be improved by simple selection. Correlation and path analysis studies revealed that the seed cotton yield was highly influenced by lint yield per plant in both normal and saline-alkaline condition. Significant positive correlations exists between Bartlett's rate index with uniformity ratio, 2.5 percent span length with bundle strength, uniformity ratio with micronaire and elongation percent, specific leaf area with leaf area index. These results clearly indicated that selection for any one of these traits might lead to concurrent improvement of other traits as well as seed cotton yield. The characters boll weight (-0.347), ginning out turn (-0.528), 2.5% span length (-0.312) and uniformity ratio (-0.440) registered high order negative direct effect on seed cotton yield. This result further confirms the negative association between the quality and yield.

Frydrych (2012) reported a progress in cotton fiber measurement methods. In new millennium it started a new era of fully automized high volume instruments giving new possibilities for users.

2.8 Quality estimation of cotton fiber

Rahman (2004) initiated a field study to estimate the genetic variability among 16 genotypes of Upland cotton (*Gossypium hirsutum* L.) and to determine associations between different traits as well as to estimate stability of performance of the tested genotypes. It was carried out in six environments, viz. Shambat in seasons 2000/01, 2001/02and 2002/03, Wad Medani in seasons 2001/02 and 2002/03and Rahad in season 2001/02. A randomized complete block design with four replications was used in each environment, and data on four morphological traits, yield, yield components and fibre characteristics were collected. In all environments, significant differences among the evaluated genotypes were detected for plant height, yield, yield components and fibre characteristics. On the other hand, the first flowering node, days to 50% flowering, period of boll development and uniformity ratio showed non-significant differences over all environments. The genotype x location interaction was significant for number of bolls/m^2, seed index, lint index, seed cotton yield, lint yield, ginning out-turn (GOT), 2.5% span length (2.5% SL) and fibre attachment force (FAF), whereas genotype x season interaction was significant for lint yield and GOT. The season x location x genotype interaction was significant for lint yield, GOT and 2.5% SL Significant differences in FAF were detected among the sixteen genotypes. The cultivar Shambat B exhibited the strongest FAF over all environments in contrast to the other tested genotypes, which showed weak (desirable) FAF. FAF had significant negative associations with seed cotton yield, lint yield and lint index. It was also negatively correlated with fibre strength. The Associations between FAF and other traits were non-significant. In all environments, significant differences were obtained among the 16 genotypes for GOT. In addition to significant first order and second order interactions. The analysis of genotype x environment interaction for GOT showed that the major part of the variance could be attributed to the linear components rather than the non-linear ones. In all environments, GOT had significant and positive association with lint yield, lint index and micronaire value. On the contrary, it displayed a negative and significant association, at the genotypic and phenotypic levels, with 2.5% SL, fibre strength and FAF. Generally, associations with other plant traits were not significant.

Wang *et al.* (2014b) developed a simulation model of cotton growth and development, CottonXL to quantify this response of cotton fiber quality to environment and management. Simulation of cotton fiber quality (strength, length and micronaire) was implemented at the level of each individual fruit, in relation to thermal time (represented by physiological age of the fruit) and prevailing temperature during development of each fruit. Field experiments were conducted in China in 2007 to determine model parameters, and independent data on cotton fiber quality in three cotton producing regions in China were used for model validation. Simulated values for fiber quality closely corresponded to experimental data. Scenario studies simulating a range of management practices predicted that delaying topping times can significantly decrease fiber quality, while sowing date and film mulching had no significant effect. We conclude that Cotton XL may be used to explore options for optimizing cotton fiber quality by matching cotton management to the environment, taking into account responses at the level of the individual fruits. The model may be used at plant, crop and regional levels to address climate and land use change scenarios.

Dutt *et al.* (2004) compared three types of coloured fibre cottons, i.e. white, brown and green, for their fibre quality and yield. The comparison of fibre quality suggested that coloured fibre cotton was inferior as compared with white fibre cotton. To understand the effect of cellulose, mineral elements [nitrogen (N), phosphorus (P) and potassium (K)] and pH of fibre cells on the quality of fibre, these components were studied at different fibre cell developed stages in all three fibre cotton types. The cellulose content is closely associated with the quality of fibre. The higher fibre quality of white fibre cotton might be the result of the high cellulose content in it compared with coloured fibre cotton. A rapid and slow decrease in pH in white and coloured cottons, respectively, might have some effects on fibre elongation. Among the mineral contents, potassium is positively correlated with the fibre quality traits. The pigment development patterns in brown and green fibre cottons are not similar. In green fibre cotton it takes more time to deepen in colour as compared with brown fibre cotton. Possible strategies for the improvement in quality of coloured fibre cotton are discussed. The results of heterosis studies in coloured fibre cotton suggest that heterosis could improve yield and quality of coloured fibre cotton. In the present study, the hybrids between ZJU12A × ZJU05R and

ZJU18A × ZJU01R, having an acceptable lint colour types plus better fibre quality and high yield performance, may be exploited further for their heterotic advantages.

Messiry and Abd-Ellatif (2013) studied the quality of Egyptian cotton varieties in terms of morphological investigation, single fibre tensile properties and other tuft properties determined by HVI. Finally, a new "modified fibre quality index (MFQI)" for the characterization of the quality is presented and compared with the spinning consistency index. This index in most cases gives the real potential of the cotton variety according to its physical properties.

There exists a plenty of standard and HVI techniques for characterization of cotton fibers. It is known that there are some differences in the principles of measurements and the results of AFIS and HVI spectrum apparatus. The differences exist between measurements of fiber strengths based on the bundles concept or single fiber concept as well. Despite of these differences it is possible to specify basic cotton fiber properties having potential influence to the cotton quality or spinning ability. The main problem with utilization of these properties for quality characterization is multivariate character of information, various units and lack of proper aggregation to utility scale. According to the general definition, the quality is characterized by several properties expressing the ability of a product to fulfill functions it was designed for. The degree of quality (complex criterion) is often expressed as cotton quality index U. The method for complex evaluation of cotton fiber performance based on this idea was presented by Militky (2013). The results of HVI measurements are used as input data. The other empirical complex characteristic of cotton fiber quality is computed as well. The program QCOTTON written in MATLAB is briefly mentioned. The comparison of selected complex criteria is demonstrated on the real data of results of the crop study of 1997 and 1998, which includes 33 sets of cottons.

Two field experiments were conducted by Long *et al.* (2010) to assess the fiber quality and yarn performance of Australian bred cotton (five *Gossypium hirsutum* L. and one *G. barbadense* L.) genotypes. The work included the novel measurement of fiber maturity ratio, fiber linear density, and fiber diameter (ribbon width). The strongest yarns were produced using genotypes with the longest and the finest fiber, for example, the strength of 20 tex yarns for the *G. barbadense* L. cultivar Sipima 280 (length = 36.6 mm, linear density = 143 mtex, ribbon width = 13.7 µm) was 25.4 cN tex^{-1} cf. the *G. hirsutum* L. cultivar Sicala 350B (length = 32.5 mm, linear density = 185 mtex, ribbon width = 14.5 µm) yarn strength of 18.1

cN tex^{-1} Micronaire was an inferior indicator of yarn performance, for example, the *G. hirsutum* L. breeding lines CHQX12B and CHQX377 each had micronaire values of 4.4, but CHQX377 spun stronger yarns due to its finer and more mature fiber. Lint cleaning had the greatest influence on nep (fiber knot) generation for *G. hirsutum* L. genotypes, generating on average 104 neps g^{-1} per lint cleaner passage. There was a negative association between fiber quality and yield, and a cost benefit analysis showed that fiber yield was the dominant economic factor compared to price premiums for better fiber quality. Alternative methods of determining fiber fineness will improve the value of Australian cotton.

Dinakarana *et al.* (2012) reported that cotton being an important cash crop of India plays a distinguished role in energizing the economy of the country by fetching appreciable amount of foreign exchange annually. The cotton production of country is improving significantly but the yield per unit area is still lower than that of the other countries due to some biotic and abiotic factors. Amongst the abiotic stresses, salinity is a serious threat next to drought. Keeping in view, the present study was conducted to assess the salt tolerance of 32 popular upland varieties released for general cultivation between 1980 and 2001 in India. The study was carried out in normal as well as saline-alkaline condition; in which salinity were created using bore well water irrigation and the average electrical conductivity level of bore well water is 3.10 ds/m. The 32 upland cotton genotypes under both salinity and normal conditions revealed high GCV and genetic gain for number of bolls per plant, boll weight, lint yield per plant, 2.5 percent span length, leaf area index, Na-K ratio and seed cotton yield and these traits could be improved by simple selection. Correlation and path analysis studies revealed that the seed cotton yield was highly influenced by lint yield per plant in both normal and salinealkaline condition. Significant positive correlations exists between Bartlett's rate index with uniformity ratio, 2.5 percent span length with bundle strength, uniformity ratio with micronaire and elongation percent, specific leaf area with leaf area index. These results clearly indicated that selection for any one of these traits might lead to concurrent improvement of other traits as well as seed cotton yield. The characters boll weight (-0.347), ginning out turn (-0.528), 2.5% span length (-0.312) and uniformity ratio (-0.440) registered high order negative direct effect on seed cotton yield. This result further confirms the negative association between the quality and yield.

2.9 Biometrical quality analysis of cotton fiber

Malagouda *et al.* (2014) carried out an investigation to study genetic parameters of fibre quality traits in diploid cotton comprising of *G. herbacium* var. Jayadhar and *G. arboreum* var. DLSa17 along with their recombinant inbred lines (RILs). Results revealed highest variance for uniformity ratio (3.30) and the lowest for micronaire (0.20). All the traits exhibited low estimates of phenotypic and genotypic coefficients of variation. Among the traits lowest GCV and PCV were observed for uniformity ratio whereas highest GCV was recorded for fibre elongation and highest PCV for micronaire. 2.5 percent span length and fibre elongation exhibited high heritability coupled with moderate genetic advance as percent mean whereas fibre strength recorded moderate heritability with low genetic advance as percent mean. Low heritability coupled with low genetic advance was observed for micronaire indicating that this trait is controlled by non-additive genes and simple selection would not be effective.

Farooq *et al.* (2014) designed an experiment to determine genotypic, phenotypic correlation coefficients and path analysis between seed cotton yield, earliness, fiber and yield contributing traits in 53 cotton cultivars. Heritability and genetic advance was computed to determine the selection procedure for the material studied. Maximum value of GCV% and PCV % was observed in CLCuV% and seed cotton yield. Maximum broad sense heritability was found in traits like FS (99%) followed by BW (98%) GOT% (97%) and FF (96%). Moderate estimates of heritability were found for nodes to 1st fruiting branch (35%) monopodia per plant (34%) and sympodia per plant (43%). Regarding correlation studies seed cotton yield have positive genotypic correlation with bolls per plant, plant height, boll weight, staple length and strength, earliness index and GOT%. Path coefficient analysis results revealed that the traits like earliness index% showed maximum positive direct effect on yield (0.63) followed by days taken to 1st square (0.17), GOT% (0.16) plant height (0.15), boll weight (0.15) and sympodia per plant (0.11). The traits like EI% and boll weight showed positive correlation, higher heritability estimates and positive direct effect on yield thus may be used as selection criteria to increase yield.

Correlation and path coefficient analysis were carried by Rao and Gopinath (2013) on 28 interspecific hybrids and 8 parents of *G. hirsutum* cotton. Genotypic correlation studies revealed that number of bolls per plant, boll weight, number of monopodia per plant, number of sympodia per plant, seed index, lint index and plant height have significant association with seed cotton yield per plant. Path coefficient analysis showed that number of bolls per plant exhibited maximum direct effect on seed cotton yield per plant followed by boll weight, number of sympodia per plant and lint index. The maximum positive indirect effect on seed cotton yield per plant was observed through number of bolls per plant. Thus due emphasis should be given to number of bolls per plant, boll weight and lint index for improvement in seed cotton yield.

Karademir *et al.* (2010) conducted a field trial to determine the relationship between yield, fiber length and other fiber related traits in advanced cotton strains, derived from a cotton breeding program. The experiments were conducted in the Southeastern Anatolia Agricultural Research Institute's experimental area according to randomized complete block design (RCBD) with four replications during 2007 and 2008 cotton growing season. In the study, 9 advanced cotton strains and 2 check varieties ('GW-Teks' and 'Stoneville 468') were used as plant materials. The results of the statistical analysis indicated that the advanced cotton strains had significant differences in terms of the investigated characteristics when compared to the check varieties. The highest seed cotton yield (4087.0 kg ha-1) and fiber yield (1632.2 kg ha-1) were obtained from 'SET-34' cotton strain which had acceptable fiber quality properties. However, the highest fiber length (32.33 mm) was obtained from 'ERA-85'. The correlation analysis indicated that there were significant negative correlations between fiber length and seed cotton yield, lint yield and ginning percentage, while there were positive and significant correlations between fiber length and fiber strength.

Hussain *et al.* (2010) studied that fifty nine varieties/genotypes of cotton (*Gossypium hirsutum* L.) collected from various cotton research institutes in Pakistan were grown in the field. Five cotton cultivars were selected out of this germplasm contrasting for three fiber quality traits viz; staple length, fiber strength and fiber fineness. Three crosses were made using these five genotypes each between two varieties contrasting for one fiber quality trait, cross CIM-707×4-F for staple length designated as cross-I, cross NIAB-111×RH-1 for fiber strength designated as cross-II and cross MS-40×4-F for fiber fineness designated as cross-III. Four generations P_1, P_2, F_1 and F_2 of each cross were developed and evaluated in the field. Measurements were made relating to various seed cotton yield and fiber quality components. Results revealed significant differences for all the traits under study. The correlation among different pairs of plant traits in three crosses indicated that seed cotton yield can be improved by increasing number of bolls per plant and boll weight. Seed cotton yield has positive association with staple length and fiber fineness. Seed cotton yield and fiber strength showed negative association in three crosses indicating less gain through selection. The simultaneous improvement in fiber strength and seed cotton yield could be achieved through intermating in early generations along with selection of desirable segregants in the following generations and repeating the process till desirable results obtained. The simultaneous improvement in staple length and fiber strength seemed possible as observed from correlations among them in cross II (RH-1×NIAB-111) and cross III (4-F×MS-40).

Ahuja *et al.* (2006) reported that improvement in fibre length is important for the textile industry in utilizing high speed yarn spinning technology and in expanding the array of yarn products. High tensile strength fibre is needed for good spinning, especially with fast modern spinning machines. The usual practice of estimating correlation coefficients and the direct and indirect effects of component traits of seed cotton yield is without grouping the genetic material on the basis of fibre length and strength. Hence, the present investigation was carried out on these aspects by grouping the 20 F_1 hybrids into 3 sets on the basis of fibre length and strength, viz, (i) 10 hybrids of low fibre strength ($\leq$20 g tex^{-1}) and medium staple length ($\leq$25.0 mm), (ii) 10 hybrids of high fibre strength ($\geq$24 g tex^{-1}) and longer fibre length ($\geq$28 mm), and (iv) 20 hybrids, i.e. all the 10 hybrids of set 1 and set 2 of *Gossypium hirsutum* L. cotton for agronomic and fibre quality traits. Significant genotypic difference existed among the hybrids in all the sets for all the characters studied. The direction of association coefficient of the traits and direct effects on seed cotton yield differed for all the traits except for the number of bolls per plant, boll weight and fibre strength in set 1 and set 2. Set 1 gave the same direction of association with seed cotton yield as obtained in set 3 of usual practice except for the traits ginning out turn (GOT) and days to flowering, whereas set two gave similar information to the usual practice for the traits days to flowering, total bolls, boll weight and GOT, and differed for other traits. The present study, therefore, indicates that the hybrid population needs to be grouped on the basis of fibre length and fibre strength prior to estimation of correlation coefficients and direct and indirect effects of other traits on seed cotton yield.

Araújo *et al.* (2012) showed the relative contribution of agronomic and technological components on the fiber yield in upland cotton cultivars. The experiment was carried out with 11 upland cotton cultivars in a completely randomized blocks design with three replications.

Initially, we performed analysis of variance, with the F test at 5% probability for the effect of cultivar as fixed effects as well as block and environment effects as random. Then the values were ordered according to cluster test Scott-Knott, at 5% probability level. The significance of the null hypothesis that all possible canonical correlations are null was evaluated using the chi-square test. The correlations were estimated through the path analysis. By examining the canonical correlations there was dependence between the two groups of variables and therefore it is possible to promote changes in certain characteristics through the selection of others correlated. Plants of upland cotton with higher fiber yield were influenced by the decrease in average weight of the cotton boll. When there is a reduced fiber yield, there is also an increase in uniformity and strength thereof. The fiber resistance had negative indirect effects on the fiber uniformity and length.

Correlation studies conducted by Ashokkumar and Ravikesavan (2010) using 4 lines, 7 testers and their 28 made with parents F_1's of upland cotton (*Gossypium hirsutum* L.) revealed that seed cotton yield has positive significant correlation with days to fifty percent flowering, number of sympodia per plant, number of bolls per plant, boll weight, number of seed per boll, ginning out turn, lint index, seed index, and micronaire. In parents and hybrids, seed oil had negative correlation with seed cotton yield and days to first flowering. Seed oil had positive correlation with number of sympodia per plant, boll weight, number of seeds per boll, lint index, seed index and 2.5 percent span length. Path analysis revealed that boll weight, number of sympodia per plant, lint index and number of seeds per boll directly influenced the seed cotton yield with high direct effects. Seed oil influenced the seed cotton yield negatively. The result of this study indicate that sympodia per plant, boll weight, number of seeds per boll, lint index, seed index and 2.5 percent span length has been affected seed oil improvement in cotton. It was concluded that these characters should be considered as significant selection criteria for seed oil improvement in cotton.

Farooq *et al.* (2013) performed an experiment to find out genotypic, phenotypic correlation coefficients and path analysis at the genotypic level between seed cotton yield, earliness, fiber and yield contributing traits in 31 cotton cultivars under CLCuV intensive conditions. The material was sown on 15th of June to observe their tolerance ability against Cotton leaf curl virus and influence of late sown conditions on association among fiber, earliness and yield related traits. Heritability was estimated to determine the selection criteria under virus intensive conditions for the studied traits. Phenotypic coefficient of variation (PCV%) was higher in magnitude than the genotypic coefficient of variation (GCV%) for all the traits. Heritability (broad sense) revealed higher estimates of fiber strength (97%), CLCuV% (97%), fiber fineness (91%), yield kg/ha (91%), boll weight (90%), plant height (87%), bolls per plant (86%), days taken to 1st flower (84%), Days taken to 1st bud (82%) while for nodes to 1st fruiting branch (56%), staple length (46%), monopodia per plant (42%) moderate but for GOT% (32%) and sympodia per plant (28%) low estimates were found. Regarding correlation studies seed cotton yield had only positive genotypic association with bolls per plant, plant height and sympodia per plant. Path coefficient analysis results revealed that all the traits indirectly influenced seed cotton yield. The traits like plant height, bolls per plant and sympodia per plant may be considered for selection in virus intensive conditions as they showed higher estimates of broad sense heritability along with positive and significant genotypic correlation with seed cotton yield.

Ahmad *et al.* (2008) carried out a field trial to determine the genetic variability, correlation and regression coefficient of the seed cotton yield with various morphological and yield contributing traits in five upland cotton cultivars. The cultivars viz; CIM-473, CIM-496, CIM-499, CIM-506 and CIM-707 were sown in a randomized complete block (RCB) design with four replications at NWFP Agricultural University, Peshawar, Pakistan during May 2005. All the genotypes revealed highly significant differences (P_0.01) for monopodia and sympodia per plant, bolls per plant and seeds per boll, while the plant height, first internode length, boll weight and seed cotton yield per plant manifested significant variations among the cultivars. Boll per sympodia showed non-significant differences in mean values. All the parameters manifested positive correlation with seed cotton yield except monopodia per plant and first internode length. Cultivar CIM-499 performed well by having better boll set, early maturity and increased seed cotton yield, while other four cultivars were having statistically at par seed cotton yield. During future breeding programme the yield related traits may also be kept in mind during making selection as they were the major attributes of the seed cotton yield.

CHAPTER III

MATERIALS AND METHODS

Stable production of cotton is a major concern in rainfed and irrigated areas that are affected by different environmental factors. Growing adapted cultivars with high yield stability is an effective strategy for reducing environmental effects on production of seed cotton yield in different areas. To develop suitable cultivars, evaluation of improved genotypes is a critical phase in cotton breeding programs, because great numbers of genotypes need to be evaluated across locations over several years. Studying the response of genotypes under different conditions may significantly increase their productivity potential and performance. Therefore, plant breeders aim to develop new cotton cultivars that consistently have high yield in a variety of environments. The adaptability of a variety is usually tested by the degree of its interaction with different environments. A variety or genotype is considered to be more adaptive or stable if it has a high mean yield with low degree of fluctuation in yielding ability grown over diverse climatic conditions. Therefore, the present research works carried out in the Cotton Research, Training and Seed Multiplication Farm, Dinajpur (25°13´ N latitude and 88°23´E longitude at 37.5m altitude), Cotton Research Center, Mahiganj, Rangpur (25° 39′ N latitude and 89° 50′ E longitude at 34m altitude) and Cotton Research, Training and Seed Multiplication Farm, Jessore (23° 17′30″ N latitude and 89°4′57″ E longitude at 9m altitude) in every cropping season (July- March) from 2010-13. The experiments were sequentially completed according to the frame work of the study.

3.1 List of the experimental materials

A total of 20 genetically diverged genotypes of cotton (*Gossypium hirsutum* L.) were used in this study. The advanced generations were obtained from Cotton Development Board (CDB), Dhaka.

3.2 List of the experiments

Three experiments were conducted during the year from 2010 to 2015. The field trials were carried out in every cropping season in the speculated period of the investigation. The list of the experiments with their conducting seasons or time is presented in Table 3.1. In the first experiment of the investigation the inherent potential of the 20 lines under optimal condition was assessed for yield and yield contributing characters and then the other experiment was accordingly completed to conclude on the rational and real features of the selected 20 lines.

Table 3.1 List of the experiments

Expt. No.	**Name of the experiments**	**Period of completion**
I	Evaluation of 20 cotton genotypes	Cropping season (2010-2011)
II	Selection of stable and high seed cotton yielding lines.	Cropping season (2011-2014)
III	Assessment of quality traits in cotton	Cropping season (2014-2015)

3.3 Description of the experimental sites

3.3.1 Locations

Experiment I: Cotton Research, Training and Seed Multiplication Farms under Jessore, Dinajpur and Cotton Research Center, Mahiganj, Rangpur

Experiment II: Cotton Research, Training and Seed Multiplication Farms under Jessore, Dinajpur and Cotton Research Center, Mahiganj, Rangpur

Experiment IIII: Cotton Research, Training and Seed Multiplication Farms under Jessore, Dinajpur and Cotton Research Center, Mahiganj, Rangpur.

3.3.2 Climates and soils

The climates of the experimental sites were characterized by average temperature (^{0}C) and rainfall (mm) and the soils were characterized by p^H and texture. The detailed of climates and soils characteristics of the experimental sites are presented in Appendices X.

3.4 Experimental materials

The experimental materials for the experiments are presented in Table 3.2 including seventeen advanced lines and three check varieties. Qualitative characters of twenty genotypes are presented in Table 3.3.

Table 3.2 List of the selected advanced lines and three check varieties

Sl No	Name	Source of Collection
1	JA-08/A	Cotton Research, Training and Seed Multiplication Farm, Jessore
2	JA-08/B	
3	JA-08/C	
4	JA-08/D	
5	JA-08/E	
6	JA-08/9	
7	JA-0541	
8	JA-0510	
9	JA-054	
10	JA-0526	
11	BC-088	Cotton Research Center, Mahiganj, Rangpur
12	BC-0303	
13	BC-0406	
14	BC-051	
15	BC-0342	
16	BC-037	
17	BC-0188	
18	CB-9	Cotton Research, Training and Seed Multiplication Farm, Gazipur
19	CB-10	Cotton Research Center, Mahiganj, Rangpur
20	CB-11	Cotton Research, Training and Seed Multiplication Farm, Gazipur

Table 3.3 Qualitative characteristics of twenty cotton genotypes

Genotypes	Growth Habit	Colour of plant	Hairiness	Leaf shape	Petal colour	Petal spot	Pollen colour	Boll shape	Boll opening	Seed fuzz	Fuzz colour	Lint colour
JA-08/A	Erect	Green	Glabrous	Entire	Cream	Absent	Cream	Conical	Normal	Fuzzy	Grey	White
JA-08/B	Erect	Green	Glabrous	Entire	Cream	Absent	Cream	Oval	Normal	Fuzzy	Grey	White
JA-08/C	Erect	Green	Glabrous	Entire	Cream	Absent	Cream	Conical	Normal	Fuzzy	Grey	White
JA-08/D	Erect	Green	Short hair	Entire	Cream	Absent	Cream	Conical	Normal	Fuzzy	Grey	White
JA-08/E	Erect	Green	Glabrous	Entire	Cream	Absent	Cream	Conical	Normal	Fuzzy	Grey	White
JA-08/9	Erect	Green	Glabrous	Entire	White	Absent	Cream	Oval	Normal	Fuzzy	Grey	White
JA-0541	Erect	Green	Glabrous	Entire	White	Absent	Cream	Oval	Normal	Fuzzy	Grey	White
JA-0510	Erect	Green	Short hair	Entire	Cream	Absent	Cream	Oval	Normal	Fuzzy	Grey	White
JA-054	Erect	Green	Short hair	Entire	Cream	Absent	Yellow	Oval	Normal	Fuzzy	Grey	White
JA-0526	Erect	Green	Glabrous	Entire	Cream	Absent	Yellow	Conical	Normal	Fuzzy	Grey	White
BC-088	Erect	Green	Short hair	Entire	White	Absent	Cream	Conical	Normal	Fuzzy	Grey	White
BC-0303	Erect	Green	Short hair	Entire	Cream	Absent	Yellow	Conical	Normal	Fuzzy	Grey	White
BC-0406	Erect	Green	Glabrous	Entire	Cream	Absent	Cream	Oval	Normal	Fuzzy	Grey	White
BC-051	Erect	Green	Short hair	Entire	Cream	Absent	Cream	Conical	Normal	Fuzzy	Grey	White
BC-0342	Erect	Green	Glabrous	Entire	Cream	Absent	Yellow	Conical	Normal	Fuzzy	Grey	White
BC-037	Erect	Green	Short hair	Entire	Cream	Absent	Yellow	Oval	Normal	Fuzzy	Grey	White
BC-0188	Erect	Green	Glabrous	Entire	Cream	Absent	Cream	Conical	Normal	Fuzzy	Grey	White
CB-9	Erect	Green	Long hair	Entire	Cream	Absent	Cream	Conical	Normal	Fuzzy	Grey	White
CB-10	Erect	Green	Glabrous	Entire	Cream	Absent	Cream	Oval	Normal	Fuzzy	Grey	White
CB-11	Erect	Green	Glabrous	Entire	White	Absent	Cream	Conical	Normal	Fuzzy	Grey	White

3.5 Experimental design and layout

The field experiments were laid out in a RCBD with three replications. The plot size was 1.8 m x 5m. The row length was 5m long and 90 cm and 45 cm distances between rows and plants, respectively. The cultivars were randomly distributed to each of the plots within a block.

3.6 Field and other operations

3.6.1 Land preparation

The land was prepared by two ploughings and one cross ploughing with a tractor mounted disc plough. Three days later the land was again ploughed and cross ploughed with the country plough followed by laddering to get a good puddle condition. Weeds and stubbles were removed from the field prior to sowing of seeds. Manures and fertilizers were applied as per the recommended doses and irrigation channels were made around each block.

3.6.2 Seeds sowing

Experimental seeds were sown @ 8kg ha^{-1} in each location at July 15 in each cropping season.

3.6.3 Intercultural operations

The trials were conducted under irrigated condition. The following necessary intercultural operations were taken during entire cropping period for proper growth and development of the plants and to receive a good harvest.

3.6.3.1 Weeding

Weeding was done during first two side dressings of urea to break the soil crust, to keep the plots free from weeds and to incorporate the urea properly into the soil which reduced the loss of urea through de-nitrification and leaching.

3.6.3.2 Fertilizer Application

Fertilizers were applied @ 250-175-175-100-10-10-10-6000 kg ha^{-1} as Urea-TSP-MOP-Gypsum-Borax-Zinc Sulphate-$MgSO_4$-Cow dung, respectively (Table 3.4) as recommended by CDB (2010-11). The total cow dung was applied at the beginning of land preparation. The fertilizers such as Urea, TSP and MOP were applied in the row at the rate of 50, 125 and 45 Kg/ha, respectively at basal dose during the final land preparation. After three (3) weeks at 1st side dressing Urea, Gypsum and Zinc sulphate were applied at the rate of 50-30 and 10 Kg/ha, respectively. After six (6) weeks at 2nd side dressing Urea, TSP, MOP, Gypsum and Borax were applied at the rate of 50-50-50-30 and 10 Kg/ha. After nine (9) weeks at 3rd side dressing Urea, MOP, Gypsum and Magnesium sulphate were applied at the rate of 50,60,40 and 10 Kg/ha, respectively. Another Urea and MOP were applied at the rate of 50 and 20 Kg/ha in 4th side dressing (within 12 weeks).

Table 3.4 Rate and method of application of fertilizers and manures in the experiments

Fertilizers and Manures	Rate (Kg ha^{-1})	Application				
		Basal	3 WAS	6 WAS	9 WAS	12 WAS
Cowdung	6000	6000	-	-	-	-
Urea	250	50	50	50	50	50
TSP	175	125	-	50	-	-
MOP	175	45	-	50	60	20
Gypsum	100	-	30	30	40	
Zinc Sulphate	10	-	10	-	-	-
MgSO4	10	-	-	-	10	-
Borax	10	-	-	10	-	-

Source: CDB 2010-11 WAS = Week After Sowing

3.6.3.3 Irrigation

Experimental plots were irrigated twice at all the locations. 1st irrigation was done at 1st week of November and 2nd irrigation was done at 3rd week of November.

3.7 Harvesting

Maturity of bolls was determined when the bolls became 80% physiologically mature. The picking of seed cotton was done on 20-25 December when nearly 50-60% seed cotton were harvested. The second picking of seed cotton was done on 15-20 January when near about 25-30 % seed cotton were harvested and rest of the seed cotton were harvested on 15-20 February in the cropping seasons. The seed cotton were separately bundled, properly tagged and then brought to the threshing floor. The yield of seed cotton was recorded after thoroughly drying in the sun.

3.8 Processing

After harvesting, the seed cotton was carefully threshed, cleaned and sun dried to record the seed cotton yield (kg ha^{-1}). The seeds were adjusted to 12% moisture content for preservation. The dried seed cotton was brought to ginning machine. After ginning, the seed and fiber were separated from seed cotton.

3.8.1 Ginning process

The total process of ginning is described below-

1. Raw cotton from the storage hall is manually transported to an intake separator where the cotton is screened out and allowed to pass to the next machine. Modern separators have rotating sealed wheels and curved screens which permit the air currents to pass directly to a fan. The separation process involves equipment like the separator, feeding hopper, and fan with tubular air ducts.

2. After the seed cotton (raw cotton) is separated from foreign materials (possibly carried over from cotton farms and during transportation), it is then passed to a hot gas drier. Here the seed cotton that is damp or wet will be dried. If seed cotton is wet some of the lint will be cut by the saws or packed into small dense tufts. The saws may become so clogged that the gin will not run at all. Hot gas dryers can be by passed when ginning during dry weather.

3. Cleaners are types of machines having concave screens or grid bars utilizing beater cylinders and are frequently supplied with a down wash of hot air. Cleaners would, therefore, clean the seed cotton by threshing over screens.

4. Extractors are equipment that employ a toothed "carding" action on the locks of cotton in conjunction with stripper cylinders that beat off the hulls, burs and stems, while the lock passes into a doffing brush. Extractors perform functions of cleaning and extracting of large piece of foreign materials.

5. Cotton gins (ginneries) use mechanical forms of distribution between overhead machinery and the feeders on the gin stands. Each gin stand in a multiple of gin stands is supplied with all the cottons it can handle. Distributors thus supply cotton to all gin stands installed in the ginnery.

6. Feeders are devices, located over each gin stand, that supply the gin saws with regulated streams of clean, dry seed cotton. Feeder takes the form of regulated rollers with spiked drum and screen.

7. Ginning is the process of separating the seed from the lint. This is accomplished by gin saws. These are steel disks approximately 0.037 inch thick and provided with about seven teeth per inch of periphery. Improved huller gins use saws 12 inches in diameter, having from 264 to 282 teeth and running at speeds from 650 to 700 revolutions per minute for maximum capacity.

8. Ribs of tough, highly polished iron are used in cotton gins to form grids through which the saws may pass. Ginning ribs are spaced about 1/8 inch apart, so that the saws carrying the lint may pass while the seeds are excluded.

The cotton gins employ rotating brushes to remove the cottons from the saw teeth. After the seed is separated from the lint, it is discharged in to self-cleaning belt and then in to self-cleaning blowpipe systems. The lint removed from the saws is carried by air blast to the condenser, which consists essentially of a large roller covered with wire screen and smaller wooden roller. From the condenser, the cotton drops in to the press box, over the bottom of which has been spread bale bagging. As the cotton collects in the box, it is packed every minute or so by mechanical trampers. After enough has been accumulated to make approximately 750lbs bale, heavy pressure is applied by hydraulic press. When the cotton is under pressure, the bagging is fitted over the sides of the bale and six steel ties are put around it and fastened. Pressure is then released, and the cotton expands somewhat but is held firmly in a compact bale by the bagging and ties. The bale is now complete. The seed produced is bagged in hessian sacks and are dispatched to oil mills. The project is environmentally friendly since it does not emit any toxic chemicals.

3.9 Data Collection

In each experiment observations were recorded ten randomly selected plants from each genotype in each replication for the following characters according to guide line given by Cotton Development Board, Dhaka.

(1) Vegetative branches plant $^{-1}$: Total number of vegetative branches plant^{-1} was counted from randomly selected ten plants and then mean was obtained.

(2) Node number of first fruiting branches (NFB) plant $^{-1}$: Number of main stem node of first fruiting branches plant^{-1} was counted from randomly selected ten plants and then mean was obtained.

(3) Primary fruiting branches plant $^{-1}$: The branches which were originated from stem and directly bore flowers/boll. Total number of primary fruiting branches plant^{-1} was counted from randomly selected ten plants and then mean was obtained

(4) Secondary fruiting branches plant $^{-1}$: The branches which were originated from vegetative/monopodial branches. Total number of secondary fruiting branches plant^{-1} was counted from randomly selected ten plants and then mean was obtained

(5) Days to 1st flowering (50%): Number of days required to commence flowering in each plot against each genotype was recorded.

(6) Days to 1st boll splitting (50%): Number of days required to split 50% bolls of the plants in unit plot was recorded.

(7) Bolls plant^{-1}: Total number of bolls plant^{-1} was counted from randomly selected ten plants and then mean was obtained

(8) Un-burst bolls plant^{-1}: Total number of un-burst bolls plant^{-1} was counted from randomly selected ten plants and then mean was obtained

(9) Single boll weight (g): Randomly collected 10 open sundried bolls during second harvest from the middle four rows per unit plot were weighed and then calculated as average boll weight in g.

(10) Plant height (cm): It was estimated from base to top of the plant in cm.

(11) Seeds boll^{-1}: Number of seeds boll^{-1} was counted from ten randomly selected bolls and then made average to obtain mean seeds boll^{-1}.

(12) Seed cotton yield (kg ha^{-1}): After final harvest of seed cottons from harvesting area were sun dried and then weighed in Kg. Finally, it was converted to Kg ha^{-1}.

Quality traits

(13) Ginning out turn (GOT %): Proportion of fibre in seed cotton was measured and expressed in percentage.

$$GOT = \frac{\text{Wt.of Lint}}{\text{Wt.of Seed Cotton}} X\ 100$$

(14) Seed index (g): Counted 100 dried cotton seed after ginning and then weighed in g.

(15) Lint index (g): The ratio of lint to seed in seed cotton is expressed by lint index.

$$Lint\ Index = \frac{\text{Wt.of Lint}}{\text{Wt.of Seed}} X\ S.I. \quad \text{(S. I. = Wt. of 100 seed in g)}$$

(16) Fuzz grade: Measured on eye estimation use 1 to 10 grade (1 was very less and 10 was very high).

(17) Fibre length (mm): Length of fibre was measured at final harvest by Digital Fibrograph.

(18) Fibre strength (gm/ tax): Strength of fibre measured at final harvest by pressley by a strength tester.

(19) Micrinaire value: Fineness of lint was measured at final harvest by a micronaire.

3.10 Statistical analysis

3.10.1 Analysis of variance

Analysis of variance for each environment, combined analysis of variance across the tested environments and stability parameters: regression coefficient (bi) and Mean square deviations (s^2di) from linear regression were performed by using CROPSTAT, version 7.2.

3.10.2 Estimation of genotypic coefficient of variation and phenotypic coefficient of variation

According to formulae given by (Burton and De Vane, 1953) the genotypic and phenotypic coefficients of variation were calculated as follows.

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

σ_g = genotypic standard deviation

$\bar{x}$ = population mean

$$\text{Phenotypic coefficient of variance (PCV)} = \frac{\sigma_p \times 100}{\bar{x}}$$

Where

σ_p = phenotypic standard deviation

$\bar{x}$ = population mean

3.10.3 Estimation of heritability

Broad sense heritability of all characters was estimated by the formula used by Johnson *et al.* (1955) and Hanson *et al.* (1956).

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

Where

σ_g^2 = genotypic variance

σ_p^2 = phenotypic variance

3.10.4 Estimation of genetic advance

The expected genetic advance for different characters under selection was estimated by the formula as suggested by Comstock and Robinson (1952).

$$\text{GA} = \frac{\sigma_g^2}{\sigma_p^2} \times K.\sigma_p$$

3.10.5 Genotypic and phenotypic correlation coefficients

The genotypic and phenotypic correlation coefficients of yield and its different contributing characters were estimated by the following formulae given by Johnson *et al.* (1955) and Singh and Chaudhary (2010).

Genotypic correlation coefficient: $r_{g1.2} = \frac{Cov._{g1.2}}{\sqrt{\sigma^2\ g_1 \times \sigma^2\ g_2}}$

Where,

Cov.g $_{1.2}$ = genotypic covariance between the variables x_1 and x_2.

$\sigma^2 g_1$ = genotypic variance of the variable x_1

$\sigma^2 g_2$ = genotypic variance of the variable x_2

Similarly,

Phenotypic correlation of coefficient: $r_{p1.2} = \frac{Cov._{ph1.2}}{\sqrt{\sigma^2\ ph_1 \times \sigma^2\ ph_2}}$

Where,

Cov.ph$_{1.2}$ = phenotypic covariance between the variable x_1 and x_2

$\sigma^2 ph_1$ = phenotypic variance of the variable x_1

$\sigma^2 ph_2$ = phenotypic variance of the variable x_2

3.10.6 Partition of genotypic correlation coefficients of different characters

The genotypic correlation coefficients were partitioned into direct and indirect effects with the help of path coefficient analysis. One of the variables under study was taken as the dependent variable (effect), which was assumed to be influenced by the other characters called independent characters or variables (causes). The path coefficient was estimated by solving the following sets of simultaneous equations indicating the basic relationship between correlation and path coefficients (Cyprien and Kumar, 2011).

$r_{iy} = p_{iy} + r_{i1} p_{1y} + r_{i2} p_{2y} + \ldots + r_{i(i-1)} p_{iy}$; i= 1, 2, 3….., n

where *n* was the number of independent characters (causes); r_{1y} to r_{iy} denoted coefficients of correlation between causal factors 1 to *i* and dependent character y, $r_{1.2}$ to $r_{(i-1)i}$ the coefficients of correlation among all possible combinations of causal factors and p_{1y} to p_{iy} denote the direct effects of character *1* to *i* on character y. The indirect effect of the i^{th} variable through to the j^{th} variable on y (the dependent variable) was computed as $p_{iy} \times r_{ji}$.

3.10.7 Construction of selection indices

The application of selection indices used simultaneous selection of several characters and aimed at discriminating desirable from undesirable cultivars on the basis of their phenotypic performance (Smith, 1936). The genetic worth (H) of an individual was:

$H = a_1 G_1 + a_2 G_2 + \ldots + a_n G_n$

Where,

$G_1, G_2, \ldots, G_n$ were the genotypic values of individual characters and

$a_1, a_2, \ldots, a_n$ signify their relative economic importance.

Another function (I), based on the phenotypic performance of various selected characters was defined as:

$I = b_1 p_1 + b_2 p_2 + \ldots + b_n p_n$

Where,

$b_1, b_2, \ldots, b_n$ were estimated such that the correlation between H and I, i.e., r(H,I), became maximum.

Once such a function (I) was obtained, discrimination of desirable genotypes from undesirable ones is possible on the basis of phenotypic performance, i.e., $p_1, p_2, \ldots, p_n$ directly. After calculating the SI, the expected genetic gain through selection was predicted by the following formula:

[illegible]

Where,

Z/v = intensity of selection (i)

a_i = economic weightage

b_i = regression coefficient

G_{ij} = genotypic variance-covariance matrix

P_{ij} = phenotypic variance-covariance matrix

In population improvement programs, selection is based on the phenotypic evaluation of several characters that are frequently obtained from the means of several replications. This is carried out to minimize the influence of experimental error and thus increase the precision of those means.

When considering several traits at the same time, the genotypic worth (G_j) of each genotype for the various characters should be obtained (Baker, 1986), that is:

$$G_j = a_1G_{1j} + a_2G_{2j} + \ldots + a_mG_{mj} = \sum_{i}^{m} a_iG_{ij}$$

Where,

a_i corresponds to the relative weights attributed to the various characters according to their economic importance (FAO, 2012)

If the characters have different economic weights, different scales and are correlated, the index can be calculated as the sum of the characters times their heritability (h^2), their economical weight (w) and the factor transforming the characters to the same scale (f).

Hence, the mathematical type of the equation for SI is given as:

$$I_i = f_1w_1h_1^2x_{1i} + f_2w_2h_2^2x_{2i}$$

The aim of the index is to select for a genotypic value. However, this is not possible thus phenotypic values are used. It has to be determined how a weight vector has to be chosen to maximize the correlation between genotypic and phenotypic values (Cropscience.ch, 2011).

The collected data were compiled and tabulated in proper forms for statistical analysis. Analysis of variance was performed following an RCB (Randomized Complete Block) design with the help of a MSTAT-C program (Freed, 1986).

3.10.8 Stability analysis

Stability was determined by regression of the mean grain yield of individual genotypes on environmental index and calculating the deviation from the regression according to Eberhart and Russell (1966) as:

$$Yij=Ki + biIj +s2dij;$$

Where, Yij was the mean performance of ith variety in jth environment, Ki was the mean of ith variety over all environments; bi is the regression coefficient which measured the response of ith variety to varying environment; s2dij was deviation from regression of ith variety in the jth environment, and Ij was the environmental index of jth environment. Regression coefficient (bi) was considered as an indication of the response of the genotype to varying environment. If the regression coefficient was close to one (bi = 1.0), the genotype was adapted in all environments, genotypes with bi > 1.0 were more responsive or adapted to high yielding environments, whereas any genotype with bi significantly lower than 1.0 was adapted to low yielding environments. Both AMMI and Eberhart and Russel models were computed using Agrobase software (Agrobase, 2000).

3.10.9 Additive main effect and multiplicative interaction (AMMI) model

The additive main effect and multiplicative interaction (AMMI) analysis was performed using the model suggested by Crossa *et al.* (1991) as:

$$Yij = \mu + g\ i+ e\ j+ \Sigma n=1h\ \lambda n\ \alpha ni.\gamma nj +Rij.$$

Where Yij is the yield of the ith genotype in the jth environment, μ is the grand mean, gi is the mean of the ith genotype minus the grand mean, ej is the mean of the jth environment minus the grand mean, λn is the square root of the Eigen value of the principal component analysis (PCA) axis, αni and γnj are the principal component scores for PCA axis n of the ith genotype and jth environment and Rij is the residual effects. Accordingly, genotypes with low (regardless of the sign) IPCA scores showed general or wider adaptability, while those with high IPCA scores showed specific adaptability (Gauch and Zobel, 1996).

AMMI Stability Value (ASV): The ASV is the distance from the coordinate point to the origin in a two dimensional plot of IPCA1 scores against IPCA2 scores in the AMMI model (Purchase, 1997 and Kempthorne, 1957). Because the IPCA1 score contributes more to the G x E interaction sum of squares, a weighted value is needed. This was calculated for each genotype and each environment according to the relative contribution of IPCA1 to IPCA2

$$ASV = \sqrt{\left[\frac{IPCA1 sum\ of\ squre}{IPCA2\ sum\ of\ squre}(IPCA1\ score)\right]^2 + [IPCA2\ score]^2}$$

In effect the ASV is the distance from zero in a two dimensional scattergram of IPCA 1 (Interaction Principal Component Analysis axis 1) scores against IPCA 2 scores. Since the IPCA 1 score contributes more to G x E sum of squares, it has to be weighted by the proportional difference between IPCA 1 and IPCA 2 scores to compensate for the relative contribution of IPCA 1 and IPCA 2 total G x E sum of squares. The distance from zero is then determined by using the theorem of Pythagoras.

3.10.10 The concept of GGE

The concept of GGE originates from analysis of METs of crop cultivars. The yield of a cultivar (or any other measure of cultivar performance) in an environment is a mixed effect of genotype main effect (G), environment main effect (E), and genotype x environment interaction (GE). In normal METs, E accounts for 80% of the total yield variation, and G and GE each account for about 10% (Gauch and Zobel, 1996; Yan *et al.,* 2000). For the purpose of cultivar evaluation, however, only G and GE are relevant (Gauch and Zobel, 1996). Furthermore, both G and GE must be considered in cultivar evaluation, thus the term GGE was evolved (Yan *et al.,* 2000).

3.10.11 The Model for Constructing a GGE Biplot

The GGE biplot is a biplot that displays the GGE part of MET data. The basic model for a GGE biplot is

$$Yij - \bar{Y}j = \lambda_1 \xi j_1 \acute{\eta} j_1 + \lambda_2 \xi j_2 \acute{\eta} j_2 + \acute{\eta} ij$$

Where,

Yij is the average yield of genotype *i* in environment *j*

$\bar{Y}j$ is the average yield over all genotypes in environment j

λ_1 and λ_2 are the singular values for PC1 and PC2, respectively

ξj_1 and ξj_2 are the PC1 and PC2 scores, respectively for genotype i,

$\acute{\eta} j_1$ and $\acute{\eta} j_2$ are the PC1 and PC2 scores, respectively, for environment *j*

εij is the residual of the model associated with the genotype *i* in environment *j*

3.10.12 Principles of biplot analysis

Mathematically, a biplot may be regarded as a graphical display of matrix multiplication. Given a matrix G with m rows and r columns, and a matrix E with r rows and n columns, they can be multiplied to give a third matrix P with m rows and n columns. If $r = 2$, then matrix G can be displayed as m points in a 2-D plot, with the 1st column as the abscissa (x-axis) and 2nd column the ordinate (y-axis). Similarly, matrix E can be displayed as n points in a 2-D plot, with the 1st row as the abscissa and 2nd row the ordinate. A 2-D biplot is formed if the two plots are superimposed, which would contain $m + n$ points. An interesting property of this biplot is that it not only displays matrices G and E, but also implicitly displays the m x n values of matrix P, because each element of P can be visualized as:

$$P_{ij} = x_i x'_j + y_i y'_j = g_i \bar{e}_j = |g_i||e_j| \cos \theta_{ij}$$

Where (xi, yi) are the coordinates for row i and $(x'j, y'j)$ are coordinates for column j; g_i *is* the vector for row i and $\bar{e}_i$ is the vector for column j; $|g_i|$ is the vector length for row i and $|e_j|$ is the vector length for column j. θij is the angle between the vectors of row i and column j.

Equation is referred to as the inner-product property of the biplot. It is the most important property of a biplot. It not only allows each element of matrix P to be estimated but also constitutes the basis for visualizing the patterns in matrix P, including ranking the rows relative to any column, ranking the columns relative to any row, comparing any two rows relative to individual columns, identifying the rows with largest (or smallest) values for each column, or vice versa (Yan and Kang, 2003).

3.10.13 Singular Value Decomposition and Partitioning

The practical application of a biplot in data analysis was stated most clearly by the founder of biplot (Gabriel, 1971 and Gomez and Gomez, 1984): any two-way table can be graphically analyzed using a 2-D biplot as soon as it can be sufficiently approximated by a rank-2 (i.e., $r = 2$) matrix. Given a genotype by environment two-way table P of m genotypes and n environments, biplot analysis starts with its decomposition into three matrices G, L, and E, via SVD:

$$Pm\ n = Gm,rLr,\ rE^{T}{}_{n\ r}\ \ mn,\ (\ r \leq \mathrm{min}(\mathrm{m},\ \mathrm{n}\ ))$$

CHATER IV

RESULTS AND DISCUSSION

Cotton is an important commercial crop providing lint as a fiber to the textile industry. It is an important natural fiber crop of global importance and widely referred as ‘King of fibre crops’. The cotton occupies only 2% percent of the total area and contributes about 3% to the total production. Globally, India ranks first in cotton area but occupies second position in production, next to China. Lower productivity in Bangladesh is mainly due to cultivation of more than 75% of cotton under rainfed conditions besides non-adoption of quality seeds, nutrient management and plant protection measures.

4.1 Mean performances of seed cotton yield and its related characters

Seed cotton yield with other eleven characters were considered to furnish the interpretation of the investigation. All the characters differentially responded to locations over the years. Mean genotypic performance for seed cotton yield and its components tested through Duncun’s Multiple Range Test and is presented in Table 4.1. Data revealed that genotype JA 08/D displayed highest significant seed cotton yield (3430 kgha^{-1}) followed by JA-08/C (3329 kgha^{-1}) cm). It was further noted that eight genotypes responded differently in attaining higher seed cotton yield. This may be due to their genetic makeup which resulted in higher seed cotton yield. The significant differences in seed cotton yield might be due to high sink size and strength for withdrawing the food materials and accommodating capacity from photosynthesis. Environmental effects may also be one of the reasons, leading to produce more seed cotton yield by the genotypes suitable to the prevailing climatic conditions (Khan *et al.,* 1993).

4.2 Correlation and Path analysis

Among the 20 genotypes under investigation the highest CV (%) was estimated for seed cotton yield (18.94%) and the lowest for main stem nodes plant^{-1} (6.82%). The precision of entire experimental trial specially referring data recording was reflected by CV (%); lower value indicated good precision during sampling and data recording for a particular character, hence seed cotton yield proclaimed some sort of good precision (Table 4.1) However, three genotypes namely, JA-051, JA-0541 and JA-08/9 were early flowering genotypes but were low yield potential as compared to other genotypes. The highest seeds boll^{-1} (35.0) was recorded from JA-0526 and which was significantly different from other genotypes. With increasing the number of unbrust bolls plant^{-1}, seed cotton yield was reduced in each genotype. The highest seed cotton yield was obtained from the genotype JA-08/D with 3430 kg ha^{-1} followed by JA-08/C (3320 kg ha^{-1}) and JA-08/E (3226 kg ha^{-1}). The other genotypes produced average seed cotton yield (kg ha^{-1}). Quantitative trait like seed cotton yield being polygenic is a total sum of genetic illustration of all the yield components (Larik *et al.*, 1997) and is significantly affected by environmental factors (Khan *et al.*, 2007). The overall performance of a genotype may vary due to changes in environment and the higher the heritability, the simpler the selection process and greater the response to selection (Larik *et al.*, 1997 & 2000; Soomro *et al.*, 2008). Generally, high difference between GCV and PCV reflected the effect of environment with low heritability but if the concerned characters are under major genes controlled, high heritability even may obtain over the higher difference between GCV and PCV. The highest heritability (97.46%) was estimated for plant height but high heritability (90.36%) coupled with high genetic advance (59.27%) was calculated against bolls plant^{-1} suggesting better response to selection of this character.

The lowest heritability (h^2b=61.27%) was calculated in primary fruiting branches plant^{-1}. The magnitude of variability present in a crop species is of utmost importance as it provides the basis for effective selection. The variation present in a population is measured by phenotypic, genotypic coefficient of variation; heritability and genetic advance under selection help the plant breeder in selection of elite genotypes from diverse genetic populations. and having broad genetic base. However, difference between GCV and PCV was high for the character, seed cotton yield (205.43-330.12), which were followed by days to1st boll splitting (65.94-80.45) and plant height (60.32-72.45), suggested that these three characters might affect by environmental fluctuation, hence direct selection would not be fruitful for improving seed cotton yield among the genotypes (Table 4.2) High heritability was estimated against plant height (h^2b=97.46%), followed by seeds boll^{-1} (96.48%) and boll weight (90.45%). Low heritability was measured for primary fruiting branches (61.27%). Since high heritability along with high genetic advance might provide better response in next generation for improving the character through selection, so bolls plant^{-1}, seeds boll^{-1} and seed cotton yield could obviously consider to get gain through selection for improving existing expression potentials of these characters.

The correlation co-efficient provide a reliable measure of association among the characters and help to differentiate vital associates useful in breeding from those of the non vital ones (Falconer, 1981).The genotypic correlation co-efficient between seed cotton yield with other eleven biometric characters and interpaired combinations of the characters were worked out and presented in Table 4.3. In order to enhance the yield potential of cotton varieties, an understanding of the relationship among different plant character is of more importance, besides, knowledge about the direct contribution of different characters to seed cotton yield would be highly important for formulating a selection program.

The study on genotypic and phenotypic correlation coefficients has as main goal the identification and quantification of the linear relationships between two sets of multiple variables, metrics or not. Several authors (Ashokkuma and Ravikesavan, 2010; Rao and Gopinath, 2013 and Farooq *et al.,* 2014) and argued that the great advantage of this technique is the possibility to assist the breeders in the study involving more than one dependent variables, allowing the efforts to select the traits having high heritability, easily measured, and with lower complexity in the quality cotton production breeding. The cotton breeding includes several agronomic traits, whose association may interfere in the selection process. The canonical correlations among these traits are not well addressed in this crop, justifying the importance of this study. The knowledge of these correlations allows measuring the magnitude of the relationship between several traits of the plant and determines the trait on which the selection can be based, to improve seed cotton yield.

The correlation analysis is a multivariate statistics procedure that allows examining the relationships between two sets of variables (X and Y). This analysis is widely used in exploratory studies by researchers who have a large number of variables, but are able to study those linear combinations whose correlation is higher. In light of these information, a total of 55 pairs of combinations among 12 characters were drawn both a genotypic and phenotypic levels. In general, genotypic correlation coefficient (rg) was higher than corresponding phenotypic correlation coefficient (r_p) for any pair of character combination, indicating inherent association among the combinations (Table 4.3). Vegetative branches plant^{-1} and unbrust bolls plant^{-1} showed negative and significant correlations with seed cotton yield (kg ha^{-1}) both at genotypic and phenotypic levels, suggested impediment effects of the two characters of seed cotton yield. Among the 12 characters under study secondary fruiting branches plant^{-1}, main stem nodes plant^{-1}, days to 1st flowering, bolls plant^{-1}, boll weight and seeds boll^{-1} exhibited positive and significant correlations with seed cotton yield (kg ha^{-1}). Therefore, these characters might selected for improving seed cotton yield through discriminant function analysis or might consider as important characters during selection of parents for hybridization. The correlation analysis provides a good index to predict the corresponding change which occurs in one trait at the expanse of the proportionate change in the other (Khan *et al*., 2007; Ahmad *et al*., 2008). Taohua and Haipeng (2006) and Meena *et al.* (2007) studied the adaptability and stability of *Gossypium hirsutum* varieties and observed diverse values for different agronomic, morphological and yield related traits.

Iqbal *et al.* (2003) and Wang *et al.* (2004) found genetic variation and positive correlation for seed cotton yield and yield components in *G. hirsutum.* Performance and positive association of seed cotton yield with yield components was observed in *hirsutum* cultivars (Mendez-Natera *et al*., 2012). Khan *et al.* (1999) and Khan (2003) found high genetic variability for yield and yield components in cotton. Khan *et al.* (2000) studied the earliness and agronomic traits of upland cotton cultivars using correlation analysis and found that monopodia had a negative direct effect on yield. Jost and Cothren (2000) and Badr (2003) also studied earliness and other yield contributing traits in different cotton cultivars and observed varied performance. DeGui *et al.* (2003) studied yield and yield components and found that the higher yield in cotton cultivars was mainly due to more number of bolls per plant. For a simultaneous selection of both yield and fiber quality traits, knowledge about association of yield and fiber quality traits is a prerequisite. The present study was designed to explore the genetic potential of different cotton cultivars and relationship of seed cotton yield with different seed cotton yield contributing characters.

Table 4.1 Mean performances of different characters in 20 genotypes of cotton at three locations

Genotypes	VB/P	PFB/P	SFB/P	MSN/P	DFF	DFBS	B/P	BW (g)	UBB/P	PH (cm)	S/B	SCY (kg ha^{-1})
JA-08/A	1.93	14.47	11.20	6.23	53	103	33.5	4.74	1.4	106.37	27.9	3012
JA-08/B	1.60	13.43	9.53	6.00	50	105	26.7	5.03	1.8	96.60	24.6	2641
JA-08/C	1.87	14.67	8.13	6.23	51	106	31.5	6.17	1.4	101.73	29.9	3329
JA-08/D	4.27	26.00	21.33	7.13	51	109	33.2	4.93	1.4	108.73	28.2	3430
JA-08/E	1.80	15.40	8.07	6.40	53	107	31.0	5.51	1.6	94.33	28.1	3226
JA-0541	1.47	17.37	9.50	6.07	49	108	28.2	5.46	1.5	110.07	25.5	2711
JA-08/9	1.40	17.23	6.53	5.27	48	102	31.7	4.17	2.3	91.80	26.8	2904
JA-054	1.53	14.93	9.03	5.73	51	105	24.9	5.80	1.6	101.33	26,0	2810
JA-0526	2.33	19.07	13.53	6.23	52	104	30.0	5.27	1.6	108.33	35.0	2703
JA-0510	1.97	15.10	9.00	5.93	50	104	25.0	4.75	1.0	102.13	26.3	2799
BC-088	2.30	21.97	13.50	6.33	50	106	29.0	4.95	1.5	131.20	25.0	2703
BC-0303	2.57	20.17	12.17	6.40	53	109	33.0	4.49	1.2	116.47	22,9	2580
BC-0406	3.20	22.50	16.23	6.53	51	107	37.9	4.47	1.8	130.93	27.4	3089
BC-051	2.03	16.60	13.23	6.33	47	104	34.5	4.33	1.6	118.73	25.6	2969
BC-0342	2.77	20.10	16.57	7.03	51	106	29.9	5.40	1.2	130.00	27.1	2973
BC-037	2.67	21.87	13.47	6.40	56	109	32.4	4.99	1.9	128.80	23.0	2466
BC-0188	2.13	22.17	15.13	6.73	53	107	32.7	4.36	1.5	131.27	26.5	2758
CB-9	3.17	21.20	14.73	7.73	56	115	25.6	5.97	1,5	104.70	23.3	2389
CB-10	2.63	23.33	15.50	6.57	50	116	33.4	5.07	1.7	118.67	27.0	3205
CB-11	0.67	16.13	6.63	6.27	50	105	26.9	5.34	1.5	119.73	23.3	2483
CV (%)	12.36	14.70	9.56	6.82	7.17	11.24	9.98	7.53	15.67	15.69	8.22	18.94
LSD	0.97	5.27	3.16	0.85	0.98	0.65	4.83	0.64	0.47	10.22	2.05	504.68

VB/P =Vegetative branches plant $^{-1}$ MSN/P =Main stem node plant $^{-1}$, ' PFB/P= Primary fruiting branches plant $^{-1}$,SFB/P =Secondary fruiting branches plant $^{-1}$,DFF =Days to 1st flowering (50%), DFBS= Days to 1st boll splitting (50%), B/P= Bolls plant^{-1} Un-burst bolls plant^{-1} 'BW = Boll weight (g) , PH =Plant height (cm), S/B =Seeds boll^{-1} , SCY= Seed cotton yield (kg ha^{-1})

Table 4.2 Genetic parameters of different characters in 20 genotypes of cotton at three locations

Characters		VB/P	PFB/P	SFB/P	MSN/P	DFF	DFBS	B/P	BW (g)	UBB/P	PH(cm)	S/B	SCY (kg ha^{-1})
Mean range	Min.	0.67	13.43	6.63	5.27	47	102	24.9	4.17	1.0	91.80	23	2466
	Max.	4.27	26.00	21.33	7.33	56	116	37.9	5.97	2.3	131.27	29.9	3430
GCV(%)		7.93	24.21	17.36	9.47	34.97	65.94	26.94	6.40	2.49	60.92	44.50	205.43
PCV(%)		8.36	26.42	23.54	10.73	39.05	80.45	28.60	7.30	2.96	72.45	49.48	330.12
h^2b (%)		78.35	61.27	82,63	85.45	84.96	87.40	90.36	96.45	85.35	97.46	96.48	83.58
GA		34.62	25.49	26.36	46,49	58.39	49.58	59.46	10.32	46.64	39.56	24.59	48.54
GAM(%)		21.50	7.35	35.30	9.94	23.60	32.46	39.57	48.39	17.48	9.42	60.35	30.73

GCV=Genotypic coefficient of variation, PCV=Phenotypic coefficient of variation, h^2b= Heritability in broad sense, GA=Genetic advance and GAM=Genetic advance as % of mean

VB/P =Vegetative branches plant $^{-1}$ MSN/P =Main stem node plant $^{-1}$, ' PFB/P= Primary fruiting branches plant $^{-1}$,SFB/P =Secondary fruiting branches plant $^{-1}$,DFF =Days to 1st flowering (50%), DFBS= Days to 1st boll splitting (50%), B/P= Bolls plant^{-1} Un-burst bolls plant^{-1} 'BW = Boll weight (g) , PH =Plant height (cm), S/B =Seeds boll^{-1} , SCY= Seed cotton yield (kg ha^{-}

Table 4.3 Genotypic (r_g) and phenotypic (r_p) correlation coefficients in all possible pair characters of cotton at three locations

	r	VB/P	PFB/P	SFB/P	MSN/P	DFF	DFBS	B/P	BW	UBB/P	PH	S/B	SCY
VB/P	r_g	**1.00**	-0.240	0.763 **	0.281	-0.563*	0.094	-0. 783**	0.438	-0.820**	0.095	0.275	-0850.**
	r_p	**1.00**	-0.221	0. 710**	0.259	-0.529*	0.087	-0730**	0.320	-0.794 **	0.088	0.251	-0801**.
PFB/P	r_g		**1.00**	-0.009	0.105	0.220	-0.489	0.390	0.390	0.007	0382.	0.117	0.474
	r_p		**1.00**	-0.003	0.096	0.187	-0.453	0.299	0. 354	0.006	0.321	0.111	0.457
SFB/P	r_g			**1.00**	0.304	-0.132	0.094	0.190	0.667.**	0.109	0.311	0.680**	0.889**
	r_p			**1.00**	0.295	-0.123	0.092	0.153	0.651.**	0.099	0.275	0.653.**	0.875**
MSN/P	r_g				**1.00**	0.774**	0.874**	0.136	0.082	0.472	0.768**	0.099	0.843**
	r_p				**1.00**	0.583*	0.827**	0.119	0.079	0.459	0.717**	0.093	0818.**
DFF	r_g					**1.00**	0.651**	0.765**	0.212	-0.009	0.348	0.231	0775. **
	r_p					**1.00**	0.650**	0732.**	0.200	-0.008	0.333	0.202	0.749**
DFBS	r_g						**1.00**	-0.107	0.357	0.273	0.110	0.200	0.273
	r_p						**1.00**	-0.100	0.355	0.272	0.101	0.197	0.259
B/P	rg							**1.00**	-0. 684**	0.795**	0.280	0.239	0.786**
	r_p							**1.00**	-0 666.**	0.784**	0.276	0.224	0.779**
BW	r_g								**1.00**	0.240	0.163	0.793**	0.689**
	r_p								**1.00**	0.236	0.154	0.768**	0.675**
UBB/P	r_g									**1.00**	0.300	0.107	-0.681**
	r_p									**1.00**	0.289	0.097	-0.664**
PH	r_g										**1.00**	0.361	0.351
	r_p										**1.00**	0.358	0.334
S/B	r_g											**1.00**	0.693.**
	r_p											**1.00**	0.678**
SCY	r_g												**1.00**
	r_p												**1.00**

* and ** indicate significant at 5% and 1% levels of probability, respectively.

VB/P =Vegetative branches plant $^{-1}$ MSN/P =Main stem node plant $^{-1}$, ' PFB/P= Primary fruiting branches plant $^{-1}$,SFB/P =Secondary fruiting branches plant $^{-1}$,DFF =Days to 1st flowering (50%), DFBS= Days to 1st boll splitting (50%), B/P= Bolls plant^{-1} Un-burst bolls plant^{-1} 'BW = Boll weight (g) , PH =Plant height (cm), S/B =Seeds boll^{-1} , SCY= Seed cotton yield (kg ha^{-1})

In order to enhance the yield potential of cotton varieties, an understanding of the relationship among different plant character is of more importance, besides, knowledge about the direct contribution of different characters to seed cotton yield would be highly important for formulating a selection program. The present investigation was carried out to obtain the information on correlations and direct and indirect effects of different attributes on seed cotton yield for utilization in the improvement of crop. Whatever, the highest direct effect (1.982) was paid by seeds boll^{-1}, which were followed by boll weight (1.568) and bolls plant^{-1} (1.526) (Table 4.4). The results suggested that these three characters were more influential to enhance seed cotton yield by contributing positive effects at genotypic level. Further, it is noted that none of the seed cotton yield contributing characters had not counter balance effect to modify the positive and significant correlation at genotypic level. Two characters namely, vegetative branches plant^{-1} and unbrust bolls plant^{-1} had negative direct effects, (-0.734) and (-0.872) respectively for the development of negative correlation coefficients with seed cotton yield. Other characters even failed to modify the negative direct effects of the two characters via indirect effects. Hence, seed boll^{-1}, boll weight and bolls plant^{-1} appeared as the more important seed cotton yield promoting characters and therefore, cotton breeders could exploit these characters for sustainable improvement in cotton. Path coefficients have been used to develop selection criteria for complex traits in several crop species (Wright 1921; Dewey & Lu, 1959; Fonseca & Patterson, 1968; Bhatt, 1973; Pandey & Torrie, 1973; Ivanovic & Kang *et al.,* 1983; Rosic, 1985; Gravois *et al.,* 1991; Diz *et al.,* 1994). Aiming to better understand the reasons involved in the association of characters, Wright (1921) proposed a method of unfolding the correlations into direct and indirect effects of the variables on a base variable, called path analysis, which measures the direct influence of one variable on another that is independent of the others. Then the path analysis can be done from phenotypic, genetic or environmental correlations (Cruz, 2001). Partitioning of correlations into cause and effects were furnished by several authors in different crops (Silva *et al.,* 2005; Amorim *et al*., 2008) and the method was applied by Tyagi *et al.*(1998) and Iqbal *et al.* (2003) in cotton.

Table 4.4 Path analysis at genotypic level of different characters in cotton

Characters	VB/P	PFB/P	SFB/P	MSN/P	DFF	DFBS	B/P	BW	UBB/P	PH	S/B	r_g with SCY
VB/P	**-0.754**	-0.410	0.280	0.525	0.209	-0.518	-0.362	-0.127	0.423	0.306	-0.422	-0.850**
PFB/P	-0.375	**0.149**	0.097	0.130	0.102	0.138	0.321	0.030	-0.220	-0.198	0.300	0.474
SFB/P	-0.643	0.172	**1.384**	0.277	-0.407	-0.768	0.409	-0.087	-0.557	0.626	0.503	0.889**
MSN/P	0.256	0.062	0.202	**0.163**	-0.145	-0.100	0.107	0.008	0.048	0.137	0.105	0.843**
DFF	-0.479	0.270	0.020	-0.286	**0.597**	0.518	0.291	0.135	-0.593	0.041	0.261	0.775 **
DFBS	-0.175	0.048	0.105	-0.229	0.200	**0.328**	0.261	-0.194	-0.251	0.056	0.124	0.273
B/P	-0.267	0.129	0.154	0.038	0.303	-0.389	**1.526**	-0.472	-0.150	0.171	-0.257	0.786**
BW	-0.365	0.208	0.122	-0.338	0.050	-0.487	-0.673	**1.568**	-0.290	0.243	0.651	0.689**
UBB/P	0.052	0.073	-0.104	0.111	-0.278	0.168	0.129	-0.205	**-0.872**	0.106	0.139	-0.681**
PH	-0.189	0.155	0.004	0.216	-0.316	0.107	-0.152	0.070	0.144	**0.104**	0.218	0.351
S/B	-0.156	0.263	0.105	-0.587	0.120	-0.456	-0.731	0.198	-0.149	0.104	**1.982**	0.693.**

Residual effect= 0.153

VB/P: Vegetative branches/plant, **PFB/P:** Primary fruiting branches/plant, **SFB/P:** Secondary fruiting branches/plant,

MSN/P: Main stem node/plant, **DFF:** Days to 1st flowering, **DFBS:** Days to 1st boll split, **B/P:** Bolls/plant, **BW:** Boll weight,

UBB/P: Unbrust bolls/plant, **PH:** Plant height, **S/B:** Seeds/boll, **SCY:** Seed cotton yield

4.3 Construction of selection indices

A total of 30 selection indices were constructed considering the most seed cotton yield enhancing characters. The five characters were selected based on their genetic parameters specially heritability in broad sense with genetic advance, genotypic and phenotypic correlation coefficients and path coefficient analysis of genotypic correlation coefficients of 11 characters with seed cotton yield as presented in Table 4.5. In conventional breeding usually a breeder pays attention to improve the ultimate character like seed cotton yield by simple selection or selection after hybridization. Since seed cotton yield is a complex character and contributed by several morpho-physiological characters. However, genetic worth and relative efficiency over straight selection was assessed on the selection indices.

4.3.1 Single character selection indices

Seed cotton yield (kg ha^{-1}) was considered as 100 and on which other indices were estimated. The expected genetic worth through direct selection of seed cotton yield was only 13.56. Therefore, there was scope of improvement on cotton through discriminant function analysis. The five characters under selection indices were days to 1st flowering, bolls plant^{-1}, boll weight, seeds boll^{-1} and seed cotton yield. As a single characters function, no doubt genetic worth was the highest for selection of seed cotton yield alone, which was followed by seeds boll^{-1} with relative efficiency over straight selection for seed cotton yield was 84.66%. The beneficial character was boll weight with relative efficiency of 78.24%. The results suggested that to obtain sustainable improvement of seed cotton yield breeders might apply simultaneous selection rather than single character selection in cotton.

4.3.2 Two character selection indices

Ten selection indices were developed considering all possible combinations of three characters at a time in the function. Four combinations included seed cotton yield, of which the highest relative over straight selection was observed from the index, I_{15} (index comprised with seed cotton yield and seeds boll^{-1}), thus the highest relative efficiency (110.62%) implied necessity of inclusion seeds boll^{-1} along with seed cotton yield in the integrated function. Excluding seed cotton yield, the highest genetic worth (16.09%) was realized by the combination boll weight and seeds boll^{-1} in index functions. The alternative choice of two character function excluding seed cotton yield was I_{35} (selection index comprised with bolls plant^{-1} and seeds boll^{-1}). Under uncertain environmental condition breeders might apply theses option to construct selection for improvement of cotton. It is further observed that any the two characters integrating functions yielded higher genetic worth and relative efficiency as compared to any of the single character functions. Hence, seed cotton yield enhancing characters need to include in functional analysis to construct selection indices.

4.3.3 Three character selection indices

Ten selection indices were constructed taking all possible combinations of three characters. Of the ten indices, six indices included seed cotton yield and in which the highest relative efficiency over straight selection (151.62%) was estimated in the function, I_{135} (seed cotton yield + bolls plant^{-1} + seeds boll^{-1}). Four selection functions didn't include seed cotton yield but appreciable genetic worth (19.78%) and relative efficiency (145.87%) were received from the function I_{345} (bolls plant^{-1} + boll weight + seeds boll^{-1}). When seed cotton yield assumes to be affected by adverse and unavoidable environments then the function, I_{345} might follow to improve cotton; otherwise the function like I_{135} should be judicial for sustainable improvement in cotton. It has not possible to identify individual traits that enhance seed cotton yield universally in relatively limited genetic and environmental situations. Therefore, selection indices still remain the biggest challenge so far for the improvement of seed cotton yield.

4.3.4 Four character selection indices

Four selection functions were built up taking account of all possible combinations. The highest genetic worth (20.98%) and the highest relative efficiency over direct selection were realized from I_{1245} function (seed cotton yield+ days to 1st flowering +boll weight +seeds boll^{-1}), followed by I_{2345} with 20.97% and 154.65% genetic worth and relative efficiency over straight selection for seed cotton yield respectively. Breeding for selection index aimed to enhance genetic potential by including important character to perform its optimum level. Thus, the breeders don't select seed cotton yield *per se*. In addition, the goal for increasing seed cotton yield to be improved by proper phenotypic expression of each of the characters integrated in the selection functions. The characters included in the selection indices were generally morphological, but physiological, biochemical and phonological characters should also be included.

4.3.5 Five character selection index

Only one selection index, I_{12345} was constructed taking five characters in the function. Relative efficiency over direct selection for seed cotton yield had increased with corresponding inclusion of more characters in the functions. However, the maximum genetic worth and relative efficiency over direct selection was realized by the five characters included function. The net gain from the I_{12345} was 157.22%.

A conventional plant breeder doesn’t encourage thinking of accumulation of more characters in the selection function, since the main objective of conventional breeding is to improvement of seed cotton yield. However, if the breeders have to pay more attention of each and every character then maximum genetic gain might achieve by considering the selected five characters in the construction of fruitful selection index.

Artificial selection is usually performed for multiple traits in order to select the best individual. In breeding practice, several strategies, such as tandem selection, independent culling, and index selection, can be applied to achieve this target. Theoretically, the selection index is never inferior to the other two methods (Young, 1961).

Selection index theory was firstly developed by Smith (1936) in plants and Hazel (1943) in living beings, which is generally called Smith-Hazel index now. Usually, the traits examined in the selection indices are controlled by nuclear genome (Geidel *et al*., 2000; Jannink *et al.,* 2000), while extra nuclear effects were seldom considered in this process. Also, the breeding value in the Smith-Hazel index is simply considered as additive effect for improvement of ultimate economic character in crop plants.

Table 4.5 Construction of selection indices in cotton

Index selection	Expected genetic worth	Relative efficiency over straight selection (%)
I_1=0.582 x_1	13.56	100.00
I_2=0.309 x_2	7.32	53.98
I_3=0.281 x_3	9.30	68.58
I_4=0.284 x_4	10.61	78.24
I_5=0.841x_5	11.48	84.66
I_{12}=0.481 x_1+0.459 x_2	14.34	105.75
I_{13}=0.252 x_1+0.480 x_3	14.87	109.66
I_{14}=0.376 x_1+0.978 x_4	14.95	110.25
I_{15}=0.597x_1+0.093 x_5	15.00	110.62
I_{23}=0.457 x_2+0.273 x_3	14.68	108.26
I_{24}=0.715x_2+0.783x_4	15.12	111.50
I_{25}=0.712 x_2+0.189 x_5	14.19	104.65
I_{34}=0.378 x_3+0.268 x_4	14.57	107.45
I_{35}=0.935x_3+0.837x_5	15.58	114.90
I_{45}=.982 x_4+0.579 x_5	16.09	118.66
I_{123}=0.357 x_1+ 0.582 x_2 +0.631 x_3	17.45	128.69
I_{124}=0.890 x_1+0.368 x_2+0.231 x_4	17.85	131.64
I_{125}=0.376 x_1+0.794 x_2+0.257x_5	17.93	132.23
I_{134}=0.598 x_1+1.471x_3+0.683 x_4	18.22	134.37
I_{135}=0.523 x_1+1.023 x_3+0.886 x_5	18.69	151.62
I_{145}=0.099x_1+0.685 x_4+0.780 x_5	19.54	144.10
I_{234}=0.680 x_2+0.572 x_3+0.780 x_4	18.83	138.86

Table 4.5 Construction of selection indices in cotton (cont'd)

Index selection	Expected genetic worth	Relative efficiency over straight selection (%)
I_{235}=0.571x_2+0.569 x_3+ 0.271 x_5	17.98	132.60
I_{245}=0.532 x_2+0.893 x_4+0.951 x_5	18.74	138.20
I_{345}=0.580 x_3+0.589 x_4+0.436 x_5	19.78	145.87
I_{1234}=0.562 x_1+0.537x_2+0.458 x_3+0.762 x_4	19.85	146.39
I_{1235}=0.379x_1+0.678 x_2+0.365 x_3+0.386 x_5	20.79	153.32
I_{1245}=0.589 x_1+0.379 x_2+0.893x_4+0.725 x_5	20.98	154.72
I_{2345}=0.572 x_2+0.785 x_3+0.470 x_4+0376 x_5	20.97	154.65
I_{12345}=0.673 x_1+0.786 x_2+0.575 x_3+0.689 x_4+0.358 x_5	21.36	157.22

x_1= Seed cotton yield, x_2=Days to 1st flowering, x_3=Bolls plant^{-1}, x_4=Boll weight and x_5= Seeds boll^{-1}.

Improvement of cotton yield and fiber characteristics is still the ultimate aim of most breeding programs of Egyptian cotton. Knowledge of the type and magnitude of genetic variability affecting important economical traits in cotton is essential for the development of efficient selection and breeding procedures. The phenotypic and genotypic coefficients of variation are important parameters for plant breeders inbreeding programs, particularly aiming for selecting better types from populations (Falconer and Macky, 1996 and Meena *et al.,* 2001).

Since yield is known to be a complex trait and highly affected by environmental conditions, thus, direct selection for yield is not expected to be effective. Therefore, the breeder avoids selection for yield and prefers to select for its components individually. The choice of selection and breeding procedures for genetic improvement of cotton or any crop is largely conditioned by the type and relative amount of genetic variance component in the population. The exploitation of genetically diverse stock in cross combinations helps to identify promising hybrids and/or to develop superior lines.

The associations between yield components and fiber characteristics are very important for cotton breeders. The value of the final product is determined by quality characteristics and high yielding genotypes will be low economic value if its fiber properties are not acceptable. Many studies have been carried out to determine the nature and magnitude of these associations in cotton (EL Siddig *et al.,* 2004, Desalegn *et al.,* 2009, Erande *et al.,* 2014 and Farooq *et al.,* 2014).

Since plant breeders must be concerned with the total array of economic characteristics and not just one trait, the importance of know how changes in one character by selection may cause simultaneous changes in other economic traits is self-evident. In their continuous efforts to improve both yield and fiber quality attributes, cotton breeders have realized the presence of either favorable or unfavorable associations between such major attributes.

El-Lawendey and El-Dahan (2012) studied phenotypic (PCV) and genotypic (GCV) coefficients of variability and the obtained data indicated that values of PCV and GCV were close to each other for most characters due to the high calculated estimates of genotypic variances. Abd El- Hafez *et al.* (2003) showed a decrease in phenotypic coefficients of variation from different cross generations and from self generations for all quatitative characters. However, genotypic coefficients of variation would give the best indication of the amount of genetic variance to be expected from selection; this is with agreement too (AL-Ameer 2004 and El-Mansy, 2009). Gooda (2001) found that the maximum predicted genetic advance in lint yield / plant was obtained from direct phenotypic selection for yield alone.

Six different kinds of insects like, jassid, plant bug, bollworm, aphids, thrips and whitefly were scouted in the field during growing season and among them jassid were very dangerous and secondly aphid was dangerous that acted as a vector for virus (Table 4.6). When the degree of infestation was estimated, the genotype JA-08/D appeared as highly resistant any of the visiting insects. Both infested leaves plant^{-1} (%) and infested bolls plant^{-1} were counted lower in the genotypes JA-08/A and JA-08/B. Among the 20 cotton genotypes, the highest infested bolls plant^{-1} (24.55%) was estimated in BC0303, followed by JA-0510 (23.20%) and

Table 4.6 Insect scouting method in cotton field

Insects	Scouting method
Bollworm	Randomly selected individual plants and examined carefully for presence of eggs or small (less than 1/2 inch long) larvae. Concentrate scouting primarily on the terminal area and the upper 8 to 12 inches of the plant. Eggs were usually deposited in the terminal bud or on the upper surface of newly expanded leaves, but also be sure to check for presence on eggs on outer square bracts.
Jassid	Jassid was scouted by randomly selecting expanded leaves. It attacks at the lower surface of leaves.
Aphids	When scouting for aphids, it was important to note any additional stress factors that might be affecting the crop and to be aware of predators, parasites, and pathogens that might be affecting the aphid population. Scouted by randomly selecting fully expanded leaves.
Whitefly	Scout for whiteflies by examining plant terminals and undersides of upper leaves for presence of adult and/or immature. Recorded counts as percent of terminals infested.
Thrips	Primarily a pest of seedling cotton, 4th leaf stage or younger: Examined whole seedlings for presence of thrips, concentrating on undersides of leaves and in terminal area.
Plant bug	Adult plant bugs were best quantified by using a 15 inch diameter sweep net. It needed to take several 25 sweep samples per field and recorded results as average number of plant bugs per 100 sweeps.

Table 4.7 Insect infestation in cotton twenty genotypes

Genotypes	NIP	NLP	NILP	ILPP	NBP	NIBP	IBPP
JA-08/A	4	145.35	3.7	2.55	33.5	1.8	5.37
JA-08/B	5	140.67	2.8	1.99	26.7	1.5	5.62
JA-08/C	3	145.90	4.9	3.36	31.5	2.0	6.35
JA-08/D	2	152.64	0.0	0.00	33.2	0.0	0.00
JA-08/E	2	148.78	7.3	4.91	31.0	2.2	7.00
JA-0541	5	139.98	6.1	4.36	28.2	2.8	9.93
JA-08/9	5	140.00	8.0	5.71	31.7	5.3	16.72
JA-054	5	142.56	5.0	3.51	24.9	3.8	15.20
JA-0526	5	135.06	11.2	8.29	30.0	5.2	17.33
JA-0510	5	137.48	10.5	7.64	25.0	5.8	23.20
BC-088	5	150.35	8.3	5.52	29.0	1.9	6.55
BC-0303	5	144.58	12.6	8.71	33.0	8.1	24.55
BC-0406	5	132.57	8.7	6.56	37.9	2.6	6.86
BC-051	5	147.94	9.4	6.35	34.5	4.7	13.62
BC-0342	5	150.37	8.2	5.45	29.9	3.8	12.71
BC-037	5	143.54	10.5	7.32	32.4	6.8	20.73
BC-0188	5	139.83	6.1	4.36	32.7	4.3	13.15
CB-9	5	149.79	7.6	5.07	25.6	2.9	11.60
CB-10	5	146.22	8.0	5.47	33.4	4.5	13.47
CB-11	5	138.45	5.9	4.26	26.9	1.8	6.69
CV (%)	2.41	12.65	7.94	2.90	9.98	13.38	2.57
LSD	0.67	15.87	3.89	4.00	4.83	2.45	9.46

NIP=Number of insect species visited the plots, **NLP =** Number of leaves plant^{-1}
NILP= Number of infested leaves plant^{-1} **ILPP=** Infested leaves plant^{-1} (%),
NBP= Number of bolls plant^{-1} **NIBP=**Number of infested bolls plant^{-1}
IBPP= Infested bolls plant^{-1} (%)

BC037 (20.73%). Therefore, the genotype JA-08/D might be high seed cotton yielding as well as highly in general insect resistant genotype (Table 4.7).

4.4 Genotype × Environment interaction

Over all Jessore was the most suitable environment as compared to Dinajpur and Rangpur for cultivation of cotton. Accordingly all the characters showed better performance in Jessore during three growing seasons (2010-2013) except unbrust bolls plant^{-1}. The important character days to 1st flowering was 50.67days in Dinajpur, 55.33 days in Rangpur and 60.60 days in Jessore. The trait boll weight remained almost same in three locations and ranged from 5.47-5.96g. The highest seed cotton yield was recorded in Jessore (3238 kg ha^{-1}) followed by Rangpur (3052 kg ha^{-1}) and Dinajpur (2825 kg ha^{-1}) (Table 4.8). Among the 20 genotypes, JA-08/D produced the highest seed cotton yield across the three locations and three years, which were followed by JA-08/C and JA-08/E. A considerable seed cotton yield also recorded from the genotype, CB-10 with the mean seed cotton yield ranged from 3088-3249 kg ha^{-1} (Table 4.9). The coefficient of variation (%) ranged from in Jessore (10.89) during 2012-13 to 17.61 in Rangpur during 2013-14. However, the range of CV (%) predicted average above precision over all the experiments.

The combined analysis for MS (mean squares) revealed that the selected characters showed significant variations over the locations and years. The effect of replication was significant (3.45) for unbrust bolls plant^{-1} only. Though genotype x year interaction was significant at 5% level of probability for main stem nodes plant^{-1}, days to 1st boll splitting and boll weight but other characters displayed strong significant interaction effects for genotype x environment (Table 4.10). The highest variation explained was calculated (28.36%) against for genotype followed by genotype x environment (18.66%) and year alone (13.57%).

Cotton researchers and breeders are aware of differences in performance among cotton cultivars, both geographically and yearly, indicating the presence of genotype by environment interactions. The importance of GE interactions has long been acknowledged since that, in the absence of GE interactions, the best cultivar in any one trial would yield more than all cultivars at all locations every year. Historically, various methodologies have been investigated to study GE interaction including linear regression (Mooers, 1921; Finlay and Wilkinson, 1963; Eberhart and Russell, 1966), cluster analysis (Ghaderi et al., 1982; Johnson, 1977), and principal component analysis (Freeman and Dowker, 1973; Mandel, 1971; Williams, 1952).

Table 4.8 Mean performances of different characters in three locations over three years

Characters	Dinajpur				Rangpur				Jessore			
	2010-11	2011-12	2012-13	Mean	2010-11	2011-12	2012-13	Mean	2010-11	2011-12	2012-13	Mean
VB/P	1.56	1.58	1.40	1.51	1.97	2.02	2.34	2.11	2.89	2.93	3.25	3.02
PFB/P	12.58	11.49	13.73	12.6	15.00	15.30	16.31	15.54	16.94	17.86	18.16	17.32
SFB/P	5.88	7.25	6.42	6.52	10.84	8.17	9.25	9.42	17.40	16.38	16.92	16.90
MSN/P	5.34	6.02	5.49	5.62	6.93	5.87	6.00	6.27	7.71	7.10	7.45	7.42
DFF	50.33	52.00	49.67	50.67	55.00	54.33	56.67	55.33	59.00	60.12	62.67	60.60
DFBS	112.33	115.00	114.67	114.00	119.00	120.33	118.00	119.11	120.67	121.00	120.00	120.56
B/P	25.54	26.90	25.18	25.87	27.48	28.05	29.26	28.26	34.62	35.74	33.59	34.65
BW	5.30	5.27	5.83	5.47	5.04	5.91	5.00	5.32	5.87	6.01	5.99	5.96
UBB/P	2.63	1.98	2.50	2.37	1.57	1.80	1.92	1.76	0.78	1.00	1.01	0.93
PH	98.35	100.00	97.52	98.62	110.48	115.50	120.61	115.53	125.48	122.22	124.57	121.08
S/B	27.40	28.00	28.25	27.88	28.28	27.95	27.91	28.05	29.27	30.03	29.88	29.73
SCY	2728	2907	2841	2825	3000	3157	2999	3052	3367	3209	3138	3238

Red marked figures = Mean value

VB/P: Vegetative branches/plant, **PFB/P:** Primary fruiting branches/plant, **SFB/P:** Secondary fruiting branches/plant, **MSN/P:** Main stem node/plant, **DFF:** Days to 1st flowering, **DFBS:** Days to 1st boll split, **B/P:** Bolls/plant, **BW:** Boll weight, **UBB/P:** Unbrust bolls/plant, **PH:** Plant height, **S/B:** Seeds/boll, **SCY:** Seed cotton yield

Table 4.9 Mean performances of different genotypes for seed cotton yield (kg ha^{-1}) over locations and years

Genotypes	Dinajpur				Rangpur				Jessore			
	2010-11	2011-12	2012-13	Mean	2010-11	2011-12	2012-13	Mean	2010-11	2011-12	2012-13	Mean
JA-08/A	2882	2930	3074	2962	3009	2857	2897	2921	2957	3139	3058	3051
JA-08/B	2340	2258	2510	2369	2368	2517	2249	2378	2739	2615	2753	2702
JA-08/C	3230	3374	3120	3241	3074	3228	3291	3197	3438	3540	3303	3427
JA-08/D	3430	3348	3273	3350	3408	3378	3325	3370	3481	3550	3665	3565
JA-08/E	3136	3359	3007	3167	3212	3286	3184	3227	3349	3250	3098	3232
JA-0541	2610	2520	2548	2559	2865	2585	2437	2629	2790	2682	2858	2776
JA-08/9	2835	2762	2806	2801	2758	2891	2787	2812	3051	2912	2845	2936
JA-054	2065	2138	2367	2190	2407	2297	2015	2239	2342	2137	2480	2319
JA-0526	2634	2761	2538	2644	2630	2879	2676	2728	2765	2850	2864	2826
JA-0510	2824	2745	2684	2751	2768	2777	2936	2827	2803	3048	2752	2867
BC-088	1938	2063	2158	2053	2204	2157	2378	2246	2433	2361	2562	2452
BC-0303	2853	2769	2899	2840	2905	2831	2876	2870	2989	3029	3000	3006
BC-0406	3076	3155	2958	3063	3001	3138	3056	3065	3259	2904	3127	3096
BC-051	2865	2927	2890	2894	3125	3089	2951	3055	3138	3106	3028	3090
BC-0342	2906	2866	2748	2840	2992	2867	2971	2943	3031	2858	3190	3026
BC-037	2347	2230	2331	2302	2457	2400	2275	2377	2582	2449	2468	2499
BC-0188	2717	2672	2590	2659	2685	2853	2579	2705	2657	2767	2906	2776
CB-9	2356	2224	2407	2329	2258	2471	2560	2429	2339	2480	2571	2463
CB-10	3056	3162	3048	3088	3107	3200	3166	3157	3137	3381	3229	3249
CB-11	2354	2427	2404	2305	2265	2467	2550	2427	2363	2661	2656	2560
CV (%)	13.63	14.00	11.58		15.33	14.56	17.61		14.90	10.89	16.48	
LSD	328.45	300.46	410.37		380.09	299.68	412.67		306.63	317.56	358.62	

Red marked figures = Mean value

Table 4.10 Combined analysis (MS) of different characters over locations and years

SOV	df	VB/P	PFB/P	SFB/P	MSN/P	DFF	DFBS	B/P	BW	UBB/P	PH	S/B	SCY	VE (%) for SCY
R	2	75.78	165.35	124.56	35.78	9.45	36.95	13.59	7.78	3.45	103.43	32.53	756.89	6.55
G	19	312.37	738.72	659.70	99.56	25.65	395.05	341.60	88.56	12.57	1256.89	97.56	3276.90	28.36
Y	2	87.62	549.06	327.62	76.34	29.76	65.32	154.76	35.65	9.56	948.25	65.98	1567.76	13.57
E	8	268.56	672.58	765.39	45.21	12.37	154.78	99.48	68.89	10.87	1034.89	45.69	927.54	8.03
G x Y	38	587.50	957.10	562.67	89.70	34.23	104.39	165.78	100.87	18.53	846.78	56.78	1457.17	12.61
G x E	152	549.53	687.39	870.00	25.77	25.12	298.53	209.90	60.64	21.25	1365.79	73.67	2156.57	18.66
Y x E	16	375.78	472.90	412,00	35.69	11.37	35.71	76.52	65.36	14.80	421.56	45.32	764.70	6.62
G x Y x E	304	121.47	54.87	26.56	25.05	16.59	39.65	5-.53	30.74	11.69	97.6.87	37.80	548.41	4.75
Residual	540	85.34	35.13	36.85	13.59	9.83	24.68	20.37	42.50	8.46	45.76	22.42	98.27	0.85

Red marked figures = Non-significant, **Blue marked figures =** Significant at 5% level of probability and
Black marked figures = Significant at 1% level of probability.

VB/P: Vegetative branches/plant, **PFB/P:** Primary fruiting branches/plant, **SFB/P:** Secondary fruiting branches/plant, **MSN/P:** Main stem node/plant, **DFF:** Days to 1st flowering, **DFBS:** Days to 1st boll split, **B/P:** Bolls/plant, **BW:** Boll weight, **UBB/P:** Unbrust bolls/plant, **PH:** Plant height, **S/B:** Seeds/boll, **SCY:** Seed cotton yield, **VE:** Variation explained

Table 4.11 AMMI analysis of variance of seed cotton yield and yield contributing characters

SOV	df	VB/P	PFB/P	SFB/P	MSN/P	DFF	DFBS	B/P	BW	UBB/P	PH	S/B	SCY
G	19	45.36	154.50	65.50	37.40	55.69	76.87	41.52	38.55	56.08	366.78	999.41	1209.52
Y	2	14.87	67.47	44.23	16.08	24.61	65.39	30.65	24.69	36.31	296.40	391.35	929.57
E	8	41.79	35.79	60.69	21.69	36.68	70.10	37.89	39.67	45.37	300.01	710.30	1747.87
G x Y	38	132.50	263.56	125.96	28.55	134.33	126.59	52.40	68.45	60.22	592.79	368.52	18943.80
G x E	152	96.45	121.84	101.37	68.39	114.51	105.48	48.92	61.82	55.87	890.31	490.58	1034.95
Y x E	16	34.73	37,86	53.52	14.56	26.76	38.91	29.58	51.66	38.91	128.54	234.61	793.12
G x Y x E	304	21.09	56.90	28.61	19.56	22.69	36.98	31.39	40.38	18.46	96.45	124.56	529.68
IPCA 1	45	12.78	35.76	25.59	17.50	18.56	30.25	27.45	36.79	13.52	70.65	25.67	156.42
IPCA 2	43	10.46	27.87	17.36	14.97	15.30	17.47	23.90	35.71	10.30	64.78	28.40	136.90
IPCA 3	41	7.66	18.50	15.75	12.59	13.95	13.60	19.76	30.10	7.20	57.14	`23.69	121.67
IPCA 4	39	4.69	14.76	11.83	10.32	9.54	9.93	15.67	26.83	4.85	49.76	19.53	105.38
Remainder	405	23.59	45.32	25.87	46.78	30.45	26.45	32.57	97.35	13.76	205.39	61,35	198.54
Av. error	709	15.65	21.78	26.72	26.83	27.78	31.03	39.16	111.20	25.83	199.90	49.66	202.36

Blue marked figures = Significant at 5% level of probability and **Black marked figures =** Significant at 1% level of probability

SOV: Source of variation, **G:** Genotypes, **Y:** Year, **E:** Environment, **VB/P:** Vegetative branches/plant, **PFB/P:** Primary fruiting branches/plant, **SFB/P:** Secondary fruiting branches/plant, **MSN/P:** Main stem node/plant, **DFF:** Days to 1st flowering, **DFBS:** Days to 1st boll split, **B/P:** Bolls/plant, **BW:** Boll weight, **UBB/P:** Unbrust bolls/plant, **PH:** Plant height, **S/B:** Seeds/boll, **SCY:** Seed cotton yield

4.5 AMMI Analysis

AMMI analysis was performed on seed cotton yield and its related eleven characters. The resutrs are presented from Table 4.11 to 4.23. Since, the ultimate aim of the investigation was to assess the seed cotton yield potential of the tested genotypes, hence the AMMI analysis was elaborarely studied for seed cotton yield only. AMMI analysis for different characters is presented in Table 4.11.

The three locations across the three years were significant for the studied characters. Main stem nodes plant^{-1} and boll weight showed significant variations over three years at 5% level of probability and other linear and interaction effects were significant at 1% level of probability. Four IPCAs were calculated and AMMI analysis revealed that mean squares for the PCA 1 and PCA 2 were significant at $P = 0.01$ and cumulatively contributed remarkable of the total GEI. Therefore, the postdictive evaluation using an F-test at $P \leq 0.01$ suggested that two principal component axes of the interaction were significant for the model with 45 and 43 degrees of freedom respectively. However, the prediction assessment indicated that AMMI with only two interaction principal component axes was the best predictive model (Zobel *et al.*, 1988). Conversely, Sivapalan *et al.* (2000) recommended a predictive AMMI model with the first four PCAs. Further interaction principal component axes captured mostly noise and therefore did not help to predict validation observations.

According to Gauch and Zobel, (1996) and, Yan and Rajcan, (2002), the most accurate model for AMMI can be predicted by using the first two PCAs. These results indicated that the number of the terms to be included in an AMMI model could be specified prior to trying AMMI predictive assessment. In general, factors like type of crop, diversity of the germplasm and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa *et al.*, 1990). Thus, results indicated that the AMMI model fits the data well, and justified the use of AMMI analysis. So the interaction of the 20 genotypes of cotton for 12 characters with 27 environments was best predicted by the first two principal components of genotypes and environments.

The AMMI method is used for three main purposes viz. first, AMMI is more appropriate in the initial statistical analysis of yield trials, because it provides an analytical tool for diagnosing other models for a particular set of data (Gauch, 1988). Secondly, AMMI clarifies the G x E interaction and it summarizes patterns and relationships of genotypes and environments (Zobel *et al*., 1998; Crossa *et al*., 1990) and third is used to improve the accuracy of yield estimates (Ilker *et al*., 2011).

The advantages of the AMMI model or its variants are that, they use overall fitting, impose no restrictions on the multiplicative terms and result in least square fit (Freeman, 1990). Within limits, any model may be expected to fit the data from which it was derived. However, the AMMI model has a good chance of being able to predict for new sites and new years, thus contributing a real advance (Gauch, 1988). Gauch and Zobel (1996) showed that AMMI1 with IPCA1 and IPCA2 are usually selected.

This study demonstrates the importance of applying AMMI analysis to investigate the main effects of genotypes and environment and the complex patterns of their interaction. The GEI accounted for sizable and significant portion of variability almost as twice as that of genotypes. Using AMMI model, the variability relating to GEI has been partitioned into pattern rich model represented by IPCA1 and IPCA2. Due to the limited number of environments being tackled here, the present study may not provide the ideal framework for identifying target testing environments for cotton breeding in three regions of our country.

Environments displaying the lowest interaction effect (IPCA scores) coupled with the highest yield potential are considered as the suitable environments to express of the real differences among the genotypes. However, the AMMI method is used for three main purposes. Gains have been obtained in the accuracy of yield estimates that are equivalent to increasing the number of replication by a factor of two to five (Zobel *et al*., 1988; Crossa, 1990). Such gains may be used to reduce testing cost by reducing the number of replications, to include more treatments in the experiments or to improve efficiency in selecting the best genotypes.

Using ANOVA, yield sum square was partitioned into genotype, environment and G x E interaction. G x E interaction was further partitioned by principal component analysis

4.6 Stability Performance

The AMMI model combined the analysis of variance for main effects of G and E with principal components analysis of GEI. It has proven useful in understanding complex GEI. The main effect of means vs the first Interaction Principal Component Analysis Axis (IPCA) from AMMI analysis was used to study the pattern of response of G, E, and GEI. It was also used to identify genotypes with broad or specific adaptation to target environments for seed cotton yield and its related eleven yield contributing characters (Table 4.12-4.23). All the Tables presented here have reflected IPCA scores and AMMI stability values (ASV).

4.7 IPCAs crossover and non-crossover interaction

IPCA scores of genotypes and environments displayed positive and negative values for seed cotton yield (Table 4.23). A genotype with large positive IPCA score in some environments must have large negative interaction in some other environments. Thus, these scores presented a disproportionate genotype response (Yan and Hunt, 2001; Mohammadi *et al.*, 2007), which was the major source of variation for any crossover (qualitative) interaction. This disproportionate genotype response is referred to as crossover G x E interaction for convenience. Diversely, scores with the same sign or near zero represent a non- crossover (quantitative) G x E interaction or a proportionate genotype response (Mohammadi and Amri 2008 and Farshadfar, 2008).

The highest mean seed cotton yield (3430 kg ha^{-1}) was obtained from the genotype JA-08/D which had below agerage IPCAs (2.436 and 1.475), indicated average stable in seed cotton yield over the locations and years, which were followed by JA-08/C (3329 kg ha^{-1}) and JA-08/E (3226 kg ha^{-1}) and the high yielding genotypes showed proportionate response as reflected by their corresponding IPCA1 and IPCA2 scores.

Table 4.12 AMMI and regression analysis on vegetative branches plant^{-1}

Genotypes	VB/P	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	s^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	1.93	0.895	0.337	0.58	1.49**	0.44	3.95	8	0.149	1.68
JA-08/B	1.60	0.237	0.351	0..24	0.69	1.12	2.80	5	0.968	2.88
JA-08/C	1.87	-0.318	0.586	0.95	0.34	1.16	4.36	7	1.045	3.25
JA-08/D	4.27	-0.306	-0.171	0.56	1.05	1.67	3.58	20	0.423	2.53
JA-08/E	1.80	0.394	-0.019	0.52	1.14**	1.04	2.49	6	1.070	1..88
JA-0541	1.47	0.500	0.260	0.17	0.95	1.77	2.85	3	1.341	2.58
JA-08/9	1.40	-0.328	0.216	0.19	-1.49**	1.16	2.76	2	-0.867	1.53
JA-054	1.53	1.504	0.002	0.10	0.10	0.36	0.81	4	0.246	-1.93
JA-0526	2.33	0.088	0.021	-0.53	1.72	1.29	0.90	13	0.257	-1.50
JA-0510	1.97	-0.637	0.401	0.50	-1.06	2.53	2.26	9	1.057	0.03
BC-088	2.30	0.320	0.025	0.36	1.05	0.79	1.69	12	-0.255	0.28
BC-0303	2.57	-0.186	-0.278	-2.56	1.76**	2.57	0.08	14	-1.248	-0.25
BC-0406	3.20	-0.808	-0.042	-087	--0.89	0.47	2.22	19	2.019	1.83
BC-051	2.03	-0.164	-0.1802	-0.88	0.98	0,82	1.60	10	1.313	1.28
BC-0342	2.77	-0.867	-0.251	-0.95	0.97	1.76	2.44	17	0.338	-3.03
BC-037	2.67	0.908	0.146	0.52	-1.34**	0.39	2.19	16	0.869	3.76
BC-0188	2.13	-0.917	-0.347	-0.18	-1.05	1.06	0.90	11	-0.128	0.75
CB-9	3.17	0.357	-0.935	-0.47	0.95	1.61	1.61	18	-0.467	1.60
CB-10	2.63	0.303	-0.415	0..79	1.21**	1.43	3.20	15		
CB-11	0.67	-1.346	-0.302	-0.48	0.63	0.75	2.40	1		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

VB/P: Vegetative branches/plant, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^2di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.13 AMMI and regression analysis on primary fruiting branches plant^{-1}

Genotypes	PFB/P	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	14.47	0.726	0.958	2.53	1.82**	1.28	1.33	2	0.528	1.55
JA-08/B	13.43	0.939	0.279	2.86	1.97**	2.21	1.21	1	0.865	3.36
JA-08/C	14.67	0.168	0.186	2.38	1.07*	1.64	1.38	3	0.571	1.65
JA-08/D	26.00	0.581	0.367	1.37	1.87**	1.26	1.55	20	0.219	1.39
JA-08/E	15.40	0.698	0.342	2.78	1.37**	2.18	0.99	6	0.880	2.38
JA-0541	17.37	0.665	0.5003	2.85	1.04	1.46	0.89	10	0.503	2.73
JA-08/9	17.23	-0.956	0.284	0.79	0.83	0.89	0.16	9	-1.349	1.43
JA-054	14.93	-0.725	1.503	2.01	1.02	0.91	1.82	4	0.873	-2.34
JA-0526	19.07	-0.267	0.883	1.05	1.07*	0.60	0.54	11	-1.317	-1.18
JA-0510	15.10	-0.991	-0.363	0.80	1.54**	0.03	0.628	5	0.045	0.40
BC-088	21.97	-0.591	-0.203	0.29	1.34**	1.28	2.06	16	0.368	-1.08
BC-0303	20.17	0.836	-0.169	0.47	1.16*	2.34	0.30	13	-0.322	-1.80
BC-0406	22.50	-0.291	-0.084	0.91	0.95	2.51	0.89	18	-0.050	-1.07
BC-051	16.60	-0.286	-0.165	-1.72	0. 69	1.39	0.95	8	0.188	-2.30
BC-0342	20.10	0.256	-0.867	-1.50	0.92	1.74	0.91	12	0.457	-2.09
BC-037	21.87	0.449	0.908	0.66	1.07*	3.54	0.51	15	0.347	1.15
BC-0188	22.17	-0.183	-0.919	-1.90	0.98	1.94	0.97	17	0.662	-0.76
CB-9	21.20	-0.496	0.571	0.57	1.03	1.33	0.24	14	-0.189	-1.47
CB-10	23.33	0.151	0.303	-1.62	0.93	1.09	1.52	19		
CB-11	16.13	0.395	-1.347	-1.18	0.97	0.79	1.34	7		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

PFB/P: Primary fruiting branches/plant, **IPCA:** Interaction principal component analysis,

bi: Regression coefficient, **S^2di:** Deviation from regression coefficient,

ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.14 AMMI and regression analysis on secondary fruiting branches plant^{-1}

Genotypes	SFB/P	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	11.20	0.411	1.675	1.93	0.95	2.64	1.54	9	0.383	1.25
JA-08/B	9.53	0.176	0.201	1..27	1.63**	3.02	1.31	8	0.236	1.05
JA-08/C	8.13	0.282	1.214	2.35	1.28	1.73	1.25	4	1.078	0.38
JA-08/D	21.33	0.214	0.781	1.76	0.69	4.72	0.71	20	0.025	0.93
JA-08/E	8.07	0.652	0.321	1.45	1.05	1.08	1.35	3	-0.075	-0.60
JA-0541	9.50	0.133	0.182	1.35	0.98	1.01	0.20	7	-0.497	-0.12
JA-08/9	6.53	-0.257	1.552	-0.05	0.26	1.25	1.81	1	-1. 710	1.00
JA-054	9.03	0.346	0.952	2.24	0.16	0.39	1.03	6	0.954	-1.60
JA-0526	13.53	1.305	-0.075	0.34	0.81	0.14	2.13	14	1.151	-1.10
JA-0510	9.00	0.111	-0.423	-1.65	1.08*	0.03	0.29	15	-1.640	1.45
BC-088	13.50	0.252	-1.326	-0.79	0.73	1.52	1.57	13	-2.119	1.63
BC-0303	12.17	0.602	1..321	5.19	1.62**	0.35	1.58	10	-1.852	0.73
BC-0406	16.23	0.341	1.313	2.17	1.00	0.27	1.87	18	-0.457	-2.72
BC-051	13.23	-1.115	1.133	-1.51	1.43**	1.55	1.62	11	1.950	-1.18
BC-0342	16.57	-0.549	-1.546	-2.07	0.63	0.37	1.98	19	2.826	-0.95
BC-037	13.47	0.108	0.412	3.10	1.15*	1.13	0.25	12	1.684	1.17
BC-0188	15.13	-1.062	0.611	-1.32	0.55	1.79	1.90	16	0.131	0.85
CB-9	14.73	-1.038	-1.227	1.67	0.53	3.51	0.22	15	-0.480	-1.13
CB-10	15.50	0.172	0.118	1.50	1.63**	2.82	1.62	17		
CB-11	6.63	-1.127	-0.123	-2.95	1.77**	2.17	156	2		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

SFB/P: Secondary fruiting branches/plant, **IPCA:** Interaction principal component analysis, **bi:** Regression coefficient, **S^2di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.15 AMMI and regression analysis on main stem nodes plant^{-1}

Genotypes	MSN/P	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	6.23	1.534	0. 553	1.65	0.87	0.77	2.45	6	1.226	0.33
JA-08/B	6.00	2.514	1.626	1.48	0.92	0.89	4.89	4	0.048	1.5.6
JA-08/C	6.23	3.615	2.575	3.72	0. 73	0.89	1.48	6	1.047	2.71
JA-08/D	7.13	1.350	1.784	1.82	0.86	1.28	4.72	14	2.085	0.71
JA-08/E	6.40	0.626	0.184	2.25	1.29**	1.26	1.39	9	1.761	2.64
JA-0541	6.07	2..217	1.279	1.15	1.13*	2.03	1.28	5	3.087	-1.36
JA-08/9	5.27	0.393	1.143	.181	0.89	0.79	1321	1	-3.356	1.88
JA-054	5.73	-1.015	4.100	-0/59	0.36	2.67	1.32	2	-1.206	1.45
JA-0526	6.23	2.159	-3.971	2.77	1.24**	1.03	0.13	6	-0.536	-0.53
JA-0510	5.93	-2.067	0. 214	0.56	0.51	0.72	4.24	3	2.640	1.52
BC-088	6.33	-2.175	1.175	1.29	0.91	1.76	1.92	8	2.252	0.36
BC-0303	6.40	2.113	-5.073	1.02	1.18*	1.06.	1.11	9	2.187	0.56
BC-0406	6.53	1.016	-0. 551	-2.68	1.38**	0.77	3.31	10	-0.048	-2.31
BC-051	6.33	2.079	2.665	-2.80	0.79	1.85	1.74	8	3.875	-0.51
BC-0342	7.03	0.907	0. 212	-.2707	1.19*	0.71	4.74	13	1.672	-0.97
BC-037	6.40	1.986	-4.243	0.14.	1.32**	0.96	2.44	9	0.953	1.12
BC-0188	6.73	0.842	-1.601	-10.4	1.68**	3.73	1.76	12	2.187	-.0.84
CB-9	7.73	-1.114	0.486	-2.18	0.95	0.73	2.00	15	-3.726	0.76
CB-10	6.57	-0.747	0.437	-1.01	0.55	0.61	0.77	11		
CB-11	6.27	2.494	1.374	-2.83	0.79	0.95	2.79	7		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

MSN/P: Main stem node/plant, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^2di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.16 AMMI and regression analysis on days to 1^{st} flowering

Genotypes	DFF	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	53	1.564	0.553	3.57	0.87	0.79	2.55	7	1.256	3.30
JA-08/B	50	2.548	1.646	4.52	0.56	0.80	4.89	4	0.028	3.27
JA-08/C	51	1.665	-2.415	3.76	0.97	0.89	2.43	5	1.057	2.73
JA-08/D	51	1.158	3.704	5.18	0.89	0.28	4.32	5	1.058	0.71
JA-08/E	53	0.726	-0.549	2.27	1.35**	1.26	1.30	7	1.752	264
JA-0541	49	5.239	-3.279	5.12	1.16*	1.20	2.82	3	3.083	3.67
JA-08/9	48	0.393	1.133	-1.83	0.79	0.79	1.32	2	-3.333	1.88
JA-054	51	-1.011	1.185	3.52	0.36	2.67	1.65	5	-1.286	1.47
JA-0526	52	-2.952	-3.082	2.75	1.24**	1.03	5.21	6	-3.526	2.38
JA-0510	50	-2.367	0.214	1.60	0.51	0.72	2.24	4	2.471	5.23
BC-088	50	-2.145	1.375	1.25	0.91	1.76	1.17	4	2.272	3.67
BC-0303	53	2.117	-2.075	1.02	1.18*	1.10	0.63	7	2.188	0.56
BC-0406	51	2.036	-0.651	3.67	1.18*	0.77	3.31	5	-0.798	-2.30
BC-051	47	4.051	2.656	-2.80	0.72	1.85	1.16	1	5.071	-5.13
BC-0342	51	2.507	0.212	-2.71	1.59**	0.71	4.74	5	1.672	-2.76
BC-037	56	2.786	-4.280	1.43	1.32**	0.96	2.49	8	-0.352	1.12
BC-0188	53	2.840	-1.201	-4.15	1.06*	3.73	2.76	7	2.182	0.84
CB-9	56	-1.115	0.786	-2.12	0.95	0.73	2.00	8	1.788	2.76
CB-10	50	-0.747	0.403	-1.09	0.95	2.14.	0.727	4		
CB-11	50	2.424	2.331	-2.89	0.71	0.95	2.79	4		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

DFF: Days to 1^{st} flowering, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^2di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.17 AMMI and regression analysis on days to 1st boll splitting

Genotypes	DFBS	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	103	0.259	0.266	7.93	0.74	0.75	0.74	2	0.142	6.02
JA-08/B	105	0.826	0.257	9.05	1.42**	0.59	1.09	2	0.164	4.03
JA-08/C	106	0.296	0.436	10.18	0.95	056	0.75	4	0.501	4.19
JA-08/D	109	0.812	-0.520	11.87	1.58**	0.87	1.14	7	0.803	7.16
JA-08/E	107	-0.165	-1.024	8.16	1.38**	0.55	1.20	5	0.616	3.48
JA-0541	108	0.139	0.103	7.67	0.74	0.47	0.36	6	0.577	-6.64
JA-08/9	102	0.337	-0.734	6.47	1.92**	0.84	0.95	1	-1.716	2.80
JA-054	105	0.084	0.456	-5.82	0.65	0.47	0.46	2	-0.864	3.47
JA-0526	104	0.347	0.815	4.62	0.89	0.71	0.80	3	0.318	-6.40
JA-0510	104	-0.275	0.087	6.45	0.92	0.55	1.22	3	-0.518	1.36
BC-088	106	-0.704	0.849	0.93	0.57	0.88	1.34	4	0.584	-4.45
BC-0303	109	0.173	-0.654	2.38	1.25**	0.59	0.50	7	0.326	-3.83
BC-0406	107	1.381	-0.878	-5.38	0.86	0.65	1.73	5	-0.142	1.97
BC-051	104	-0.534	0.392	5.25	1.36**	0.79	0.92	3	0.343	-5.76
BC-0342	106	0.618	0.305	2.36	0.94	0.68	0.86	4	0.459	-2.10
BC-037	109	0.462	0.727	-6.19	0.59	0.59	0.93	7	-0.840	1.18
BC-0188	107	-0.815	-0.615	2.20	1.14	0.44	0.16	5	0.058	2.83
CB-9	115	-0.742	-0.543	5.48	1.44	0.57	1.25	8	-0.864	3.92
CB-10	116	0.896	-0.185	8.92	1.05	0.65	0.37	9		
CB-11	105	0.237	-0.186	-7.23	0.96	0.78	0.86	2		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

DFBS: Days to 1st boll split, **IPCA:** Interaction principal component analysis, **bi:** Regression coefficient, **S^2di:** Deviation from regression coefficient, **ASV:** Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.18 AMMI and regression analysis on bolls plant^{-1}

Genotypes	B/P	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^{2}di	ASV	Rank	SI	E. index (Ei)
JA-08/A	33.5	0.432	1.261	3.88	0.89	0.84	1.24	18	0.349	3.86
JA-08/B	26.7	1.817	1.332	2.36	1. 77**	1.46	2.91	4	0.718	4.60
JA-08/C	31.5	1.175	1.175	2.09	0.96	1.64	2.16	12	1.69	3.56
JA-08/D	33.2	1.249	1.799	4.38	1.06*	1.29	2.99	17	1.449	6.49
JA-08/E	31.0	1.377	1.484	2.37	1.55**	1.25	2.91	11	1.375	1.47
JA-0541	28.2	1.845	0.567	-3.55	0.81	1.36	2.18	6	-1.981	1.64
JA-08/9	31.7	1.024	2.179	1.97	0.86	1.98	2.56	13	-0.758	4.37
JA-054	24.9	0.189	1.326	1.30	0.98	0.67	1.34	1	0.783	-3.37
JA-0526	30.0	1.412	0.777	-2.96	0.75	1.18	2.90	10	-0.154	-3.85
JA-0510	25.0	1.586	1.756	-1.79	0.73	1.37	2.89	2	-0.325	3.30
BC-088	29.0	1.459	2.043	2.08	1.09*	1.02	3.37	7	-0.669	-2.71
BC-0303	33.0	0.884	1.191	-2.73	1.13*	0.84	1.78	16	-0.892	-1.07
BC-0406	37.9	1.326	0.769	3.0	1.23**	1.41	2.19	20	1.736	2.06
BC-051	34.5	0.637	0.712	0.3	1.03	0.46	0.28	19	2.130	-2.59
BC-0342	29.9	0.607	0.478	2.00	0.93	1.16	3.81	8	3.257	-4.14
BC-037	32.4	2.107	2.704	-1.65	1.32	1.96	3.74	14	1.423	3.77
BC-0188	32.7	0.157	0.184	3.61	0.87	0.56	0.24	15	-0.141	3.15
CB-9	25.6	0.750	0.204	1.89	1.16*	0.83	1.14	3	0.466	-1.78
CB-10	33.4	0.877	0.869	2.85	1.38**	0.47	1.69	18		
CB-11	26.9	0.483	1.094	-1.04	0.96	1.88	1.24	5		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

B/P: Bolls/plant, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^{2}di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.19 AMMI and regression analysis on boll weight

Genotypes	BW	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	4.74	0.145	0.135	0.53	0. 76	0.63	2.29	6	1.357	1.83
JA-08/B	5.03	1.649	1.475	0.83	1.74**	1.22	2.79	11	1.128	1.81
JA-08/C	6.17	1.326	1.534	0.89	0.94	1.07	2.16	20	0.577	0.98
JA-08/D	4.93	1.435	1.645	1.48	2.87**	1.92	1.15	8	1.124	2.18
JA-08/E	5.51	0.763	1.272	0.63	1.16*	1.70	1.72	17	1.287	1.28
JA-0541	5.46	-0.923	-1.592	1.23	0.18	0.65	-0.78	16	1.271	0.95
JA-08/9	4.17	1.923	-1.265	0.55	1.21	0.75	1.11	1	2.789	1.11
JA-054	5.80	0.607	0.411	-1.07	0.97	1.21	0.11	18	-2.314	-1.54
JA-0526	5.27	1.022	1.345	0.86	0.18	1.30	1.45	13	0.815	-0.91
JA-0510	4.75	-1.761	-0.646	-0.25	1.85**	0.71	0.401	7	4.846	0.65
BC-088	4.95	0.482	-0.255	-0.58	1.75**	1.41	3.40	9	-3.087	-464.26
BC-0303	4.49	-2.173	-1.228	-1.46	0.98	1.17	2.26	5	-5.471	-1.39
BC-0406	4.47	0.672	1.257	-2.68	0.95	0.09	1.79	4	2.311	1.29
BC-051	4.33	1.735	1.382	0.67	1.14*	1.40	1.96	2	-1.973	-1.45
BC-0342	5.40	1.465	-1.456	-1.02	0.75	0.28	1.84	15	-1..385	-0.90
BC-037	4.99	1.126	0.152	0.69	1.09	0.57	1.58	10	0.249	1.51
BC-0188	4.36	1.098	1.287	0.37	0.98	1.47	1.17	3	1.747	-1.79
CB-9	5.97	0.816	1.042	0.28	1.67**	0.41	1.06	19	-1.461	-1.27
CB-10	5.07	1.513	1.831	1.29	0.54	1.41	1.66	12		
CB-11	5.34	-1.603	1.721	-1.21	0.36	2.18	1.32	14		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

BW: Boll weight, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^2di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.20 AMMI and regression analysis on unburst bolls plant^{-1}

Genotypes	UBB/ P	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^{2}di	ASV	Rank	SI	E. index (Ei)
JA-08/A	1.4	-0.537	-0.240	0.28	0.98	1.04	0.83	3	0.275	0.94
JA-08/B	1.8	1.317	1.146	0.67	1.40**	1.42	1.19	7	1.204	0.97
JA-08/C	1.4	0.648	0.387	0.54	1.09*	0.81	1.90	3	1.136	0.47
JA-08/D	1.4	-0.992	-1.446	0.98	0.78	1.23	1.54	3	0.555	083
JA-08/E	1.6	-0.626	0.378	0.54	1. 09*	1.09	0.79	5	1.147	0.29
JA-0541	1.5	-0.292	1.724	-0.54	1.07*	1.04	1.84	4	-0.068	-0.16
JA-08/9	2.3	0.814	-0.697	-0.16	0.95	0.96	1.12	9	0.437	0.19
JA-054	1.6	-0.236	-0.961	-0.19	0.89	0.61	0.59	5	0.830	-0.70
JA-0526	1.6	1.536	-1.665	0.95	1.08	0.85	2.78	5	-0.422	-0.95
JA-0510	1.0	-0.591	0.551	-0.97	0.96	0.93	1.61	1	0.383	0.19
BC-088	1.5	-0.537	1.426	-0.28	1.84**	0.53	1.96	4	-0.136	-0.78
BC-0303	1.2	-1.024	-0.946	-0.53	0.81	1.28	1.69	2	0.899	-0.09
BC-0406	1.8	0.552	0.843	0.68	1.20**	1.62	1.18	7	0.345	0.84
BC-051	1.6	-1.034	1.083	-0.32	1.30**	081	1.094	5	0.678	0.11
BC-0342	1.2	-0.939	-1.083	0.08	0.81	0.51	2.08	2	0.793	-0.85
BC-037	1.9	-0.212	1.580	-0.89	1.18*	4.07	1.62	8	0.580	0.78
BC-0188	1.5	0.878	-0.753	0.33	1.63**	3.04	1.09	4	0.912	-0.04
CB-9	1.5	-0.959	-1.617	0.36	0.70	1.73	2.92	4	0.267	-0.56
CB-10	1.7	-1.621	0.952	0.73	0.57	0.59	2.57	6		
CB-11	1.5	-0.520	-0.238	0.51	0.99	0.85	0.85	4		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

UBB/P: Unbrust bolls/plant, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^{2}di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.21 AMMI and regression analysis on plant height

Genotypes	PH	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	106.37	3.185	2.128	5.36	0.95	1.56	1.27	8	5373	5.83
JA-08/B	96.60	2.693	1.447	3.57	0.74	1.25	2.27	3	3.658	3.49
JA-08/C	101.73	1.345	1.194	2.48	0.96	1.13	2.16	5	4.578	3.67
JA-08/D	108.73	2.426	1.475	6.49	0.97	0.54	1.15	10	7.104	6.72
JA-08/E	94.33	0.643	-1.698	2.63	1.06*	0.87	1.17	2	1.187	2.79
JA-0541	110.07	-2.163	-1.597	1.26	0.98	0.83	3.57	11	5.941	-5.28
JA-08/9	91.80	1.620	-1.786	2.56	1.24**	0.15	1.10	1	2.273	4.86
JA-054	101.33	4.102	-3.4186	-1.05	0.94	1.95	5.51	4	-2.154	-2.64
JA-0526	108.33	-1.082	1.745	1.76	0.98	2.91	2.35	9	0.918	-2.51
JA-0510	102.13	2.278	-1.676	2.56	1.68**	0.56	3.07	6	2.484	1.67
BC-088	131.20	3.242	-2.255	-3.82	1.27	1.36	4.30	19	-9.058	-4.22
BC-0303	116.47	-8.117	-1.428	-3.78	0.91	1.62	2.15	12	-5.581	-2.90
BC-0406	130.93	-4.621	5.578	1.68	0.99	0.57	1.84	18	5.111	0.87
BC-051	118.73	4.135	1.857	-1.65	1.14*	2.80	1.96	14	-1.973	-4.41
BC-0342	130.00	-1.392	-2.406	-1.52	0.77	0.75	1.95	17	-1.574	-1.76
BC-037	128.80	2.816	3.354	2.68	1.19*	0.99	1.57	16	6.049	5.35
BC-0188	131.27	-2.438	1.257	-1.35	0.98	382.94	1.27	20	-1.734	-3.10
CB-9	104.70	3.126	1.082	1.92	1.27**	0.35	1.15	7	-1.261	-2..74
CB-10	118.67	1.532	3.034	2.97	0.45	0.93	2.66	13		
CB-11	119.73	-1.203	0.719	-1.83	0.84	0.86	1.80	15		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

PH: Plant height, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^2di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.22 AMMI and regression analysis on seeds boll^{-1}

Genotypes	S/B	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	27.9	3.480	2.401	2.45	0.95	0.57	3.68	15	1.472	2.47
JA-08/B	24.6	1.295	2.654	2.67	0.89	0.82	2.41	4	3.563	2.51
JA-08/C	29.9	1.325	-1.195	3.57	0.94	1.01	2.16	18	0.572	1.65
JA-08/D	28.2	-2.416	-1.477	5.62	0.97	0.42	1.55	17	4.184	2.74
JA-08/E	28.1	0.663	-1.169	3.58	1.06*	0.57	1.22	16	1.287	2.70
JA-0541	25.5	-2.143	-1.597	-2.92	0.78	1.32	1.78	6	1.071	1.28
JA-08/9	26.8	0.699	-1.765	1,68	1.21**	1.15	1.01	11	2.278	1.89
JA-054	26.0	4.206	2.418	-3.52	0.97	0.98	1.11	8	-2.454	1.65
JA-0526	35.0	-1.682	1.545	2.22	0.91	1.92	2.34	19	0.218	1.59
JA-0510	26.3	2.279	-1.637	-2.37	1.18*	0.56	0.40	9	2.464	1.69
BC-088	25.0	3.243	-2.215	2.88	1.52**	0.36	3.45	5	-2.088	1.26
BC-0303	22.9	-2.118	-1.284	-3.31	0.84	5.62	2.12	1	-5.578	2.94
BC-0406	27.4	-6.621	6.575	-2.19	0.92	1.65	1.89	14	1.317	0.82
BC-051	25.6	4.125	3.847	3.48	1.14*	2.84	1.24	7	-.1976	4.41
BC-0342	27.1	-1.371	-2.416	1.52	0.78	0.74	1.84	12	-1.5.35	1.79
BC-037	23.0	4.826	3.372	1.76	1.19*	4.42	1.58	2	3..249	2.31
BC-0188	26.5	-2.418	1.027	-2.58	0.68	2.94	1.14	10	-1.147	3.13
CB-9	23.3	3.156	1.572	1.009	1.07*	0.35	1.03	3	-1.159	-2.04
CB-10	27.17	-1.581	3.031	4.376	0.95	1.96	3.66	13		
CB-11	23.3	-1.2.09	1.716	1.487	0.64	131	1.88	3		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

S/B: Seeds/boll, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^2di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

Table 4.23 AMMI and regression analysis on seed cotton yield (kg ha^{-1})

Genotypes	SCY	IPCA1 Score	IPCA2 Score	Phenotypic index (Pi)	bi	S^2di	ASV	Rank	SI	E. index (Ei)
JA-08/A	3012	2.185	1.328	153.68	0.91	0.39	7.29	14	2.363	18.384
JA-08/B	2641	5.659	3.413	89.65	0.94	1.22	12.29	5	1.628	181.49
JA-08/C	3329	1.345	1.194	80.39	0.84	1.02	11.60	18	0.057	281.63
JA-08/D	3430	2.436	1.475	149.16	0.97	5.42	15.15	19	2.134	114.75
JA-08/E	3226	1.643	1.169	126.39	1.06*	0.77	11.22	17	1.284	112.79
JA-0541	2711	2.155	6.532	126.80	0.88	2.32	7.18	7	5.971	157.21
JA-08/9	2904	2.623	-1.766	105.67	1.24**	3.15	21.01	11	2.789	114.89
JA-054	2810	4.186	4.181	-105.6	0.97	5.96	5.51	10	-2.354	-154.64
JA-0526	2703	-1.058	1.845	76.89	0.98*	3.92	2.35	6	0.814	-216.51
JA-0510	2799	2.271	-0.676	25.63	1.18*	2.56	20.01	9	2.480	65.64
BC-088	2703	3.242	-2.245	-382.96	1.52**	3.69	23.50	6	-4.088	-404.26
BC-0303	2580	-4.811	-1.828	-378.92	0.84	1.15	21.26	4	-5.574	-132.94
BC-0406	3089	-6.625	1.657	168.18	0.92	1.16	18.91	15	5.711	129.81
BC-051	2969	4.125	1.852	-65.79	1.01	2.84	9.64	12	-19.276	-214.41
BC-0342	2973	-3.139	-5.046	-52.00	0.78	0.71	9.84	13	-15.834	-207.79
BC-037	2466	3.892	2.352	208.61	1.19*	4.42	5.68	2	5.949	151.31
BC-0188	2758	-2.408	1.227	153.57	0.98	443.94	2.714	8	10.44	-309.13
CB-9	2389	3.112	1.072	192.14	1.27**	0.35	11.53	1	-16.41	-272.04
CB-10	3205	-1.733	3.037	297.58	0.94	1.96	3.60	16		
CB-11	2483	-1.209	4.716	-183.15	0.86	3.15	8.80	3		

* and ** indicate significant at 5% and 1% levels of probability, respectively.

SCY: Seed cotton yield, **IPCA:** Interaction principal component analysis,
bi: Regression coefficient, **S^2di:** Deviation from regression coefficient,
ASV: Average stability value, **SI:** Selection index, **Ei:** Environmental index

4.8 AMMI stability value (ASV)

The AMMI model did not make provision for a quantitative stability measure, such a measure is essential in order to quantify and rank genotypes according to their yield stability, the ASV measure was proposed by Purchase *et al.* (2000) to cope with this problem. In fact, ASV is the distance from zero in a two dimensional scattergram of IPCA1 (interaction principal component analysis axis 1) score against IPCA2 score. Since the IPCA1 score contributed more to G x E sum of square for seed cotton yield (Table 4.23), it has to be weighted by the proportional difference between IPCA1 and IPCA2 scores to compensate for the relative contribution of IPCA1 and IPCA2 to the total G x E sum of squares. The distance from zero was then determined using the theorem of Pythagoras (Purchase *et al.*, 2000). In ASV method, a genotype with least ASV score was the most stable, accordingly, among the four high seed cotton yielding genotypes, CB-10 (ASV=3.60) appeared as the most stable followed by the genotypes JA-08/E (ASV=11.22) and JA-08/C (ASV=11.60) but only the highest seed cotton yielding genotype, JA-08/D produced averagely higher ASV (15.15) yield as compared to other stable genotypes across the environments. Therefore, as a selection criterion in breeding programs, in general the importance of AMMI model was in reduction of noise even if principal components did not cover much of the G x E sum of squares.

This measure is essential in order to quantify and rank genotypes according to their yield stability, the least Genotype Stability Index (GSI) was considered as the most stable with high seed cotton yield (Farshadfar, 2008). Based on the GSI, the most desirable genotype might select considering both stability and high seed cotton yield. Not only was that estimation of environmental indices (Ij) used to classify environments into three classes: positive significant as good (favorable environments), positive or negative non significant as average environments and negatively significant as poor (unfavorable) environments.

The combined analysis of variance revealed that effects of genotype (G), environment (E), and G × E interaction were highly significant. Significant G × E interaction indicated that at least one cotton genotype behaved differently in at least one of the test environments; it implied genetic variability and the possibility of selecting genotypes with high seed cotton yield and good yield stability. Therefore, it is possible to proceed to estimate phenotypic stability (Annicchiarico, 1997; Gauch *et al.*, 2008). Genotype × environment interaction makes it difficult to select the best performing, most suitable genotype with good seed cotton yield stability because it reduces the efficiency of selection in plant breeding programs.

4.9 Genotype x Environment interaction through regression analysis

The analysis of variance revealed that genotypes (G), environments (E) and the G x E 'interaction mean squares were significant for seed cotton yield (Table 4.10). Pooled analysis of variance showed highly significant differences among genotypes and environments (Table 4.11), indicating the presence of genetic and environmental variability among the studied genotypes. The G × E interaction was further partitioned into linear and non-linear (pooled deviation) components. Mean squares for both components were found highly significant, indicating that both predictable and un-predictable components shared G x E interaction.

The linear interaction was highly significant when tested against pooled deviation, showing genetic differences among genotypes for their regression on the environmental-index. These results are in accordance with those of Finlay and Wilkinson (1963) and Perkins and Jinks (1968). In the present investigation, the regression coefficients of 13 genotypes were not significantly different from unity. Therefore, the stable performance of these genotypes in this case was predicted on the basis of other two parameters, i.e., deviation from regression and average yield over all the environments (Zubair *et al.*, 2002). The simultaneous consideration of three stability parameters for the individual genotype revealed that JA-08/D, JA-08/C, JA-08/E and CB-10 had higher seed cotton yield over the grand mean seed cotton yield with the regression coefficients (bi) 0.97, 0.84, 1.06* and 0.94 respectively and only the bi of JA-08/E differed significantly from unity (±1.0) (Table 4.23). Due to greater value of regression coefficient (bi > 1.0), JA-08/E expected to give good yield under favorable environmental conditions.

The genotypes, JA-08/A and BC-0406 seemed to be specifically adapted to wide environmental conditions having appreciable seed cotton yield ((3012 and 3089 kg ha^{-1} respectively) but the genotype, JA-08/A had low deviation from regression ($s^2di=0.39$), suggested less sensitive and the genotype, BC-0406 had high deviation from regression ($S^2di=1.16$), suggested highly sensitive change of year as well as locations. Eberhart and Russel, (1966) proposed that the genotypes having average high yield and high s^2di are very sensitive to changing environment and suitable only for favorable environment. Similar results were also reported by other investigators (Arain and Siddiqi, 1977; Sial *et al.*, 1999;

Shindin and Lokteva, 2000). Regression values above 1.0 described genotypes with higher sensitivity to environmental change (below average stability) and greater specificity of adaptability to high yielding environments. A regression coefficient below 1.0 provided a measurement of greater resistance to environmental change (above average stability), and thus increased the specificity of adaptability to low yielding environments (Wachira et al., 2002). Linear regression for the average seed cotton yield of a single genotype on the average yield of all genotypes in each environment resulted in regression coefficients (bi values). The large variation in regression coefficients indicated different responses of genotypes to environmental changes.

The nine environments were developed in three locations of the country and based on the seed cotton yield the environments were subjected to GGE biplot analysis (Fig.4.1). The environmental mean for the character settled of the ordinate of the diagram, indicating superiority of the prevailing environment in Jessore for cultivation of cotton.Moreover, the environmental for the character felt on the ordinate against Jessore, hence this location obviously might for cotton cultivation. When the stability of the genotypes separated according to their performance, the genotypes JA–08/A (1), BC–051(14), BC–342 (15) and BC–0303 (12) had the most stability, besides the genotype JA-08/D (4) followed by JA–08/C (3) had the highest yield and based on GGE biplot their yield was more than environmental mean, therefore the genotypes JA-08/D (4) and JA–08/C (3) considered as genotypes with both high yield and stability performance.

The other genotypes on the right side of the line with double arrows (BC-051(14) and JA-08/D (4)) displayed yield performance greater than mean yield and the genotypes on the left side of this line indicated yield less than mean yield. Genotype JA–0526 (9) showed the lowest yield and genotypes JA–08/9 (7) and JA–0526 (9) exhibited the lowest stability. Overall, genotypes with above-average means were very sensitive to changing of environments, while genotypes with below-average means were stable across the environments. Genotypic stability is quite crucial in addition to genotype yield mean.

The IPCA I scores (70.09%) of a genotype were interpreted in conjunction with the IPCA 1 scores of the individual environments, the adaptability of the genotype might largely be determined by characterization of the environments, for example, whether they be low potential (unfavorable) environments, high potential (favorable) environments, due to drought conditions, high temperature conditions, or whatever the limiting production factor may be present in a particular environment. The relative distance of the individual mean of the genotype for the character has shown (Fig.4.2). The genotypes settled around the zero appeared as stable across the environments.

In general, AMMI and joint regression were found to be useful in assessing the stability of cotton genotypes under the studied environments under study. AMMI was found to be more informative in depicting the adaptive response of the genotypes (Peterson *et al.*, 1989), the joint regression analysis also remains a good option (Eberhart and Russell, 1966; Singh and Singh, 2001). By modeling the above shown AMMI1 results, the effects of the experiment locations were removed, and the yields of the genotypes were calculated according to the scores of the first principal component (Fig. 4.2). The stations were presented on the y-axis according to their scores on the principal component of AMMI1, and the nominal yield is represented on the y-axis. The grouping of the experiment sites is shown. The environment (2010-11) proceeded by 2011-12 and 2012-13 under jessore appeared as favorable environments. The genotypes JA - 08/D (4) and JA - 08/C (3) produced high yield (kg ha^{-1}) at the favorable environments. The genotypes JA– 054 (8) and CB - 11 (20) high IPCA 1 scores, indicated sensitive to mega- environmental changes.

The best genotype with respect to environment was genotype JA-08/D (4). Genotypes JA-08/C (3) and JA-08/E (5) were best for site Jessore; genotypes JA–08/A (1), BC–0406 (13) and BC–051 (14) were best for sites Rangpur. Genotypes located near the plot origin were less responsive than the vertex genotypes. Genotypes JA-08/D (4) and CB-10 (19) gave the highest average yield (largest IPCA 1 scores), but JA-08/D was not stable over the sites, due to the fact that it did not give small absolute IPCA 2 score. In contrast, the non-adapted genotypes JA–08/B (2) and BC-088 (11) yielded poorly at all sites, as indicated by their small IPCA 1 scores (low yielding) and relatively small IPCA 2 scores (relatively stable). The average yield of genotypes CB–10 (19) was below average (IPCA 1 score < 0) and highly unstable (large absolute IPCA 2 score). The biplot showed not only the average yield of a those with above-average means. The ranking of 20 genotypes based on their mean yield and stability performance was exhibited in Fig. 4.3. The line passing through the biplot origin is called the average tester coordinate (ATC), which is defined by the average IPCA 1 and IPCA 2 scores of all environments (Yan and Kang, 2003). When ATC line is parallel to X-axis (IPCA 1) the contribution of G and G x E in the GGESS is equal. This situation can also be observed in normal MEYTs. If ATC line has the increasing form, the contribution of G in the GGESS is more than G x E and decreasing form of ATC indicated that the contribution of G x E in the GGESS was more than G. As Fig. 4.3 revealed increasing form of ATC, therefore contribution of G in the GGESS was more than G x E. This result was confirmed by combined analysis of variance. The line which passes through the origin and is perpendicular to the ATC with double arrows represents the stability of genotypes. Either direction away from the biplot origin on this axis indicated greater G x E interaction and reduced stability. However the stable genotypes have a shorter vector from the ATC and yielder genotypes have the most distance on the right side of biplot from the confluence point of ATC and double arrow lines.

According to Duarte and Vencovsky (1999), stability is evaluated in the x-axis (IPCA 1) by AMMI1, whilst y-axis ((IPCA 2) by AMMI2 analysis revealed stable environments and genotypes located near the origin, with low scores for the two axes of the interaction. In the AMMI analysis for yield, the first two principal components account for G×E interaction variability (IPCA 1 27.09 % and IPCA 2 20.92 %). The results in a graph (Fig. 4.4) showing the environmental effect on each genotype (Gauch and Zobel, 1996; Burgueño *et al.*, 2000; Yan and Hunt, 2001; Kaya *et al.*, 2002). This bidimensional Figure (Fig.4.3) was divided into four sections in which cultivars and environments are distributed according to the sign of their respective vectors obtained in the analysis (Tarakanovas and Ruzgas, 2006; Kaya *et al.*, 2006). In general, cultivars exhibit a high degree of yield variability reflected by high dispersion in the biplot. Thus, interesting cultivars are those with IPCA 1 values higher than zero and classified as high yield, while those with IPCA1 values lower than zero are classified as low yield and low adaptability (Kaya *et al.*, 2006). Low yield genotypes and environments are located in quadrants III and IV while, high yield genotypes are located in quadrants I and II. The genotypes JA–0526 (9), CB–10 (19) and CB–11 (20) had low IPCA 1 scores, indicated low adaptability and the lowest yield. On the other hand, genotypes that were stable or less sensitive to environmental influences were found near the biplot point of origin (Mahalingam *et al.*, 2006; Kaya *et al.*, 2006). Das *et al.* (2010), and Kulsum *et al.*

4.10 Which-Won-Where Pattern of genotypes

The ranking of the nine environments were summarized by considering means of the specific locations for seed cotton yield. The location, Dinajpur fell on the lower slopping diagonal line, seemed the location has average suitability for cultivation of cotton. Again, the three locations have not shown speedy deviation on the performances of the genotypes, since the upper slopping line is far away from the environmental means. One of the smartest facial appearances of a GGE biplot is its facility to show the which-won-where model of a genotype by environment dataset (Fig. 4.5). Many researchers find this use of a biplot intriguing, as it graphically addresses important concepts such as crossover G × E, mega environment differentiation, particular adaptation, etc (Yan and Tinker, 2005). The most accurate model for AMMI can be predicted by using the first two PCAs (Gauch and Zobel, 1996; Yan *et al.*, 2002). Conversely, Sivapalan *et al.* (2000) recommended a predictive AMMI model with the first four PCAs.

These results indicate that the number of the terms to be included in an AMMI model cannot be specified a priori without first trying AMMI predictive assessment. In general, factors like type of crop, diversity of the germplasm, and range of environmental conditions will affect the degree of complexity of the best predictive model (Crossa *et al.,* 1990). A biplot is generated using genotypic and environmental scores of the first two AMMI components (Vargas and Crossa, 2000). A biplot has four sections, depending upon signs of the genotypic and environmental scores. In the Fig. 4.5, the sites fell into four sectors. The polygon is created by involving the markers of the genotypes that are further away from the biplot source such that all other genotypes are restricted in the polygon. Genotypes located on the vertices of the polygon performed either the best or the poorest in one or more environments since they had the long distance from the origin of biplot. The perpendicular lines are equality lines between adjacent genotypes on the polygon, which facilitate visual comparison of them.

Hence, it is important in the selection of genotypes across several environments, besides calculating the average performance of the genotypes under evaluation (Gauch and Zobel, 1997).

4.11 Fibre quality analysis

The quality of fiber was assessed through eight characters as presented in Table 4.24. The highest GOT (ginning out turn) percentage was recorded from the genotype; JA-08/D (43.05%) followed by JA-08/C (42.33) and JA-08/A (41.60) and were significantly higher than other genotypes. The lowest GOT (%) was recorded from CB-11 (33.74%). The highest seed index was also obtained from JA-08/D (12.26) followed by JA-08/E (11.30) and JA-08/B (10.42). The lowest seed index was recorded from JA-0526 (7.78). The range of lint index varied from 4.36-7.90 and the highest value of this trait was estimated in CB-10, which were followed by JA-08/B (7.84) and BC-097 (7.67). Three genotypes namely, JA-08/D, CB-10 and CB-11 showed same fuzz grade (8) and it was significantly higher than other genotypes. The lowest fuzz grade (5) also recorded from two genotypes (JA-054 and BC-0342). The highest 2.5% span length (1.19 inch) was obtained from JA-08/D which were followed by three genotypes viz. JA-0526, JA-0510 and CB-10, each with the value of 1.18 inch for the trait. The lowest 2.5% span length (1.10 inch) was estimated in CB-11. The highest Presley strength (Psi) was recorded by the genotype JA-O8/D and the lowest was recorded by the control variety CB-9 respectively. The highest micronaire value (4.39) was estimated in JA-08/D, which was followed by two genotypes, each the value of 4.28 for the trait. The lowest micronaire value (4.02) was recorded in CB-11.

To maximize fiber length, proper management and good growing conditions must be available during the elongation phase of fiber development. Fiber elongation takes place in the first 16 to 25 days after boll development. During this time, high temperatures, water stress and potassium deficiency can result in shorter fibers (Liakatas,1998). Fiber length can also be affected by the ginning process. If cotton moisture is low during ginning, fiber length can be compromised due to breakage. The ideal ginning moisture range is 6 to 8%. When lint moisture is below 5%, each percentage point lower is equivalent to 1/100 of an inch reduction in length (Delhom and Rodgers, 2016). Fiber strength is primarily determined by the variety; however, environment can have some affect on strength. Certain cultural practices can increase or decrease the lint strength. Severe potassium deficiency can decrease lint strength and extreme weather conditions may cause physical or microbial damage to fiber, resulting in reduced strength.

Table 4.24 Characteristics of cotton fibers in 20 genotypes

Genotypes	G.OT (%)	Seed index (g)	Lint index (%)	Fuzz grade	50% Span length (inch)	2.5% Span length (inch)	2.5% Span length (mm)	Presley strength (psi)	Micronaire value
JA-08/A	41.60	8.56	6.57	6	0.5	1.13	28.7	84.7	4.17
JA-08/B	42.00	10.42	7.84	7	0.58	1.14	28.96	83.87	4.28
JA-08/C	42.33	8.68	6.26	6	0.57	1.16	29.46	84.63	4.16
JA-08/D	43.05	12.26	7.59	8	0.59	1.19	30.23	85.58	4.39
JA-08/E	39.97	11.30	5.80	7	0.58	1.15	29.21	83.79	4.05
JA-0541	4118	9.57	5.43	6	0.56	1.16	29.46	84.97	4.16
JA-08/9	39.63	8.99	6.08	6	0.53	1.11	28.19	83.03	4.25
JA-054	37.13	9.25	6.12	5	0.55	1.13	28.7	84.25	4.28
JA-0526	37.31	7.78	5.58	6	0.51	1.18	29.97	84.33	4.16
JA-0510	36.48	8.71	6.8	6	0.52	1.18	29.97	84.70	4.03
BC-088	35.15	9.56	6.72	7	0.50	1.15	29.21	83.59	4.12
BC-0303	36.48	9.72	4.47	6	0.54	1.16	29.46	84.61	4.27
BC-0406	34.42	9.58	5.88	6	0.55	1.17	29.72	83.87	4.18
BC-051	34.98	9.99	5.95	6	0.57	1.15	29.21	84.34	4.14
BC-0342	35.47	9.16	4.36	5	0.58	1.13	28.7	84.58	4.12
BC-037	36.90	9.45	7.67	7	0.53	1.14	28.96	84.70	4.23
BC-0188	35.58	9.50	6.20	5	0.52	1.16	29.46	83.85	4.16
CB-9	34.68	9.26	6.88	7	0.57	1.16	29.46	82.62	4.25
CB-10	37.52	10.52	7.90	8	0.58	1.18	29.97	84.50	4.13
CB-11	33.74	9.39	6.55	8	0.53	1.10	27.94	84.18	4.02
CV (%)	7.23	8.46	7.21	6.89	6.29	6.48	6.48	8.22	5.90
LSD	2.375	1,842	1.736	0.815	0.025	0.007	0.007	0.002	0.012

G.O.T: Ginning out turn

CHAPTER V

SUMMARY AND CONCLUSION

Cotton is currently the leading plant fibre crop worldwide and is grown commercially in the temperate and tropical regions of more than 50 countries. Specific areas of production include countries such as USA, India, China, America, the Middle East and Australia, where climatic conditions suit the natural growth requirements of cotton, including periods of hot and dry weather and where adequate moisture is available, often obtained through irrigation. Cotton is primarily grown as fibre crop. It is harvested as 'seed cotton' which is then 'ginned' to separate the seed and lint. The long 'lint' fibres are further processed by spinning to produce yarn that is knitted or woven into fabrics. The ginned seed is covered in short, fuzzy fibres, known as 'linters'. These must be removed before the seed can be used for planting or crushed for oil, and are used in a variety of products including foods. The linters are produced as first-cut or second cut linters. The first-cut linters have a longer fibre length and are used in the production of mattresses, furniture upholstery and mops. The second-cut linters have a much shorter fibre length and are a major source of cellulose for both chemical and food uses. They are used as a cellulose base in products such as high fibre dietary products as well as a viscosity enhancer (thickener) in ice cream, salad dressings and toothpaste. In the chemical industry the second-cut linters are used with other compounds to produce cellulose derivatives such as cellulose acetate, nitrocellulose and a wide range of other compounds. However, the findings of the entire investigation are described below-

5.1 Mean performances of the characters

The mean performances of 12 characters revealed significant variation for each of studied characters in 20 genotypes of cotton. Among the genotypes, days to 1st flowering ranged from 47-56 and the genotype, BC-051 was appeared the earliest and BC-037 was the late flowering genotypes. The character like boll weight remarkably varied among the genotypes. And the range was 4.17g (JA-08/9) to 6.17 (JA-08/C) with increase of un-brust boll plant^{-1} reduced seed cotton yield. The plant height among the genotypes varied from 91.80 cm (JA-08/9) to 131.27 (JA-0188). The highest seed cotton yield (3430 kg ha^{-1}) was obtained from JA-08/D followed by JA-08/C (3329 kg ha^{-1}), JA-08/E (3226 kg ha^{-1}) and CB-10 (3205 kg ha^{-1}).

Though the highest CV (%) was estimated in seed cotton yield (19.94%) but other characters had reasonable CV (%).

5.2 Genetic parameters of the characters

The characters under study were polygenitically controlled, hence the expression of the characters were influenced by environments (locations and years). The PCV for particular character was higher than corresponding GCV, suggested influence of environments. A wide difference between GCV and PCV was measured for days to 1st boll splitting, plant height and seed cotton yield, therefore theses characters were more affected environmental fluctuations. High heritability coupled with high genetic advance (h^2b=90.36% and GA=58.49) was estimated against bolls plant^{-1}. Moderate heritability (h^2b=83.58%) and moderate genetic advance (GA=48.54) were estimated for seed cotton yield, therefore, theses two characters might exploit to improve seed cotton yield through selection and discriminant function analysis.

5.3 Correlation coefficient analysis

A total of 55 pairs of correlation coefficients (r_g and r_p) were computed considering 12 characters. The genotypic correlation coefficient (r_g) of a particular character was higher than corresponding phenotypic correlation coefficient (r_p) suggested that the relationship among the characters were primarily genetically controlled. The characters like vegetative branches plant^{-1} and un-brust bolls plant^{-1} showed negative and significant association with seed cotton yield and six characters viz, secondary fruiting branches plant^{-1}, main stem nodes plant^{-1}, days to 1st flowering, bolls plant^{-1}, boll weight (g) and seeds boll^{-1} exhibited positive and significant correlation with seed cotton yield both at genotypic and phenotypic levels, hence these characters might promote seed cotton yield through appropriate breeding programs. Three characters namely primary fruiting branches plant^{-1}, plant height and days to 1st boll splitting showed positive but nonsignificant correlation with seed cotton yield.

5.4 Path coefficient analysis

Since the association among the characters was primarily genetically controlled, only genotypic correlation coefficients were separated through path coefficient analysis. The highest direct effect (1.982) was exerted by seeds boll^{-1} followed by boll weight (1.568) and bolls plant^{-1} to develop strong and positive correlation with seed cotton yield. The characters like vegetative branches plant^{-1} and unbrust bolls plant^{-1} showed negative and significant association with seed cotton yield. The cumulative indirect effects other characters had not change the direction of association with seed cotton yield.

5.5 Selection index

A total of 30 selection indices were constructed considering five characters namely days to 1st flowering, bolls plant^{-1}, boll weight, seeds boll^{-1} and seed cotton yield. The characters were selected based on genetic parameters, genotypic and phenotypic correlation coefficients and causes and effects to develop genotypic correlation with seed cotton yield. Seed cotton yield alone considered as 100% and based on this assumption other selection functions were analyzed. Among the single character function, seeds boll^{-1} exaggerated 11.48% genetic worth and 84.66% relative efficiency over straight selection. Of the two character combination functions, the highest relative efficiency (118.66%) was realized by the combination of boll weight and seeds boll^{-1} but when seed cotton yield was included with others. The function I_{15} produced the highest genetic worth of 15.00% due to combined with seeds boll^{-1}. Usually the relative efficiency was increased with corresponding increase of more characters in the functions and accordingly, the index I_{135}(seed cotton yield+ bolls plant^{-1} + seeds boll-^{1}) offered the highest relative efficiency among the five functions where seed cotton yield was included in every index. However, of the 10 functions comprising with possible four characters integration, the highest relative efficiency (154.72%) was obtained from I_{1245} (seed cotton yield+ days to 1st flowering+ boll weight+ seeds boll^{-1}). At the end the functional analysis the genetic worth of the five characters combination was realized where the highest relative efficiency was estimated to 157.22%. Since a conventional breeder, always thinks to develop high seed cotton yielding variety, simultaneous consideration of these five characters must be emphasized to develop sustainable and high seed cotton yielding variety.

5.6 Insect infestation in cotton

Five insects such as thrips, cotton bug, bollworm, aphids and whitefly frequently visited cotton field during cropping season. It is noted that Bt cotton has been developed against insect but cotton bollworm was not a major insect in cotton as compared to other visiting insects. None of the genotypes was found insect free but JA-08/D did not attack by any insect. Number of infested leaves plant^{-1} varied from 0.0-12.6 and the highest infestation of leaves was recorded in BC-0303, which was followed by JA-0526 (11.2) and JA-0510 and

BC-037 with each of 10.1. The highest number of infested bolls plant^{-1} (8.1) was recorded from BC-0303 followed by BC-037 (6.8) but did not significantly differ.

5.7 Mean performances over locations and years

Among the three locations, Jessore was more suitable for cotton cultivation as compared to Rangpur and Dinajpur for expression of all the characters except unbrust bolls plant^{-1}. The magnitude of unbrust bolls plant^{-1} was only 0.93 in Jessore. The highest yield over the years was obtained in Jessore (3238 kg ha^{-1}) followed by the seed cotton yield obtained in the Rangpur (3052 kg ha^{-1}) and Dinajpur (2825 kg ha^{-1}). The genotypes flowered earlier (50.67 days) in Dinajpur as compared to Rangpur (55.33 days) and Jessore (60.60 days). Though bolls plant^{-1} differed remarkably in three locations over three years but the highest bolls plant^{-1} was observed in Jessore. Boll weight did not appreciably vary in three locations. However, genotype, JA-08/D performed better in three locations over three years, which were followed by JA-08/C and JA-08/E.

5.8 Combined analysis of variance

Combined analysis revealed significant effects of genotypes, locations and years and their possible interactions on the characters. Usually replication did not show significant variation but unbrust bolls plant^{-1} showed significant effect over the locations and years. The highest variation expected accounted 28.36% for genotype followed by genotype x environment (18.68%) and year (13.57%). The changes of locations and years caused such types of interaction effects of the expression of the characters. Genotype x year interaction was also significant at 5% level of probability for main stem nodes plant^{-1}, days to 1st boll splitting and unbrust bolls plant^{-1} and other multiplicative interactions were significant at 1% level of probability. For precise G x E interaction the data were subjected to AMMI analysis. All kinds of additive and multiplicative interactions were significant. Four IPCAs were calculated and the G x E interactions was estimated mainly based on IPCA1 and IPCA2 values. Two IPCA scores, bi (regression coefficient), s^2di (deviation from regression) and average stability value were simultaneously considered to assess response and stability of 20 genotypes over three locations and across three years. Out of four high seed cotton yielding genotypes (JA-08/D, JA-08/C, JA-08/E and CB-10) were stable but JA-08/E was relatively unstable over the locations and years due to significant bi=1.06*.

5.9 Estimation of fiber quality

The highest GOT (Ginning Out Turn) was recorded in JA-08/D (43.05%) followed by JA-08/C (42.33%) and JA-08/B (42.00%). Lint index was the highest in CB-10 (7.37). Three genotypes had same fuzz grade as 8.0 in JA-08/D, CB-10 and CB-11.

Genotype x environment interaction continues to be a challenging issue among plant breeders, geneticists, and production agronomists who conduct drop performance trials across diverse environments. GEI can reduce progress from selection. The methods of partitioning GEI into components attributable to each genotype measure the contribution of each genotype to GEI. A universally acceptable selection criterion that takes GEI into consideration does not exist. Whenever an interaction is significant, the use of main effects, e.g. overall genotypes means across environment is questionable. Stability of performance should be considered an important aspect of yield trials. Researchers need a statistic that provides a reliable measure of stability or consistency of performance across a range of environments, particularly one that reflects the contribution of each genotype to the total GEI. However, the stability measure alone is of limited use to be of practical utility in a breeding or cultivar testing programme, both stability and yield (or any other trait) must be considered simultaneously so as to make selection of genotypes more precise and reliable. Also integration of stability of performance with yield through suitable measures will reduce the effect of GEI and will help in selecting cultivars in a more refined manner.

5.10 Recommendation

1. The selected twelve characters including seed cotton yield differentially responsed to three locations over three years.
2. Bolls plant^{-1}, Seeds boll^{-1} and boll weight were the more seed cotton yield enhancing characters. So breeders might exploit these three characters for improvement of cotton.
3. Jessore was the best location for cotton cultivation; therefore, the farmers' of this belt might include to PPB (Participatory Plant Breeding) or PVS (Participatory Variety Selection) methods. to find out high seed cotton yielding genotypes.
4. Though five insects such as thrips, cotton bug, bollworm, aphids and whitefly frequently visited during cropping season but JA-08/D showed complete resistant to insect attack.
5. Any of the four high seed cotton yielding genotypes JA-08/D, JA-08/C, JA-08/E and CB-10 might advance in further breeding programs with a view to develop high yielding cotton varieties.

CHAPTER VI

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Appendix I: Monthly average maximum temperature (^{0}C) in different locations (2010)

Location	July	August	September	October	November	December
Jessore	36.7	34.6	33.8	30.2	27.0	23.6
Dinajpur	32.7	32.7	32.3	30.7	30.1	25.5
Rangpur	33.2	31.1	32.5	31.3	29.2	25.2

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix II: Monthly average minimum temperature (^{0}C) in different locations (2010)

Location	July	August	September	October	November	December
Jessore	25.5	25.0	24.2	21.7	17.7	9.9
Dinajpur	26.3	25.8	25.5	20.4	18.3	11.3
Rangpur	23.3	26.7	27.3	21.1	17.5	10.1

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix III: Monthly total rainfall (mm) in different locations (2010)

Location	July	August	September	October	November	December
Jessore	123.7	35.6	202.4	99.3	0.0	41.5
Dinajpur	256.0	115.0	151.0	69.0	0.0	0.0
Rangpur	290.0	141.0	115.0	43.0	15.0	0.0

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix IV: Monthly average maximum temperature (^{0}C) in different locations (2011)

Location	July	August	September	October	November	December
Jessore	33.2	34.1	34.7	32.3	29.5	23.0
Dinajpur	32.6	32.7	31.3	32.0	29.6	21.9
Rangpur	31.5	33.9	30.1	31.5	28.3	19.9

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix V: Monthly average minimum temperature (^{0}C) in different locations (2011)

Location	July	August	September	October	November	December
Jessore	13.7	13.4	14.1	18.9	15.2	10.0
Dinajpur	25.7	25.5	25.7	23.0	15.9	10.9
Rangpur	24.5	27.3	24.8	23.9	14.2	9.9

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix VI: Monthly total rainfall (mm) in different locations (2011)

Location	July	August	September	October	November	December
Jessore	224.9	381.1	268.8	11.8	0.0	94.6
Dinajpur	328.0	499.0	278.0	46.0	0.0	0.0
Rangpur	290.0	430.0	310.0	60.0	10.0	0.0

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix VII: Monthly average maximum temperature (^{0}C) in different locations (2012)

Location	July	August	September	October	November	December
Jessore	31.8	32.2	30.9	28.8	24.9	23.3
Dinajpur	31.8	33.0	32.4	31.8	28.7	21.4
Rangpur	30.3	32.8	31.9	30.7	29.6	20.1

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix VIII: Monthly average minimum temperature (^{0}C) in different locations (2012)

Location	July	August	September	October	November	December
Jessore	26.9	26.9	26.4	22.7	17.2	11.2
Dinajpur	26.4	26.0	25.4	22.1	15.1	11.5
Rangpur	25.3	27.0	23.2	21.2	14.5	12.2

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix IX: Monthly total rainfall (mm) in different locations (2012)

Location	July	August	September	October	November	December
Jessore	289.8	249.6	174.1	55.8	76.2	0.0
Dinajpur	528.0	102.0	424.0	15.0	0.0	0.0
Rangpur	490.0	120.0	450.0	40.0	25.0	0.0

Source:

1. Meteorological department, Regional Agriculture Research Station, Jessore
2. Meteorological department, Wheat Research Center, Nashipur, Dinajpur
3. Meteorological department, Cotton Research Center, Mahiganj, Rangpur

Appendix X: Soil Characterization of Different Locations

Items	Locations		
	Jessore	Dinajpur	Rangpur
Soil Type	Sandy to sandy loam	Sandy loam	Sandy loam to loam
P^H	6.0 – 6.5	4.5 – 5.5	6.5 – 7.0
AEZ	11	03	03
Description of AEZ	The site is situated approximately between $23^0 17'30''$latitude north and between $89^0 4'7''$ longitude east	The site is situated approximately between $25^0 13'$ latitude north and between $88^0 23'$ longitude east	The site is situated approximately between $25^0 39'$ and $25^0 59'$latitude north and between $89^0 5'$ and $89^0 20'$ longitude east

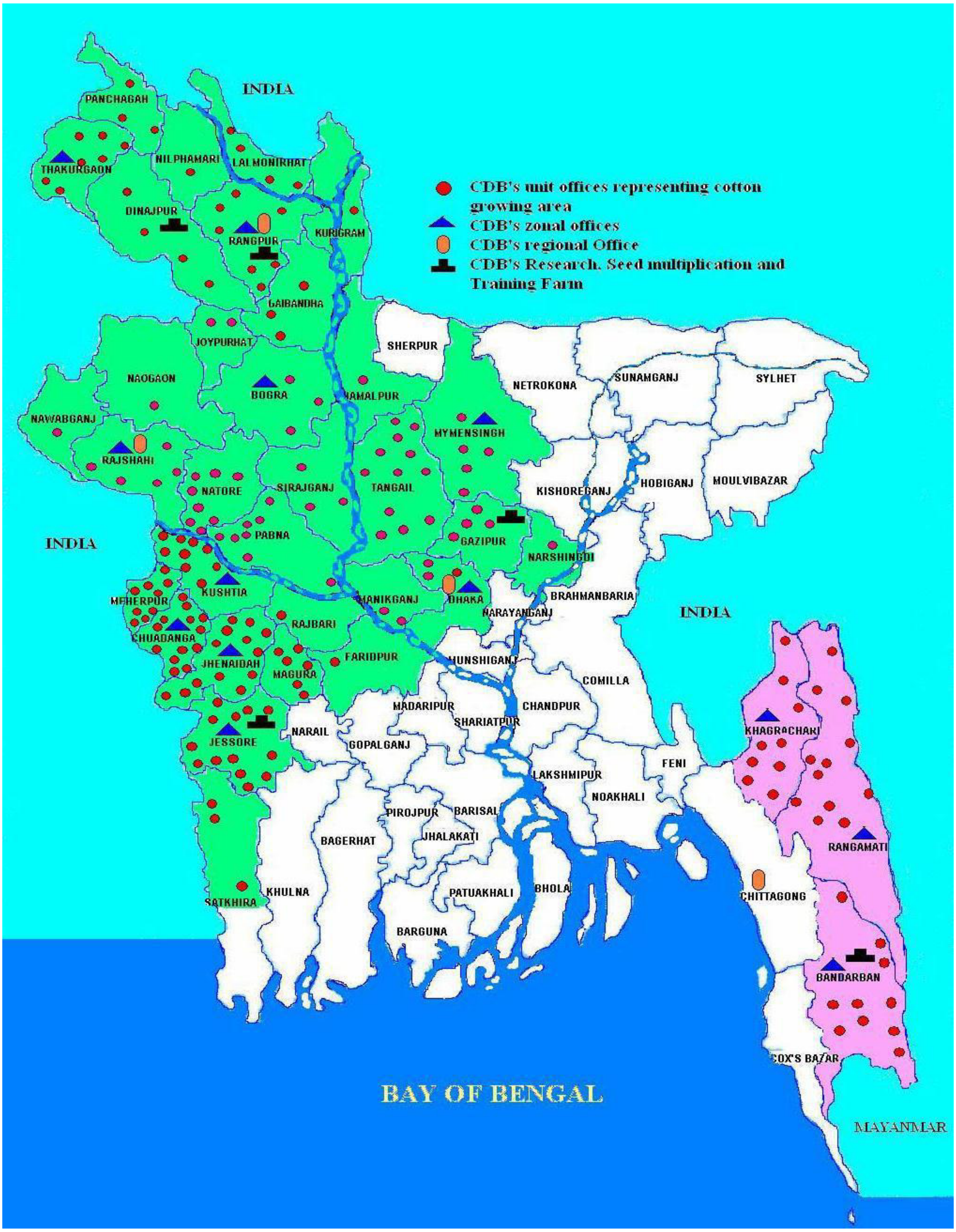

Fig. 1.1.1 Cotton growing areas in Bangladesh

Fig. 3.3.1.1 Map of Bangladesh

Fig. 3.6.2.1 Pictorial view of seed sowing in the research field at Cotton Research, Training and Seed Multiplication Farm, Jagodishpur, Jessore

Fig 3.6.2.2 Pictorial view of seed sowing in the research field at Cotton Research, Training and Seed Multiplication Farm, Sadarpur, Dinajpur

Fig 3.6.2.3 Pictorial view of seed sowing in the research field at Cotton Research Center, Mahigonj, Rangpur

Fig 3.6.3.2.1 Pictorial view of application of cowdung at the experimental plot

3.6.3.4 Mulching

Mulching was done after 40 days of sowing to make easy aeration of soil and to conserve moisture, which ultimately ensured better growth and development. Breaking of crust of the soil, when needed was done through mulching.

3.6.3.5 Plant Protection

After 30-35 days of sowing, first spray of choloropyriphose was applied against sucking pests such as Jassid, Aphid etc. Other seven (7) sprays of chloropyriphose were applied in combination with pyrethorid to control sucking and chewing (Boll worm, spoted boll warm, spodoptera etc) pests. In all cases scouting based spray was followed. Boll worm and spodoptra attack was controlled by taking different control measures. Hand picking and Pheromone trap also used to kill larva and moths of the insets. As a result, more or less insect reproduction were stopped which encouraged friendly agro-ecosystem to some extent.

To protect the fungal diseases, Dythane-M-45 and Bavistin were sprayed about three times at seedling and after boll formation stages of the plant. Insect attack and disease incident was keenly observed line wise.

Fig 3.6.3.5.1 Application of fungicide by napsack sprayer at seedling stage

Fig 3.6.3.5.2 Application of inter-row cultivator for weed control and fertilizer Management

Fig 3.6.3.5.3 Spraying of chemical insecticide by power spray

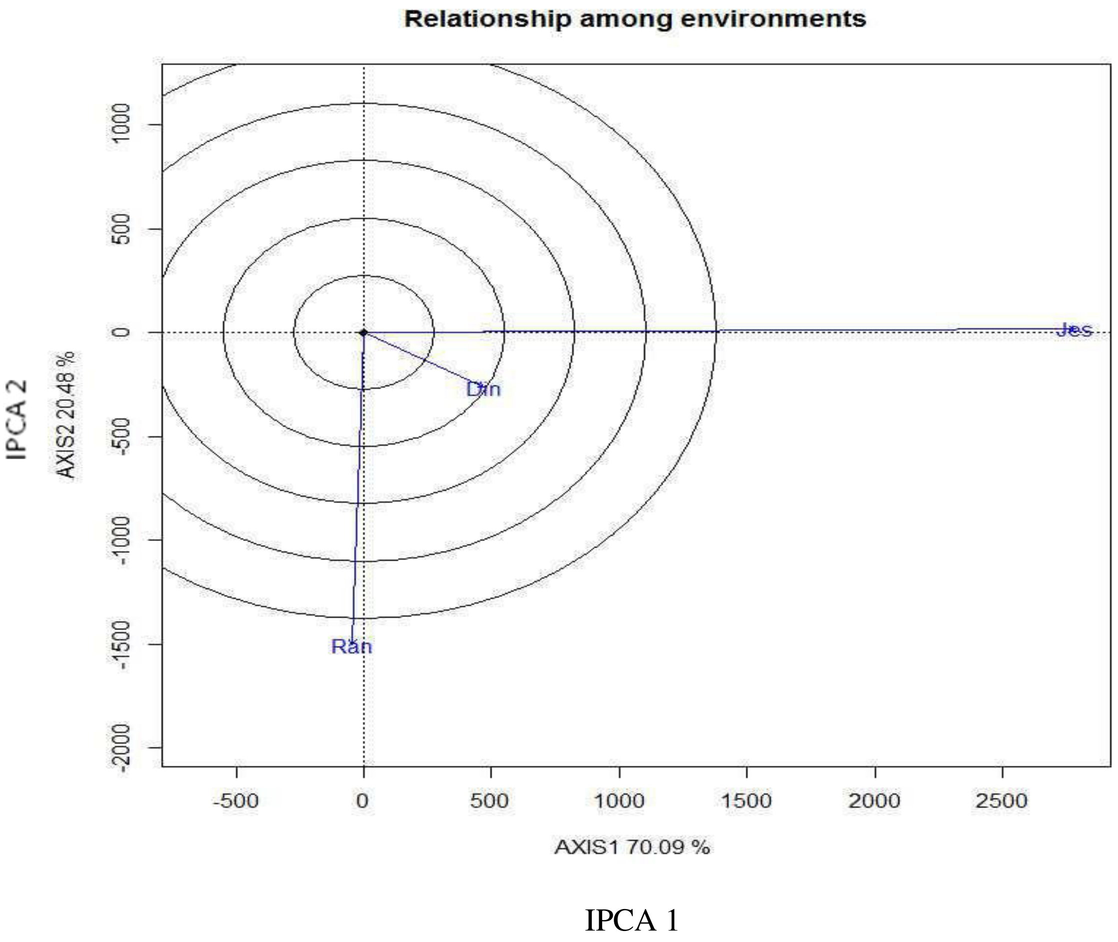

Fig. 4.1 GGE biplot analysis based environment focused sealing for comparison seed cotton yield (kg ha^{-1})

IPCA: Interaction principal component analysis through two axes
Ordinate= Jessore (1st quardant)
Abcissa= Rangpur (3rd quardant)
Between Ordinate and Abcissa= Dinajpur (4th quardant)

The ideal genotype should have the highest mean performance and be absolutely stable (Yan and Kang, 2003), which is represented by the dot with an arrow pointing to it (Fig. 4.1). Such an ideal genotype is defined by having the greatest vector length of the high yielding genotypes and with zero GEI. Concentric circles were drawn to help visualize the distance between each genotype and the ideal genotype; a genotype is more desirable if it is located closer to the ideal genotype. The highest genotype JA-08/D (4) followed by JA–08/C (3) and JA-08/E (5) were appeared as ideal genotypes and closer cluster of this group included BC - 0406 (13) and JA–08/A (1) across the environments Jessore, Rangpur and Dinajpur, respectively.

The presence of main effect variation was observed. However, according to IPCA1 genotype array, significant G x E interaction occurred. The genotype JA–08/C (3) had the smallest interaction effect, while the genotype BC-0406 (13) followed by JA–08/B (2) responded vigorously to amelioration. The genotypes JA-08/D (4), JA-08/C (3) and JA-08/E (5) gave averagely high yield and showed stable over the environmental modifications. The other two genotypes, CB-9 (18) and CB-11 (20) exhibited great reduction of yield potential under unfavorable environment (Fig. 4.1) A remarkable seed cotton yield variation explained by environments indicated that environments tested in the study were diverse, with large differences among environmental effects causing the most variation in seed cotton yields of cotton genotypes (Dimitrijevic *et al.*, 2005).

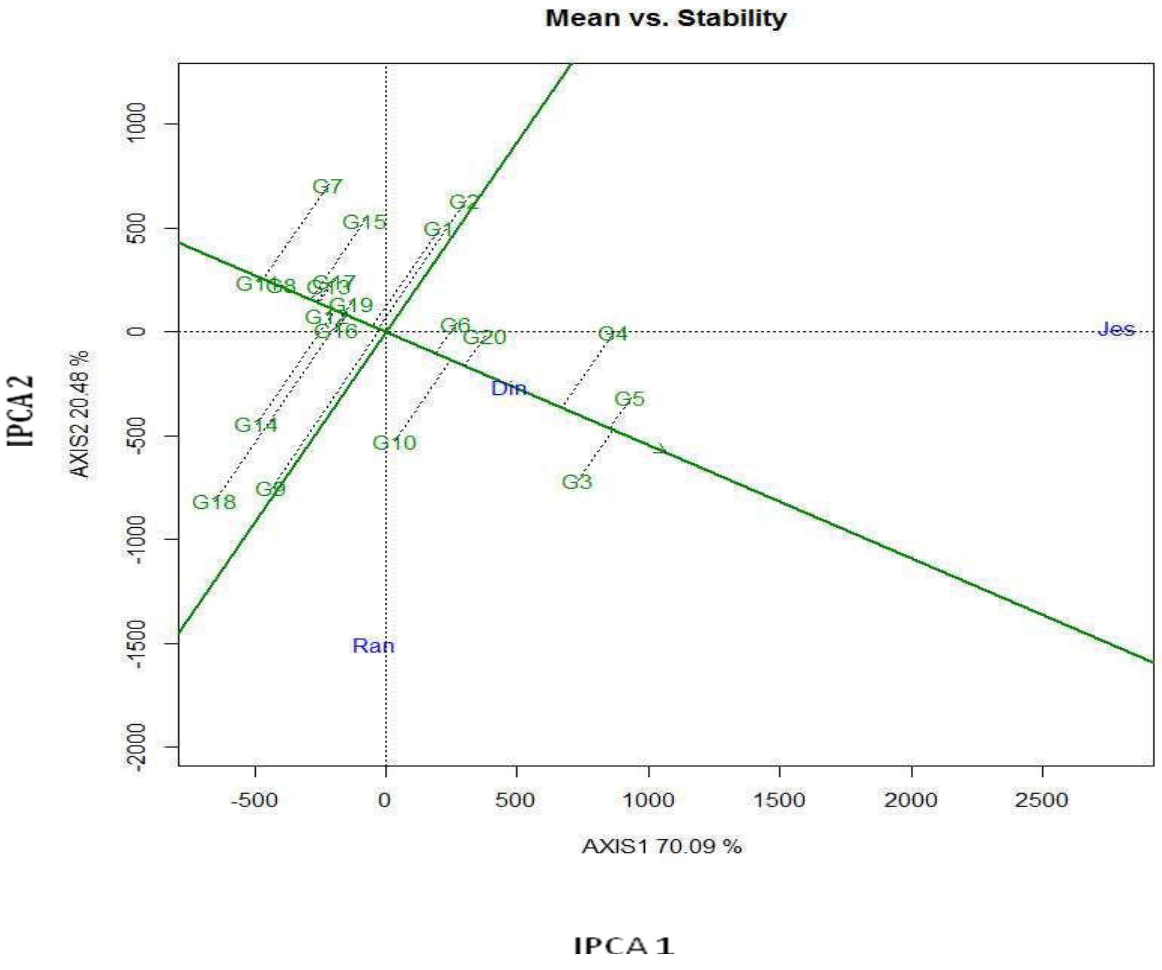

Fig. 4.2 AMMI Model for seed cotton yield (kg ha^{-1}) showing the means of genotypes and locations against their respective IPCA scores

IPCA: Interaction principal component analysis through two axes
Green color indicate = Distribution of 20 genotypes
Purple color indicate = Locations

genotype (IPCA 1 and IPCA 2 effects), but also how it was achieved. That is, the biplot also showed the yield of a genotype at individual sites.

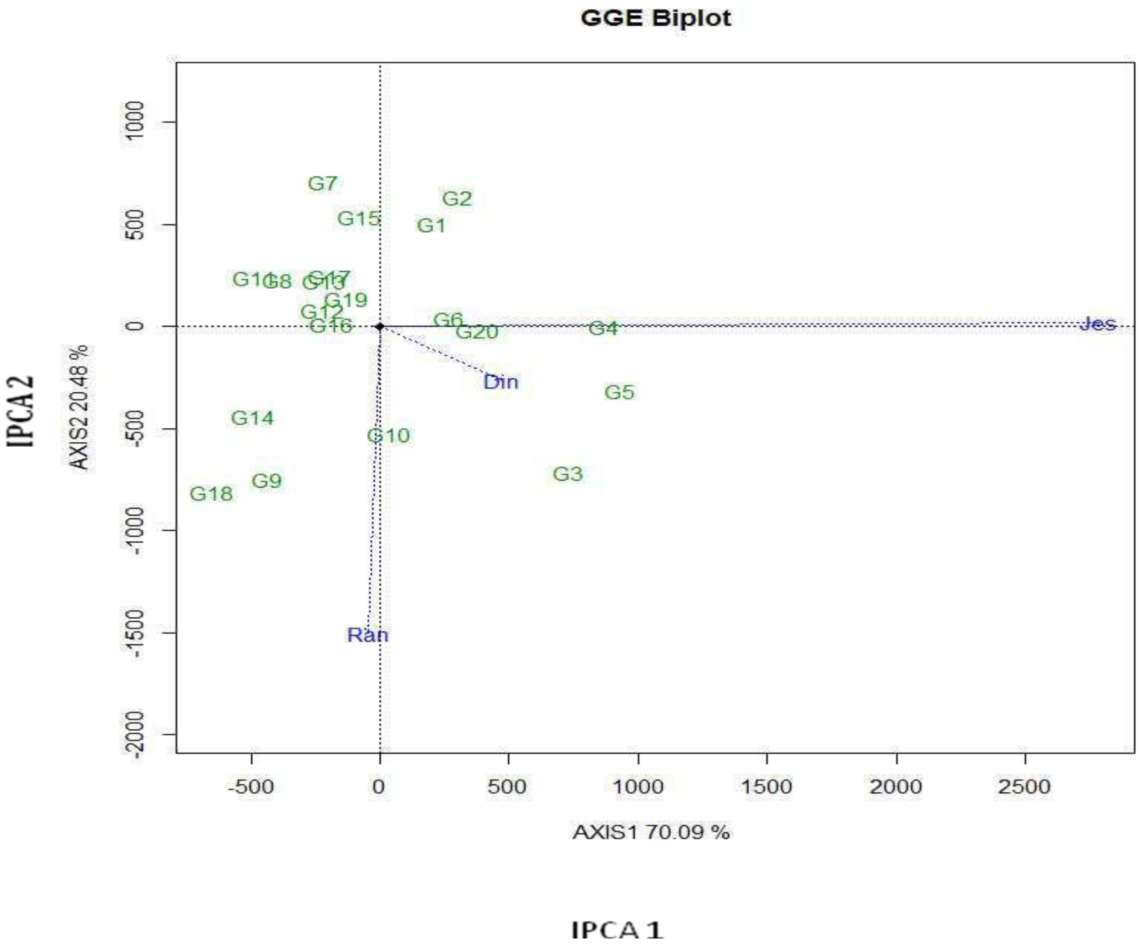

Fig. 4.3 Average tester coordinator (ATC) views of the GGE biplot based on environmental focused sealing for seed cotton yield (kg ha^{-1}) and stability of the genotypes

IPCA: Interaction principal component analysis through two axes
Green color indicate = Distribution of 20 genotypes
Purple color indicate = Locations

The yield stability of genotypes was evaluated by an average environment coordination (AEC) method (Yan, 2001; Yan and Hunt, 2000; Yan, 2002). In this method, the average principal components were be used in all environments, as depicted in (Fig. 4.3). A line was then drawn through this average environment and the biplot origin; this line was called the average environment axis and serves as the abscissa of the AEC. Unlike the AEC abscissa, this has one direction, with the arrow pointing to a greater genotype main effect; the AEC ordinate and either direction away from the biplot origin indicated greater GEI effect and reduced stability. The AEC ordinate separates genotypes with below-average means from

(2013) reported that since, the environments with positive IPCA 1 score near zero had small interaction effects indicating that all the genotypes performed well in that location. Adugna *et al*. (2007) and Anandan *et al.* (2009) reported similar pattern of interactions. However, the genotypes distributed around the nill point and covered by same periphery supposed to high performance over the environments.

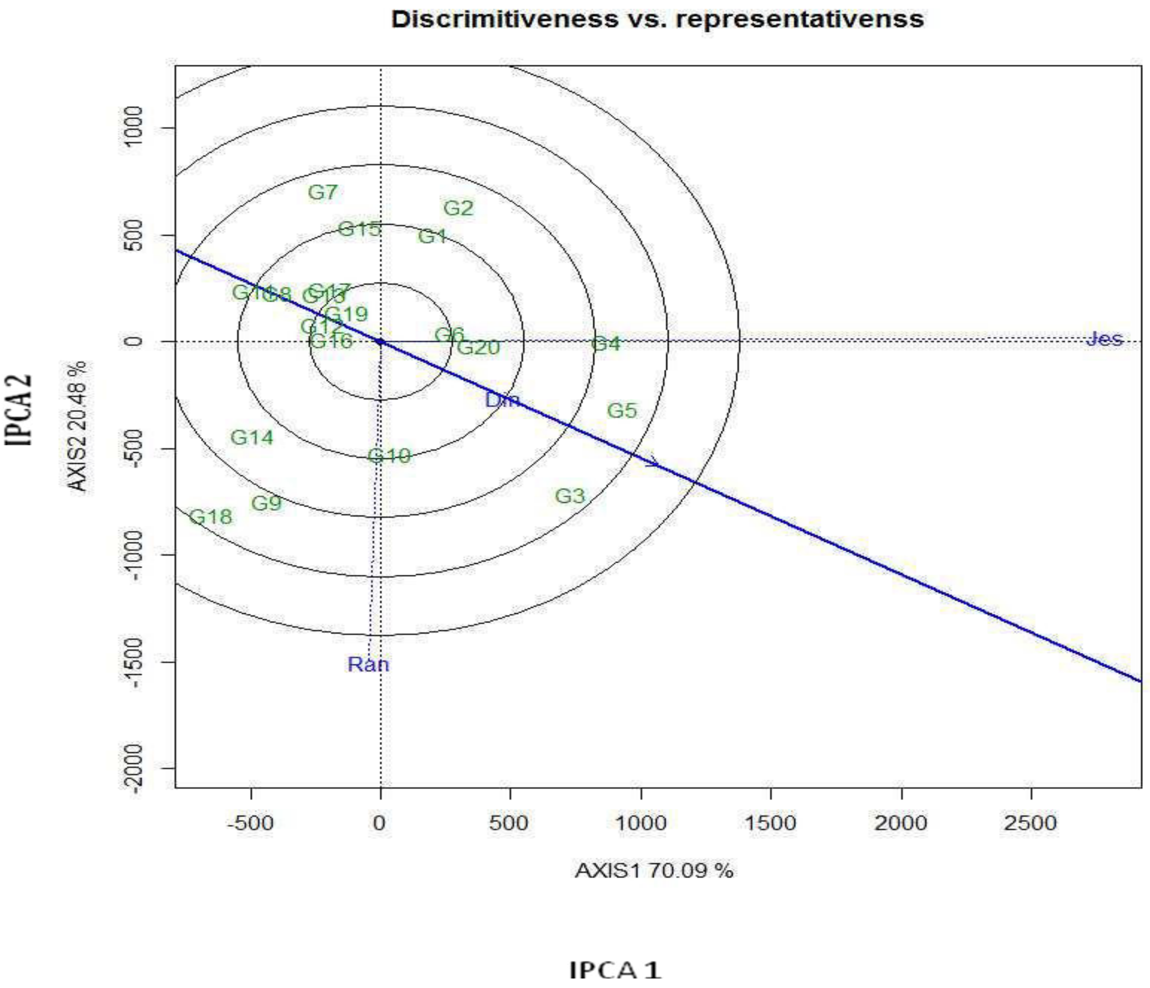

Fig. 4.4 AMMI Model for seed cotton yield (kg ha^{-1}) showing IPCA 1vs IPCA 2 scores of cotton genotypes sown across the locations

IPCA: Interaction principal component analysis through two axes
Green color indicate = Distribution of 20 genotypes
Purple color indicate = Locations
Purple diagonal line= Average G x E with relative distributions of the genotypes and environments.

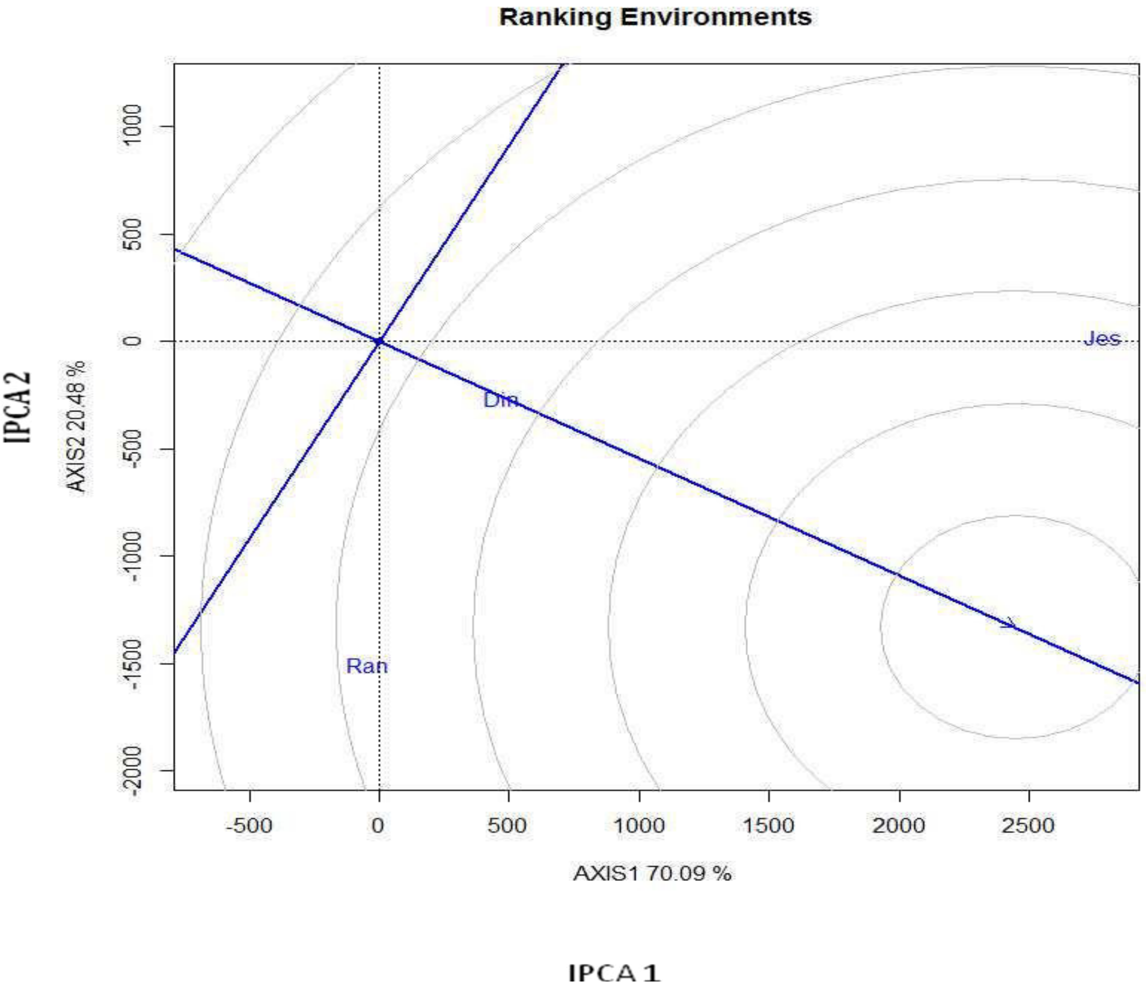

Fig. 4.5 GGE biplot analysis based on environmental means focusing comparison seed cotton yield (kg ha^{-1})

IPCA: Interaction principal component analysis through two axes
Purple color indicate = Locations
Purple lines = Upper slopping line is more sensitive to lower slopping line

For instance, adaptable genotypes or higher yielding in environment Jessore may also show similar responses to environments Rangpur and Dinajpur, as well as indirect selection for non-stress environments. An environment is more desirable if it is located closer to the ideal environment. Thus, using the ideal environment as the centre, concentric circles were drawn to help visualize the distance between each environment and the ideal environment (Yan *et al.,* 2000; Yan and Rajcan, 2002).

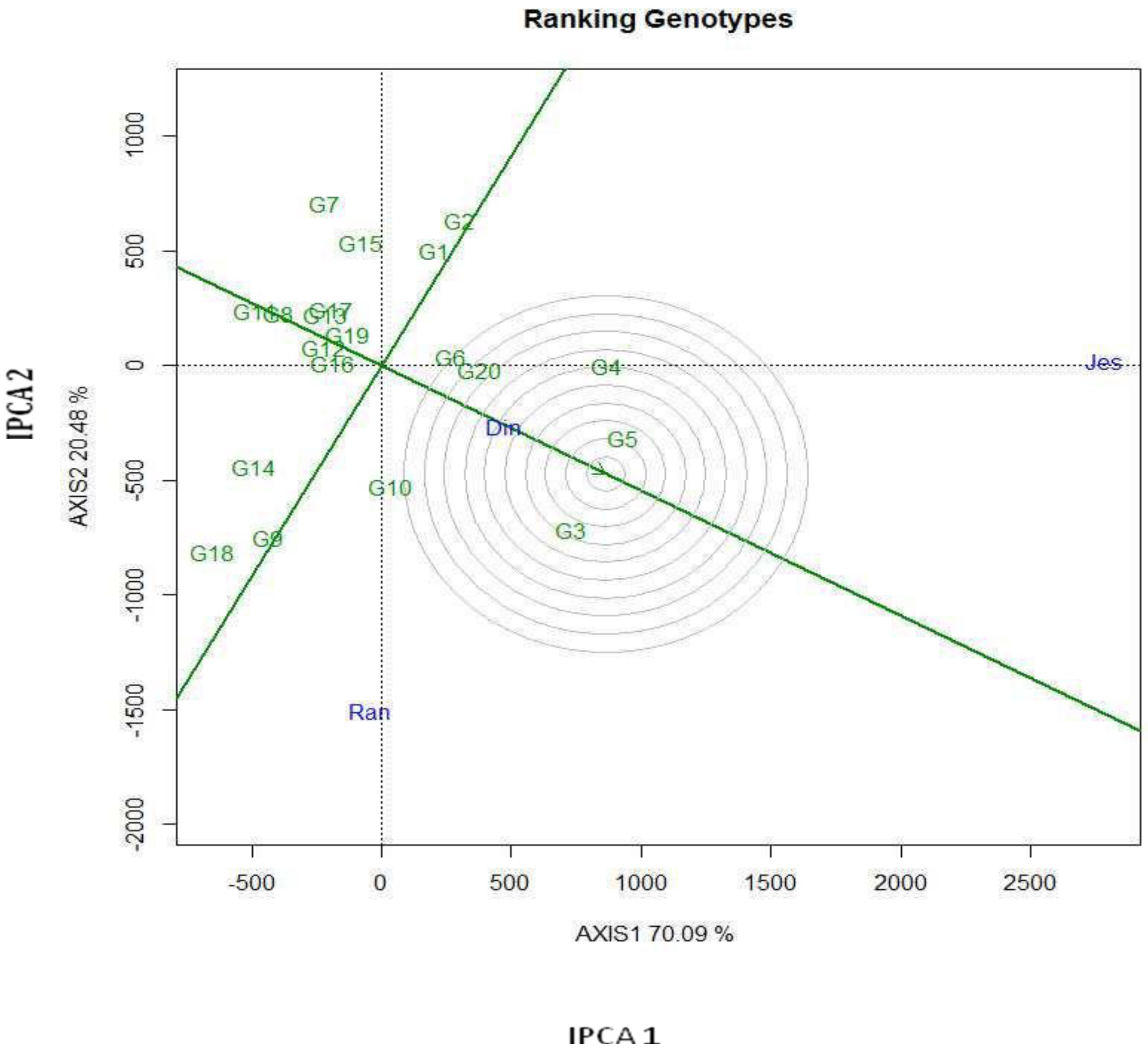

Fig. 4.6 GGE biplot of ideal location and comparison of the location with genotypes for seed cotton yield (kg ha^{-1})

IPCA: Interaction principal component analysis through two axes
Purple color indicate = Locations
Purple lines= Upper slopping line is more sensitive to lower slopping line

The relative positions of the genotypes in respect of average stable diagonal and high sensitive line are presented in Fig. 4.6. The results indicated that the seed cotton yield performance was highly influenced by GE interaction effects; the magnitude of environment effect was higher that of genotype effect. There were desirable genotypes in terms of high mean yields, for example genotype JA-08/D (4) and JA–08/C (3). These results were also similar to those obtained by Castillo *et al.* (2012) and Kaya *et al.* (2002). When environmental differences were larger as in three locations (Dinajpur, Rangpur and Jessore), might expect appreciable G x E interaction. As result, one genotype might have the highest yield in some locations over the sowing times, while another genotype might excel in others.