T.R.

KAHRAMANMARAS SUTCU IMAM UNIVERSITY

GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCE

ASSOCIATION ANALYSIS AND MAPPING OF FIBER QUALITY IN COTTON

KHEZIR HAYAT BHATTI

DOCTORATE THESIS

DEPARTMENT OF BIOENGINEERING AND SCIENCES

KAHRAMANMARAŞ 2018

T.R.

KAHRAMANMARAS SUTCU IMAM UNIVERSITY

GRADUATE SCHOOL OF NATURAL AND APPLIED SCIENCE

ASSOCIATION ANALYSIS AND MAPPING OF FIBER QUALITY IN COTTON

KHEZIR HAYAT BHATTI

This thesis

prepared at the

DEPARTMENT OF BIOENGINEERING & SCIENCES

for the degree of

DOCTOR OF PHILOSOPHY

KAHRAMANMARAS 2018

"Association Analysis and Mapping of Fiber Quality in Cotton" named this thesis prepared by Kahramanmaraş Sutcu Imam University Graduate School of Natural and Applied Science student Khezir Hayat BHATTI, was accepted as a Doctorate Thesis by our jury at the date of 04/01/2018 unanimously / by majority of the votes in the Department of Bioengineering & Sciences.

Assoc. Prof. Dr. İsmail AKYOL (SUPERVISOR)

Agriculture Biotechnolgy, Kahramanmaras Sutcu Imam Univesity

Assist. Prof. Dr. Adem BARDAK (CO-SUPERVISOR)

Agriculture Biotechnolgy, Kahramanmaras Sutcu Imam Univesity

Assoc. Prof. Ziya Dulumpinar (MEMBER)

Agriculture Biotechnolgy, Kahramanmaras Sutcu Imam Univesity

Assoc. Prof. Dr. Oktay ERDOĞAN (MEMBER)

Biosystem Engineering, Neveshir Haci Bektas Veli University

Assist. Prof. Dr. Faheem Shehzad Baloch (MEMBER)

Field Crops, Abant Izzet Baysal University, Bolu

Assist. Prof. Dr. Remzi EKINCI (MEMBER)

Field Crops, Dicle University Diaybakir

Assist. Prof. Dr. Ramazan Sadet GUVERCIN (MEMBER)

Medical & Aromatic Plants, Kahramanmaras Sutcu Imam University

I confirm that the signatures above belong to mentioned academic members.

Assoc. Prof. Dr. Mustafa Şekkeli …….

Director of Graduate School of Natural and Applied Science

THESIS NOTIFICATION

I declare and guarantee that all information in this document has been obtained and presented in accordance with academic rules and ethical conduct. Based on these rules and conduct, I have fully cited and referenced all material and results that are not original to this work.

(Signature)
(**Khezir Hayat BHATTI**)

This study supported by Scientific Research Project Unit of Kahramanaras Sutcu Imam University.
Project Number: 2017/2-58M; 2017/4-24D

PAMUKTA İLİŞKİLENDİRME HARİTALAMASI YÖNTEMİYLE LİF KALİTE ÖZELLİKLERİ İLE İLİŞKİLİ MARKÖR BELİRLEME

(DOKTORA)

KHEZIR HAYAT BHATTI

ÖZET

Gossipum cinsi tüm dünyadaki en iyi doğal lif kaynağıdır. Ekonomik değeri yüksek olan karakterlerlerin kalıtımının karmaşık olması ve bunlar hakkında yeterli bilginin bulunmamasından dolayı, klasik ıslah proğramları ile genetik ilerleme sınırlı kalmaktadır. DNA polimorfizmlerinin belirlenmesi ve açıklanmasında moleküler markörlerin kullanılması etkin bir seleksiyon için en önemli anahtarlardan bir tanesidir. Sekanslama yoluyla genotipleme (GBS) germplazmlardaki genetikvaryosyonun açıklanmasında kullanılabilir. Bağlantı denksizliği (LD) kullanılarak ilişkilendirme haritalarının yapılması, tüm bitkilerde kantitatif özellik lokuslarının (QTLs) belirlenmesi için en önemli amaçtır. Bu çalışmada, lif kalitesi özellikleri ile markör ilişkilerini belirlemek için 286 genotip taranmıştır. Biz Acala Maxxa, Paymaster2379 (USA), Delcerro (Venezuela), Carmeen (Australia), NSCH777 (India) gibi küresel koleksiyonlardan ve Türkiye'den Carla, Nazilli84S, Flora gibi elit çeşitleri içeren genotipleri inceledik. Fenotipik analizler sonucunda AB-80, Flora ve Delcerro çırçır randımanı, lif uzunluğu ve lif mukavemetinin arttırılması için potansiyel ebeveyn olarak kullanılabilir. İlikilendirme haritalaması için 4730 tek nükleotid polimorhizmi (SNPs) alleli kullanılmıştır. 95 tane SNP markörü çok önemli ($p<0.001$) bulunmuştur. Toplam 32 QTL belirlenmiş olup, 19. Kromozomda qFL-chr19-1, qFl-Chr19-2, qGOT-Chr-19-5, qUI-Chr19-9, qMIC-Chr-19-10, qFSChr-19-11, gibi 12 QTL belirlenirken, 11 yeni QTL'in kromozom lokasyonu belirlenememiştir. Sonuç olarak belirlenen yeni QTL'lerin doğrulaması yapılarak markör destekli seleksiyonda kullanımları mümkün olacaktır.

Anahtar Kelimeler: Pamuk, Lif kalitesi, Moleküler markör, NGS, GBS, İlişkilendirme Analizi

Kahramanmaraş Sütçü İmam Üniversitesi
Fen Bilimleri Enstitüsü
Bioengineering & Sciences, OCAK / 2018

Danışman: Dr. Ismail AKYOL

Eş Danışman: Yrd. Doç. Dr. Adem BARDAK

Sayfa sayısı: 169

ASSOCIATION ANALYSIS AND MAPPING OF FIBER QUALITY IN COTTON

(Ph.D. THESIS)

KHEZIR HAYAT BHATTI

ABSTRACT

Gossypium genus is the ultimate source of natural fiber all over the globe. Limitations in conventional breeding program for genetic improvement are due to the complexity of the genetic pattern for economically important traits. The use of molecular markers for the detection and exploitation of DNA polymorphism is one of the most significant key for effective selection. Genotyping-by-sequencing (GBS) can be used to explore genetic variation in germplasms. Association mapping using linkage disequilibrium is the most important goal for searching QTLs in all crops. In the present study, 286 genotypes were screened for determining marker-trait associations related to fiber quality. We investigated genotypes from global collection such as Acala Maxa, Paymaster2379 (USA), Delcerro (Venezuela), Carmeen (Australia), NSCH777 (India) and elite cultivars from Turkey including Carla, Nazilli84S, Flora. Phenotypically analysis resulted that AB-80, Flora and Delcerro can be used as potential parents for increasing ginning outturn, fiber length and strength. 4730 single nucleotide polymorphsims (SNPs) allels used for association mapping. 95 highly informative SNPs identified at ($p<0.001$). 32 QTLs found; particularly multiple QTLs on chromosome 19 such as qFL-chr19-1, qFl-Chr19-2, qGOT-Chr-19-5, qUI-Chr19-9, qMIC-Chr-19-10, qFSChr-19-11, while 11 were novel. It was concluded that the new QTLs will be validated which will ultimately contribute to marker-asisted selection.

Key Words: Cotton, Fiber quality, Molecular Markers, NGS, GBS, Association mapping

Kahramanmaraş Sütçü İmam University
Institute for Graduate Studies in Science and Technology
JANUARY/ 2018

Supervisor: Assoc. Prof. Dr. İsmail AKYOL

Co-supervisor: Asst. Prof. Dr. Adem BARDAK

Page number: 169

ACKNOWLEDGMENTS

Foremost, gratefulness of ALLAH Almighty, with His help I am able to complete Doctor of Philosophy dissertation. Firstly, I am thankful to worthy Assoc. Prof. Dr. Ismail AKYOL for offering me his mentorship, and providing me with support and a fantastic intellectual environment. His cooperative realtion and energetic nature continuously stimulated me on right way.

Exceptional appreciation and profound regard to my second advisor, Assist. Prof. Dr. Adem BARDAK for enabling me to learn molecular breeding approaches under his guidance. The fulfilment of dissertation would not have been achieveable without his outstanding direction. I am highly pleased to acknowldge Assoc. Prof. Dr. Ziya DULUMPINAR for his advice and vital role. I would like to pay my attribute to Assoc. Prof. Dr. Oktay ERDOGAN for intellectual guidance during research. My special acknowledgement to my admirable thesis committee members for providing me valuable suggestions for compiling thesis; Assist. Prof. Dr. Remzi EKINCI for execution of field trial, Assist. Prof. Dr. Ramzan Sadet GUVERCIN who helped me for data analysis. I am also thankful to Assist. Prof. Dr. Mucahit PAKSOY and Assist. Prof. Dr. Sabahattin COMERTPAY who always supported me.

I have learned a lot from those who worked with me during my whole studies. I am particularly thankful to Halil TEKEREK, Done PARLAK, Fatih Mehmet KILINC, Sadettin CELIK, Ali Can SEVER, Ridvan UCAR, Elif COSKUN DAGGECEN.

Finally, sincere thanks to my family for continuous support throughout my studies. I have no words that can describe everlasting love of my mother. It would be meaningless not to mention my wife, your cooperation and sacrifices have blessed my life. Sons; Fouzan, you are an innocent child and Faran, your cuteness and the cartoons you draw for Baba kept me going even the situations were tough.

I am pleased to say special thanks to Kahramanmaras Sutcu Imam University for offering me BAP Fellowship for conducting thesis work. Thanks also goes to Pakistan Central Cotton Committee, Ministery of Textile Industry Government of Pakistan for allowing me to do PhD abroad.

Khezir Hayat BHATTI
JANUARY, 2018

TABLE OF CONTENTS

Page

ÖZET I

ABSTRACT II

ACKNOWLEDGMENTS III

TABLE OF CONTENTS IV

LIST OF SYMBOLS AND ABBREVIATIONS VII

LIST OF FIGURES IX

LIST OF TABLES XIII

1. INTRODUCTION 1
   1.1. Phenotyping of germplasm for fiber quality 3
   1.2. Marker Assisted Selection 5
   1.3. Association Mapping of Fiber Traits Using Genotyping by Sequencing (GBS) 7
   1.4. QTLs for Fiber Quality 11

2. LITERATURE REVIEW 13
   2.1. Phenotyping of germplasm for fiber quality 13
   2.2. Marker assisted selection 15
   2.3. Association mapping of fiber traits Using Genotyping by Sequencing (GBS) 19

3. MATERIAL AND METOD 25
   3.1. Phenotypic screening for fiber quality 25
      3.1.1. Plant material 25
      3.1.2. Climatic Conditions of area 29
      3.1.3. Soil preparation 30
      3.1.4. Sowing 30
      3.1.5. Agronomic practices, fertigation and pest control measures 31
      3.1.6. Recording of data related to fiber quality 31
         3.1.6.1.1. Ginning outturn (GOT%) 31
         3.1.6.1.2. Fiber analysis using High Volume Instrument 32
         3.1.6.1.3. Fiber length (mm) 32
         3.1.6.1.4. Fiber Uniformity index (UI) 32
         3.1.6.1.5. Fiber fineness (µg $inch^{-1}$) 33
         3.1.6.1.6. Maturity coefficient 33
         3.1.6.1.7. Fiber Strength (FS) (g tex^{-1}) 33
         3.1.6.1.8. Fiber elongation (FE) 33

3.2. Association Mapping for Fiber Quality 33
3.2.1. Plant material 33
3.2.2. DNA marker analysis 34
3.2.3. Leaves collection 34
3.2.4. DNA extraction 34
3.2.5. Mortar and paste of leaves 35
3.2.6. DNA extraction 36
3.2.7. DNA quantification 37
3.2.8. Genotyping by sequencing 38
3.2.8.1. Bioinformatic analysis via GBS 39
3.2.8.2. SNPs calling 40
3.2.9. Population structure 40
3.2.10. Pairwise linkage disequilibrium and LD decay 41
3.2.11. Marker-traits associations 41
3.2.12. Alignment to NCBI 41
3.3. Statistical analysis 41
3.3.1. Heritability 42
4. RESULTS AND DISCUSSIONS 43
4.1. Phenotypic Screening for Fiber Quality 43
4.1.1. Phenotyping in Kahramanmaras 43
4.1.1.1. Analysis of variance 43
4.1.1.2. Descripitive statistics for fiber traits 44
4.1.1.3. Performance of genotypes for fiber 45
4.1.1.3.1. Ginning outturn (%) 45
4.1.1.3.2. Fiber length (mm) 46
4.1.1.3.3. Uniformity index (%) 47
4.1.1.3.4. Fiber fineness (µg inch^{-1}) 48
4.1.1.3.5. Maturity (%) 50
4.1.1.3.6. Strength (g tex^{-1}) 50
4.1.1.3.7. Elongation (%) 52
4.1.1.4. Correlation 53
4.1.2. Phenotyping in Diyarbakir 54
4.1.2.1. Analysis of variance 54
4.1.2.2. Descripitive statistics and variability parameters for fiber fiber traits in Diyarbakir 55
4.1.2.3. Performance of genotypes for fiber 56
4.1.2.3.1. Ginning outturn (%) 56
4.1.2.3.2. Fiber length (mm) 57
4.1.2.3.3. Uniformity (%) 58
4.1.2.3.4. Micronaire (µg inch^{-1}) 60
4.1.2.3.5. Maturity (%) 61
4.1.2.3.6. Strength (g tex^{-1}) 62
4.1.2.3.7. Elongation (%) 64
4.1.2.4. Correlation for fiber traits 65
4.1.3. Combined Phenotypic Analysis 66
4.1.3.1. Analysis of variance 66

4.1.3.2. Descripitive stattictics and variability for fiber traits 67
4.1.3.3. Performance of genotypes for fiber 68
4.1.3.3.1. Ginning outturn (%) 68
4.1.3.3.2. Fiber length (mm) 69
4.1.3.3.3. Uniformity index 70
4.1.3.3.4. Fiber fineness (µg $inch^{-1}$) 72
4.1.3.3.5. Maturity (%) 74
4.1.3.3.6. Strength (g tex^{-1}) 86
4.1.3.3.7. Elongation (%) 87
4.1.4. Combined correlation 89
4.1.5. Conclusion 90
4.2. Association mapping using genotyping by sequencing 92
4.2.1.1. DNA isolation 92
4.2.1.1.1. Leaves grinding and DNA extraction 92
4.2.1.2. Sequencing of libraries 92
4.2.1.2.1. Processing raw sequences from illumnia 92
4.2.1.2.2. Filtering of SNPs 92
4.2.1.2.3. Genotyping for association mapping 93
4.2.1.2.4. Population structure 93
4.2.1.2.5. Kinship 94
4.2.1.2.6. Linkage disequilibrium and LD decay 95
4.2.1.2.7. Association analysis 96
4.2.1.2.8. GLM using TASSEL 97
4.2.1.2.9. MLM using TASSEL 104
5. CONCLUSION AND RECOMENDATIONS 118
REFERENCES 122
CURRICULUM VITAE 146
APPENDIES 149

LIST OF SYMBOLS AND ABBREVIATIONS

QTLs	**:**	Quantitative trait loci
LD	**:**	Linkage disequlibrium
GBS	**:**	Genotyping by sequencing
PCR	**:**	Polymerase chain reaction
RAPDs:	**:**	Random amplified polymorphic DNA
RFLP	**:**	Restriction fragment length polymorphism
AFLP	**:**	Amplified polymorphic DNA
SSR	**:**	Simple sequence repeats
SRAP	**:**	Sequence repeat amplified polymorphism
ISSR	**:**	Inter simple sequence repeat
STS	**:**	Sequence tag site
CAP	**:**	Cleaved amplified polymorphism
ESTSSR	**:**	Expressed sequence tag
SSCP	**:**	Single strand conformation polymorphic
SNP	**:**	Single nucleotide polymorphism
RRL	**:**	Reduced representation libraries
RAD	**:**	Restriction ite associated DNA
BC	**:**	Backcross
CMD	**:**	Cotton marker database
cM	**:**	Centi Morgan
AM	**:**	Association mapping
r^2	**:**	Coefficient of determination
RILs	**:**	Recombinant inbred lines
Mbp	**:**	Mega base pair
GLM	**:**	General linear model
MLM	**:**	Mixed linear model
N	**:**	Nitrogen
GOT%	**:**	Ginning outturn percentage
HVI	**:**	High volüme instrument
RH	**:**	Relative humidity
UHML	**:**	Upper half mean length
UI	**:**	Uniformity index
MIC	**:**	Micronaire
CTAB	**:**	Ceytl-trimethy ethidium bromide
NaCl	**:**	Sodium chloride
HCl	**:**	Hydrochloric acid
EDTA	**:**	Ethylelediammine tetra acetic disodiumsalt
PVP	**:**	Polyvinyl-pyrrolidone
TAE	**:**	Tris-acetate-EDTA
EtBr	**:**	Ehtidium bromide

UV : Ultra-violet light
bp : Base-pair
GWAS : Genome-wide association

LIST OF FIGURES

Page No

Figure 1.1. Allopolyploid Cotton 2

Figure 1.2. Fiber Quality Traits 4

Figure 3.1. Layout and sowing 30

Figure 3.2. Ginning of samples for fiber analysis 31

Figure 3.3. HVI M-1000 Usterhouse Switzerland 32

Figure 3.4. Leaves storage at -80^{0}C 34

Figure 3.5. Mortar & Paste of leaves 35

Figure. 3.6. DNA pellet 36

Figure 3.7. Centrifugation for precipitating DNA 37

Figure 3.8. Gel Electrophoresis for DNA quantification 37

Figure 3.9. Gel photograph of genomic DNA 38

Figure 3.10. Spectrometer quantification of DNA 38

Figure 3.11. Library Constrcution using GBS 39

Figure 3.12. Bioinformatic analysis via GBS 40

Figure 4.1. Frequency distribution for GOT (%) 45

Figure 4.2. Fiber length classification 46

Figure 4.3. Fiber length frequency distribution 46

Figure 4.4. Uniformity classification 47

Figure 4.5. Uniformity frequency distribution 48

Figure 4.6. Micronaire classification 49

Figure 4.7. Micronaire frequency distribution 49

Figure 4.8. Maturity ratio distribution 50

Figure 4.9: Strength classification 51

Figure 4.10. Strength frequency distribution 51

Figure 4.11. Elongation classification 52

Figure 4.12. Elongation frequency distribution 52

Figure 4.13. Ginning outturn distribution 57

Figure 4.14. Fiber length classification 57

Figure 4.15. Fiber length distribution 58

Figure 4.16. Uniformity classification 59

Figure 4.17. Uniformity distribution 59

Figure 4.18. Micronaire classification 60

Figure 4.19. Micronaire frequency distribution 61

Figure 4.20. Maturity frequency ditribution 62

Figure 4.21. Fiber strength classification 63

Figure 4.22. Stregnth frequency distribution 63

Figure 4.23. Elongation classification 64

Figure 4.24. Elongation frequency distribution 65

Figure 4.25. Ginning outturn distribution 68

Figure 4.26. Fiber length classification 70

Figure 4.27. Fiber length frequency distribution 70

Figure 4.28. Uniformity classification 71

Figure 4.29. Uniformity frequency distribution 71

Figure 4.30. Micronaire classification 72

Figure 4.31. Micronaire frequency distribution 73

Figure 4.32. Maturity ratio distribution 74

Figure 4.33. Combined strength classification 86

Figure 4.34. Strength frquency distribution 87

Figure 4.35. Combined elongation classification 88

Figure 4.36. Elongation frequency distribution 88

Figure 4.37. Kinship coefficient in germplasm 94

Figure 4.38. LD decay in germplasm 95

Figure 4.39. LD Scatter diagram. Below $r^2 = 0.1$ LD decay is determined. 96

Figure 4.40. Q-Q Plots for fiber traits using GLM 98

Figure 4.41. Manhutton Plot for fiber length in GLM 98

Figure 4.42. Manhutton Plot for Ginning outturn in GLM 99

Figure 4.43. Manhutton plot for unifomity in GLM 99

Figure 4.44. Manhutton plot for micronaire in GLM 100

Figure 4.45. Manhutton plot for maturity in GLM 100

Figure 4.46. Manhutton plot for strength in GLM 101

Figure 4.47. Manhutton plot for strength in GLM 101

Figure 4.48. Q-Q plot for fiber traits using MLM 105

Figure 4.49. Manhutton plot for fiber length using MLM 107

Figure 4.50. Manhutton plot for ginning outturn using MLM 111

Figure 4.51. Manhutton plot for uniformity using MLM 112

Figure 4.52. Manhutton plot for micronaire using MLM 113

Figure 4.53. Manhutton plot for maturity using MLM 114

Figure 4.54. Manhutton plot for fiber stregth strength using MLM 114

Figure 4.55. Manhutton plot for fiber elongation using MLM 115

LIST OF TABLES

Page No

Table 3.1. Germplasm collection for fiber quality 25
Table 3.2. Meteorological data during experiment at Kahramanmaras and Diyarbakir 29
Table 4.1. Means squares for fiber quality 44
Table 4.2. Descripitive statistics for fiber..... 44
Table 4.3. Correlation for fiber quality traits..... 54
Table 4.4. Means squares for fiber quality 55
Table 4.5. Descripitive statistics and variability for fiber traits 56
Table 4.6. Correlation for fiber quality traits..... 66
Table 4.7. Means squares for fiber traits 66
Table 4.8. Descripitive statistics for fiber traits..... 67
Table 4.9. Means for fiber quality traits 75
Table 4.10. Correlation for fiber quality traits..... 89
Table 4.11. Significant associations of SNP loci with fiber traits identified by GLM..... 102
Table 4.12. Significant associations of SNP loci with fiber traits identified by MLM..... 108

1. INTRODUCTION

Cotton is a crop of immense importance as being a dominant source of fiber and oil from cottonseed all over the world (Bardak and Bolek, 2012). The improvement of cotton fiber quality has become more important because of changes in spinning technology and ever-increasing demands of fibre. Cotton is grown in more than 80 countries, and contributes to the world economy as a raw material for textile industry (Tan et al., 2014).

In 2017, cotton was sown on an area of 29.27 million hectare with production of 105.34 million bales all over the globe while India, China, United States of America, Pakistan and Brazil were the top growers. (USDA, 2017). In Turkey, cotton covers 416,000 ha area and is sown in four main regions; Agean, Anatalya, Cukrova and Southeastern Anatolia. The overall lint production of 756.000 tons achieved from these areas (USDA, 2017). 2.5% of global fiber yield is shared by Turkey which is ranked 7th.

"*Gossypium*" genus is made up of about 57 species of which 50 are diploid and 7 are as allotetraploids (Fryxall, 1979; 1992; Stewart, 1995; Grover et al., 2015; Gallagher et al., 2017). It has been differentiated into 8 genomes A, B, C, D, E, F, G, K upon the basis of chromosomes homology (Endrizzi et al., 1985; Percival et al., 1999; Wendel and Cron, 2003). Of all the species of the genus, two most common diploids are *G. arboreum* L., *G. herbaceum* L., while *G. hirsutum* L., and *G. barbadense* L. are considered as the most commercially valuable tetraploids.

G. hirsutum, is characterized by high yield, moderate fiber quality and wide adaptability contributes for 95% of overall cotton production (Cai et al. 2014); while *G. barbadense* (Pima, and Egyptian) increases superior fiber quality (Ulloa et al., 2005; Gore et al., 2014). About million years ago allopolyploid cottons appear to have evolved, as a result of A-genome taxon through trans-oceanic dispersal to the New World and succeeded by mating with an indigenous D-genome diploid (Figure 1.1). Eventually as developed, three recent species formed due to allopolyploids, consisting of widely grown species *G. hirsutum* L. and *G. barbadense* L., (Wendel and Albert, 1992; Meredith, 2000; Wendel and Cronn, 2003).

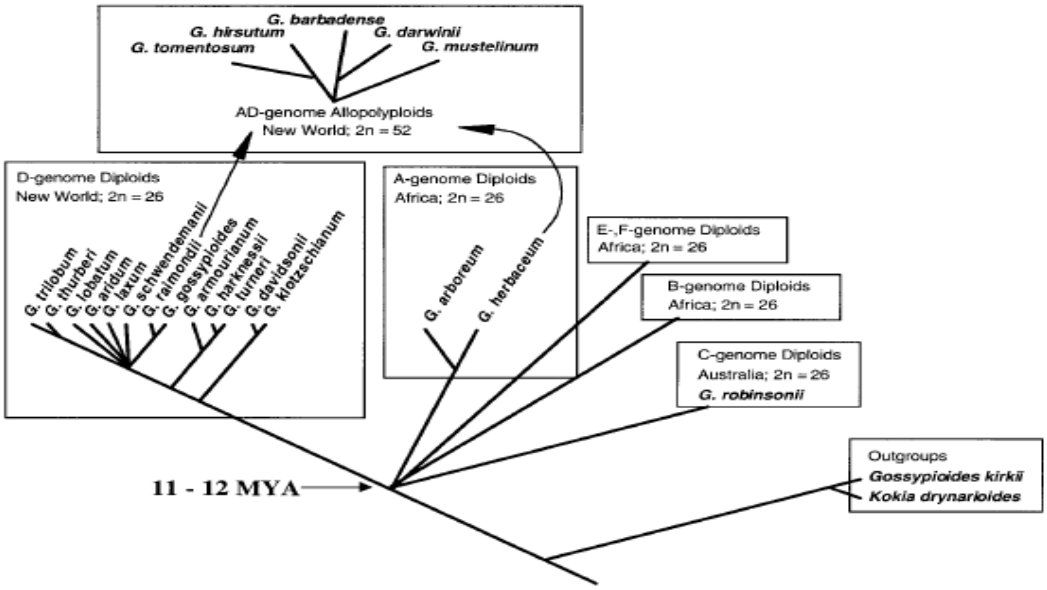

Figure 1.1. Allopolyploid Cotton (Wendel and Albert, 1992, Seelanan, 1997, Small, 1998, Wendel and Cronn, 2003)

Efforts for broadening the genetic base of *Gossypium* genus have not generated successful outcomes due to the complex and large genetic architecture of its genome. Moreover, owing to its developmental barriers, genetic studies have not yet been able to produce the required traits in cotton (Rahman et al., 2008). Association among markers and characters can be used for fastening the breeding program. The hereditary variation present among the gene pool land races can be exploited by applying the mapping based on linkage disequilibrium. It will speed up the cotton breeding through identification of markers among trait of interest and ensure molecular breeding. Single reproducibility of genetic marker which govern a specific appearance on sequence of nucleotides can be analyzed with genome wide association (Cerda and Cloutier, 2016). Association mapping relies upon the magnitude of different pair of genes for population analysis. Moreover, this mapping shows powerful connection between required character and a genetic marker while nonrandom combination between two quantitative trait loci or markers manifests linkage disequilibrium (Cai et al., 2014). The valuable information about the origin of an individual is determined with the degree and the size of the population (Nordborg and Tavare 2002; Slatkin, 2008). Many loci relating to polygenic characters have been determined via genetic maps and linkage disequilibrium (LD) was measured in humans through diverse analysis methods (Weis and Clark, 2002; Kruglyak, 2008). Population based polygenic characters mapping for desired traits became a widely used technique thanks to the innovations in omics and availability of

advanced bioinformatic tools for analysing genetic variations (Zhu et al., 2008). The ultimate benefits of this technique includes the ability to work with a large number of loci, producibilty of highly saturated maps, its speed and its low cost (Flint-Garcia et al., 2003).

1.1. Phenotyping of germplasm for fiber quality

Single cell elongation of ovule in cottonseed outer layer forms a natural fiber known as "trichome" which contains about 89-100% cellulose. (Basara and Malik, 1984; Ryser, 1985; Delmer and Amor, 1995; Haigler et al., 2005). As little as, 30% of lint primordia have the ability to be differentiated as mature fibers forming about 20,000 of it within a single ovule (Berlin, 1986; Tiwari and Wilkins, 1995). The ideal cotton fiber should be white like frozen vapor, durable like iron, attractive like silk and stretched as a wool (Bradow and Davidonis, 2000). Nonetheless it is hard to include all these qualities within a breeding program for cotton production, but efforts have been made to obtain the most desired ones. Fiber quality is an array of quantitative traits (length, fineness, strength, uniformity and elongation) (Figure 1.2) that enhance yarn value during spinning (Dutt et al., 2004; Ali et al., 2008; Shen et al., 2011). Fiber quality is a difficult association of physiology and genetic make-up of plant within a growing season of cotton (Rehman et al., 2007; Ali et al., 2008). It is well documented that among major fiber traits lint percentage, strength and fiber length have complex relationship (Smith and Coyle, 1997; Ali et al., 2009). Accordingly, researchers have accomplished enormous objectives for many years to improve hereditary via conventional breeding, genetic transformation and molecular biology based techniques (Badignnavar, 2010).

Fiber quality enhancement through genetics is the ultimate objective of breeding strategy in cotton. Cotton scientists have been involved in fiber quality improvement for a long time due to the increase in demand for multiple products from cotton. The critical goals of all cotton related techniques are fiber yield and quality, and the precise parameters which contribute its economic value on global level. Spinning automation renders fiber improvement according to interests of textile sector, as a result fiber quality measurements for breeders are considered. As an instance, prevailing spinning automation highly signify strength instead of fiber length and fineness (Shen et al., 2005). Moreover, fiber quality improvement is a demanding task as it is determined after harvesting of crop.

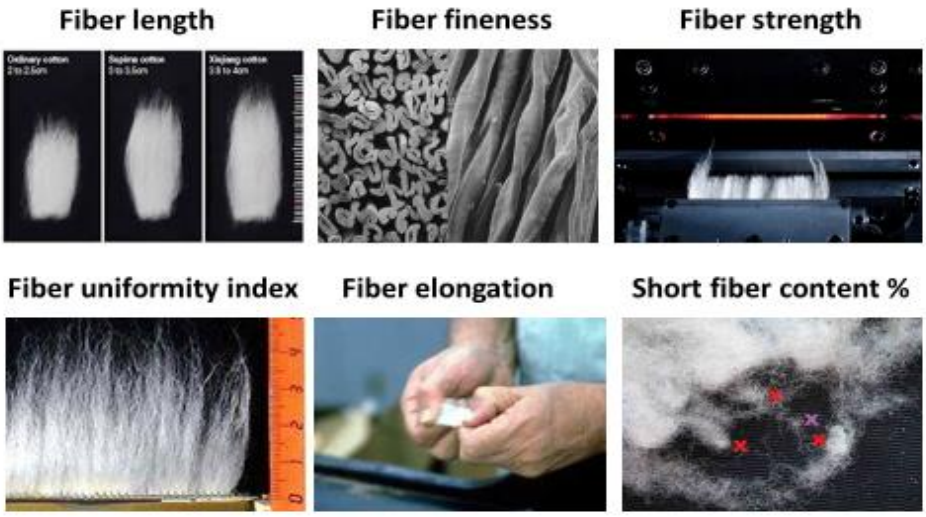

Figure 1.2. Fiber Quality Traits (www.cirad.fr)

Hussain et al. (2010) showed the existence of dominance effects instead of the additive ones among genotypes. They observed highly significant differences for fiber traits consisting of fiber length, strength, fineness and fiber uniformity ratio screened under normal agronomic practices. Likewise, in sealand cotton accessions, non-additive gene action was observed for fiber length, strength and fineness (Meredith and Bridge, 1972). While Mingbaoa et al., (2008) showed that both additive and dominance effects were found in fiber length although the dominance effect was little higher than the additive effect. However, the other traits including fiber uniformity, fiber fineness and fiber strength produced higher additive and lack of dominance effects. Moreover, non-additive type of gene action was also observed for fiber quality traits (Ahmad et al., 1997; Iqbal et al., 2005).

The main goal of all genetic improvement is to increase yield. Lint yield manifested stable increase till 1980s (Bridge et al., 1971; Bridge and Meredith, 1983; Bassett and Heyer, 1985; Culp and Green, 1992). The intensity of improvement for lint production has deteriorated since the 1980s (Meredith et al., 1997; Meredith, 2002; Bayles et al., 2005). Transgenic variety development is the main drawback for enhancing production in cotton as backcross methodology is used having too few recurrent parents and a narrow genetic variation in upland cotton genetic stock (Meredith et al., 1997; Meredith, 2006). Nonetheless, genetic diversity has increased at the start of 21st century (Kerby and Hugie, 2006; Kuraparthy and Bowman, 2013).

It has been well documented that tight negative relationship is found among essential fiber traits and lint production (Al-Jibouri et al., 1958; Meredith and Bridge, 1971). The utmost important relationship is observed between yield and fiber strength as it was revealed from earlier studies; the extent of connection is population based. Owing to limited genetic diversity in elite cotton cultivars (Iqbal et al., 2001; Rungis et al., 2005; Lacape et al., 2007, Abdurakhmonov et al., 2008) and contradictory affiliation of yield and quality (Culp and Lewis, 1973), the advancement to enhance fiber production and upgrade quality through traditional breeding methods has been confined (Smith and Coyle, 1997). Furthermore, conventional ways would be tiresome and stagnant (Shen et al., 2005). Hence, the modern plant improvement methods should be integrated.

1.2. Marker Assisted Selection

As mentioned above; due to the inverse relationship between seedcotton yield and fiber quality, and the complicated involvement of multiple genes in traits demand breeders to evolve varieties through more useful methods. In the past textile industry flourished principally via selection of new recombinants among germplasm entries with traditional breeding approaches (Green et al., 1990; Zhang et al., 2012). Elite grown cotton genotypes have narrow genetic base, therefore it has been thought that germplasm should be used for improvement of traits. Some of popular characters such as disease and insect resistance have been enhanced by introgression (McCarty and Percy, 2001). The advent of DNA markers paved the way for plant breeders to fasten breeding process through fast, authentic and substitutive techniques instead of the traditional methods for the selection to develop both agronomic and economic characters of plants (Tanksley and Hewitt, 1988).

Molecular marker is a specific DNA portion with a known position on the chromosome (Kumar, 1999), or a gene whose phenotypic expression is frequently easily distinguished and used to detect an individual (King and Stansfield, 1990; Schulmann, 2007). Genetic markers are divided into three groups: (1) morphological markers which themselves have phenotypic characters; (2) biochemical markers, having allelic variants of enzymes called isozymes; and (3) DNA markers, which show sites of variation in DNA (Joshi and Nguyen, 1993; Winter and Kahl, 1995; Jones et al., 1997; Gupta et al., 1999 DNA markers are having the property of polymorphism which can be used for the differentiation of homozygotes and heterozygotes (Roychowdhury et al., 2014). DNA markers having high

polymorphism in germplasm collections are desired in marker assisted selection (Bolek, 2003).

Marker assisted selection has a great amont of advantages over conventional breeding, reviewed by many researchers (Collard and Mackill, 2008; Kumpatla et al., 2012; Waqas et al., 2014). Plant breeders utilize DNA markers for selection of desirable traits on molecular basis in spite of observing them phenotypically (Helentjaris et al., 1986), furnishing the basis for using the molecular assisted selection (Welsh and McClelland 1990; Vos et al.,1995; Struss and Plieske, 1998). Molecular markers are desired for improving traits in many essential crops; rice (Mackill et al., 1999), wheat (Koebner and Summers, 2003), maize (Stuber et al., 1999; Tuberosa et al., 2003) and barley (Thomas, 2003; Williams, 2003). Cotton is an important cash crop at global level and marker assisted selection has not got desired goals because of compatibility barriers through historic domestication and insufficient polymorphism (Iqbal et al., 2001; Rahman et al., 2005; Abdurakhmonov et al., 2008).

Molecular characterization is the way to transfer required traits into modern genotypes (Paterson et al., 1991; Mohan et al., 1997; Zhu and Cruch, 2008; Collard and McKill, 2008, Bolek et al., 2016). Quantitative trait loci (QTLs) allow gene pyramiding for yield and fiber quality through evolution of linkage maps. Association mapping using linkage disequilibrium on genome wide level is the most valuable strategy among scientists for searching QTLs in crop sciences. The association among trait of interest and germplasm entries is observed using population construction information and linkage disequilibrium (LD) with association mapping (Thornsberry et al., 2001). LD mapping is highly popular thanks to the sophistication of mathematical methods and accessibility of large number of DNA markers.

The traits controlled by multiple genes such as fiber quality can be studied more precisely with linkage maps after the availability of new genomic data of Gossypium spp. like *Gossypium raimondii* Ulbrich Wang et al., (2012); Paterson et al., (2012), *Gossypium arboreum* L. Li et al., (2014) and *Gossypium hirsutum* L. (Li et al., 2015, Zhang et al., 2015). Chen et al., (2007) revealed that tetraploid species derived from crossing of two diploid species *Gossypium arboreum* L. (A genome) and *Gossypium raimondii* Ulbrich (D genome) about 1-2 million years ago. Moreover, it may pave the way for fiber improvements as higher

number of QTLs assigned to the D_t sub-genome compared to A_t sub-genome in hawian cotton (Jiang et al., 2000; Paterson et al., 2003; Rong et al., 2007).

Many researchers have observed QTLs for seedcotton yield and its components (Shappley et al., 1998; Ulloa et al., 2002, 2005; He et al., 2005, Fang et al., 2014, Zhang et al., 2015, Said et al., 2016). But, mostly filial generations were used for QTLs. Quantitative trait loci are highly effected by low heritability and more experimental error which are high in such plant materials, hence it is need of the day that a useful way should be employed for the development of stable populations for overcoming these obstacles. The accuracy of QTL determination relies upon allelic frequency among QTL of the desired character and related marker (Mackay and Powell, 2007). Molecular breeding methods designed with the information obtained through quantitative trait loci analysis in association mapping creates valuable genetic variation from stable populations (Breseghello and Sorrells, 2006).

1.3. Association Mapping of Fiber Traits Using Genotyping by Sequencing (GBS)

Molecular markers are highly favored for linkage map development because they are polymorphic, easily transferred to next generation with Mendelian ratio and do not show epistasis. Molecular breeding with highly saturated maps having QTLs connected with economic traits through impactful genetic markers provides a good source for cotton improvement (Bolek et al., 2016). Genomic analysis in many crop species including cotton has been done using populations derived from hybridization of only two ancestors; which is major drawback for omics information. Therefore, there has been hindrance in applying QTL information gained from such populations to accomplishing breeding objectives, as, in these populations, the genetic aspects are the same owing to the share of genetically similar backgrounds.

The foundation of association mapping is on hypothesis about occurrence of markers as a panel in which the alleles are found almost adjacent to the required traits with co-segregation and thought to be in linkage disequilibrium. Germplasm entries are used for determining QTLs of interest using genome wide association mapping (Nordborg et al., 2002). There are many agents including type of copulation, gene flow frequency and population structure can affect such mapping approach (Flint-Garcia et al., 2003). Association mapping allows to overcome drawbacks found in bi-parental mapping from traditional methods which include using populations which are found as well-established

genotypes, detects only the required gene and identify high polymorphism (Abdurakhmonov and Abdukarimov, 2008; Abdurakhmonov et al., 2008; Abdurakhmonov et al., 2009). This methodology also urges to use knowledge based on linkage disequilibrium instead of linkage mapping.

Marker assisted breeding involves recent approaches of genomics combined with traditional breeding procedures for improving traits in crop sciences. For this reproducibility is essential among genetic markers. Morphological characters grading and genotyping with molecular markers is accomplished (Lande and Thompson, 1990). Molecular markers are very effective for identifying and overcoming problems for transfer of traits from other species such as segregation distortion (Chee et al., 2005). Genetic markers are effective for determing genetic variation in *Gossypium* gene pool. Kumar et al. (2009) classified DNA markers into groups: 1) non-hybridization based; which include Amplified Fragment Length Polymorphism (AFLP), Ssimple Sequence Repeats (SSR), Sequence Repeat Amplified polymorphism (SRAP), İnter-Simple Sequence Repeats (ISSR), Expressed Sequence Tag (EST-SSR), Single Nucleotide Polymorphism (SNPs) etc. Numerous linkage maps have been developed in allotetraploid cotton employing diverse mapping populations and different DNA markers techniques (Reinisch et al., 1994; Ulloa et al., 2002; Rong et al. ,2004; Mei et al., 2004; Nguyen et al., 2004; Han et al., 2004). Numerous SSRs and SNPs have been evolved in cotton (Guo et al., 2007; Lacape et al., 2009; Blenda et al., 2012; Fang and Yu, 2012; Yu et al., 2012). Saturated genetic maps development through loci information of SSR and SNPs in cotton paves the way for ascertaining quantitative traits related to breeder objectives (Zhu et al., 2011; Marathi et al., 2012; Lacape et al., 2013; Li et al., 2013). Nonetheless, association analysis and very fine mapping is not possible owing to less information from these maps. It is need of the day that highly saturated mapping should be devised in cotton for overcoming the sequencing drawbacks and fastening the variety development.

Availability of microsatellites (SSR) and single-nucleotide polymorphisms (SNPs) have fastened genome mapping owing to their wider applicability in diverse populations derived from discrete genetic backgrounds (Guo et al., 2007; Lacape et al., 2009; Nguyen et al., 2004; Reddy et al., 2001; Van Deynze et al., 2009; Xiao et al., 2009; Yu et al., 2012).

Thanks to advances in genotyping and SNPs calling tools; broadening of genetic base is being explored excessively in plants owing to availability of valuable loci information

(McCouch et al., 2010; Davey et al., 2011; Feuillet et al., 2011; Morrell et al., 2012; Poland and Rife, 2012; Chen et al., 2013b; Huang et al., 2013).

Single nucleotide polymorphisms are distinct points of nucleotides on chromosomes between two genotypes differentiated by a single base (Bolek et al., 2016). Gupta et al. (2001) speculated that each SNP is found after 100-300bp in any genome while Canal et al. (2009) revealed that such genetic markers are highest in occurrence than any other marker and manifest higher degree compared to microsatellites. These are the most frequent variations as depicted in every 1000 bases among genotypes. These are alterations in bases either transitions (C/T or G/A) or transversions (C/G, A/T, C/A, or T/G). Moreover, such variations can be induced due to insertions and deletions (Collins et al., 1998). SNPs are popular for genomic studies owing to efficiency, abruptness and economic level (Rafalski, 2002). These are the ultimate ample variations being utilized in omics among different plant species like maize and rice (Wang et al., 2015).

SNPs can be formed rapidly with economical cost owing to availability of high-throughput tools for genotyping (Maughan et al., 2009). Assessment of gene expression (Harper et al., 2012; Naoumkina et al., 2014), genome wide association (Xu et al.,2011; Li et al., 2014) and SNPs detection has been carried among the individuals having different sizes of genomes and also polyploid species having limited genetic variation like cotton Byers et al. (2012); Gore et al. (2014) and wheat Poland et al. (2012) through low-cost high-throughput genotyping tools. SNPs have been explored and genotyped among different species via diverse ways (Elshire et al., 2011; Byers et al., 2012; Poland et al., 2012; Gore et al., 2014).

Genotyping-by-sequencing (GBS) is powerful and easy approach which paves the way for the discovery of numerous SNPs concurrently among large number of genotypes (Islam et al., 2015). Restriction enzymes with methyl sensitivity are used to mark the flanking restriction sites in the genome for the development of reduced representation of the genome via GBS (Elshire et al., 2011; Poland et al., 2012). GBS method is much easier, requires lower amount of DNA and library preparation is achieved in just two steps on plates, circumvents DNA fragment analysis preceded by PCR amplification of pooled library in contrast to reduced representation libraries (RRL) and restriction site associated DNA (RAD) (Elshire et al., 2011). The discovery and verification of reproducibility is not required in this procedure and can be applied in any species having polymorphism or mapping

population with diverse size (Schnable et al., 2013). A number of SNPs has been discovered in many species using GBS like maize Elshire et al., (2011), wheat, barley Poland et al. (2012), sorghum Ma et al. (2012), rice Spindel et al. (2013), soybean Sonah et al. (2013), oat Huang et al. (2014) and cotton (Gore et al., 2014; Islam et al., 2016; Said et al., 2016).

Association mapping furnishes saturated map of desired trait in contrast to pair of genes harboring a required character (Yang et al., 2007). Therefore, verification of QTLs is compulsory for mapping. Association mapping is the way to examine genetic variation of required characters; integrates the variation of the desired characters through reproducibility of the alleles and genetic markers are selected connected to economic traits using linkage disequilibrium extent (Nie et al., 2016). Moreover, LD elaborates the ancestral pattern through information among populations and ecology (Gould and Johnston, 1972; Roesti et al., 2013).

LD based association mapping has been applied by using different strategies for determining genetic diversity contributing source pattern and design of population (Pritchard et al., 2000; Peleg et al., 2008). Grouping of population individuals with combined genetic distance among the entries established via LD (Nei, 1972; Rogers, 1972; Nei, 1978). LD extent among natural population is not contributed by linked loci but non-homologous chromosomes are also involved, accountable to selection, behavior of population and hybridization. Owing to which immense care should be considered for analyzing such relations. Reproducibility in a sequence controlling a specific character is the property of this mapping (Yan et al., 2010). Moreover, considerable concern is prevailed among association studies and linkage mapping relating to depth and precision of QTLs, the magnitude of knowledge and evaluating procedures (Nie et al., 2016).

In spite of the fact, statistical analysis is not appropriate with LD derived tools. Natural population partitioned into distinct categories with model-based procedures (Badiganavar, 2013). Bayesian modeling is used widely for assessing the probability of a genotype related to a specific population category through allele repetition. With this technique the genotypes are allotted to particular population which can be interspersed into statistical methods for association mapping with population organization. The population framework is analyzed by using STRUCTURE software Pritchard et al. (2000) which has been used for association studies in many plants. Various studies have been conducted in cotton for different aspects in cotton through association mapping like seedcotton yield and

components (Mei et al., 2013; Zhang et al., 2013, Qin et al., 2015), fiber quality (Abdurakhmonov et al., 2008; Zeng et al., 2009; Cai et al., 2014; Nie et al., 2016, Iqbal and Rahman, 2017; Sun et al. 2017), salt tolerance (Saeed et al., 2014), architecture of plant (Li et al. 2016b), earliness (Li et al. 2016b) and protein and oil contents (Liu et al., 2015).

1.4. QTLs for Fiber Quality

Cotton fiber quality as whole involves diverse fiber characters. As association among number of fibers is observed during spinning then high convolution is created. Cotton researchers screen many traits for getting desirable fiber quality including number of fibers, fiber length, elongation, strength, uniformity and fiber fineness (Meritt, 2014). Plant breeders chiefly observe combined lint production and other economic characters for advancing fiber quality. Fiber production is of high value among these quantitatively controlled parameters from grower point of view while fiber length, fiber elongation, fiber uniformity, fiber strength and fiber fineness (micronaire) matters a lot for textile. Commonly, within standard cultural measures fiber quality parameters heritability values are higher than seedcotton yield (Percy et al., 2006; Ulloa, 2006). Therefore, the extent of phenotypic variation between the individuals in breeding material contributed to genetic properties likely to be less for lint. As a consequence, fiber characters like fiber production having low heritability are influenced by ecological factors a lot as are limited responsive to selection.

Variety development and commercialization of cotton requires special emphasis on fiber improvement. Marker assisted breeding through QTLs offers a wonderful opportunity for improving multigenic traits related to disease, yield and fiber value; developing high resolution maps (Iqbal and Rahman, 2017). Within breeding program under specific climate; major task is to relate a genotype with specific character. The analysis of polygenic trait variation produced through germplasm entries intends to locate loci which are connected to desired trait.

Quantitative characters connected to fiber quality have been observed in cotton through LD mapping (Abdurakhmonov and Abdukarimov, 2008; Kantartzi and Stewart, 2008; Abdurakhmonov et al., 2008, 2009; Zeng et al., 2009; Zhang et al., 2012, 2013; Cai et al., 2014; Fang et al., 2014).

However, the materials were limited in these studies, which originated from limited cotton regions whose representations were not sufficient. The markers used in association analysis did not uniformly distribute on each chromosome, so they could not cover the whole cotton genome.

From breeding perspectives in order to boost yield, it's compulsory to have information related to variability pattern and degree of relationship among multiple characters. As mostly traits of interest in cotton are governed by multiple factors therefore it's a perquisite to divide the total observed variation into its parts using heritability and coefficient of variation. Moreover, it is recommended that other parameters should be evaluated jointly with yield. It is advisable to consider yield components which had high heritability. Awareness about relationship among yield and yield component traits are of huge favor for breeders to advance populations in the same time with polygenic traits of value. Moreover, simple correlation information is also necessary.

The study was conducted during 2016-17 at two locations Kahramanmaras Agriculture Research Center, Kahramanmaras and at farmer field at Bismil, Diyarbakker with the goal to observe association among entries and determine molecular markers related to fiber quality. The germplasm accessions serve as a good source for conducting mapping studies.

Keeping in view of this information, present study on "Association Analysis and Mapping of Fiber Quality in Cotton" was done with the following objectives.

(1): Phenotyping of germplasm for fiber quality traits.

(2): To design an "association mapping" study with population structure analysis between germplasm entries to find biologically meaningful marker-trait associations using Single Nucleotide polymorphism (SNPs)

(3) To assign QTLs for traits related to high fiber quality (1- Ginning outturn (%), 2- Fiber length, 3- Fiber fineness (micronaire), 4- Fiber strength, 5- Fiber uniformity index, 6- fiber maturity, 7-Fiber elongation).

(4) To be used as a framework for developing cotton cultivars with superior quality.

2. LITERATURE REVIEW

2.1. Phenotyping of germplasm for fiber quality

There are two tetraploid species of *Gossypium* which share a considerable area all over the world; one of which is Egyptian cotton with long staple fiber while the other widely sown and highest contributing with very high yield potential genetically (Percy et al., 2006). In contrast to *Gossypium barbadense* L. (pima); upland cotton is highly desired owing to tremendous efforts made for increasing yield and fabric properties (McCreight, 1992; Felkner, 2001).

Gulati (1929); Damp, (1994); Brubaker et al. (1999) reported that about 5000 to 7000 B.C in India and America, human exercises has affected natural material of fiber originated from *Gossypium* genus for the development of yarn and fabrics.

Cotton fiber enhancement has been the main objective of breeders (Braden, 2005), spinning produces variety of materials and it is also used as seedcake and oil. Fabric is used for diverse kinds of products in textile industry like dresses, paper bags, nets (Smith, 2001; Cotton Incorporated, 2013). Anyway, thirst for development of polygenic characters has been on process. Accelerated selection for improving lint yield and acclimatization in upland cotton for harvest duration has diminished genetic diversity a lot (May, 2000; Percival, 1987; Percy et al., 2006). Therefore, synthetic fiber development demands more fine fiber from the breeders to compete at global level (Joy et al., 2010).

Outer primordial of cottonseed ovule produce fibers $\pm$ 3 days after pollination (Fang et al., 2014; Gilbert et al., 2014). Fast track innovations in woven industry has forced a lot to improve fiber parameters. Fiber length, fiber strength, fiber fineness, fiber elongation etc. constitutes fiber quality (Poehlman and Sleper, 1995; Ali et al., 2008; Islam et al., 2016). Nonetheless, inverse relationship is prevalent among yield and fiber quality, the highly effective strategy is to be observed through refinement of the traits. As a whole fiber quality is accomplished as joint contribution of all fiber quality traits in a precise way (Meritt, 2014).

OK- 86 and Acla-44 were used for observing variation and revealed irregular heritability on single plant basis in advance generations F_1, F_2, BC_1, BC_2, F_3 and BC_2F_4 (Murray and Verhalen, 1969).

But response to selection of BC_2F_4 with progeny rows depicted that fiber length trait improvement should be carried in latter generation while yield improvement better in advance populations. Yang et al. (2009) studied the relationship among fiber traits and yield components. They found high genotypic correlation among yield and fiber characters. The magnitude of dominant correlation was diverse among all traits while phenotypic, genotypic and additive correlation was almost same in all characters. They concluded that additive correlation can be utilized for devising any breeding strategy.

Genetic characteristics for fiber quality were observed in different strains of upland cotton (Akhtar et al., 2010). Researchers showed that incomplete dominance is prevalent among fiber fineness and fiber strength while complete dominance found for fiber length; moreover, no occurrence of epistasis between all traits.

Hussain et al. (2010) studied fiber quality traits relationship among germplasm entries. They found positive relation between staple length and strength while micronaire showed negative relation with fiber length and strength. They concluded that it will be best to study genetic pattern of fiber trait for improving quality.

Fiber quality analyzed using elite cultivars for enhancing the genetic variation under different climatic conditions (Zeng et al., 2011). They showed that the entries can be valuable source for improving multiple traits at a same time like SP192, SP224 for lint percentage, fiber length and fineness while SP192, SP205 and JC65 for fiber lint production, fineness and elongation and SP156 & SP224 for ginning out turn and fiber strength.

Yield and fiber traits are inversely correlated with each as it prevailed from the analysis among two continents under different years (Clement et al., 2012). They observed higher yield potential in Australian region as compared to American but yield was inversely associated with fiber length and fiber strength. As a whole, fiber quality attributes like length and strength were significantly inverse correlated with yield while maturity showed positive relation to yield. They verified the presence of inverse association among fiber traits and yield and this relationship can be overwhelmed through genetic mapping. They deduced that the strains having good fiber traits with yield should be selected, population size should be more and screening should be carried in contrasting climate for fastening the breeding program.

Lint yield and fiber quality parameter's genetic variation and gene action was observed in pima cotton (Swamy et al., 2013). They observed that both additive and non-additive effect economical characters a lot.

Genetic variation was observed in different genotypes of cotton (Bolek et al., 2014). They found that fiber length, micronaire, strength was contributed by dominant effects as well as short fiber scoring, uniformity and elongation produced by dominance.

Akiscan and Gencer (2015), screened cotton genotypes (VD-4, PAUM-15, Cukurova 1518, VD-18, Stoneville 468 and Nazilli 84S) for determining genetic pattern of fiber quality. They revealed the presence of dominance of additive genes among all traits. The cultivars could be used for improving different traits like fiber length, fiber strength, fiber finess and spinning consistency index using VD-18, PAMU15, Nazilii 84S and VD-4 respectively

Yaqoob et al. (2016) observed association yield and fiber characters in American cotton. They found direct relation among yield and fiber traits. Moreover, they predicted negative association among fiber length with fiber strength and seed cotton yield.

Relationship among fiber quality and yield components were observed using promising varieties from the germplasm (Imran et al., 2016). They observed lack of epistasis for fiber length, fiber strength and fiber finess. It was revealed that additive gene effects is more than non-additive and range of narrow-sense heritability from low to high can be used for variety development.

Campbell et al. (2016) screened genotypes for observing variation of polygenic traits involved in lint production and genetic behavior. Additive genetic effects were dominantly involved for fiber traits among the breeding material. They deducted that "MD15" is a diverse source with maximum additive nature and can be utilized for fiber quality refinement.

2.2. Marker assisted selection

Molecular markers are highly favored for breeding purposes as having qualities which overcome phenotypically selected characters (Tanksley, 1983).

These include individuals can be observed on genomic level using any tissue or cell; alleles intensity is naturally more at loci, all available combinations can be compared as mostly DNA markers are co-dominant, and having the capability of less interaction of epistasis.

Availability of DNA markers allow to develop cultivars with good fiber yield in cotton (Paterson et al., 1988). Molecular breeding is of immense value for transferring of genes of interest in crop sciences. DNA markers serve as a tool for fastening the breeding program via identification of QTLs. Marker assisted selection facilitates the improvement of characters with desirable QTLs from breeder perspectives. Genetic map development is the highly desired implementation of molecular markers and are utilized for assessment of traits of economic value.

Meredith (1992) used RFLP for determing parentage and hybrid vigor in American cotton. Broadening of genetic base through utilizing the available variation among diverse entries of the germplasm is a thirst among all cotton researchers via genomic studies.

Reinisch et al. (1994) used introgressed F_2 mapping population derived from *G. hirsutum* race palmeri and "K101" of *G. barbadense* with RFLP. They developed the pioneer genetic map consisting of 41 linkage groups.

RAPDs were used for determining the variation among promising cultivars of cotton (Iqbal et al., 1997). Genepool consisting of 22 cultivars from *G. hirsutum* and 1 originated from *G. arboreum* were screened with fifty markers. They observed reproducibility among 49 markers in whole panel and as a whole reproducibility of 89.1%. The *G. arboreum* cultivar Ravi manifested 55.7% coincidence to tetraploids.

Brubakar et al. (1999) used RFLPs for the identification of loci related to diploid and allotetraploid genomes. They developed genetic map and analyzed the genomic development among diploid and tetraploid species with parallel RFLP mapping. As a whole they observed 19 loci between the species.

Simple sequence repeats (SSRs) utilized and 70 polymorphic loci were observed in cotton (Liu et al., 2000). They postulated that these primers can be used in genetic mapping with other genetic markers for observing cotton genomic structure at whole genome.

Fiber quality QTLs observed in a mapping population evolved from introgression of long staple (*G. barbadense*) 3-79 and TM-1 (*G. hirsutum*) using RAPDs (Kohel et al., 2001).

As a whole 13 QTLs were observed; out of which three QTLs related to fiber length, 6 to fiber fineness and 4 connected to fiber strength. All of these were found on different loci and as a whole contributed to about 30-60% of phenotypic expression for fiber quality in mapping population.

Recombinant inbred lines evolved from introgression among Egyptian to Hawaiian cotton utilizing American cotton "NM 24016" as a parent (Yingzhi et al., 2004). As a whole about 500 primers including RAPDs, AFLPs, STSs, SRAPs and SSRs were screened among two populations (TM-1 x NM24016 and 3-79 x NM24016). RAPDs were transformed to STSs and found polymorphic markers related to yield, agronomic and fiber characters.

Ninety eight microsatellites were genotyped among 56- gene pool entries of *G. arboreum* for different fiber quality traits developed from 9 zones of Asia, Africa and Europe (Kanthrtzi and Stewart, 2008). Most of the primers manifested polymorphism in most entries. Six separate subgroups were found using structure analysis which proofed the origin of all entries from different regions with diverse genetic make-up. Marker-trait relations were calculated using single marker analysis and relation among morphological characters observed with population formation

Lu et al. (2009) observed genetic diversity among upland cotton and *G. barbadense* (pima) cotton cultivars for yield and fiber quality traits at genome wide level. They applied sequence tag sights (STS), cleavage amplified polymorphism (CAP) and SNPs developed from single strand conformation polymorphic (SSCP) markers for the assessment of polymorphism. As a whole 75 primers were found polymorphic. 48 primer pairs were related to SSCP, 27 were evolved between the species, 6 were present in intra-specific and 15 found both in intra-specific and interspecific combination. They found 18 SNPs with sequencing having mean length of 350bp and 1.3 SNPs per fragment. 78% of the SNPs were related to alteration in nucleotides and 8 of total SNPs observed among species while 4 Indels produced polymorphism in such combinations. Restriction enzyme digestion verified 6 SNPs. They concluded that genetic mapping can be accomplished at whole genome level by using SSCP markers as SNPs can be developed by using such DNA markers.

Microsatellites used for the development of saturated linkage maps for fastening breeding efforts in cotton (Xio et al., 2009).

Polymorphic loci with microsatellites obtained from easily access two public sources Cotton DB (http://cottondb.org/) and CMD (http://cottonmarker.org) databases. Genetic map spans to 4140cM with 207 loci which seems like cotton genome. Monsanto has been engaged for providing the required information like chromosome location, sequence etc via precise database for 945 SSR markers and commercially available 615 SSRs which will ultimately a source for researchers to overcome all problems in upland cotton.

The high density map developed in cotton collecting information from six highly saturated genetic maps using sequence-based marker redundancy. The genetic map encompassed to 4070 cM in 8254 loci derived from 6669 markers with a mean of 2 cM per marker (Blenda et al., 2012). They concluded that highly saturated genetic map can used as a base for map-based cloning related to economic characters, QTL mapping among diverse populations and for further genomic analysis among *Gossypium* species.

Wang et al. (2013) constructed a genetic map in mapping population developed from *G. barbadense* (Hai7124 x 3-79). They used 15971 gSSRs, EST-SSRs, SRAPs and SSCP SNPs for determining loci related to economic traits in Egyptian cotton. The map spanned to 2140.37 cM with an average of 6.26cM per marker. 337 loci were mapped on 52- linked groups and 35 groups assigned to 20 chromosomes. As a whole they observed 23 and 12 QTLs for yield contributing and fiber quality respectively.

Wang et al. (2015) used intra-hirsutum population derived from DH-962 and Jimin-5 evaluated under multiple locations for determining loci related to yield and fiber traits through construction of genetic map. The map covered 2016.44 cM with a mean of 3.27 cM among each marker having 616 loci. As a whole they observed 134QTLs for yield and fiber traits, out of which 70 were related to yield and 64 for fiber with phonological variation of 4.40-15.28% in different climatic zones for six years. They found 22 and 19 new QTLs in joint analysis and 9 common QTLs in more than one climate. They observed 26 QTLs on 13 loci and 2- large linked groups, also a few QTLs bunches designated to yield and fiber characters. They deduced that precision in QTLs for polyploid plants, needs to screen the populations in multi-climatic zones in order to intensify merits of molecular breeding.

Shang et al. (2015) observed QTLs related to fiber quality in mapping population screened in multiple locations.

They found 20 QTLs for fiber length, strength, micronaire and elongation. They showed 2 stable QTLs for fiber length, strength and micronaire (qFL-Chr5-2 and qFL-Chr10-1), qFS-chr1 and qFM-chr19-1 respectively.

Koebernick et al. (2015) found that owing to less intra-specific reproducibility there are less mapping reports in upland cotton, but omics developments are on peak due to breakthrough of single nucleotide polymorphisms which will ultimately has fasten polygenic traits studies. They also pointed that fiber traits can be analyzed more precisely using such high-through put techniques and applying marker trait associations.

Jamshed et al. (2016) observed fiber quality in cotton using SSR in mapping population evaluated under different climatic conditions for several years. As a whole 28861 used for screening among 0–153 and sGK9708 cultivars and out which 851 were polymorphic. The genetic map covered about 93% of cotton genome and spanned to 4110 cM with mean of 5.2 cM among markers. As a whole 165 QTLs were found for fiber and out of which 47 were same in more than one climatic zone. They further revealed that 75 QTLs are new and 90 QTLs are in accordance to earlier studies. They observed high heritability 0.93, 0.92, 0.85 and 0.80 respectively among fiber traits fiber length, strength, micronaire and uniformity.

2.3. Association mapping of fiber traits Using Genotyping by Sequencing (GBS)

In-contrast to genetic mapping in populations developed from hybridization of parents using conventional ways are not saturated, labor intensive, always in danger, high investment for development and more work after evaluating numerous genotypes of gene pool (Abdurakhmonov et al., 2007). Nonetheless, association mapping use LD and overcomes the requirement of bi-parental populations by utilizing the extent of genetic variation present within the available stable populations like cultivars, accessions developed with the time and maintained as gene pool. Association mapping on whole genome has been studied in Arabidopsis (Atwell et al., 2010); rice (Huang et al., 2012) for observing loci connected to economical characters. Association studies allow the development of highly saturated maps via determination of QTLs related to economic characters at whole genome level in permanent mapping populations. Molecular breeding methods can be used more efficiently by using markers with high number of markers on maps at whole genome level (Timmerman-Vaughan et al., 2004; Burstin et al., 2007; Lejeune-henaut et al., 2008).

Genotyping-By-Sequencing has a potential to assist the researchers involved in cotton to determine the QTLs related to yield and fiber traits being the thirst for a long time. Molecular breeding require numerous and valuable SNPs which can saturate the map for the detection of QTLs connected to desired traits and further genomic studies (Young, 2013). The evolution of single nucleotide polymorphism has speed up due to availability of high-through put sequencing ways which allow the development of highly saturated maps for searching loci related to yield and fiber quality traits.

Seed protein and oil contents were analyzed in soybean germplasm collection at whole genome level using association mapping and loci observed related to these economical traits (Huwang et al., 2014). As a whole large variation found among all genotypes when association was determined. Illumnia and GoldenGate assays performed to genotype the whole germplasm with 55159 SNPs and 31954 primers screened with minor allele frequency>0.10 for calculation of LD among the loci. The association results prevailed that 40 SNPs were connected to protein contents on 17 separate locations in the genome 25 SNPs investigated in 13 distinct loci connected to oil contents. 7 of total SNPs were significantly correlated to both oil and protein contents. They postulated that association mapping not only confirm earlier QTLs but also determined new locations on chromosomes in a shorter distance which will contribute a lot to devise new plans for improving dietary value in soybean

Abdurakhmonov et al. (2008) used association analysis for observing association among fiber traits in cotton among germplasm entries for utilizing the genetic variation in marker-based breeding. Linkage disequilibrium based association mapping determined in the germplasm having diverse genotypes from all over the world. 95 SSR were screened among all germplasm entries for ascertaining QTLs at whole genome level associated with fiber properties. They found about 11-12% LD among all SSRs. They also observed significant population orientation among all entries. They employed mixed linear model and general linear model using kinship and population structure and as a whole determined 6 & 13 % pair of primers related to fiber quality. They concluded that the markers selected in this study can be used for refinement of fiber using hidden sources of genetic variability.

Genetic variation, population behavior and LD based association analysis for fiber conducted in germplasm under two different climatic zones (Abdurakhmonov et al., 2009). The upland gene pool containing 335 elite entries screened with 202 SSRs.

Mean of LD prolonged to 25 cM at whole genome level among all genotypes at 0.01 probability. They found that LD dropped to about 5 cM at ($r^2 > 0.2$) showing potential for association among genotypes for yield contributing characters. They performed mixed linear model and population analysis for observing association contributing to permutation significance and population pattern. As a whole developed many common markers for fiber traits among genotypes in both locations. They revealed that mixed linear model associations ranged from 7 to 43% having strong to very strong relation to fiber properties as confirmed by Bayes factor which will be a very effective source for association analysis of yield improvement in marker based breeding techniques.

Wang et al. (2013), found association among yield and fiber characters in using mixed linear model in pima cotton germplasm entries. They observed 72 loci, out of which 46 were connected to fiber while 26 related to cotton. They concluded that marker-associations among fiber characters are of vital value for enhancing quality.

Fang et al. (2014), used multi-parents population for observing association among yield and fiber quality traits. They revealed that common and new QTLs deducted in this study can be used for overcoming problems in fiber quality enhancement. They screened 1582 polymorphic microsatellites among 275 RILs in first set developed from diverse parents for screening QTLs connected to fiber. 131 QTLs found for fiber quality sharing characters via association analysis with TASSEL while same QTLs verified in second set of 275 RILs with 270 SSR. The distinction showed that 54 new QTLs and 77 QTLs are in accordance to previous studies.

Genetic map constructed using RIL developed from transference of superior fiber quality from *G. barbadense* (TM-1) to *G. hirsutum* cv. NM24016 and relationship determined among yield components and fiber. 429 SSR and 412 GBS-based single nucleotides were involved in the development of map which spanned to about half length of upland cotton genome (Gore et al., 2014). They revealed that all makers are distributed randomly among all loci of the genome. The yield components and fiber characters showed extreme phenotypic expression under multiple locations. They found 28 QTLs which are useful from breeding perspectives for agronomic and fiber properties.

Cai et al. (2014) used 99 upland cotton genotypes to ascertain the association for fiber traits. The relationship among fiber components determined with 97 polymorphic

microsatellites. The genomic regions associated with fiber were 107 including 70 in 2 or more than 2 zones and 37 found in just one. It was revealed that most of the associations were reliable as verified from earlier findings for fiber quality. They also observed genomic regions related with 2 or more characters and assumed that such regions derived from the genotypes which are having minor allele frequency less than five, from local sources or acclimatized in china. They concluded that fiber traits can be renovated by using such loci from diverse resources.

Islam et al. (2015), carried GBS for observing SNPs which can be used for improving economic traits in cotton gene pool. RILs and 11 contrasting parents were used in the study with two separate methods were applied for determing SNPs with variant allele frequency of >0.1. SNPs quality control performed and calling done with available *G. raimondii* Ulbrich genome. As a whole 1071 and 1223 SNPs observed among At and Dt genomes respective. Moreover these SNPs were found in coding region usually in higher frequency. GBS was conducted in germplasm consisting of 154 accessions for the verification of 111 of total SNPs and the SNPs verified in all parents and none of the genotype was found with same SNP. They revealed that SNPs can be determined in *G. hirsutum* with ease and genetic improvement can be done after getting true SNPs.

Association among fiber traits conducted in germplasm collection of Hawaiian cotton consisting of 503 genotypes (Nie et al., 2016). They used 494 microsatellites at whole genome and as a whole 179 replicable SSRs were screened among genotypes under diverse climatic conditions. Population pattern and LD used for observing association among various fiber traits with mixed linear model via TASSEL program. The QTLs were selected among markers and phenological characters with association values. 426 alleles were evolved and germplasm was differentiated into seven subgroups upon the basis of hybridization, climate and topographical pattern. 216 polymorphic loci were associated with fiber contributing characters having mean of 2.7% and showed phenotypic variation from 0.58-5.12%. LD decreased significantly to 0-5cM and observed 13 QTLs which are same to earlier findings and 3 connected to similar character while 7 QTLs were corresponded to fiber formation. They concluded that novel alleles identified based association mapping based LD for fiber quality can be applied in breeding cultivars for tagging genes of interest.

GBS carried in a population evolved using various parents for overcoming the inverse relation among yield and fiber traits (Islam et al., 2016).

They assumed that GBS will serve as a valuable source for the development of high saturated map with the development of large frequency of SNPs. Association analysis via mixed linear model in TASSEL observed among fiber traits in four separate climates with 5071 SNPs developed from GBS and 223 SSRs from 547 RILs. One QTL cluster related to fiber traits including length, short fiber content, strength and uniformity found and verified on locus A07. They also studied the ultimate genes connected to fiber traits and revealed that SNP (CFBid0004) formed from deletion of 10bp GhRBB1_A07 is directly associated with fiber traits among RIL and 104 approved american varieties. Moreover, GhRBB1_A07 can be used in MAS for the improvement of fiber traits among germplasm entries.

Sun et al. (2017), studied the genetic architecture of major fiber traits in cotton germplasm using association mapping under different climatic zones. The mixed linear model association analysis showed that fiber length, strength and uniformity had 16, 10 and 7 SNPs respectively while *G. raimondii* 7^{th} chromosome had two main genomic locations and fiber length contributing four genes were also observed. Moreover population structure showed that populations from low peaks were having less genetic variation among accessions compared to high peaks. The valuable allelic frequency was more in genotypes from less elevation in-contrast to high. They concluded that the desired allelic number among genotypes can be used for enhancement of fiber.

Association was observed for plant ideotype, heat tolerance, yield contributing traits and fiber quality among germplasm collection under different climatic conditions for consecutive three years at whole genome (Gapare et al., 2017). The genetic stock associations were observed using SNPs. Fiber characters were found to be low to highly heritable as value ranged from 0.26-0.89 for boradsense heritability as compared to yield components having 0.14-0.43. Phylogenetic analysis showed that the genotypes were developed from diverse parents having multiple characters from breeding perspectives. They pointed that less number of informative markers can be used for association mapping studies as LD value found upto 5Mbp which decreased to 2Mbp at $r^2 \geq 0.2$. 17 significant SNPs connected fiber length while 50 SNPs for fineness were observed using mixed linear model. The results revealed that associations among most of the characters at whole genome were non-significant as numerous SNPs impact on phenotype was found lower than 5% and assumed this to be due to low reproducibility of markers among cotton or SNP Chip less coverage in the germplasm.

Sun et al. (2017) used association analysis in germplasm containing wide variation among genotypes at multiple locations for fiber quality traits. Illumnia SNP array was used for genome-wide study for quality analysis. They found 10511 SNPs which were distributed over all loci and 46 SNPs associated with fiber quality with significance. They observed two QTLs for strength and length on At07 and Dt11.

Association among fiber quality traits observed in genetic stock containing 185 genotypes using SSR (Iqbal and Rahman, 2017). As whole 382 markers were screened in 10 elite cultivars with good fiber and found 95 being polymorphic which ultimately used among all germplasm. The traits including lint percentage, fiber length, strength, uniformity and boll weight showed highly significant differences among all genotypes. The mean polymorphic value and genetic diversity were 0.175 and 0.191 respectively while four main-groups found using STRUCTURE program, Principal component analysis and Unweighted pair group with arithmetic mean. Grouping done using Ward's method among germplasm entries gave better results than principal component analysis. Phylogeny tree showed that 47 genotypes were derived from same parents. As a whole 75 associations were observed among genotypes using phenotypic data which included 18, 18, 8, 3, 15 and 13 for lint percentage, fiber length, fineness, strength, uniformity and boll weight alternatively. MGHES-51 marker found in all associations. LD value showed significant linkage among primers as 6.8% and 4.4% at ($r^2 \geq 0.05$) and ($r^2 \geq 0.1$) respectively. They postulated that most of the associations were new and can be a good source for speeding up the molecular breeding with new high-through put technologies.

3. MATERIAL AND METOD

The work done related to association analysis of fiber quality in germplasm collection of cotton from all over the world maintained at Kahramanmaras Sutcu Imam University, Kahramanmaras Turkey. The gene pool screened for analyzing genetic diversity, population structure and quantitative trait loci assessment by phenotyping in the field at two locations during 2016. Each step explained in sequence:

3.1. Phenotypic screening for fiber quality

3.1.1. Plant material

In 2016, the *Gossypium* germplasm consisting of 286 genotypes including accessions, obsolete or modern registered cultivars, introgressed lines, elite breeding strains, and representatives of genomes used for association analysis related to fiber traits. The germplasm used for association mapping is given in (Table 3.1). The trials were grown at on 24th April, 2016 sown at the East Mediterranean Transitional Zone Agricultural Research Institute Kahramanmaras Turkey using augmented design while at farmer field using same experimental layout on 23rd April, 2016 in Diyarbakir at grower filed.

Table 3.1. Germplasm collection for fiber quality

Genotype	Species	Origin	Genotype	Species	Origin
1118-Glandless	*G. hirsutum L.*	USA	Corina	*G. hirsutum L.*	Spain
152-F	*G. hirsutum L.*	Russia	Crincle Leaf	*G. hirsutum L.*	USA
153-F	*G. hirsutum L.*	Russia	Cırpan 603	*G. hirsutum L.*	Bulgaria
2421-A	*G. hirsutum L.*	Russia	Cukurova-1518	*G. hirsutum L*	Turkey
308 (CAMPO)	*G. hirsutum L.*	Turkey	Cun S-1	*G. hirsutum L.*	USA.
4SP	*G. hirsutum L.*	Albania	Delcerro	*G. hirsutum L.*	Venzevle
919 (LİDER)	*G. hirsutum L.*		Delta Opal	*G. hirsutum L.*	USA
93 FF 01	*G. hirsutum L.*		DP-388	*G. hirsutum L.*	USA
YB10	*G. hirsutum L.*	USA.	DPL-20	*G. hirsutum L.*	USA
Acala-172	*G. hirsutum L.*	USA	DPL-50	*G. hirsutum L.*	USA
Acala-552	*G. hirsutum L.*	USA	DPL-5409	*G. hirsutum L.*	USA
AK-4	*G. hirsutum L.*	Russia	DPL-5614	*G. hirsutum L.*	USA.
Aktas-3	*G. hirsutum L.*	Azerbaijan	AB80	*G. hirsutum L.*	Turkey
Albania-6172	*G. hirsutum L.*	Albania	EUROPA-1752	*G. hirsutum L.*	.
Aleppo 1	*G. hirsutum L.*	Syria	Fibermax 819	*G. hirsutum L.*	USA
Aleppo 40	*G. hirsutum L.*	Syria	Fibermax 832	*G. hirsutum L.*	USA
Aydın-110	*G. hirsutum L.*	Turkey	Fibermax 958	*G. hirsutum L.*	USA
Azerbaycan 3038	*G. hirsutum L.*	Azerbhaican	Garant	*G. hirsutum L.*	Albania.
Beli İzvor-432	*G. hirsutum L.*	Bulgaria	Gedera-5	*G. hirsutum L.*	Turkey

Table 3.1. Continue

Genotype	Species	Origin	Genotype	Species	Origin
Belserroms-30	*G. hirsutum L.*	Turkey	Golda	*G. hirsutum L*	Turkey
BSC-4	*G. hirsutum L.*	USA	Gurbeyms34/1	*G. hirsutum L*	Turkey
CA-228	*G. hirsutum L.*	Africa	IS-2	*Gossypium Sp.*	Israil
Carmen	*G. hirsutum L.*	Australia	Kahinath	*Gossypium Sp.*	India
Caskot BR-1	*G. hirsutum L.*	USA	Lachata	*G. hirsutum L.*	Spain
Maras92	*G. hirsutum*	Tukrey	H-88029	*G. hirsutum*	Turkey
Marcel leaf	*G. hirsutum*	USA	Hint Ç.9	*G. hirsutum*	Turkey
McNair-235-612	*G. hirsutum*	USA	HYC-76/59	*G. hirsutum*	Turkey
MC NAMARA	*G. hirsutum*	USA	İs 4	*Gossypium sp.*	Israil
NAKBC1-14/2	*G. hirsutum*	Turkey	İs 8	*Gossypium sp.*	Israil
NATA	*G. hirsutum*	Spain	Kurak-1	*G. hirsutum*	Turkey
Nazilli 342	*G. hirsutum*	Turkey	Lockette	*G. hirsutum*	Turkey
Nazilli 84S	*G. hirsutum*	Turkey.	Nazilli 87	*G. hirsutum*	Turkey
Nazilli M-503	*G. hirsutum*	Turkey	Özbek 142	*G. hirsutum*	Turkey
Nazilli (93-7)	*G. hirsutum*	Turkey	Visalia Elmer	*G. hirsutum*	Turkey
Nectar free	*G. hirsutum*	Turkey.	Sealand 542	*G. hirsutum*	USA
Nieves	*G. hirsutum*	Australia	Siokra 133	*G. hirsutum*	USA
NSCH-777	*Gossyp. Sp.*	India	STN. K311	*G. hirsutum*	USA
Okra 201	*G. hirsutum*	Fildisi	Stonville 506	*G. hirsutum*	USA
Okra 204	*G. hirsutum*	Fildisi	YB141	*G. hirsutum*	Turkey
Okra-frego	*G. hirsutum*	USA	Acala 44	*G. hirsutum*	USA
P.D. 0648	*G. hirsutum*	USA	Acala Royale	*G. hirsutum*	USA
Paymaster 2379	*G. hirsutum*	USA	Acala1517-99	*G. hirsutum*	USA
Paymaster 330	*G. hirsutum*	USA	Acala Prema	*G. hirsutum*	USA
R-5 (STG-6)	*G. hirsutum*	Turkey	Acala1517-95	*G. hirsutum*	USA
RKNR 261	*G. hirsutum*	Turkey	Stoneville 132	*G. hirsutum*	USA
SAHEL 1	*G. hirsutum*	Turkey	YB149	*G. hirsutum*	Turkey
SAYAR-314	*G. hirsutum*	Turkey	YB150	*G. hirsutum*	Turkey
Semer. Uzbek	*G. hirsutum*	Ozbekis.	YB151	*G. hirsutum*	Turkey
Semu SS7G	*G. hirsutum*	Australia	YB152	*G. hirsutum*	Turkey
SG 404	*G. hirsutum*	USA	YB1535	*G. hirsutum*	Turkey
SG 501	*G. hirsutum*	USA	YB154	*G. hirsutum*	Turkey
Sindos 80	*G. hirsutum*	Greece	YB155	*G. hirsutum*	Turkey
Siocra	*G. hirsutum*	Australia	YB156	*G. hirsutum*	Turkey
Sivon	*G. hirsutum*	USA	YB157	*G. hirsutum*	Turkey
Sphinx V	*G. hirsutum*	USA	YB158	*G. hirsutum*	Turkey
STG 14	*G. hirsutum*	USA	YB159	*G. hirsutum*	Turkey
Stn 8a	*G. hirsutum*	USA	YB160	*G. hirsutum*	Turkey
Stoneville-453	*G. hirsutum*	USA	YB161	*G. hirsutum*	Turkey
Suregrow 125	*G. hirsutum*	USA	Gosspollfree	*G. hirsutum*	Turkey
Sahin 2000	*G. hirsutum*	Turkey	PI 528420	*G. hirsutum*	USA

Table 3.1. Continue

Genotype	Species	Origin	Genotype	Species	Origin
Tamcot CABCS	*G. hirsutum*	USA	NP-ozbek 100	*G. hirsutum*	Turkey
Tamcot Luxor	*G. hirsutum*	USA	TX 0175-2	*G. hirsutum*	USA
Tamcot Pyramid	*G. hirsutum*	USA	Özbek 105	*G. hirsutum*	Turkey
Tamcot SP 37-N	*G. hirsutum*	USA	TX 0175-1	*G. hirsutum*	USA
Tamcot Sphinx	*G. hirsutum*	USA	TX 0061-2	*G. hirsutum*	USA
Taskend-6	*G. hirsutum*	Ozbekist.	Nazilli 07	*G. hirsutum*	Turkey
YB101	*G. hirsutum*	Turkey	Sezener 76	*G. hirsutum*	Turkey
TKY-9409	*G. hirsutum*	USA	TX 0060-2	*G. hirsutum*	USA
Togo	*G. hirsutum*	Africa	TX 0091-1	*G. hirsutum*	USA
Veramine	*G. hirsutum*	Iran	İpek 607	*G. hirsutum*	Turkey
Zeta 2	*G. hirsutum*	Greece	PI 528426	*G. hirsutum*	USA
YB106	*G. hirsutum*	Turkey	NP EGE 2009	*G. hirsutum*	Turkey
Kurak 2	*G. hirsutum*	Turkey	PI 173332	*G. hirsutum*	USA
NGF-63	*G. hirsutum*	Turkey	PI 529128	*G. hirsutum*	USA
Naked	*G. hirsutum*	Turkey	STN498	*G. hirsutum*	USA
Orgosta 644	*G. hirsutum*		TX 0091-2	*G. hirsutum*	USA
İs 10	*Gossp.sp.*	Israil	GAİA	*G. hirsutum*	Turkey
Samon	*G. hirsutum*	USA	PI 165325	*G. hirsutum*	USA
Ujchi 2 Uzbek	*G. hirsutum*	Turkey	ZN243	*G. hirsutum*	Turkey
108F	*G. hirsutum*	Russia	PI 528429	*G. hirsutum*	USA
Acala 3080	*G. hirsutum*	USA	PI 528450	*G. hirsutum*	USA
Acala S.J. 2	*G. hirsutum*	USA	PI 528525	*G. hirsutum*	USA
Coker 413/68	*G. hirsutum*	USA	GAPEAM1	*G. hirsutum*	Turkey
DPL 15/21	*G. hirsutum*	USA	PI 529869	*G. hirsutum*	USA
DPL529	*G. hirsutum*	USA	Spears3(967)	*G. hirsutum*	USA
DPL 90	*G. hirsutum*	USA	YB193	*G. hirsutum*	Turkey
Ege-69	*G. hirsutum*	Turkey	YB194	*G. hirsutum*	Turkey
Extreme Okra	*G. hirsutum*	Tureky	YB195	*G. hirsutum*	Turkey
Eksi-91	*G. hirsutum*	Turkey	YB196	*G. hirsutum*	Turkey
Gossypollfree86	*G. hirsutum*	Turkey	YB198	*G. hirsutum*	Turkey
TX0175-1	*G. hirsutum*	USA	DP419	*G. hirsutum*	USA
TX 0175-2	*G. hirsutum*	USA	Primera	*G. hirsutum*	USA
528875	*G. hirsutum*	USA	Veret	*G. hirsutum*	Turkey
Acala wild 1517	*G. hirsutum*	USA	BA 525	*G. hirsutum*	Turkey
Ugur	*G. hirsutum*	Turkey	DP 5690	*G. hirsutum*	USA
Acala 1517-99	*G. hirsutum*	USA	SJU 86	*G. hirsutum*	USA
TX 0091-2	*G. hirsutum*	USA	Blightmaster	*G. hirsutum*	USA
YB214	*G. hirsutum*	Turkey	Sicala 33	*G. hirsutum*	USA
YB215	*G. hirsutum*	Turkey	HT2	*G. hirsutum*	Turkey
YB216	*G. hirsutum*	Turkey	Dicle 2002	*G. hirsutum*	Turkey

Table 3.1. Continue

Genotype	Species	Origin	Genotype	Species	Origin
PI 163722	*G. hirsutum*	USA	Semu 55/6	*G. hirsutum*	Turkey
PI 163615	*G. hirsutum*	USA	Tropical 225	*G. hirsutum*	Turkey
163615	*G. hirsutum*	USA	STV 373	*G. hirsutum*	USA
YB225	*G. hirsutum*	Turkey	Naz 84	*G. hirsutum*	Turkey
Krem	*G. hirsutum*	Turkey	4 SB	*G. hirsutum*	Turkey
Acala 1517 D	*G. hirsutum*	USA	İdeal	*G. hirsutum*	Turkey
ADN 123	*G. hirsutum*	USA	Vurcano	*G. hirsutum*	USA
Sealand 1	*Gossy. Sp.*	USA	STV 478	*G. hirsutum*	USA
TMN 170	*G. hirsutum*	USA	SG 1001	*G. hirsutum*	USA
TM-1	*G. hirsutum*	USA	Barut 2005	*G. hirsutum*	Lebanon
Coker 312	*G. hirsutum*	USA	Nazilli 303	*G. hirsutum*	Turkey
Sicala 3/2	*G. hirsutum*		Siokra 1/4	*G. hirsutum*	Australia
Tamcot H 0 95	*G. hirsutum*	ABD	YB289	*G. hirsutum*	USA
Gossy. Nazilli	*G. hirsutum*	Turkey	STV 474	*G. hirsutum*	USA
Cooker 100 Ahıl	*G. hirsutum*	USA	Fantom	*G. hirsutum*	Turkey
Naz. 954	*G. hirsutum*	Turkey	Famosa	*G. hirsutum*	Turkey
Paymaster 404	*G. hirsutum*	USA	TMK 122	*G. hirsutum*	Turkey
GSN 12	*G. hirsutum*	Turkey	ADN 710	*G. hirsutum*	Turkey
HT1	*G. hirsutum*	Turkey	TMN 16	*G. hirsutum*	Turkey
Naz 143	*G. hirsutum*	Turkey	TMS 108/2	*G. hirsutum*	Turkey
Emand 542	*G. hirsutum*	Turkey	ADN 712	*G. hirsutum*	Turkey
Flora	*G. hirsutum*	Turkey	TMN 199	*G. hirsutum*	Turkey
Napa	*G. hirsutum*	Turkey	BEREN	*G. hirsutum*	Turkey
YB247	*G. hirsutum*	Turkey	Sarı Gelin	*G. hirsutum*	Turkey
DP 493	*G. hirsutum*	Turkey	Nihal	*G. hirsutum*	Turkey
H- 23	*G. hirsutum*	Turkey	Gelincik	*G. hirsutum*	Turkey
GSN 22	*G. hirsutum*	Turkey	TMN 18	*G. hirsutum*	Turkey
G. hirsutum	*G. hirsutum*	USA	ADN 413	*G. hirsutum*	Turkey
Cooker 100 A 2	*G. hirsutum*	USA	Ozaltın 112	*G. hirsutum*	Turkey
Cabu cs 2-1-8-3	*G. hirsutum*	USA	Özaltın 404	*G. hirsutum*	Turkey
Menderes 2005	*G. hirsutum*	USA	Lodos	*G. hirsutum*	Turkey
S-9	*G. hirsutum*	Turkey	Flash	*G. hirsutum*	Turkey
H-10	*G. hirsutum*	Turkey	Carisma	*G. hirsutum*	Turkey
DP 5111	*G. hirsutum*	USA	Aksel	*G. hirsutum*	Turkey
SG 96	*G. hirsutum*	USA	BA 440	*G. hirsutum*	Turkey
Adana 98	*G. hirsutum*	Turkey	BA 811	*G. hirsutum*	Turkey
Cun S-2	*G. hirsutum*	Turkey	Lydia	*G. hirsutum*	Turkey
Tamcot SP 21-9	*G. hirsutum*	USA	PG 2018	*G. hirsutum*	Turkey
Siokra L 22	*G. hirsutum*	USA	Julia	*G. hirsutum*	Turkey
Coskun-1	*G. hirsutum*	Turkey	Claudia	*G. hirsutum*	Turkey

Table 3.1. Continue

Genotype	Species	Origin	Genotype	Species	Origin
DKG 658	*G. hirsutum*	Turkey	Carla	*G. hirsutum*	Turkey
Naz M 39	*G. hirsutum*	Turkey	Candia	*G. hirsutum*	Turkey
DP 396	*G. hirsutum*	USA	Gloria	*G. hirsutum*	Turkey

3.1.2. Climatic Conditions of area

The experimental farm of Kahramamaras Sutcu Imam University, East Mediterranean Transitional Zone Agricultural Research Institute Kahramanmaras located at east 37-38º parallel to 36-37º towards north. Maximum temperature varied from 30.8-42.8^{0}C during cropping season in-contrast to 21.2-36^{0}C since years (Table 3.2) while mean ranged 15.5-28.5^{0}C with 90.6mm rainfall.

Table 3.2. Meteorological data during experiment at Kahramanmaras and Diyarbakır

Year	Climatic parameters	Months													
		April		May		June		July		August		September		October	
		KM	DB	KM	DB	KM	DB	KM	DB	KM	DB	KM	DB	KM	DB
1950-2015	Max. Temp. (ºC)	21.2	35.3	26.7	38.1	31.9	42	35.6	45	36.0	45.9	32.4	42	26	35.7
	Min. Temp. (ºC)	9.9	-6.1	14.1	0.8	18.8	6.0	22.1	11	22.2	13.8	18.4	5.2	12.9	-1.2
	Av. Temp. (ºC)	15.5	13.8	20.3	19.2	25.2	26.2	28.4	31.1	28.5	30.4	25.2	24.9	19	17.2
	Rainfall (mm)	72.7	11.7	40	9.3	6.8	2.9	1	0.5	0.9	0.3	8.9	1.2	45.4	5.8
	Humidity (%)	57.7	13.8	54.4	19.2	49	26.3	50.5	31.1	51.9	30.4	49.2	38.7	53.8	41.3
	Wind intensity (ms^{-1})	2.1	68.4	2.4	44.4	3.4	8.8	3.9	0.5	3.4	0.4	2.5	4.2	1.3	33
2016	Max. Temp. (ºC)	30.8	28	35.5	33	41.3	34.4	42	38.9	42.8	40.3	38.7	31.7	32.5	26.5
	Min. Temp. (ºC)	8.6	6.8	9.7	11.2	14	17.2	19.8	22.4	21.4	21.9	11.3	23.6	9.2	10.7
	Av. Temp. (ºC)	18.8	15.1	21.8	19.2	26.8	25.8	29.7	30.7	30.7	31	24.9	15.2	19.3	18.6
	Rainfall (mm)	17.6	0.5	18.7	1.1	17.9	14.5	1.0	0	1.0	0.3	23.7	0	10.7	0.8
	Humidity (%)	41.2	55.1	47.9	51.1	40.3	31.2	36.5	22.3	40.9	21.8	39.2	28.9	38.9	35.5
	Wind intensity (ms^{-1})	1.32	9.3	1.7	10.9	1.9	12.4	2.1	14.9	1.86	9.6	1.7	12.4	1.1	7.2

KM: Kahramanmaraş, DB: Diyarbakır

The secong trial conducted at Diyarbakır which is the southeastern part of Turkey and located at east 37-40 º and 20-41 º and parallel to towards north 38-43º. As a whole climate is harsh as it very hot in summer and too much cold in the winter. Maximum temperature 48.4^{0}C observed in the city during 1946 while lowest temperature -25^{0}C in

1933. Annually 496mm rainfall recorded for the region out of which more than 50% is in summer (Anonim, 2016b).

3.1.3. Soil preparation

Double ploughing done for eradication of weeds before sowing. Nitrogen (N) and phosphorous (P_2O_5) fertilizer applied @ 70kg ha $^{-1}$ (20:20:0) for restoration of soil fertility about 1-week before sowing.

3.1.4. Sowing

Federer (1956) developed a type of experimental design designated as augmented design, to overcome problems produced from non-replicated trials for germplasm screening. The perquisite of this design is to include check varieties for which enough material is available and within a proper experimental layout repeat the checks. Check varieties are placed in blocks in each replication (relies upon design whether complete or incomplete) and the genotypes to be screened are allotted to plots that are not found in blocks. Observed values of genotypes to be screened are adjusted using block effects and significance of the genotype differences is assessed with error.

The genetic stock consisting of all entries described in (Table 1) was sown in an augmented design during 2016 on 24th April 2016 at the farm of Kahramanmaras Sutcu Imam University, Kahramanmaras having plot length 6m and planting distance 0.2m x 0.7m between plants and rows and 1m left as a path among the blocks (Figure 3.1). While at farmer field in Diyarbaker on 24th April 2016 using same experimemtal layout.

Figure 3.1. Layout and sowing

3.1.5. Agronomic practices, fertigation and pest control measures

After one week of sowing manual weeding was done for ensuring weed control in Kahramanmaras. First irrigation was applied after 7-days of sowing, subsequent were applied each after 6-days and as a whole about 9-irrigations were applied until maturity. Before first irrigation, ammonium sulphate (21%) was applied @60kg ha^{-1} . Last application of fertilizer as 46% Nitrogen was applied @ 60kg ha^{-1} before 5th irrigation. Normal agronomic practices carried out. Dimethoate was applied @ 1000ml per ha^{-1} for thrips control during first week of June. On 1st and 25th July, 2016 Indoxacarb was used to control *Heliothis armigera* @ 450ml per ha^{-1}.

3.1.6. Recording of data related to fiber quality

3.1.6.1.1. Ginning outturn (GOT%)

As a whole 50 opened bolls were harvested manually from 10 consecutive plants leaving the border plants from each entry at both locations. The samples were ginned manually using roller gin at "Agriculture Biotechnology Department Faculty of Agriculture, Kahramanmaras Sutcu Imam University (Figure 3.2). Lint percentage calculated by expressing the fiber component weight as a percentage of the total weight of the seed and fiber components (Singh, 2004).

$$GOT\ (\%) = \frac{Lint}{Seed\ cotton} \times 100$$

Figure 3.2. Ginning of samples for fiber analysis

Approximately 150 g of fiber from each entry used for the determination of fiber properties.

The fiber quality characters like fiber length (mm), fiber uniformity (UI), micronaire (fiber finess) (µg inch^{-1}), fiber maturity, fiber strength (g tex^{-1}), fiber elongation (FE) were recorded.

3.1.6.1.2. Fiber analysis using High Volume Instrument

The analyses of all fiber samples performed with a HVI M-1000 (Usterhouse Switzerland) in a controlled condition (20 ^{0}C and 65 % RH) at the Test Center of Cotton Fiber Quality at Kahramanmaras (Figure 3.3). The fiber traits determined using HVI were fiber length (mm) as upper half mean length (UHML), uniformity index, fiber strength (g tex^{-1}), micronaire value (µg inch^{-1}), maturity and elongation expressed as percentage.

Figure 3.3. HVI M-1000 Usterhouse Switzerland

3.1.6.1.3. Fiber length (mm)

The 2.5 per cent span length (mm) is defined as the distance spanned by the longest 50% of fibers being measured and also designated as upper half mean length. It is expressed as hundreds or 32'^{s} of an inch. The present fibre length at 2.5 per cent span was estimated by using HVI and expressed in millimeters.

3.1.6.1.4. Fiber Uniformity index (UI)

Ratio as a percent of mean length to the upper mean length (Anthony, 1999). Fiber length uniformity is expressed with uniformity index. HVI measured uniformity index in percentage using the following formula:

$$Uniformity\ ratio\ (\%) = \frac{50\%\ span\ length}{2.5\%\ span\ length} \times 100$$

3.1.6.1.5. Fiber fineness (µg inch^{-1})

Micronaire is an attribute of fiber determines the volume of air passing through a fiber under pressure in compressed cotton fibers (Anthony, 1999). Fiber fineness and maturity are measured using micronaire. It is expressed in micrograms per inch.

3.1.6.1.6. Maturity coefficient

Fiber maturity index measures the degree of fiber growth. The extent of secondary thickening of fiber effects directly maturity. The mature fiber ratio is lower than 1 among lumen and cell wall, partially mature fiber from 1-2 and un-ripened fiber has more than 2 maturity ratio. Fibre maturity was determined by using HVI.

3.1.6.1.7. Fiber Strength (FS) (g tex^{-1})

Fiber strength is determined as a force in grams required to partition a bunch of fibers one tex unit in size. Tex indicate weight in grams of 1000 fibers. It is calculated as g tex-1 via HVI.

3.1.6.1.8. Fiber elongation (FE)

It is the ratio of elongated length and initial length and determined in percentage. It is defined as the capability to stretch before breakage and considered as a vital component for yarn quality.

$$\text{Elongation (\%)} = \frac{\text{Apparant length} - \text{initial length}}{\text{initial length}} \times 100$$

Phenotypic measurements recorded on each location and then averaged across two locations germplasm using augmented design with three standards.

3.2. Association Mapping for Fiber Quality

Association mapping conducted among 90 genotypes in an association panel of upland cotton for ascertaining association among fiber traits. Each step for this analysis is described as follows.

3.2.1. Plant material

Germplasm collection consisting of 90 genotypes having diverse material from all over the world was used for association analysis using genotyping by sequencing.

3.2.2. DNA marker analysis

Genomic DNA extracted from fresh young leaf tissue of individual cotton plants of germplasm entries grown in the field in accordance with the modified CTAB DNA extraction procedure as described by Zhang and Stewart (2002).

3.2.3. Leaves collection

On an average. 4-5 fresh leaves from selected from each entry of the germplasm (Figure) in the field. The leaves were washed with distilled water, put in plastic bag having plant number and saved in the box with dry ice for maintaining temperature of -80^{0}C. Collected leaves were stored in Agriculture Biotechnology laboratory in refrigerator purchased from New Brunswick Scientific @ -80^{0}C. (Figure 3.4) till DNA extraction.

Figure 3.4. Leaves storage at -80^{0}C

3.2.4. DNA extraction

DNA extracted from leaves of each entry of germplasm following Zhang & Stewart, 2000. Briefly the protocol used for isolation of DNA is as follows:

DNA of each accession isolated from fresh young leaves harvested. DNA was isolated according to (Zhang & Stewart, 2000). Briefly fresh leaf material (about 0.5 g) was homogenized in 0.5 mL extraction buffer {0.1 M Tris-HCI (pH:8), 1 M NaCl, 0.02 M EDTA(pH:8), 2% w/v CTAB, 2% Polyvinyl-pyrrolidone-40, 1 mM, 0.2% P-mercaptoethanol}.

Homogenization was followed by placing samples in a hot water bath (65 °C) for 60 min with shaking each after 10min. Plant debris was then separated using centrifuging (20 min. a@ 12000 r.p.m) after adding a 0.6ml 24:1 chloroform [Chloroform: iso-Amyl Alcohol]) was used to separate proteins. The supernatant was then discarded to 1ml Eppendorf tubes and Ice-cold isopropanol (800 µL) was added to each 1000 µL isolated upper part supernatant. Depending on the amount of the precipitated DNA, the solution was left at -20 °C for 60 min for incubation. The solution was centrifuged @ 12000 rpm for 10 min and pellet was cleaned. 500 µL of 70% ethanol was added to pellet the DNA before another centrifugation @ 13000 rpm for 2-min followed by 100% ethanol for 2-min to get clear pellet. The pellet left at room temperature for drying then 300 µl Tris-EDTA solution {10 mM Tris (pH:8), 1 mM EDTA (pH:8), 1 M NaCl} added before storage at -20 °C. 2 µL of Rnase-A (10 mg/mol). The DNA samples were diluted to a concentration of 20 ng/µL with TE0.1 (10 mM Tris-HCl pH 8.0; 0.1 mM DTA) to be used as a working solution for Genotyping by sequencing.

Stepwise procedure used for isolation is mentioned below.

3.2.5. Mortar and paste of leaves

The leaves collected from germplasm were used for getting the proper tissue for DNA extraction using liquid nitrogen followed by grinding the frozen tissue with a mortar and pestle to break the plant cells open allowing the DNA to freely leave the cell. The paste was transferred into two 15ml falcon tubes and stored at -80^{0}C (Figure 3.5).

Figure 3.5. Mortar and Paste of leaves

3.2.6. DNA extraction

7ml extraction buffer [(0.1 M Tris-HCI (pH:8), 1 M NaCl, 0.02 M EDTA (pH:8), 2% w/v CTAB, 2% Polyvinyl-pyrrolidone-40, 1 mM 1,10-Phenanthroline monohydrate, % 0.2 mercaptoethanol)] was added to falcon tube having paste of leaf after shaking gently from top and bottom. The falcon tubes were placed in water bath for 1-hr @ 65^0C and shaking done gently each after 10min from both sides. 7ml Chloroform-isoamyl alcohol (24:1) was added, mixed slowly from top to bottom and centrifuged @12000 for 10min for precipitation of DNA. After this, the tubes were took outside with immense care to avoid two layers and upper layer having precipitate transferred to new 2ml Eppendorf tubes each having 1ml of supernatant. Latter on 800ml isopropanol stored at -20^0C added to each tubes, mixed very gently until homogeneity observed and put tubes at -20^0C for 1-hr in a freezer (Figure 3.6).

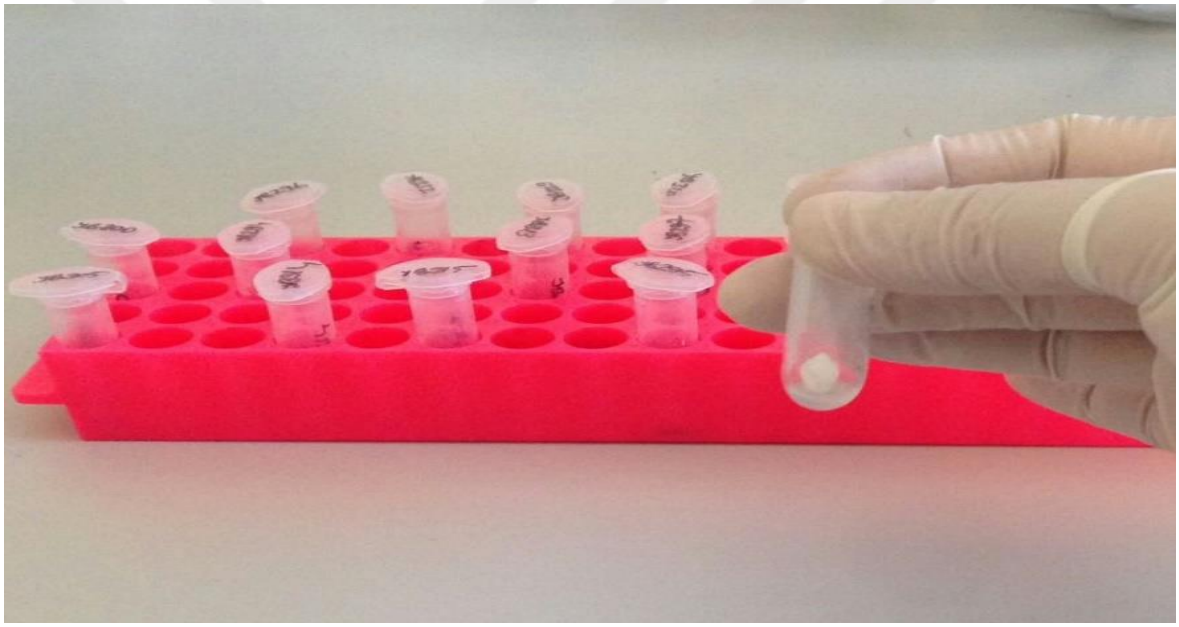

Figure. 3.6. DNA pellet

For purification of DNA, eppendorf tubes were centrifuged @ 12000rpm for 10min (Figure 3.9). Then isopropanol was discarded and 500µl 70% ethanol and centrifuged @13000rpm for 2min (Figure 3.7). Followed by 500 µl addition of 100% and same centrifigation. Allow DNA to dry at room temperature.

Figure 3.7. Centrifugation for precipitating DNA

3.2.7. DNA quantification

Two methods were used to identify and quantify the quality of DNA samples. DNA quantity and quality was observed with an agarose gel 1% electrophoresis method (Figure 3.10).

Figure 3.8. Gel electrophoresis for DNA quantification

All samples DNA concentration of genomic DNA was calculated using size of each band of the sample corresponding with those of DNA ladder (Promega) under ultra violet light after putting gel in ethibidium bromide (EBR) for 20min (Figure 3.9).

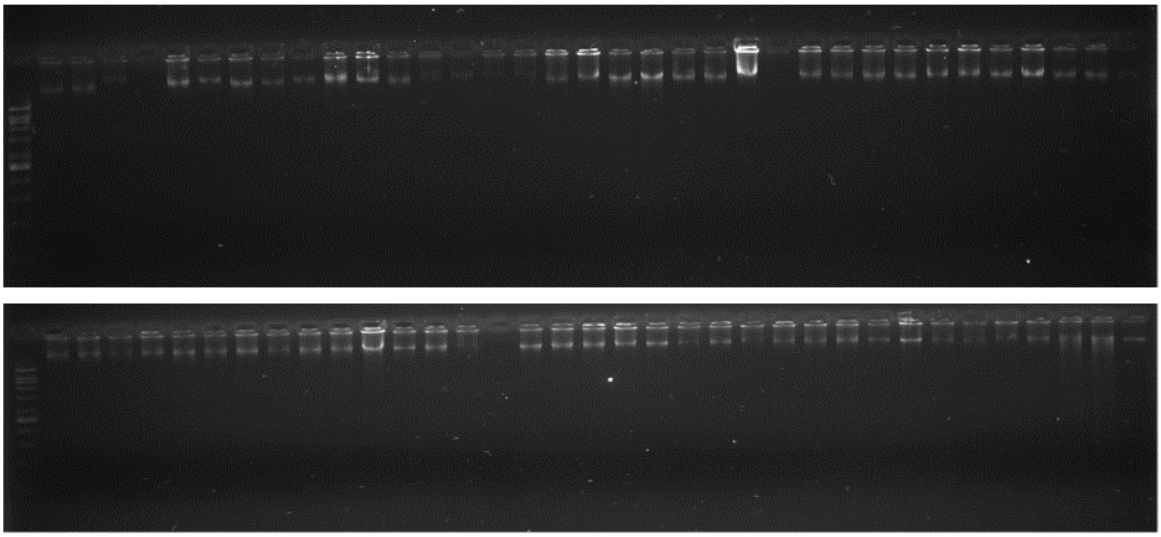

Figure 3.9. Gel photograph of genomic DNA

Spectrophotometry was used for quantification and quality checking depending on A260/A280 (Figure 3.10).

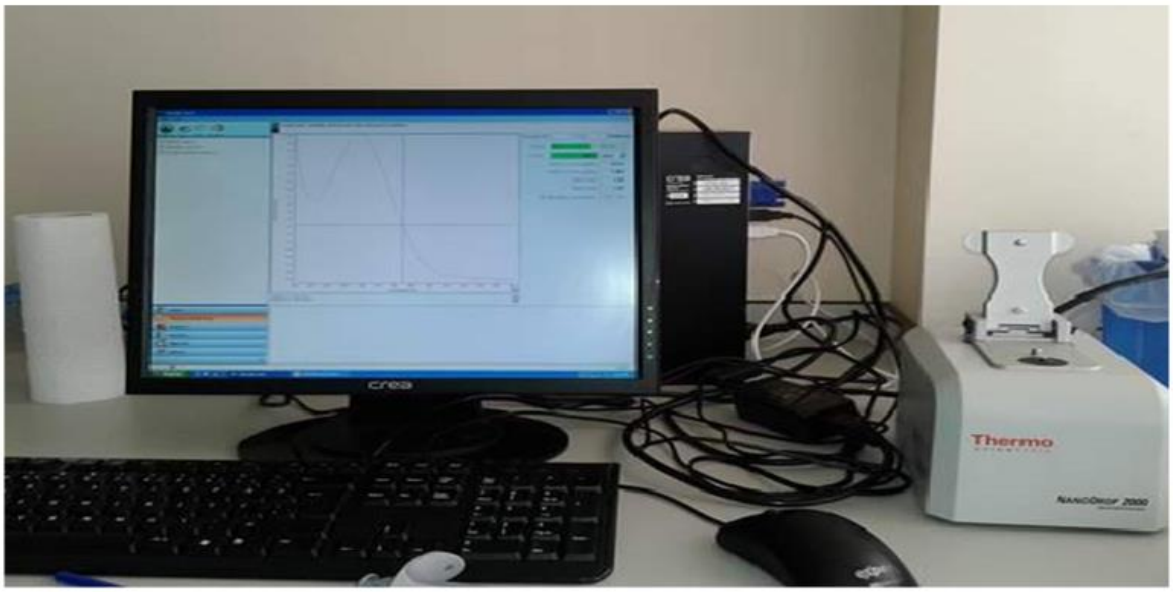

Figure 3.10. Spectrometer quantification of DNA

3.2.8. Genotyping by sequencing

Thanks to advances in next generation sequencing, it is now possible to produce reduced representation of genomes via construction of libraries in Illumnia sequencing platform using Genotyping by Sequencing (GBS).

GBS develops large number of single nucleotide polymorphism (SNPs) for mapping. As a whole GBS libraries were constructed in Bejing Genomic Institute (BGI), China. The GBS libraries were constructed in 95-plex using the P1 & P2 adaptor set (Poland et al., 2012). The stepwise library construction procedure is as follows:

(1). DNA digestion: Restriction enzyme, e.g., ApeKI used for digestion of genomic DNA.

(2). Adapter ligation: Fragments were ligated using P1 and P2 adapters. Forward amplification primer site, an Illumnia sequencing primer site and a barcode are included in P1 adapter.

(3). End Pair and add A: The selected fragments were subjected to end-repair and then was 3‘adenylated.

(4). PCR: P1 and P2 specific primers are used for amplification of sequences with polymerase chain reaction (PCR).

(5). Library quality control: Library was validating on the Agilent Technologies 2100 Bio-analyzer and the ABI StepOnePlus Real-Time PCR System (Figure 3.11).

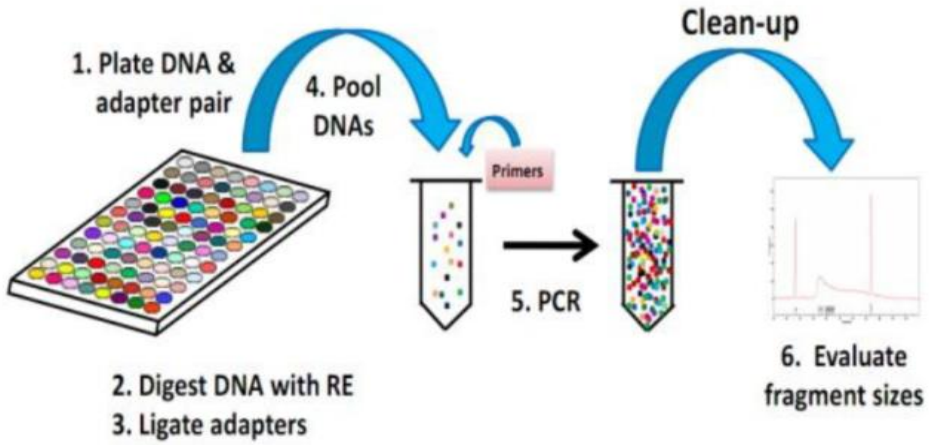

Figure 3.11. Library constrcution using GBS

3.2.8.1. Bioinformatic analysis via GBS

Bioinformatic tools conducted for the development of SNPs using GBS in BGI is as shown in Figure 3.12.

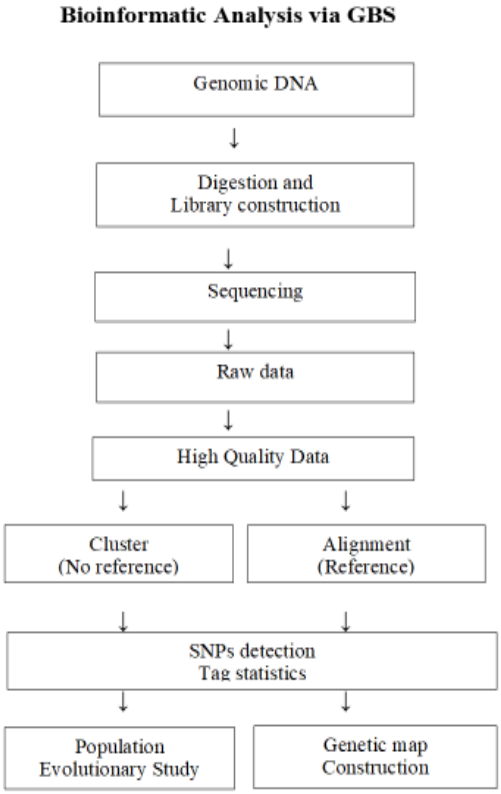

Figure 3.12. Bioinformatic analysis via GBS

3.2.8.2. SNPs calling

SNPs were filtered among population individuals using minor allele frequency (MAF) of 0.05. We supposed that the unique sequences were allelic. Owing to sequencing problems, homologue sequences on separate genomes and duplications, the two alleles are found in observed in same individual for putative SNPs.

3.2.9. Population structure

STRUCTURE V.2 Pritchard et al. (2000) program used to develop subgroups among the populations with Bayesian population subgrouping methodology to form the number of subgroups (K) and to designate individuals to sub-groups depending on kinship magnitude in each sub-group. Bayesian sub-grouping permits determination of pairwise values from dominant markers and no need of earlier information about selfing (Holsinger et al., 2002; Holsinger and Lewis, 2003). 2 independent runs were carried in STRUCTURE for K= 3–7 and a mean log likelihood values for each K was determined along runs. Mean log likelihood used for the determination of posterior probability.

Hence, the allocation of members of subgroups depending upon participant magnitude designated as, the Q matrix; was determined as the 24 mean of the three runs for k=5. across runs was estimated for each K.

3.2.10. Pairwise linkage disequilibrium and LD decay

Genome-wide LD decay was determined using r^2 of LD was used in graph as cM to mark estimate of genetic distance. Within 50 cM distance the significant association were observed ($r^2 \geq 0.05$) among SNPs. The genetic distance in the range of 0-25 cM quickly decreased as genome-wide LD was $r^2 \geq 0.1$. Therefore, at $r^2 \geq 0.2$ was decreased to 6-8 cM, showing value for association analysis.

3.2.11. Marker-traits associations

Type 1 error are involved in the creation of false associations during association studies and these should be analyzed according to statistical measures with utmost care. True marker-trait associations can be can be enhanced using the outcomes of population structure and principal component analysis. TASSEL Software (v.5.1, http://www.maizegenetics.net) were used for the determination of marker-trait associations. Yu et al. (2006) methodology for General linear model (GLM) and Mixed linear model (MLM) used in TASSEL for estimating associations using kinship and population matrix. "K" was estimated via STRUCTURE software and the covariances values of the population (Q) were determined. "P-value" was assigned to marker if a QTL was associated to the marker and "R^2" designated to the magnitude of QTL effects (Agrama et al., 2007). Two loci relatedness is described by "R^2", which is of immense value from association mapping perspectives (Kantartzi et al., 2008).

3.2.12. Alignment to NCBI

SNPs identified for marker-trait associations aligned using Best Linear Alignment Tool (BLAST) using NCBI and QTLs identified.

3.3. Statistical analysis

Analysis of variance (ANOVA), variability parameters and Pearson coefficient of correlation analysis of fiber quality determined using JMP 7 software (https://www.jmp.com/en_dk/software.html).

Frequency curves constructed using Microsoft Excel for each location and then pooled data used for combined frequency distribution.

3.3.1. Heritability

Broadsense heritability was calculated according to Johnson et al., (1955) using genotypic and phenotypic variance.

$$Heritability\ (bs) = \frac{Vg}{Vp} \times 100$$

Where;

bs Broadsense heritability

Vg= Genetic variance

Vp= Phenotypic variance

4. RESULTS AND DISCUSSIONS

4.1. Phenotypic Screening for Fiber Quality

Cotton is a crop of warm climate as it is grown in tropical and sub-tropical regions of the world. Elevated temperatures and unequal distribution of rainfall adversely affect the production of cotton on global level. Temperature is an important attribute being involved in cotton morphology and fruit development (Reddy et al., 1991). When day/night temperatures are greater than the optimum i.e 30/22-35/27 °C then cotton plant growth is disturbed and results in reduction of lint production.

The environmental data related to daily minimum and maximum air temperature during cropping season of 2016 were shown in (Table 3.2). It was demonstrated that the average the highest and the lowest temperatures was similar to the long term average while the avarage rainfall was also the same during flowering conditions but found high during establishment of crop. Long term rainfall is 174.7mm which is 84mm more than cropping season (Table 3.2).

Fiber quality traits were analyzed using each location separately and then jointly for observing genetic variability and effect of different ecological conditions. Likewise, frequency distribution was determined through means of each genotype. Variability parameters were used for determining heritability pattern of all characters. Mean values of each trait were used for correlation and significance was calculated with Pearson coefficient.

4.1.1. Phenotyping in Kahramanmaras

4.1.1.1. Analysis of variance

Highly significant differences were found for ginning outturn, fiber length, uniformity index, maturity, micronaire from analysis of variance (p=0.01) while significant differences were observed for strength and elongation (p=0.05) in germplasm collection (Table 4.1).

Table 4.1. Means squares for fiber quality

Source	DF	GOT	UHML	UI	FF	MAT	STR	ELT
Genotype	288	16.5**	3.95**	2.78**	0.24**	0.0002**	12.7*	0.48*
Block	7	1.18	0.41	1.6	0.07	0.00004	12.6	0.39
Error	14	1.57	0.76	0.49	0.02	0.00002	6.02	0.19
Total	309	5525.4	1175.9	839.4	75.3	0.0654	3797.7	151.5

**, P <0.01; *, P <0.05; df: degree of freedom; GOT: Ginning of outturn (%); UHML: Fiber length (mm); UIN: Uniformity Index (%); FF: Fiber fineness (µg inch^{-1}); STR: Fiber strength (g tex^{-1}); MT: Maturity (ratio); ET: Elongation (%).

4.1.1.2. Descripitive statistics for fiber traits

The genotypes were screened for fiber quality traits with 3-checks (BA119, STV468 and TEX) replicated randomly among entries in each block of germplasm. The descriptive statistics including range, means, variance, standard deviation and variability related to the heritability are shown in Table 4.2.

Table 4.2. Descripitive statistics for fiber

	GOT	FL	UI	FF	MAT	STR	ELT
Mean ± SE	37.0±0.28	28.6±0.11	83.4±0.1	4.7±0.03	0.88±0.00	31.9±0.23	4.9±0.04
S. D	4.77	2.03	1.84	0.53	0.01	3.96	0.71
Minimum	4.35	21.1	76.0	2.72	0.81	28.7	3.02
Maximum	47.6	36.03	88.1	6.24	0.92	49.0	7.77
CV	3.4	3.0	0.83	3.1	1.6	7.7	8.9
h^2 (bs)	54.3	34.3	36.8	49.3	45.8	12.0	16.0

S.E: standard error; S.D: standard deviation; h^2 (bs): Broad sense heritability
GOT: Ginning of outturn (%); UHML: Fiber length (mm); UIN: Uniformity Index (%); FF: Fiber fineness (µg inch^{-1}); STR: Fiber strength (g tex^{-1}); MT: Maturity (ratio); ET: Elongation (%).

Table 4.2 showed wide genetic variability among fiber traits as the highest range was observed for ginning outturn varying from 4.3% to 47.6% with moderate heritability (54.3%) with a mean of 37.0±0.28. Fiber length was found to range from 21.1 to 36.0mm with heritability value of 34.3% and the mean was 28.6±0.11. Moderately-high heritability values 49.3% were found for micronaire with mean of 4.7±0.03 ranging from 2.7 to 6.2 among the genotypes. Uniformity index and maturity had means of 83.4±0.01, 0.88±0.1 with moderate heritability 36.8 and 45.8 respectively while strength and elongation were calculated as means of 31.9±0.23 and 4.9±0.04 in respect to their order. Coefficient of variation varied from 0.83 to 8.9% as maximum found in elongation followed by 7.7% for strength.

4.1.1.3. Performance of genotypes for fiber

The means for all fiber traits were used for comparisons using JMP Software (V.7.0) APPENDIX (1). Performance of genotypes for each fiber trait determined.

4.1.1.3.1. Ginning outturn (%)

Ginning outturn means varied from 4.35% to 47.6% among germplasm entries as compared to standards. The maximum ginning outturn was found in genotypes of AB80, Carla and BA440 with 47.6%, 46.2%, 44.6% respectively as the best standard STV468 had 41.4% (Table 4.2). The improvement of fiber yield and quality is a difficult way as these are influenced by agronomic and climatic conditions. Ginning outturn is a vital component for fiber yield as it is directly associated with lint and it should be analyzed with care for fiber quality improvement. It has been reported that yield can be boosted 3% with 1% rise in ginning outturn (Saleem et al., 2010). Phenotypical screening of polygenic characters is highly influenced by climatic factors and many genes which all contribute to decrease in heritable portion. The germplasm screening showed that wide variation is present among genotypes for ginning outturn (Appendix II). Our findings are in accordance with Sezner et al. 2006; Karademir et al. 2011; Wang et al., 2013; Sezener et al., 2015.

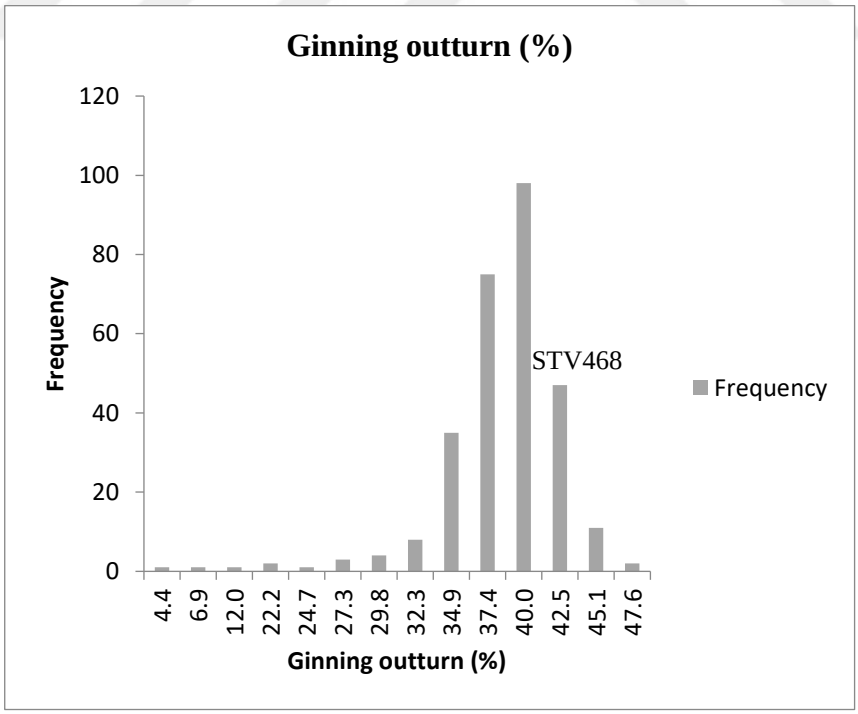

Figure 4.1. Frequency distribution for GOT (%)

4.1.1.3.2. Fiber length (mm)

28.6±0.11 mean value was observed for fiber length. Flora had maximum fiber length of 36.0mm and Zeta2 with 21.1mm whereas standards GW-TEX, BA119 and STV468 were measured 29.1mm, 28.3mm and 28.2mm respectively (APPENDIX-I). The germplasm collections were classified into different groups according to Bradow and Davidnois, (2000). Genotypes included in each category showed that most of the genotypes were found in medium-long class (Figure 4.2). Most of the genotypes were included in long staple category as frequency curve was developed (Figure 4.3).

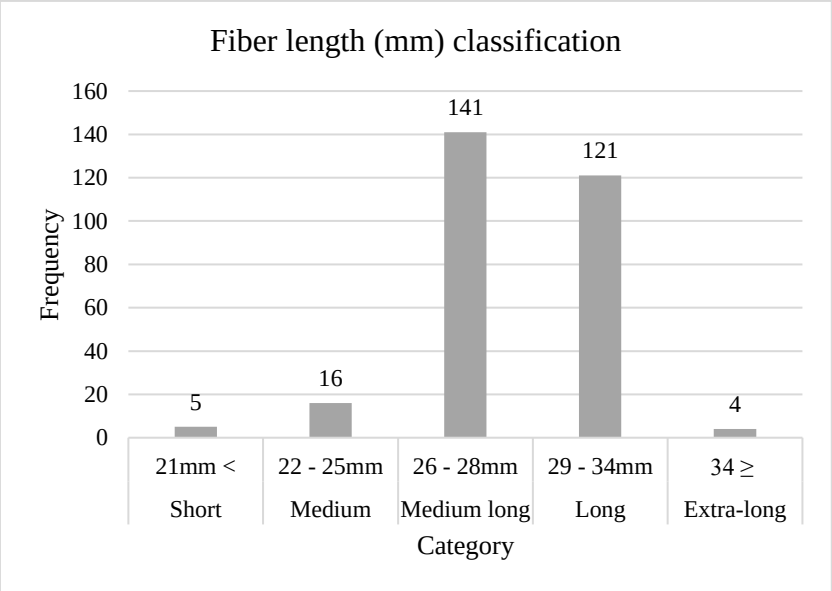

Figure 4.2. Fiber length classification

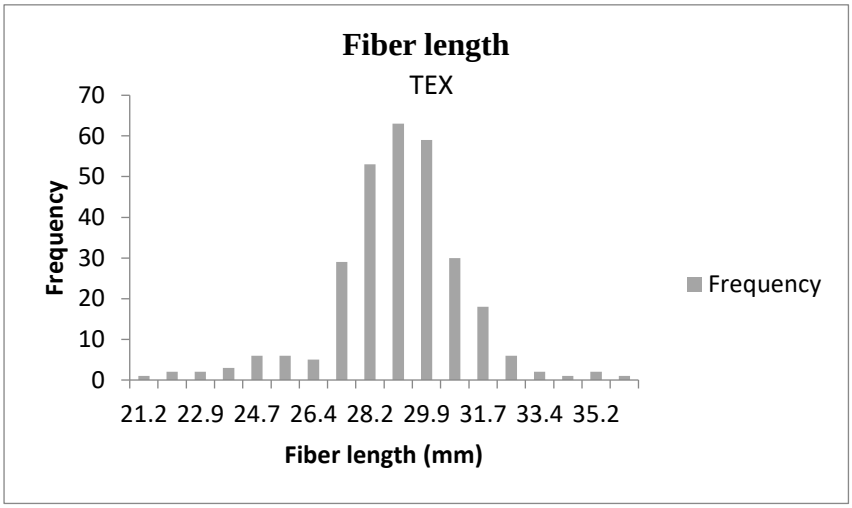

Figure 4.3. Fiber length frequency distribution

The features of the material which corresponds to capability of fiber spinning and responsible for effective industry output are designated as fiber quality. The essential components of this include fiber length, strength and micronaire. As the most important of all, fiber length is calculated as the mean of the longer one-half of fibers which affects the strength of yarn and highly influence processing of fiber. In our study, the phenological parameters depicted useful variability among germplasm entries for upland cotton which revealed that germplasm collection is having diverse source for fiber related traits. There results are in accordance with what was observed by Karademir et al. (2011), Wang et al. (2013); Elci et al. (2014).

4.1.1.3.3. Uniformity index (%)

The means for uniformity index varied from 76.0% to 88.1% with mean value of 83.4±0.1 whilst the checks STV468, BA119 and GW-TEX with 84.9%, 84.4%, 84.2% respectively (Appendix I). The sub-grouping showed that 18.6% of the genotypes were found in high range (Figure 4.4). The frequency curve showed the presence of most genotypes in high-class of fiber maturity (Figure 4.5).

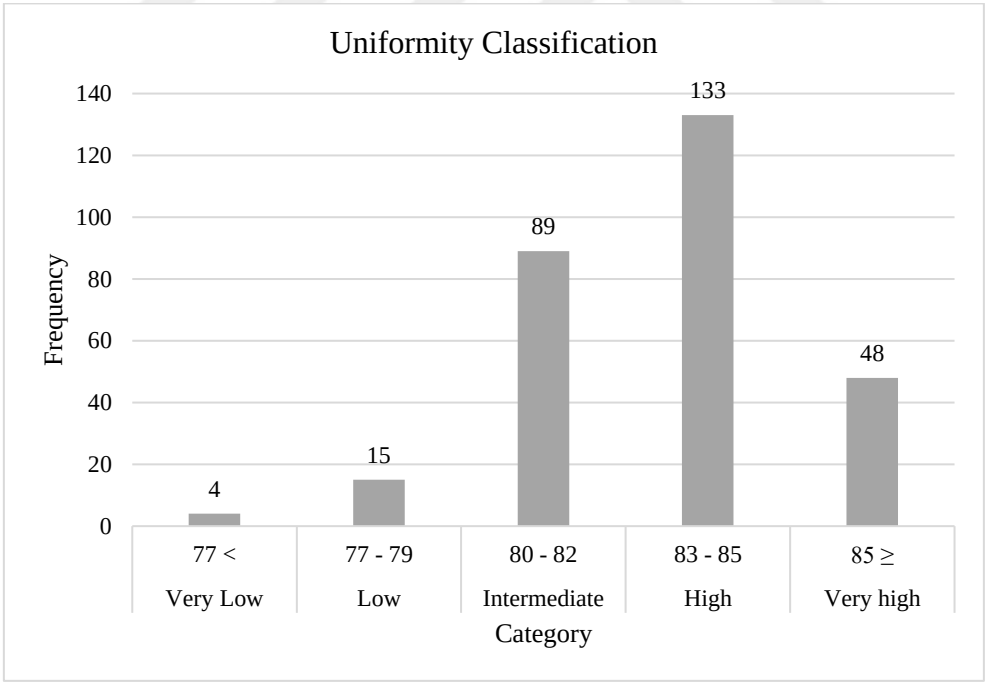

Figure 4.4. Uniformity classification

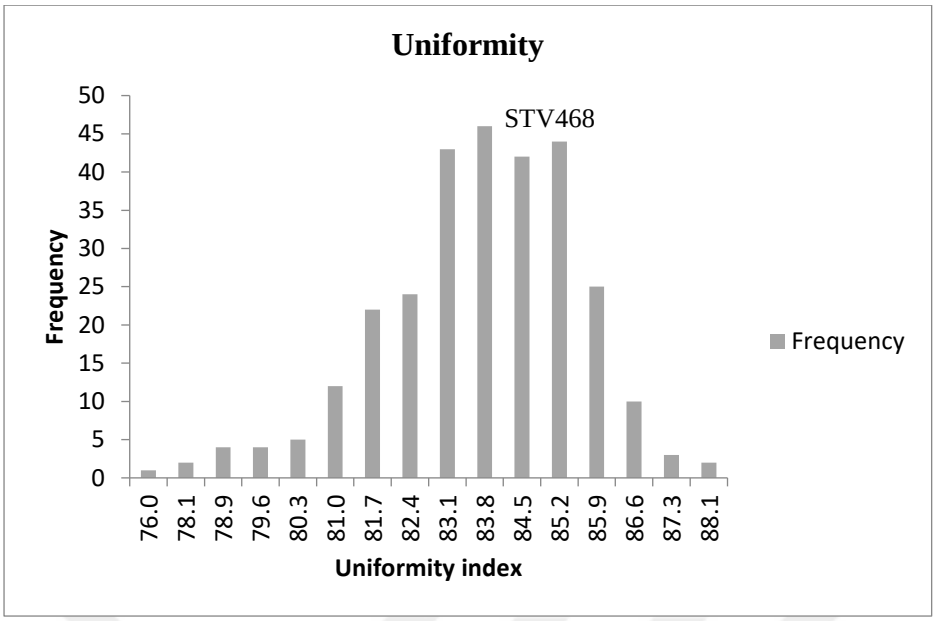

Figure 4.5. Uniformity frequency distribution

Uniformity index is a trait of fiber which describes the difference of average span length to 2.5% pan length. Uniformity ratio of high value is desirable since an individual having identical upper half mean length with low uniformity will show the presence of high quantity of short fibers. We observed a high uniformity index in the germplasm and this result matched with previous studies.

4.1.1.3.4. Fiber fineness (µg inch^{-1})

The genotypic means varied from 2.7(µg inch^{-1}) to 6.2 (µg inch^{-1}) as comapred to best standard GW-TEX with a value of 4.76 (µg inch^{-1}) for micronaire while mean was 4.74±0.03. The genotypes were further partitioned into different groups using standard classification which revealed that most of the genotypes were in average class (Figure 4.6). The frequency curve were constructed using means for each accession (Figure 4.7) which showed asymmetrical distribution.

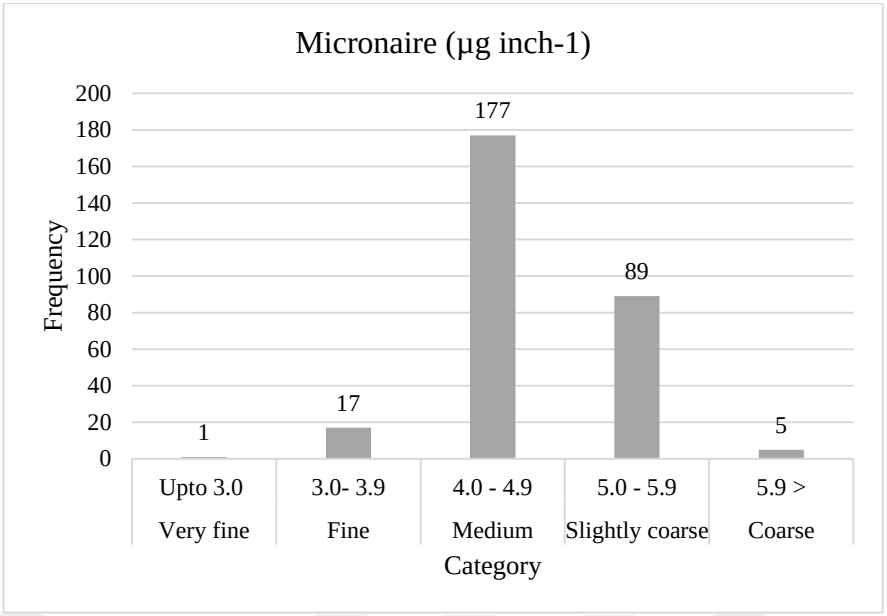

Figure 4.6. Micronaire classification

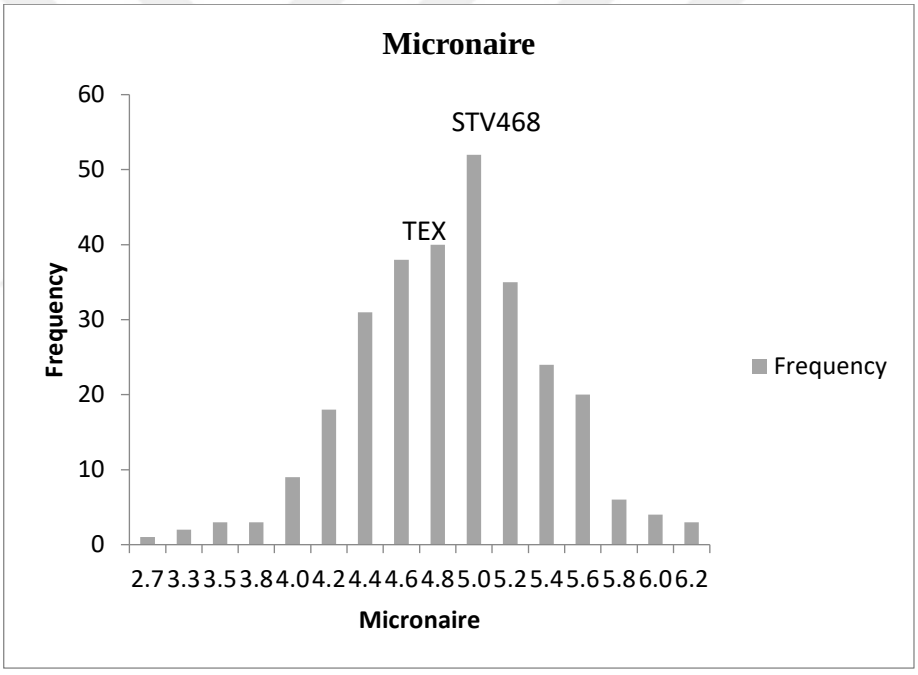

Figure 4.7. Micronaire frequency distribution

Micronaire is a parameter which determines fiber fineness and maturity which play an important part during processing of fiber. Micronaire is expressed as weight per unit length of fiber. From our observations, it was found that most of the genotypes were in the acceptable range of textile since it has been suggested that germplasm sources should have micronaire in the range of 3.9-4.5 for fulfilling the requirements of textile. Our results are similar to Karademir et al. (2010, 2011), Augado et al. (2010), and Zeng et al. (2014).

4.1.1.3.5. Maturity (%)

Means ranged from 0.81% to 0.92% among genotypes for maturity with an average of 0.88±0.00. The genotypes with high maturity includes YB157, TX 0091-2, and Allepo40 as compared to GW-TEX with mean value of 0.88% (Appendix-1). Frequency curves were developed from mean value (Figure 4.8). Maturity is a fiber component which is determined by diameter of secondary wall thickening and it plays vital role in spinning. It is expressed as a ratio of unmatured fiber to mature fiber and it should be less than 1. If the value is higher than 1, then it shows that fiber is fully mature and it will cause problems in dying which will ultimately produce neps in the yarn. In the present study, maturity ratio was found to be in acceptable range and can be used as a material for developing good cultivars, and these results were similar to the observations of Zeng et al. (2009).

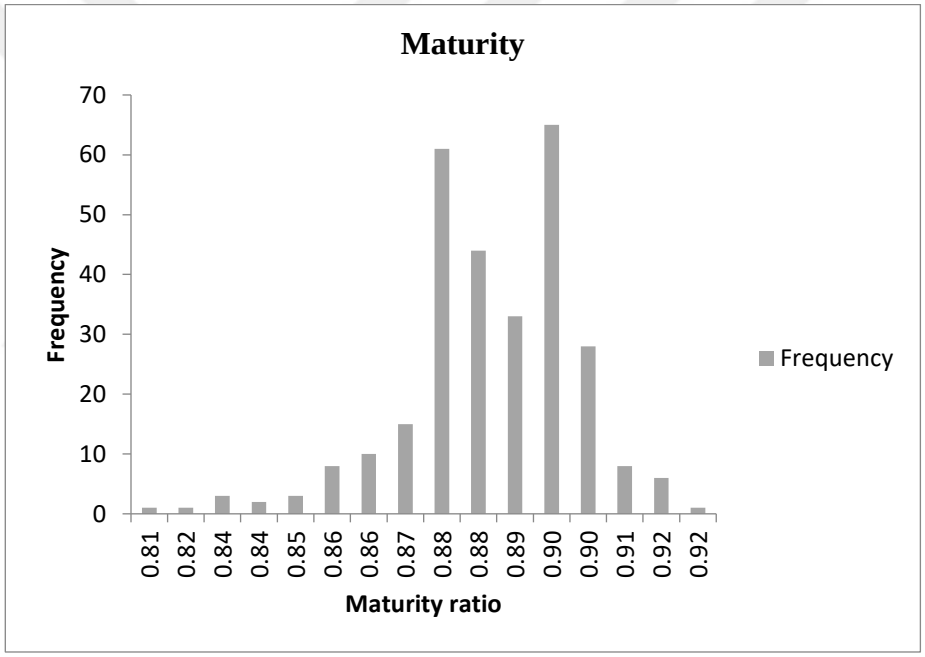

Figure 4.8. Maturity ratio distribution

4.1.1.3.6. Strength (g tex^{-1})

Delcerro had the highest fiber strength 49.1 (g tex^{-1}) while the best standard GW-TEX was with 34.0 g tex^{-1} followed by Menderes2005 and YB162 with 42.3(g tex^{-1}) and 41.2 (g tex^{-1}) respectively. While means varied from 28.7 to 49.0 among genotypes. Moreover, 26.2% of the genotypes had higher strength than the best check (Figure 4.9). The distribution of entries showed an asymmeterical distribution and most of our samples were in middle of the peak (Figure 4.10).

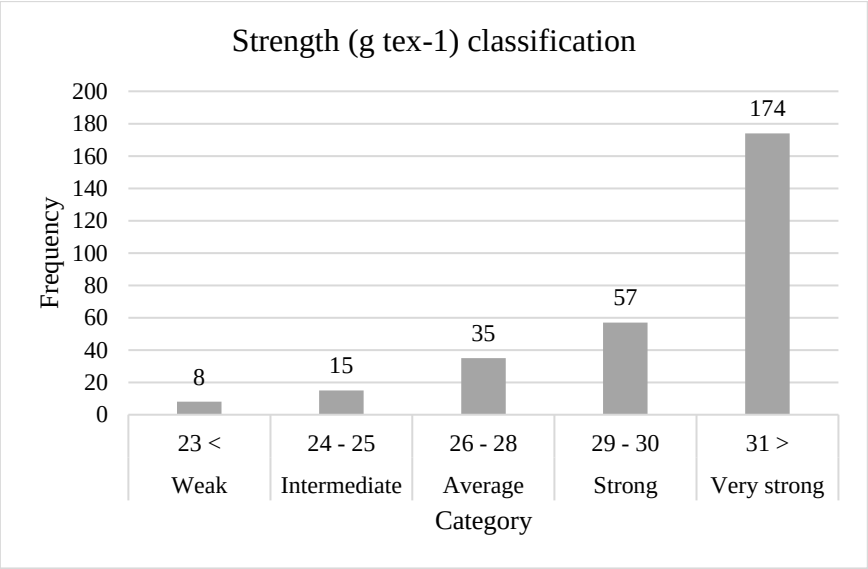

Figure 4.9. Strength classification

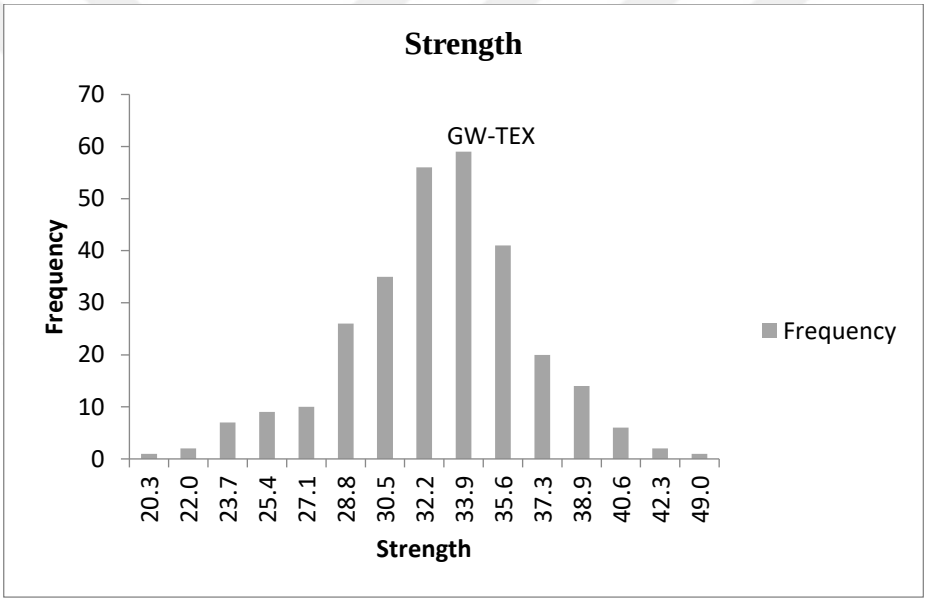

Figure 4.10. Strength frequency distribution

The advancement of fiber requires the production of fiber with other quality characters. Among these characters, fiber length is on the top and it is followed by tenacity and micronaire. Our results showed that the genotypes had wide differences regarding to fiber strength. It has been reported in earlier studies that strength varied among cultivars (Osman, 2006; Karademir et al., 2010; Hauge et al., 2011). The germplasm entries we investigated here manifested considerable variation which indicates a potential for the fiber improvement.

4.1.1.3.7. Elongation (%)

Means ranged from 3.02 to 7.8% among genotypes for fiber quality. The highest elongation was found in STG14 followed by NSCH777 and YB154 with elongation percentage of 7.7%, 7.6% and 6.9%, respectively. The standards, STV468, BA119 and TEX, on the other hand, presented the values of 5.6, 5.6, and 4.9, respectively (APPENDIX I). 13.2% was found to have higher elongation percentage as compared to the superior control (Figure. 4.11) and frequency distribution also used for means.

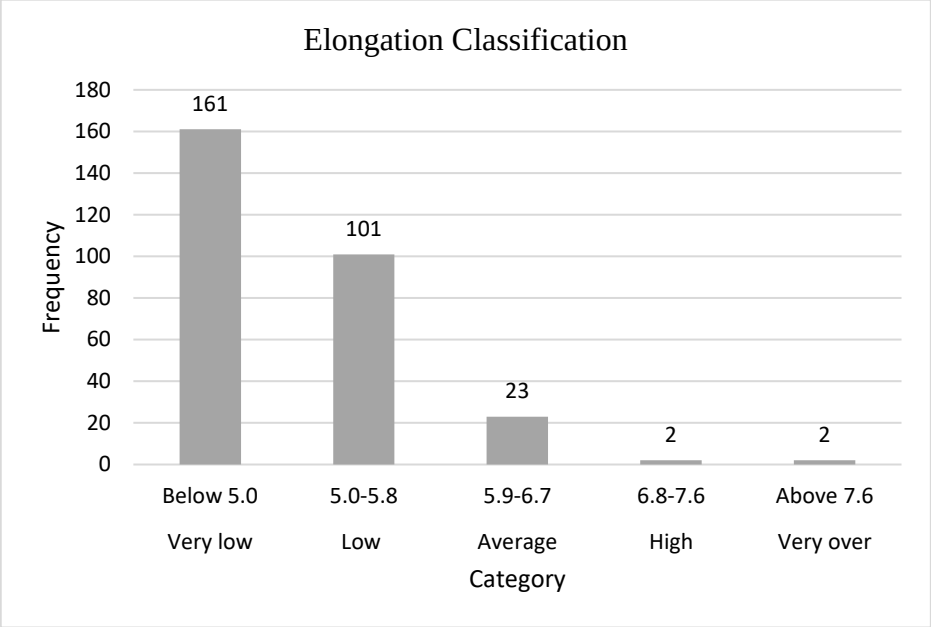

Figure 4.11. Elongation classification

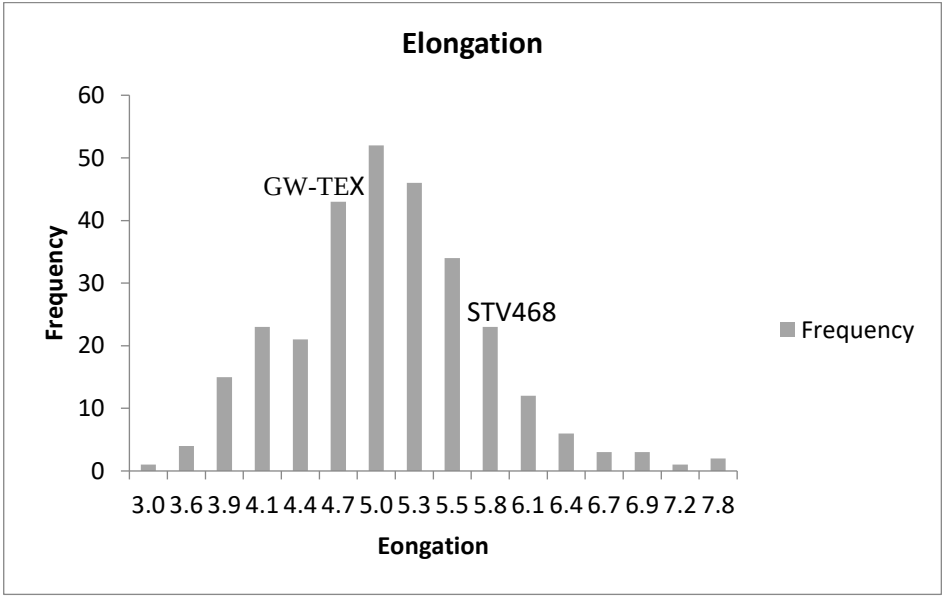

Figure 4.12. Elongation frequency distribution

It has been a practice since historically that diverse genepool collections should be used for creation of genetic diversity. As elongation is a trait which is directly associated with strength and is involved in the processing of fiber. The wide variation among germplasm entries showed that these are useful for further studies in agreement to (Zulkadir and Bolek, 2014). Stewart (1986) revealed that climatic factors are involved for this trait as after 3-15days of pollination affect elongation while 15-45 days are related with micronaire.

Genetic variation is compulsory for improvement of any economic trait. There is an increasing demand in industry that cotton should fulfill the requirements according to innovations. The results showed that genotypes had heritability from moderate to moderately high in most of the traits (Table 4.2). The occurrence of moderately high heritability for ginning out turn predicted that these traits can be enhanced through phenotypic selection. It has been found that genotypes are diverse for uniformity index and can be used as good material for breeding. Our results are in accordance to (Hauge et al., 2011). Desalegn et al. (2009) observed different values of heritability for fiber quality; moderate for uniformity ratio, micronaire and low heritability for fiber strength. Koli et al. (2014) observed low heritability for fiber strength when screened cotton germplasm for fiber. Campbell and Myer, (2015) revealed that moderate heritability is present for fiber strength. Our results are in accordance to Liu et al. (2011) who observed moderate heritability for most of fiber characters.

4.1.1.4. Correlation

Association analysis allows the selection of genotypes through valuable information about traits of interest from economical perspectives (Ali et al., 2009). Different ecological condition are vital for such studies (Baloch et al., 2012). Association analysis showed that there are many traits which are significant, but some had positive association and others had negative. While there were maximum positive associations among the traits but were non-significant (Table 4.3). Ginning outturn had positive significant association with fiber length, uniformity and maturity while negative non-significant with elongation. Our findings are in accordance to Zeng et al. (2009) as fiber length was positively associated with uniformity and strength while negative found for micronaire and elongation. This association showed that the genotypes with fiber length in long-staple category had good uniformity and strength which will contribute to good quality yarn and our findings are in accordance to (Asif et al., 2008; Basal et al., 2009; Karademir et al., 2010) who reported that good fiber should good

fiber strength and length. While fiber finess was significantly and positively related with uniformity and maturity but negatively for strength with non-significance. Fiber maturity and strength were negatively associated with elongation with significance. Moreover, occurrence of direct association among fiber length and strength and indirect association with micronaire strongly argued that these most desired traits can be analyzed jointly for improvement of fiber. Same associations were revealed by (Ulloa and Meredith, 2000; Karademir et al., 2010). But, Mei et al. (2004) reported positive correlation among fiber strength and finess.

Table 4.3. Correlation for fiber quality traits

	GOT	FL	UIN	FF	MAT	STR	FE
GOT	1						
FL	0.1314**	1					
UI	0.1782**	0.3347**	1				
FF	0.008	-0.21**	0.1274**	1			
MAT	0.1296**	-0.0623	0.1756**	0.7948**	1		
STR	0.1037	0.5353**	0.4191**	-0.0068	0.1613**	1	
FE	-0.0447	-0.2348**	-0.0112	0.0556	-0.413**	-0.1835**	1

GOT: Ginning outturn (%); FL: Fiber length (mm); UIN: Fiber uniformity index (%); FF: Fiber fineness (µg $inch^{-1}$); STR: strength (g tex^{-1}); MAT: Maturity (ratio); FE: Fiber elongation (%).

4.1.2. Phenotyping in Diyarbakır

4.1.2.1. Analysis of variance

It has been observed from analysis of variance that significant differences ($P < 0.01$) were observed among ginning outturn, fiber length, strength and elongation while non-significant for uniformity index, micronaire and fiber maturity (Table 4.4) which exhibited that variation is present among genotypes for fiber traits and it should be further analyzed for determining actual factors for this.

Table 4.4. Means squares for fiber quality

Source	DF	GOT	FL	UI	FF	MAT	STR	FE
Genotype	288	0.64	1.59	4.01	0.69	0.0002	5.61	0.074
Block	7	6.38**	4.56**	2.72^{ns}	0.25^{ns}	0.0003^{ns}	10.01**	0.893**
Error	14	0.73	0.88	2.03	0.12	0.0003	4.297	0.362
Total	309	2052.9	1177.8	824.9	76.7	0.1021	3004.2	264.6

**, P <0.01; *, P <0.05; df: degree of freedom; GOT: Ginning of outturn (%); FL: Fiber length (mm); UIN: Uniformity Index (%); FF: Fiber fineness (µg $inch^{-1}$); STR: Strength (g tex^{-1}); MAT: Maturity (ratio); FE: Fiber elongation (%).

On contrary non-significance of uniformity, micronaire and fiber maturity showed presence of limited genetic diversity. This is in accordance to the observations of (Guang and Xiong-Ming, 2006) who reported that numerous cultivars has been developed in cotton with less germplasm sources which are responsible for reduction in genetic variation. Moreover, our findings are also like Iqbal et al. (2001) as they showed less variation in the upland cotton germplasm as has been evolved from lines with minimum resources. They revealed that as most cultivars released for general cultivation has used USA germplasm which is the factor for low genetic diversity. Gilio et al., (2017) found non-significance in variance analysis which show that the genotypes are affected by the environment.

4.1.2.2. Descripitive statistics and variability parameters for fiber fiber traits in Diyarbakır

Germplasm containing diverse collection of genotypes evaluated for fiber traits with standards BA119, STV468 and GW-TEX. Descriptive statistics shown in (Table 4.5). The fiber traits had wide ranges for all traits as it ranged from 3.9% to 45.1% for ginning outturn with a mean of 37.7±0.2 and moderately high heritability. While fiber length had mean of 29.0±0.12 and varied from 0 to 36.9mm and the trait was inherited with medium value. Uniformity index ranged from 75.5 to 88.7 with mean of 83.7±0.1 and highly inherited, micronaire was moderately heritable and fluctuated from 3.0 to 5.6 µg $inch^{-1}$with an average of 4.34±0.03. Fiber strength ranged from 20.9 to 42.4g tex^{-1} with a mean of 30.3±0.19 and the character found to be highly inherited. Elongation found to be highly inherited with a mean of 6.3±0.05% (Table 4.5).

Table 4.5. Descripitive statistics and variability for fiber traits

	GOT	FL	UI	FF	MAT	STR	ELT
Mean ± SE	37.7±0.2	29.0±0.12	83.7±0.1	4.34±0.03	0.86±0.00	30.3±0.19	6.3±0.05
S. D	2.61	2.13	1.94	0.52	0.01	3.3	0.88
Minimum	3.9	20.9	75.5	3.05	0.8	20.9	4.1
Maximum	45.1	36.9	88.7	5.65	0.9	42.4	9.2
CV	2.3	3.2	1.7	7.9	2.0	6.8	9.6
h^2 (bs)	49.0	34.3	64.8	36.8	48.6	68.9	70.0

SE: Standard error; bs: Broadsense heritability

GOT: Ginning of outturn (%); FL: Fiber length (mm); UIN: Uniformity Index (%); FF: Fiber fineness (µg $inch^{-1}$); STR: Strength (g tex^{-1}); MAT: Maturity (ratio); FE: Fiber elongation (%).

Heritability is useful for breeding as it allows breeders to devise strategy about selection of traits. Hanson, (1963); Nyquist (1991) found that the outcome of the character after screening can be assessed, appropriate approach can be devised and useful for ascertaining the selection intensity. Most of the traits showed medium-high heritability which manifested that there is a good potential for quality improvement using germplasm lines which is in accordance to earlier findings (Desalegn et al., 2009).

4.1.2.3. Performance of genotypes for fiber

4.1.2.3.1. Ginning outturn (%)

The germplasm entries ranged from 3.9% to 45.1% for GOT (%) (Table 4.5). Ozbek142 had highest ginning outturn 45.1% followed by AB80, BA440 with 44.6 and 44.3 respectively in contrast to best standard STV468 with 41.3% (Appendix II). While lowest found in PI528426 with 3.9% (Figure 4.13). The availability of germplasm collections with wide genetic variability is need of the day to tackle the needs of fast blooming textile industry. The research carried out to screen germplasm having elite genotypes from all over world for fiber quality. Ginning out turn is directly associated with yield and yield components. The variation range as compared to standard showed diverse from breeding point. Sezener et al. (2006, 2007); Khan et al. (2015) observed that genotypes having high GOT% are good for devising strategy for fiber quality improvement.

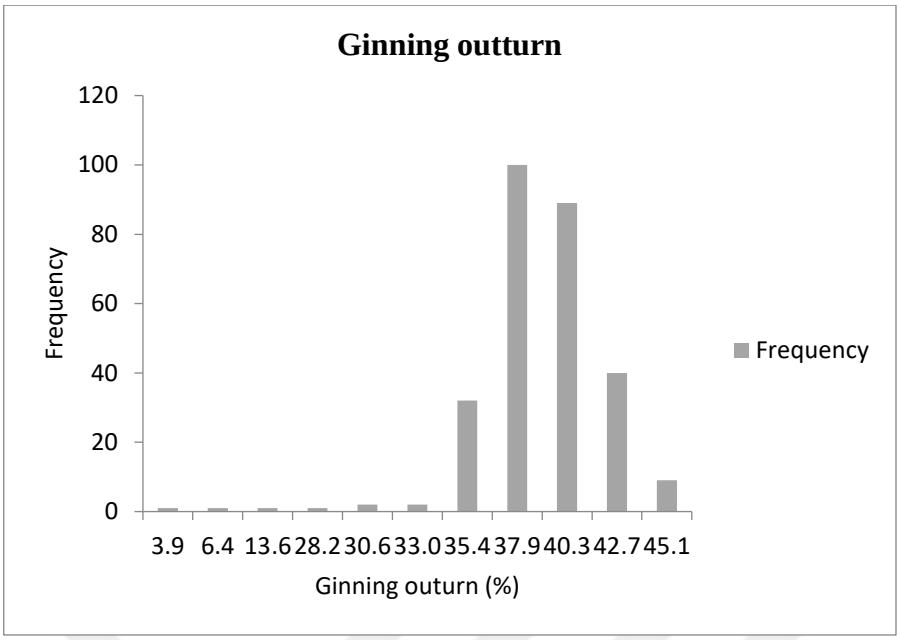

Figure 4.13. Ginning outturn distribution

4.1.2.3.2. Fiber length (mm)

Sealand1 had maximum staple length 36.9mm as compared to best standard GW-Tex with 30.78mm. Spears3(967), Acala 1517-99 and Flora found long-staple 35.5mm, 34.0mm & 33.6mm while PI528420 had 20.9mm (Appendix II). The categorization of fiber length showed that most of germplasm entries found in long-staple while 22.8% had long fiber as compare to best control (Figure 4.14). It was observed from means distribution that most of the genotypes were found to be in asymmeterically (Figure 4.15).

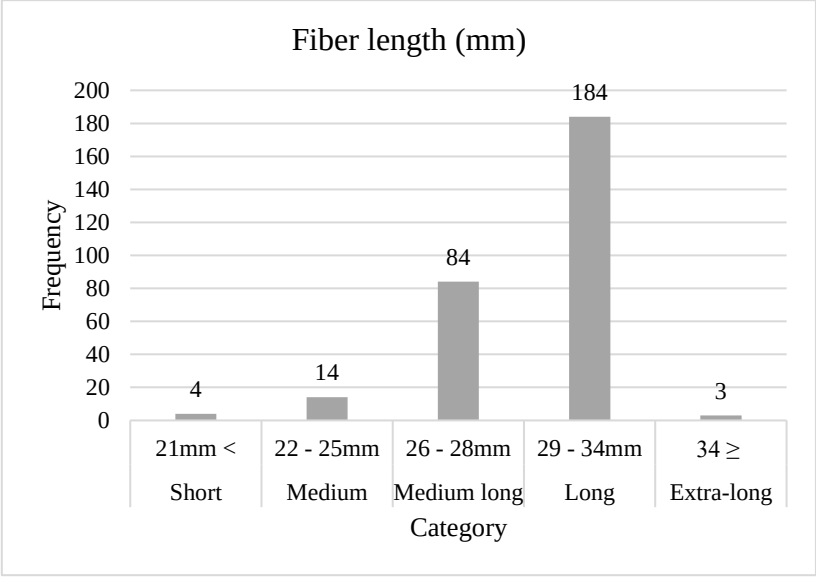

Figure 4.14. Fiber length classification

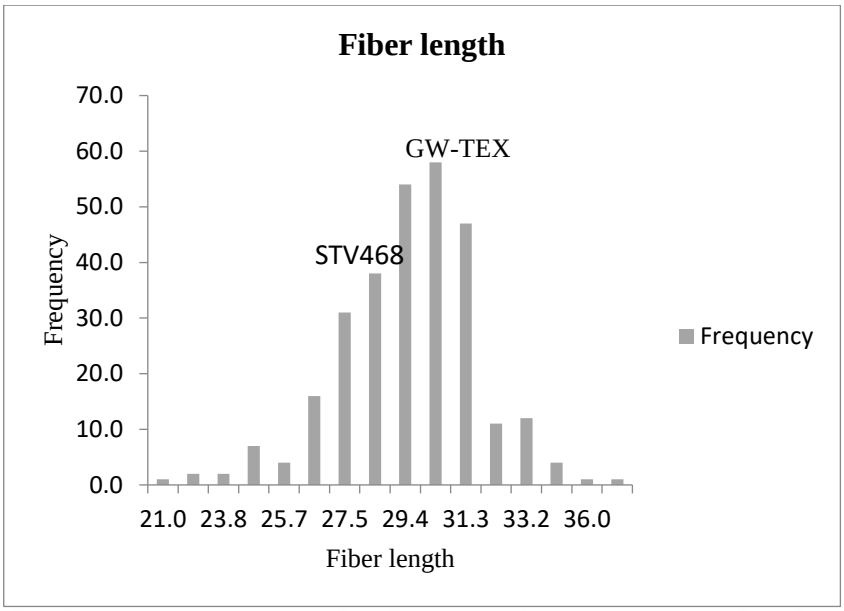

Figure 4.15. Fiber length distribution

The acquisition of any variety development approach is depends upon sufficient amount of variation. Germplasm collections evaluated for assessing genetic variation related to fiber to fiber length depicted wide diversity. The measure of typical section of fibers within a specimen of cotton is known as fiber length. The genotypes with longer fiber will produce high quality fabric and will be a source of high economic value. It has been reported that fiber length being a major component from textile perspective; can be used in breeding for boosting fiber yield. These results are in accordance to (Akiscan, 2012; Elci et al., 2014, Zulkadir et al., 2014; Guvecin et al., 2016) who shown that Turkish cotton germplasm has been refined to remarkable value and it can be a good source for the breeders.

4.1.2.3.3. Uniformity (%)

The means varied from 75.5% to 88.7% (Table 4.10). The genotypes with highest uniformity found Sicala 3/2 and Sealand1 with 88.7% and 88.5% as compared to STONEVİLLE 468, GW-TEX, BA119 with 84.8%. 84.5% & 84.1% respectively.

As two species of tetraploid origin dominates the world cotton market, but it is need of the day to enhance fiber parameters for quality specially length, micronaire, strength, elongation and uniformity ratio (McCreight, 1992). Uniformity is a parameter associated with fiber length and highly influence spinning in the textile sector. The variability among the genotypes showed that majority of the genotypes were found in the high category of fibers (Figure 4.16) as devised by (Bradow and Davidnois, 2000).

Means distribution among genotypes showed considerable variation (Figure 4.17). Our findings are similar to (Akiscan, 2012; Elci et al., 2014) which exhibited that genepool sources with rich variation for uniformity index in Turkey are the best choice for cultivar development.

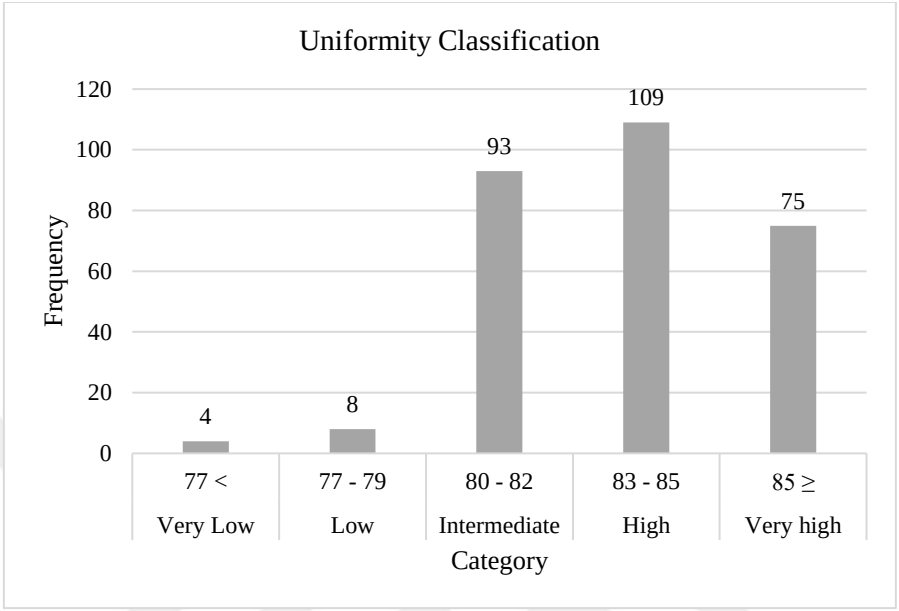

Figure 4.16. Uniformity classification

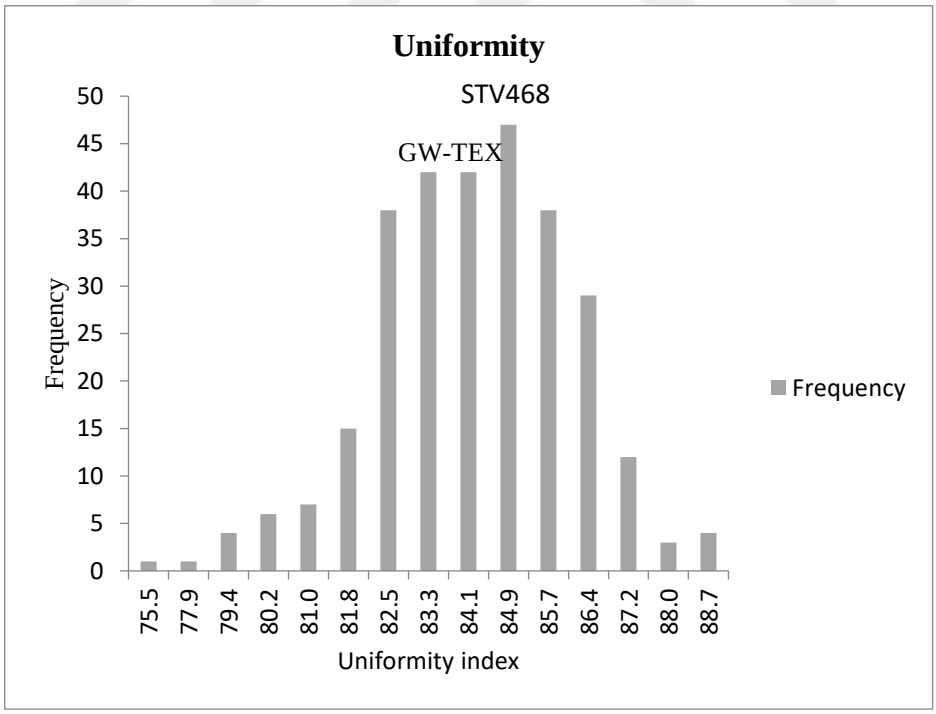

Figure 4.17. Uniformity distribution

4.1.2.3.4. Micronaire (µg inch^{-1})

The genotypes varied from 3.06 µg inch^{-1} to 5.6 µg inch^{-1} with an average of 4.3±0.03. The genotypes containing more values for micronaire include TX0091-2, YB157 and Famosa with 5.68, 5.56, 5.52 respectively (Appendix II). While most of genotypes were included in the desirable range i.e 3.9 to 4.6 µg inch-1 from textile perspectives and the best standard STONEVİLLE468 had 4.45 µg inch^{-1}. The classification of germplasm entries showed that genotypes were found in acceptable range (Figure 4.18). The means were also plotted using frequency curves and it was found that majority of the entries were present in average categiry as same pattern was also observed in the classification of genotypes (Figure 4.19).

Micronaire is a parameter which influence spinning and yarn development as it determines the ability of fibers to withstand with pressure of air within a specified area and also calculate fineness in the fiber related with maturity of fibers (Lacape et al., 2010). The variation among the genotypes showed that most of the genotypes are found in mean category of fineness. These genotypes will be good for the breeders for refinement of fiber quality based on micronaire and in accordance to findings of (Karademir et al., 2010; Elci et al., 2014; Rahman et al., 2014).

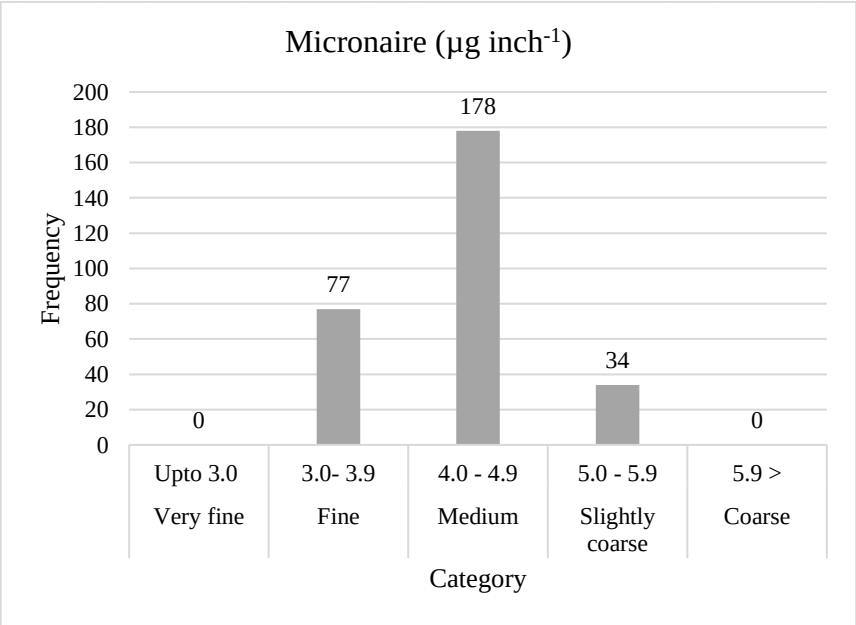

Figure 4.18. Micronaire classification

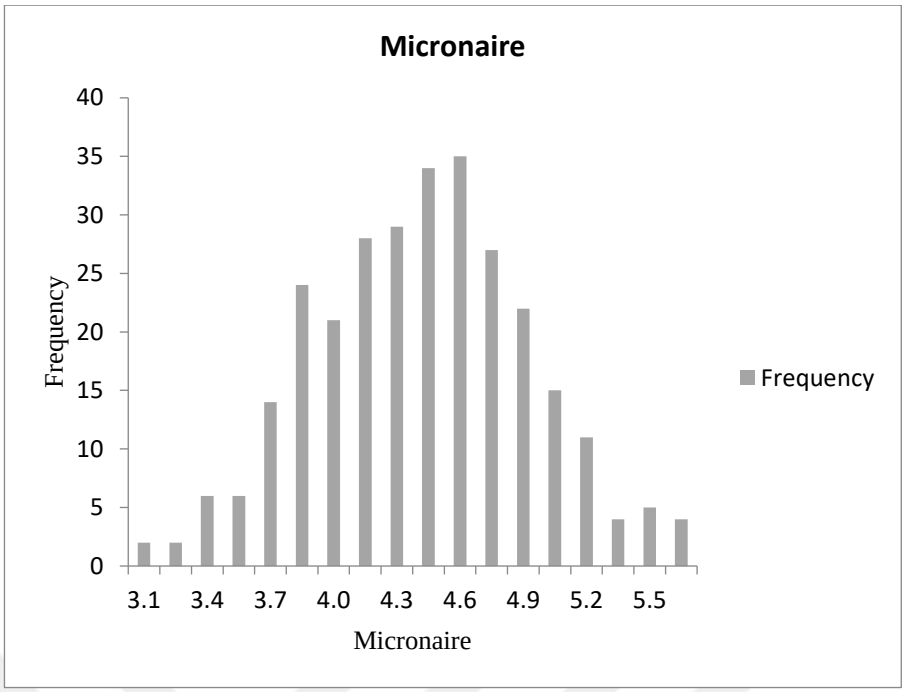

Figure 4.19. Micronaire frequency distribution

4.1.2.3.5. Maturity (%)

The values ranged from 0.8 to 0.91% for maturity ratio. The genotypes with highest maturity were Flora and TX0175-2 with 0.91% & 0.90% ratio respectively in-contrast to standards with GW-TEX, STV468 and BA119 had 0.85, 0.85, 0.84% alternatively. The extent of mature fibers is associated with fiber maturity. The genotypes found highly uniform as just few were found to be low and it clearly showed that fiber with such class can be of high value from industry goals. The means distribution also depicted as frequency curves (Figure 4.20). The fiber with high maturity results in high quality yarn. Zeng et al. (2014); Elci et al. (2014) also observed that high maturity increases the dying of the yarn which contribute towards high value of yarn and our findings are also similar as entries had maturity ratio mostly in the range of mature fiber.

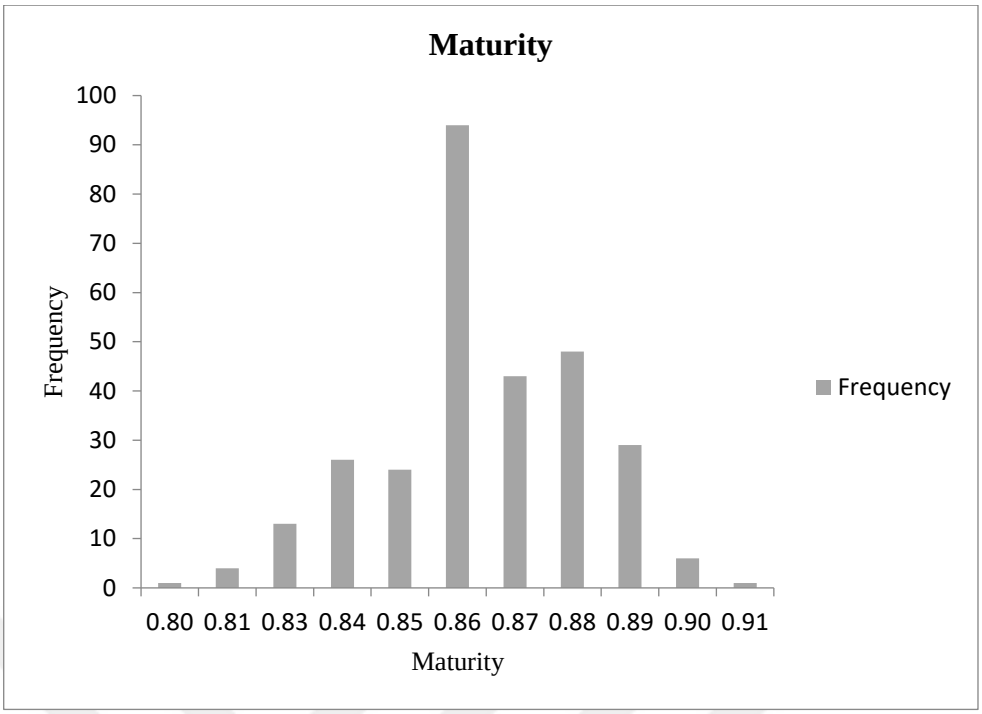

Figure 4.20. Maturity frequency ditribution

4.1.2.3.6. Strength (g tex^{-1})

The genotypes were found from 20.9 to 42.4 g tex^{-1} with a mean of 30.6±0.19. Maximum fiber strength was found in Samon followed by Delcerro with 42.2 and 40.0 g tex^{-1} as compared to the checks with 32.1 g tex^{-1}, 30.2 g tex^{-1} & 29.9 g tex^{-1} for GW-TEX, STV468 and BA119 respectively (Appendix II). It was also found that 22.5% genotypes had more strong fiber than best check (Figure 4.21). Distribution of means was also analyzed with frequency curves and asymeterical distribution was observed (Figure 4.22).

Fiber strength is a trait of fiber quality which is the major contributor of yarn durability (Meredith et al., 1991; May and Taylor, 1998). Due to different methods for processing of fiber like rotor and ring; strength has to be improved. It is the property of fiber that produce high value yarn with more firmness among single fiber. The ranges among the genotypes showed that genotypes were found mostly in high category which strongly argues to use this germplasm for breeding purpose. As strength is trait of immense value for yarn production so strong fibers should be developed for overcoming problems during processing of fiber. Sezener et al. (2006); Elci et al. (2014); Zeng et al. (2014) reported that germplasm has got diversity for fiber traits including strength that can be applied for selection of good parents for developing cultivars.

Moreover, Zumba and Meyer, (2008) explored genetic variation for fiber strength and revealed that it has precise role for textile. They found ranges among the germplasm collection which are also similar to our germplasm screening.

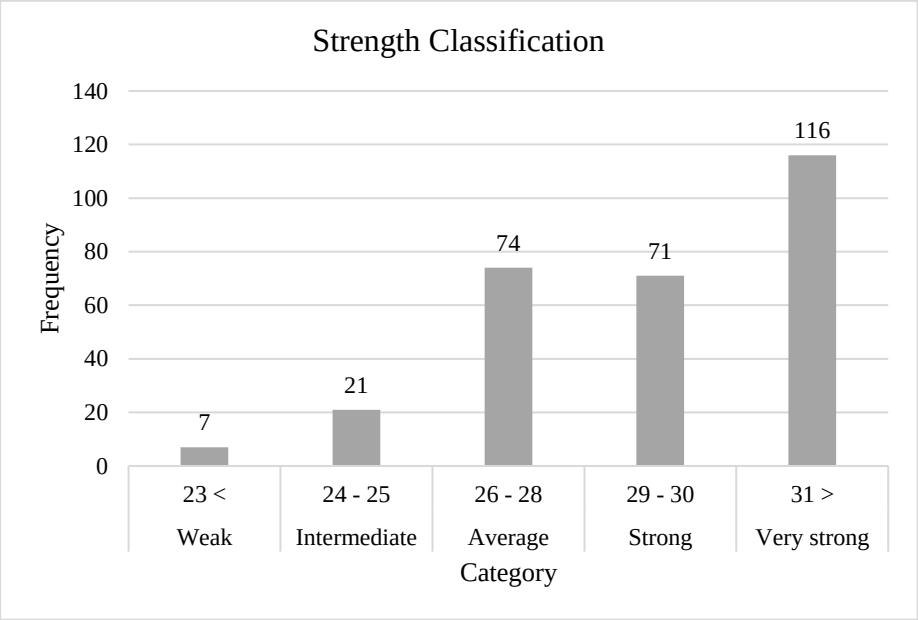

Figure 4.21. Fiber strength classification

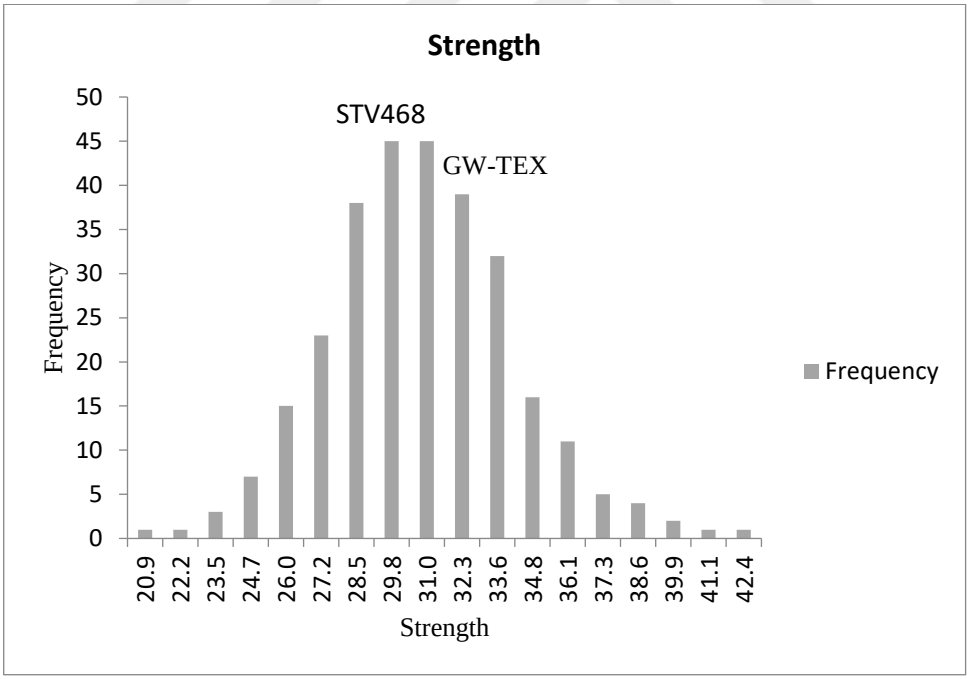

Figure 4.22. Stregnth frequency distribution

4.1.2.3.7. Elongation (%)

Mean for elongation was 6.3% as compared to GW-TEX with 5.9% and varied from 4.1 to 9.2%. Sahin2000 had maximum elongation followed by Sayar314, Carisma with 8.4% and 8.1% respectively. Moreover, the genotypes were found in all classes of elongation (Figure 4.23). Frequency distribution showed the existence of wider variability in genotypes (Figure 4.24).

Yarn tenacity can be reduced highly if there are wider fluctuations found in fiber elongation. On the other hand, if such modifications are less then will create yarn which will be highly effective from textile perspectives (Suh et al., 1993; Suh et al. 1994; Liu et al., 2005). In the present studies it has been observed that genotypes had 11.8% high elongation in germplasm as compared to best check STV468 with 7.3. These results are in accordance to previous findings (May and Taylor, 1998; Liu et al., 2005; Akiscan, 2012).

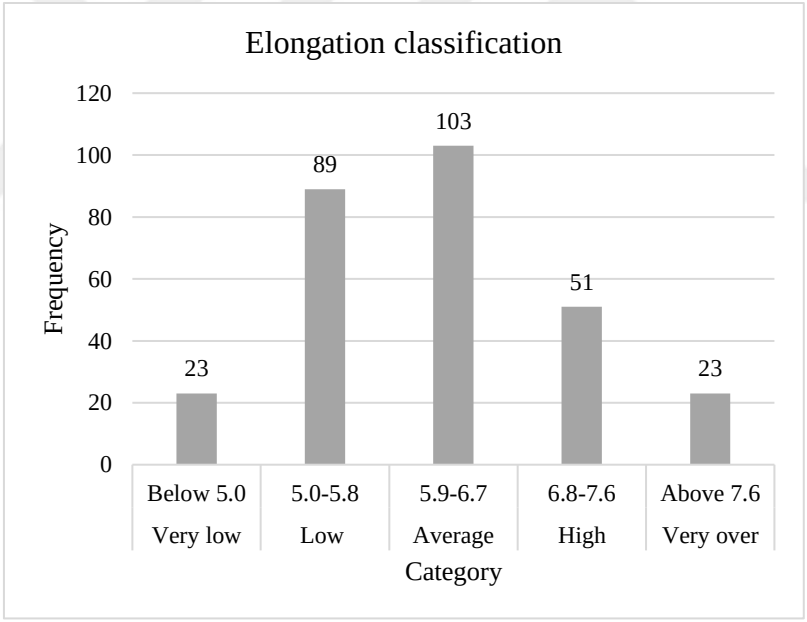

Figure 4.23. Elongation classification

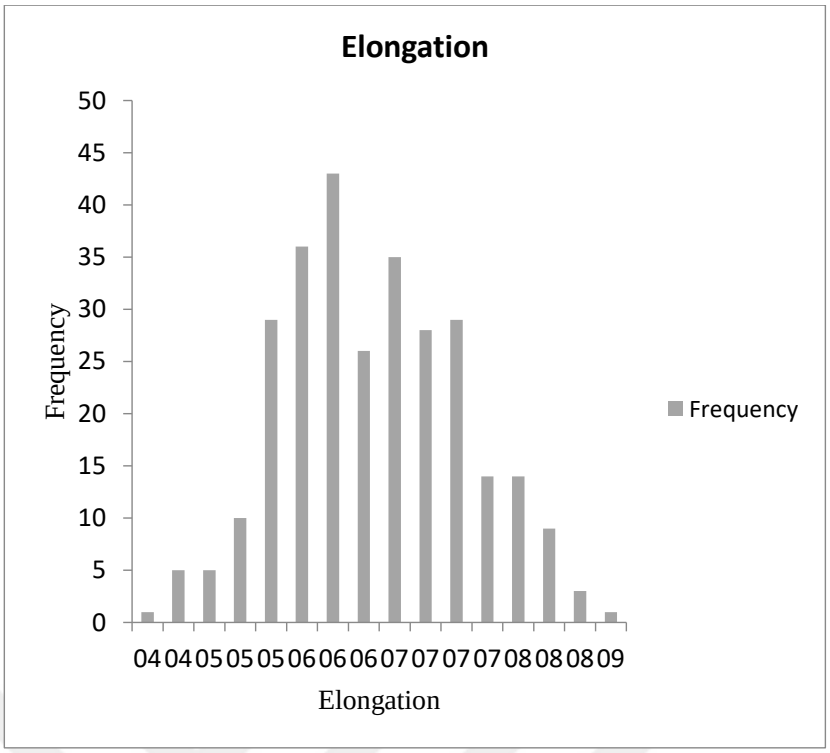

Figure 4.24. Elongation frequency distribution

4.1.2.4. Correlation for fiber traits

Associations among germplasm entries for fiber characters shown in (Table 4.6). It has been revealed from association analysis that there are significant relations in fiber quality traits. Fiber length found to be significantly and directly associated to strength and uniformity. While fiber fineness directly related with maturity and strength is positively associated with uniformity. While negative relationship with significance observed among fiber length with fineness, elongation; fineness and strength, maturity and elongation and strength with elongation. It predicted that there is confound relation among fiber quality traits. Ginning out turn found to be positively associated with uniformity with significance but with fiber length non-significance which is accordance to earlier findings that fiber length has positive relation with ginning out turn (Desalegn et al., 2009; Karademir et al., 2010). It has been a point of concern for the cotton breeders to develop varieties with good lint yield and fine quality (Meredith, 1971; Percy et al., 2006). Fiber quality can be enhanced by improving fiber length, fiber strength and fiber fineness as fiber length had highly significant positive relationship with strength and negatively related to fineness with highly significant value. These findings found similar to (Shao et al., 2016). Moreover, maturity

was positively associated with fiber fineness while significantly and indirectly associated with fiber elongation. Zeng et al. (2009) also reported same findings among fiber traits.

Table 4.6. Correlation for fiber quality traits

	GOT	FL	UIN	MIC	MAT	STR	FE
GOT	1						
FL	0.020	1					
UIN	0.115**	0.481**	1				
MIC	0.097	-0.192**	0.009	1			
MAT	0.069	-0.051	0.087	0.632**	1		
STR	0.094	0.564**	*0.463	0.004	0.0824	1	
FE	0.018	-0.181**	0.009	0.0015	-0.197**	-0.130**	1

GOT: Ginning outturn (%); FL: Fiber length (mm); UI: Uniformity Index (%); FF: Fiber fineness (µg inch-1); STR: Fiber strength (g tex^{-1}); MAT: Maturity (ratio); FE: Elongation (%).

4.1.3. Combined Phenotypic Analysis

4.1.3.1. Analysis of variance

As ultimate goal is to find genotypes with good economical traits, likewise the means were pooled and variation was observed. Analysis of variance showed highly significant differences among all fiber quality traits (Table 4.7). The genotypes were found highly significant for fiber traits. It was found that locations were highly significant for all traits. Moreover, it has been shown the quality traits are influenced by environment as the interaction among genotypes and location highly significance (p=0.01) for ginning outturn, uniformity index and maturity.

Table 4.7. Means squares for fiber traits

SOV	**DF**	**GOT**	**FL**	**UI**	**FF**	**MAT**	**STR**	**FE**
Location	1	79.79**	33.12**	26.36**	26.12**	0.0709*	384.47**	236.63**
Block	7	0.716	1.262	3.914	0.13	0.00008	5.766	0.408
Genotypes	288	18.03**	6.833**	3.513*	0.36**	0.0002**	16.424**	0.938**
Genotype*location	288	4.88**	1.156	1.993**	0.150	0.0001**	6.190	0.309
Error	35	1.142	0.767	1.353	0.06	0.0001	8.222	0.282
Total	619	7550.77	2389.96	1688.30	182.35	0.21945	7337.42	634.92

GOT (%): Ginning outturn; FL: Fiber length (mm); UIN: Uniformity Index (%); FF: Fiber fineness (µg $inch^{-1}$); STR: Fiber strength (g tex^{-1}); MAT: Maturity (ratio); FE: Fiber elongation (%).

The association among genepool entries showed that there is a considerable variability in the collection. These observations are in accordance to earlier studies (Murray

and Verhalan, 1970; Percy et al. 2006; Sezener et al. 2006) which showed differences for genotype x environment interaction for fiber properties. Similarly, slight genotype x environment interaction differences were observed among *Gossypium* species for yield and fiber characters (Zeng et al., 2007). It has been revealed from observations that acclimatization of the genetic resources for desired characters should be done before starting a breeding plan.

4.1.3.2. Descripitive stattictics and variability for fiber traits

The variation among all traits was sufficient to observe them in detail. Means, standard error and variation in the form of standard deviation for different traits on combined basis mentioned in (Table 4.8). All the characters exhibited wide variation among germplasm genotypes as ranged from 4.13 to 46.12%, 21.9 to 35.6mm, 78.4 to 87.2%, 2.92 to 5.9 µg $inch^{-1}$, 21.6 to 44.6 g tex^{-1}, 0.83 to 0.90% and 3.7 to 7.7% for ginning outturn, fiber length, uniformity index, micronaire, strength, maturity and fiber elongation. While variation on standard deviation fluctuated from 0.01 to 4.2 among all entries (Table 4.8). Micronaire, strength and uniformity index found to be highly heritable as had high broad sense heritability 91.2%, 71.2% and 65.1% respectively. Fiber length, and maturity was moderately heritable, as 49.9% and 34.0% was observed. The highest coefficient of variability 13.9% found for fiber uniformity and 9.7% fiber elongation while lowest in maturity.

Table 4.8. Descripitive statistics for fiber traits

	GOT	**FL**	**UI**	**FF**	**MAT**	**STR**	**FE**
Mean ± SE	37.35±0.24	28.83±0.11	83.57±0.08	4.55±0.03	0.87±0.00	31.05±0.17	5.56±0.04
S. D	4.22	1.92	1.52	0.45	0.012	2.91	0.64
Minimum	4.1	21.9	78.4	2.97	0.83	21.67	3.7
Maximum	46.1	35.6	87.2	5.9	0.90	44.6	7.7
CV (%)	2.9	3.0	13.9	5.4	1.1	9.2	9.7
h^2 (bs)	64.8	49.7	71.1	91	34.1	65.1	22.4

SE: Standard error; bs: Broadsense

GOT: Ginning outturn; FL: Fiber length (mm); UIN: Uniformity Index (%); FF: Fiber fineness (µg $inch^{-1}$); STR: Fiber strength (g tex^{-1}); MAT: Maturity (ratio); FE: Fiber elongation (%).

4.1.3.3. Performance of genotypes for fiber

4.1.3.3.1. Ginning outturn (%)

Mean value 37.4 found for ginning outturn among the entries being highest 46.1% in AB80 followed by BA440, Ozbek142 and Carla with 44.5%, 44.4%, 43.2% respectively while minimum 4.1% in PI528426 (Table 4.9). Means for checks STV468, TEX and BA119 were 41.3%, 41.2% and 40.9 % respectively. It is need of the day, to fulfill demands of growers and textile, breeding measures should be taken altogether for boosting yield and lint percentage. Ginning out turn varied from 4.1% to 46.1% among germplasm which showed that diverse collections are present with low to high GOT (Table 4.9). It has been revealed from the results that 20 (6.2%) genotypes had better ginning outturn than best standard STONEVILLE468 as (41.3%) (Figure 4.25). Same variation pattern for ginning outturn was observed in germplasm by (Sezener et al., 2006; Khan et al., 2010). Moreover, ginning outturn variation is in accordance to Iqbal and Rahman, 2017 which found enormous variation among germplasm entries. Since a lot of reports have been published but still it's compulsory to use sources with good lint yield and one such found AB80.

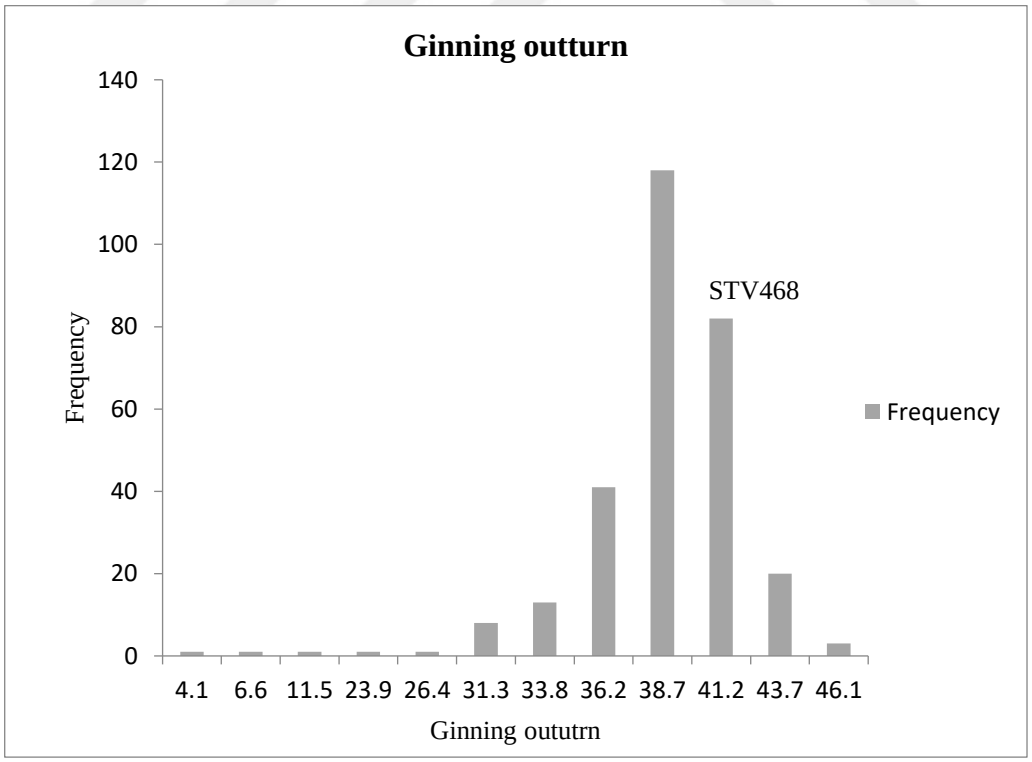

Figure 4.25. Ginning outturn distribution

4.1.3.3.2. Fiber length (mm)

Fiber length ranged from 21.9mm to 35.6mm among germplasm entries as maximum 35.6mm found in YB230 while minimum 21.9mm in PI528420. Fiber length found 28.2mm, 28.3mm and 29.9mm in STV468, BA119 and TEX respectively in contrast to Flora, SPEARS3(67), PI528875 with 34.8mm, 33.8mm, 33.6mm (Table 4.9). It has been reported that fiber length change according to genotypes and environment. Behery, (1993) revealed that it is impossible to have actual value for length of fiber and fibers vary a lot even in an individual seed as stretched fibers are found on chalzal part while small are on micropylar end. But from years fiber length has been refined according to industry demands. These variations are in accordance to (Zulkadir and Bolek, 2014; Bardak and Bolek, 2016). From textile sector demand, fiber length has been classified into 5- different classes as all specified types of garments are compulsory (Bradow and Davidson, 2000). Majority of the genotypes were included in long staple class (Figure 4.26). Frequency distribution curves were found normal for genotypes (Figure 4.27). Yarn spinning property is boosted with the increase in fiber length. (25.6%)entries were found to be long as compared to best standard GW-Tex (29.9mm). Moreover, the variability found in current studies was in accordance to (Elci et al., 2014) who revealed that there is wider variation among germplasm entries of cotton for improving fiber quality especially fiber length being a trait which has been advanced from short staple to long staple in the breeding programs. Guvercin, (2016) also observed that parents used in breeding programs should be of good fiber length and our findings also found same ranges. While heritability was moderately heritable which depicted that this trait can be improved by selecting good genotypes from the germplasm (Table 4.8). It has revealed in literature that fiber quality traits are highly affected by climatic conditions Falconer and Mackey, (1996) while varying degree of heritability has been observed as medium heritability was observed by Tang et al., (1996); McCarty et al., (1996). Our findings are also in accordance to (Qin et al., 2015).

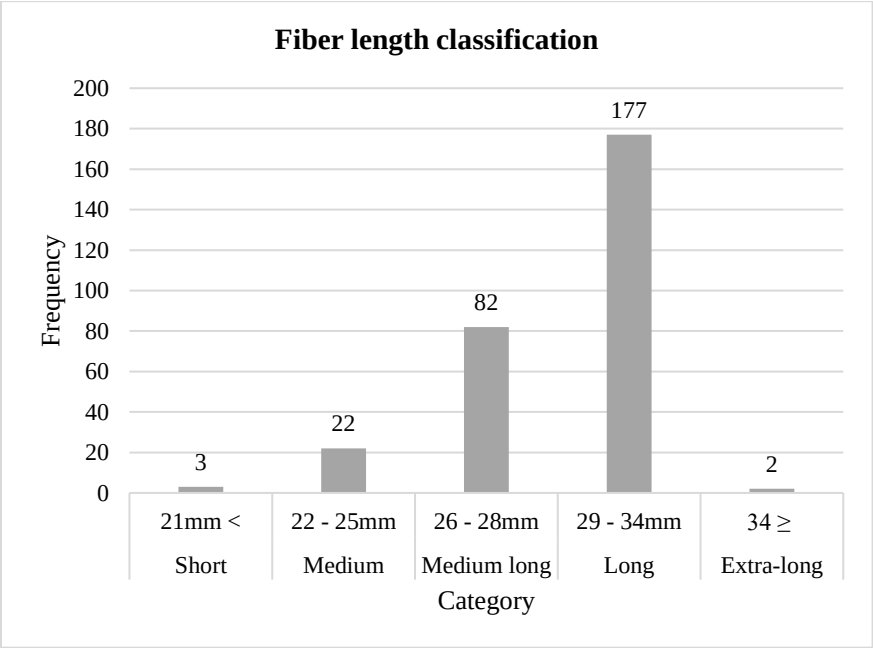

Figure 4.26. Fiber length classification

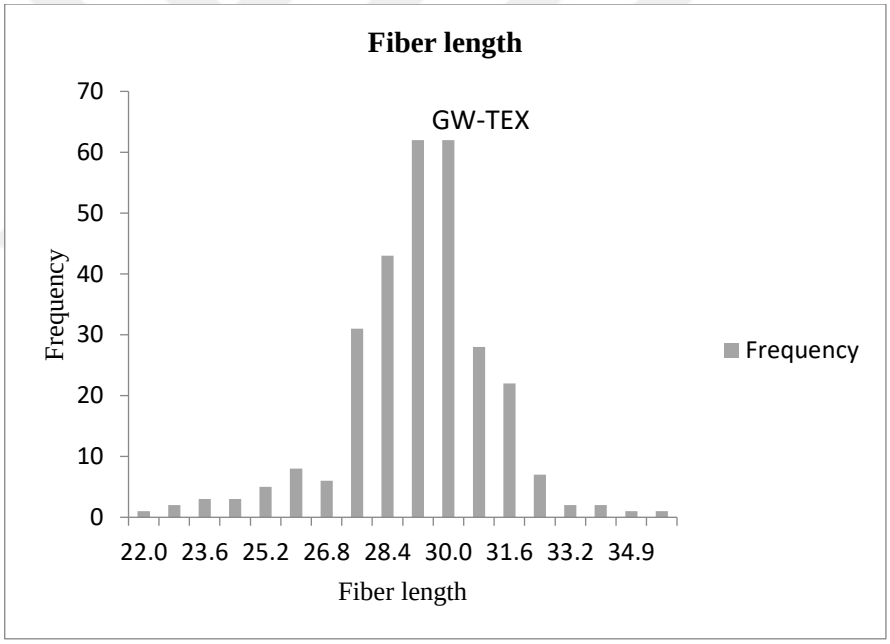

Figure 4.27. Fiber length frequency distribution

4.1.3.3.3. Uniformity index

Means for uniformity index ranged from 78.4% to 87.2% as highest found in Sealand1 while lowest in PI528450 as compared to standards. Uniformity values were almost similar i.e 84.8%, 84.3% and 84.3%, in STONEVILE468, GW-TEX, BA119 respectively (Table 4.9). Fiber uniformity is measured in percentage; the uniformity will be higher if the percentage is higher.

Uniformity index plays a major role during spinning as related with strength and smoothness of yarn. The class of garments is inferior with small uniformity ratio as it exhibits the more frequency of small fibers which ultimately affects yarn. All germplasm entries were classified into different groups according to cotton incorporated scale (Cotton Incorporated Standards).

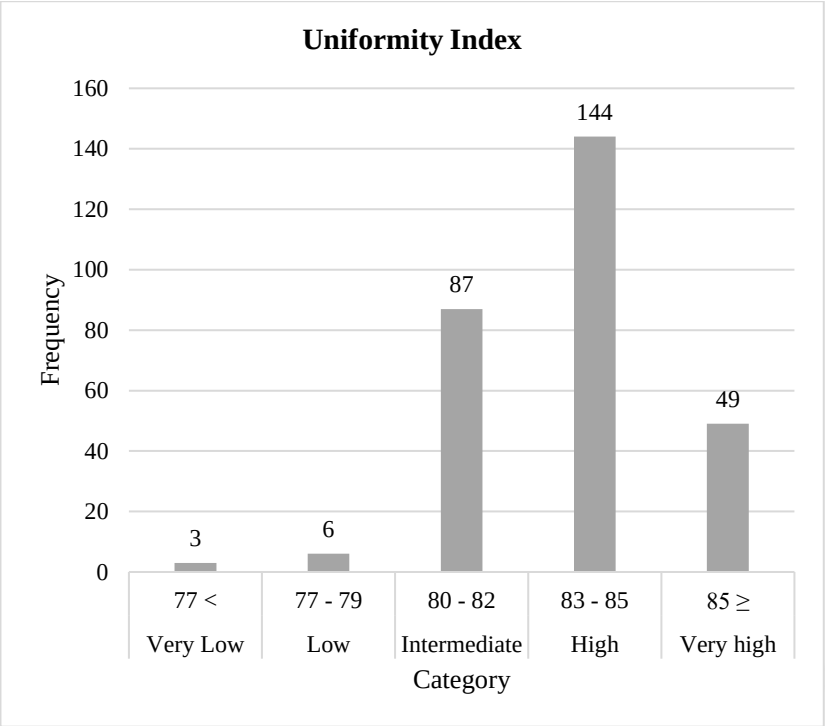

Figure 4.28. Uniformity classification

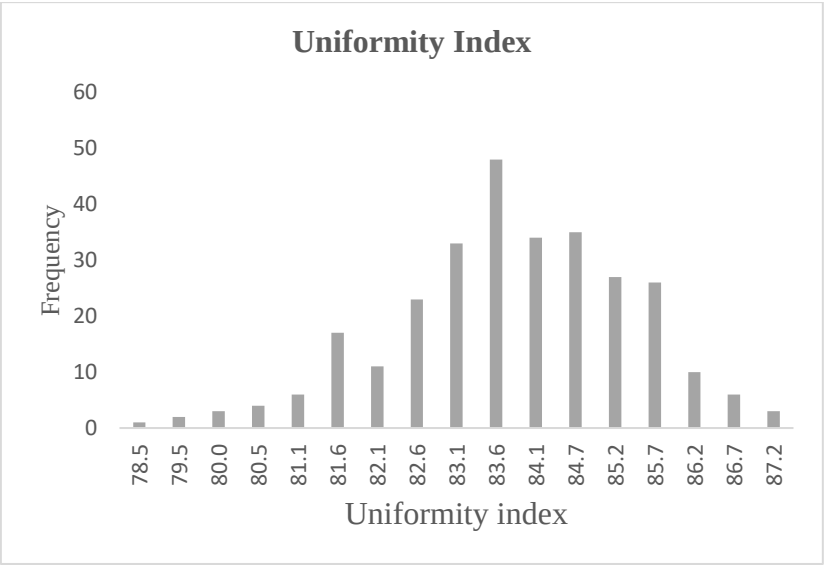

Figure 4.29. Uniformity frequency distribution

The detail of entries from very low to very high shown (Figure 4.28) which revealed that majority of the entries 144 (49.8%) were in high class and 49 of genotypes (17.1%) found very high as compared to superior standard STV468 (84.89%). Means were used for frequency distribution and it was found to be up to mark (Figure 4.29). Augedo et al., (2010); Akiscan et al., (2012); Ilci et al., (2014) also found same observations.

4.1.3.3.4. Fiber fineness (µg inch^{-1})

Micronaire values ranged from 2.9 µg inch^{-1} to 5.9 µg inch^{-1} as was highest in YB157 and Cun S-2 had minimum 3.2 µg inch^{-1}. STV468 had the highest micronaire i.e 4.7 µg inch^{-1} between controls while GW-TEX and BA119 had 4.48 µg inch^{-1} & 4.49 µg inch^{-1} respectively (Table 4.9). Statistically means of the genotypes were differentiated into different groups as from fine, medium to coarse (Ribbins and Davidnois, 2000). Coarse cultivars include TX 0091-2, Ozbek 142, Kashinat 5.8 µg inch^{-1}, 5.8 µg inch^{-1}, 5.7 µg inch^{-1}. The germplasm collections were differentiated into groups for determining the micronaire. It has been shown that the germplasm entries were found in four categories (Figure 4.30). 42.7% genotypes found better as compared to best check GW-TEX with micronaire of 4.4 µg inch^{-1}. Means distribution were also observed by frequency curves (Figure 4.31).

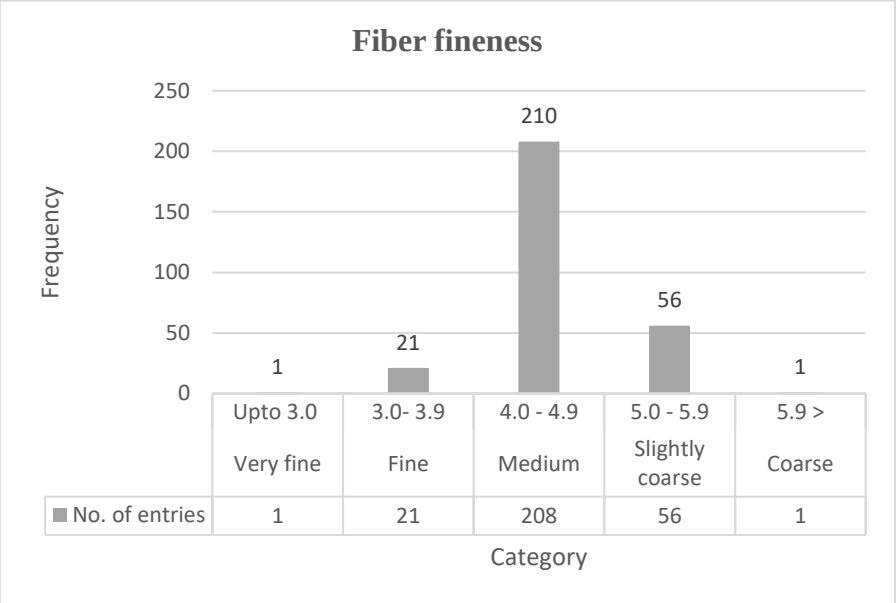

Figure 4.30. Micronaire classification

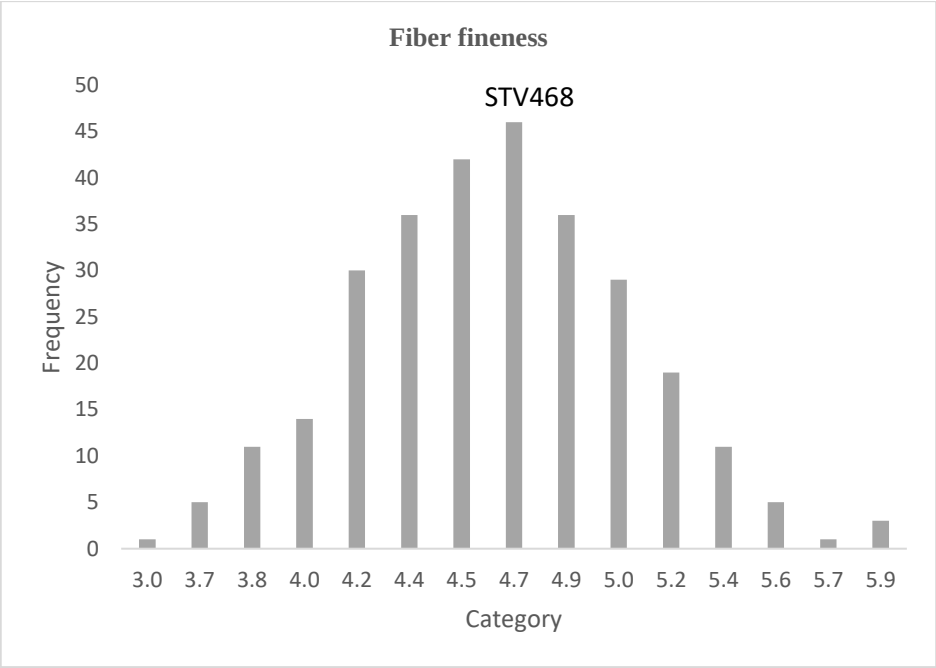

Figure 4.31. Micronaire frequency distribution

Fiber fineness and maturity are determined using micronaire values (Weber and Backe, 1994). It's a trait which is solely involved for excellent garments production in textile industry. Micronaire values should exist within the range of 3.5 to 4.9 µg inch^{-1} (Cotton Incorporated, 2013) while high value should be within range of 3.7 to 4.5 µg inch^{-1} for premium. Micronaire effects spinning and quality of yarn a lot. Yarn made from fine fibers known to be durable. Genotype, climate effect on genotype and picking method are associated with unexpected measurement value. For obtaining effective output textile industries need that fiber should be compatible during spinning (Deussen, 1992). During bale selection based on different parameters, fiber length and strength can be compromised during blending but too high micronaire is undesirable as bales cannot be further mixed (Indust, 2011). Same findings were obtained (Jenkins et al., 2009; Akiscan et al. 2012; Ilci et al. 2014). As most of the genotypes are having micronaire in the range which can be used in spinning for getting strong yarn so these resources can be used for fiber quality improvement.

4.1.3.3.5. Maturity (%)

Mean values for maturity ratio ranged from 0.83 to 0.90% as compared to best standard GW-TEX with 0.87%. Maximum ratio observed in YB157 (0.90%) followed by TX 0175-1 (0.90%) and minimum in Togo. Most of the genotypes were found to be mature as frequency curves were also constructed using means (Figure 4.32).

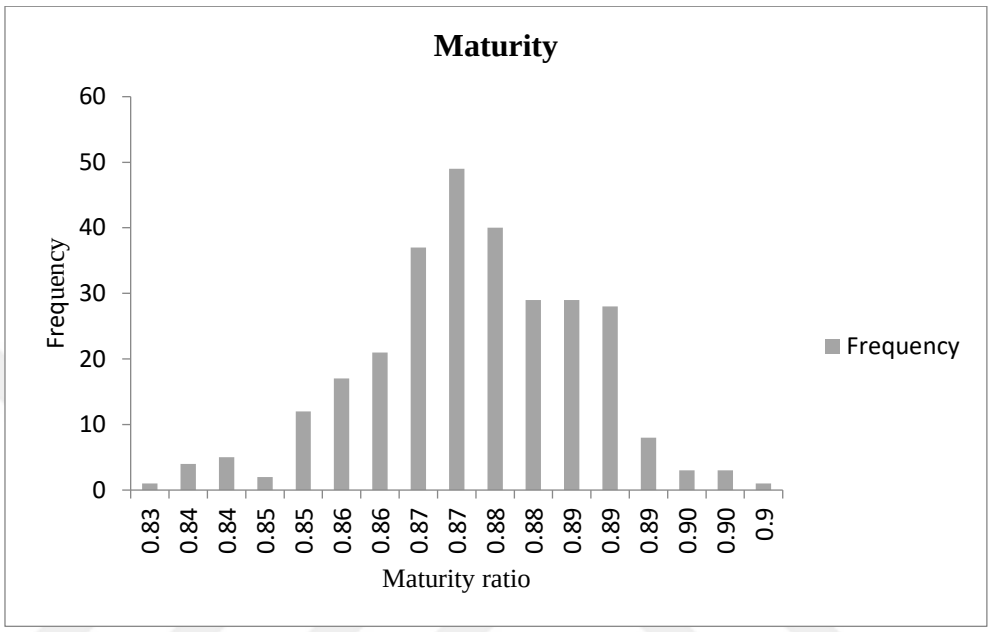

Figure 4.32. Maturity ratio distribution

Fiber maturity is defined as the ability of fiber to hold dye steadily during processing and is considered as one of the best essential trait of quality. It is expressed in ratio. During dyeing, high tearing of fiber, deformity and low absorption of dye are produced due to high immature fibers (Paudel et al., 2013). Therefore, it is compulsory that fiber should be mature to fulfill the needs of all stakeholders related to cotton. 0.71-0.77 maturity ratio was found for maturity ratio (Nagaraj and Katageri, 2011) while in the present investigations variation is higher and according to breeding objectives as high maturity results in better consistency up to the length of fiber. Karademir et al., (2010); Koli et al., (2014) also observed same variation among germplasm line.

Table 4.9. Means for fiber quality traits

	Kahramanmaras							Diyarbakir						
Genotype	**GOT %**	**FL**	**UI**	**FF**	**MAT**	**STR**	**FE**	**GOT %**	**FL**	**UI**	**FF**	**MAT**	**STR**	**FE**
11180-Glandless	35.7	28.1	81.4	5.4	0.9	34.3	5	38.5	28.3	85.3	4.8	0.86	29.7	7.77
152-F	37.1	28	83.8	5.3	0.9	32.2	4.9	39.7	30	85	4.7	0.87	31.3	7.27
153-F	42.3	27.6	82.7	5.4	0.89	28.9	6.5	38.5	28.5	82.2	4.4	0.86	26.1	7.37
2421-A	36.1	30.1	84.7	4.8	0.9	34.4	4.1	38.7	27.5	81.9	4.2	0.86	31.2	6.47
308 (CAMPO)	41.8	27.8	82.3	5.4	0.9	30.7	5.2	39.2	26.5	85.4	4.8	0.86	28.1	7.77
4SP	38.6	30.3	83.5	4.9	0.89	33.3	5.6	37.9	29.1	83	4.5	0.86	28.7	6.57
919 (LİDER)	43.1	27.3	83.5	4.9	0.9	31.1	4	40.7	28.2	85.1	4.4	0.87	31	6.07
93 FF 01	41.6	27.8	79	4.9	0.89	31.4	5.2	38.5	26.5	81.4	4.4	0.87	24.9	5.97
YB10	40.7	29	83.8	4.9	0.9	34.2	3.7	39.3	27.8	81.8	4.7	0.86	29.5	5.07
Acala-172	38.3	32.4	81	4.5	0.88	33.4	4.7	40.1	30.7	82.9	4.6	0.84	29.8	5.87
Acala-552	38.9	25.1	79.6	5.4	0.9	30.9	5.2	35.8	24.7	82.8	5	0.88	24.4	6.27
AK-4	32.2	25.7	84.2	5.2	0.9	30.9	4.5	34.1	23.5	82	5.1	0.84	27.3	5.57
Aktas-3	36.6	24.4	81.4	5.3	0.91	33.5	3.9	39.9	24	83.7	5.2	0.87	28.9	4.97
Albania-6172	37.7	27.1	81.3	5.4	0.91	28.6	3.4	38.1	27.3	83.9	4.3	0.87	28.9	5.47
Aleppo 1	36.1	27.6	81.8	4.2	0.88	29.2	4.1	35.2	26.1	82.9	4.1	0.85	23	6.67
Aleppo 40	41.1	27.3	82.5	5.9	0.92	31.1	4.7	37.8	27.5	84.3	5.1	0.87	26.8	6.97
Aydın-110	35.3	32.2	78	4.4	0.89	38.1	3.7	35.5	29.2	81.8	3.5	0.85	27.9	5.27
Azerbaycan 3038	33.6	27	81	4.4	0.88	33.2	5	36.7	28.5	83.8	4	0.86	30.2	5.67
Beli İzvor-432	36	27.5	83.2	5.4	0.91	32.3	3.5	37.4	26.1	84.4	3.6	0.85	27.9	5.57
Belserroms-30	36.5	31.6	84.1	5.1	0.9	34.3	4	38.3	28.9	84.3	3.9	0.86	30	5.67
BSC-4	39.2	27.3	83.4	5	0.89	32.5	4.8	41.4	26.1	82.6	4.5	0.87	28.3	5.71
CA-228	40.5	28.6	83.4	4.6	0.89	32.6	3.7	40.4	30.2	83.9	3.6	0.85	32.8	5.07
Carmen	39.4	29.6	83	4.7	0.89	35.5	4.1	38.1	26	83	4.2	0.86	24.3	5.67
Caskot BR-1	39	27.7	82.3	4.5	0.88	33	5	39.1	26.4	82.4	4.3	0.86	24.7	6.77
Corina	39.9	29.8	85.2	4.9	0.88	34.1	5.8	38.1	28.6	82.6	4.6	0.86	26.8	7.77

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
Crincle Leaf	40	27.8	76	3.5	0.86	22.5	4.3	36	29	82.5	3.9	0.85	25.9	6.17
Cırpan 603	32.7	27.8	85.5	5	0.89	37.5	5	37.9	28.4	82.8	5.1	0.89	34.6	5.37
Cukurova-1518	36.9	28.6	80.7	4.3	0.88	33.9	4	38.8	27.4	81.8	4.4	0.86	25.9	5.95
Cun S-1	36.3	25	83.1	5.3	0.9	30.8	5	38.6	26.3	83.1	4.8	0.88	28.4	5.67
Delcerro	34	31.3	83.6	4.6	0.9	49.1	3.9	37	32.2	84.1	4.6	0.88	40.2	5.57
Delta Opal	35.3	31.2	83.5	4.5	0.88	33.4	4.6	35.9	30.8	82.8	4.1	0.86	29.2	5.83
DP-388	37.4	28	82.1	5.1	0.89	31.6	5.1	37.2	26	82.7	4.6	0.87	27.3	6.07
DPL-20	39	26.9	83.3	5.4	0.91	35.3	4.6	36.6	27.4	85.1	4.4	0.86	32.9	6.77
DPL-50	33.6	27.2	83.2	5.6	0.91	33.4	4.8	35.9	23.8	81.6	4.6	0.87	26.9	5.47
DPL-5409	38.5	29.8	82.4	4.5	0.89	32.7	3.4	34.7	29.3	83.6	3.9	0.85	30.9	6.06
DPL-5614	36.4	29.5	80.8	4.9	0.89	33.9	4.9	37.4	28.8	84.9	4.1	0.85	32.5	6.97
AB80	47.6	29.7	84.6	5.3	0.89	32.4	5.3	44.6	27.8	82.2	3.7	0.84	25.9	6.3
Europa-1752	33.3	30.4	85.1	4.7	0.88	34.4	4.9	36.8	31.7	84	4.7	0.88	30.5	4.9
Fibermax 819	38.8	29.4	86.5	4.9	0.88	32	5.3	38.1	28.7	83.5	4.1	0.86	29.5	5.6
Fibermax 832	38.5	29.9	83	4.3	0.87	36.6	5.1	36.8	31	83.8	3.9	0.86	30.5	5.6
Fibermax 958	40.5	28.4	83.9	5.2	0.9	33.4	4.3	40.2	29.6	84.9	4.8	0.88	30.8	5.6
Garant	34.9	28.7	84	5.3	0.89	28.4	5.5	35	29.2	84.2	4.8	0.87	30	6.4
Gedera-5	40.5	29	84.2	4.4	0.87	32.1	6.1	37.3	27.8	81.8	4.1	0.85	28.9	6.6
Golda	36.7	28.3	85.2	5.8	0.9	30.7	5.3	37	29.5	80.2	4.5	0.86	30.9	7.1
Gurbeyms34/1	36	29	85.6	4.6	0.88	33.5	5.2	37.2	27.1	82	4.6	0.86	26.5	7.6
IS-2	37.1	27.9	83	5.4	0.89	30.4	6	39.5	28.8	83.2	4.7	0.87	30.4	6.4
Kahinath	37.4	28.8	84	5.9	0.91	33.6	5.3	39.1	27.5	79.8	5.6	0.87	30.4	4.4
Lachata	39.2	31	85.6	5.3	0.89	32.9	5.4	42	30.2	83.3	4.8	0.87	28.5	6.3
Maras92	37.6	29.9	82.9	5	0.89	34.9	4.7	39.2	29.9	84.2	4.4	0.87	31.3	5.8
Marcel leaf	35.6	25.5	81.9	5	0.88	27.1	5.7	39.1	27.1	80.2	4.8	0.87	26.9	6.4
McNair-235-612	38.2	29.3	84.3	5.2	0.89	34.8	5.3	37.2	29	82.1	3.8	0.85	28.3	6.1
MC Namara	35.5	28.1	84.6	5.6	0.9	32.7	5.3	35.2	26.8	81.6	4.9	0.88	24.9	5.7

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
NAKBC1-14/2	41.2	27.8	81.7	4.6	0.88	31.7	4.9	40.8	28.7	81.3	5.1	0.87	26.9	6.7
NATA	37.8	31.4	85.8	4.9	0.89	35.9	4.3	36.2	30	83.8	3.8	0.85	33	5.7
Nazilli 342	40.4	30.9	85.7	5	0.89	33.4	4.9	38.2	30.1	84.6	3.6	0.85	27.6	5.6
Nazilli 84S	38.2	29.4	82.7	4.8	0.88	32.3	5.2	38.6	29.9	83.4	3.5	0.84	31	6.7
Nazilli M-503	38.3	28.6	82.9	5.4	0.9	31.7	5.2	37.3	28.8	82.6	4.7	0.88	26.3	5.2
Nazilli (93-7)	37.2	28.3	84.5	5.4	0.9	31	4.7	40.9	30.5	83.5	4.5	0.87	31.4	5.7
Nectar free	40.3	29.6	83.7	5	0.89	33.6	4.7	39.1	29	84.2	4	0.86	28.2	5.4
Nieves	35.9	27.4	85	5.5	0.9	35.3	5.2	37.8	27.1	84.4	4.3	0.86	28.5	6.4
NSCH-777	30.7	28.3	85.2	4.9	0.88	27	7.7	35.2	26.7	82	4.6	0.85	27.3	7.9
Okra 201	34.4	27.5	82.4	4.8	0.88	30.8	6	36.5	28.4	82.5	4.2	0.87	25.9	4.7
Okra 204	36.7	26.1	82.7	4.9	0.89	30.2	4.8	37.5	28.1	83.1	5.4	0.88	29.5	6.9
Okra-frego	39.4	27	82.4	5.5	0.9	33	4.8	35.2	28.4	84.3	5.1	0.88	31.3	6.2
P.D. 0648	37.7	28	83.3	5	0.89	34.9	4.8	37.2	29.4	85.4	3.7	0.85	30.7	5.2
Paymaster 2379	37.5	28.5	84.1	5.7	0.9	38.7	6	37.8	28.4	83.8	4.9	0.87	31.8	7.4
Paymaster 330	35.2	27.8	83.3	5.4	0.9	33.2	5.3	39.1	26.8	83	5.2	0.88	29.4	6.9
R-5 (STG-6)	38.9	27.9	81.5	4.1	0.86	40.2	6.4	40.1	28.9	83.5	5.1	0.88	32.2	6.8
RKNR 261	38.1	27.9	85.5	4.6	0.87	31.1	6.1	38.1	27.4	83	3.7	0.83	27.3	7.7
SAHEL 1	36.6	27.3	86.1	6.1	0.91	32.8	5.1	38.2	27.4	83.8	4.6	0.87	33.4	5.9
SAYAR-314	37.7	31.1	85.6	5.5	0.89	29.9	6.4	39.8	30.9	86.2	3.9	0.84	29.6	8.4
Semer. Uzbek	36.6	27.3	84.6	5	0.88	31.7	6.1	39.5	27	82.1	3.8	0.84	30.1	8.1
Semu SS7G	38.7	26.7	80.5	5.2	0.88	27.6	6.3	36.9	26.6	82.1	4.4	0.85	28.6	7.57
SG 404	37.5	27.8	82.9	4.8	0.88	26.5	4.7	38.3	30	85.9	3.7	0.84	32.5	6.27
SG 501	40.4	28.6	84.4	5.1	0.89	27.4	5	38.9	30.1	85.2	4.1	0.85	33.5	6.27
Sindos 80	38.7	28.5	82.6	4.8	0.88	27.1	5.6	36.4	29.3	83.9	3.8	0.85	37.5	6.27
Siocra	39.1	30.7	84.8	4.9	0.89	24.8	4.7	41.3	31.9	83.4	3.2	0.83	32.6	5.77
Sivon	43.7	29.5	82.4	5.2	0.89	31.8	5.1	39.4	29.2	85.1	3.8	0.85	28.5	4.87
Sphinx V	36.6	28.4	82.5	4.3	0.87	24.7	4.7	36.9	29.4	83.3	3.1	0.83	28.4	5.87

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
STG 14	38.4	29.2	81.1	4.7	0.83	28.4	7.8	38.6	29.2	85.2	4.3	0.85	32.3	7.07
Stn 8a	40.1	26.6	82	4.5	0.87	22.4	5.3	37.7	28.6	84	3.8	0.84	28.6	6.47
Stoneville-453	40.2	27.7	80.9	5	0.88	22.9	6.1	38.6	27.8	81.6	4.2	0.85	26.2	6.17
Suregrow 125	41.8	27.7	83.8	5.8	0.9	23.5	5.6	37.3	27.5	84.6	5	0.88	28.8	5.57
Sahin 2000	38.1	29.2	84.1	5.2	0.89	25.5	5.5	37.2	30.7	85.2	4.3	0.83	29.9	9.27
Tamcot CABCS	40.5	29.1	82.1	3.9	0.86	29.4	5.4	38.6	28.8	84.1	3.7	0.84	32.3	6.67
Tamcot Luxor	40.8	26.3	83.4	4.3	0.87	27.8	4.8	42.7	27.4	80.9	3.9	0.82	31.6	5.37
Tamcot Pyramid	37.3	29.4	84.2	4.8	0.88	30.9	5.5	37.8	30.8	85	4.2	0.85	33.1	6.77
Tamcot SP 37-N	38.2	28.5	82.1	3.8	0.86	24.7	4.8	40.5	28.1	85.1	3.8	0.81	32.6	5.17
Tamcot Sphinx	37.1	30.2	85.5	4.8	0.88	32.5	5.3	41.1	28.4	84.5	4.6	0.86	36	6.37
Taskend-6	35.6	28.6	84.3	4.3	0.87	25.3	4.2	37.6	29.8	84.5	3.8	0.84	28.8	6.37
YB101	41.4	30	84.9	4.8	0.89	31.7	4.3	40.1	32.6	88.4	4.4	0.86	35.3	6.37
TKY-9409	36.6	28.5	84.4	5.4	0.9	28.4	4.3	36.2	30.6	85.9	4.7	0.87	34.1	5.37
Togo	38.1	30.1	80.6	4.5	0.81	27.6	6.1	37.4	29.9	85.1	4.1	0.85	32.1	5.67
Veramine	37.1	32	86.2	5	0.89	32.2	4.1	34.5	30.9	85.4	4.1	0.86	33	5.27
Zeta 2	29.9	21.1	81.8	5.7	0.9	23.1	5.3	34.4	23.8	80.7	4.4	0.85	29.9	7.07
YB106	25.4	25.2	80	4.2	0.86	20.3	5	36	26.6	80.2	3.3	0.83	27.5	6.57
Kurak 2	38.5	28.1	81.9	5	0.88	24.4	5.1	38.8	27.4	81.2	4	0.85	26.4	5.97
NGF-63	37.4	30.7	85.1	4.7	0.88	29.5	4.7	37	31.1	82.8	3.2	0.83	32.5	5.77
Naked	5.33	0	0	0	0	0	0	3.9	0	0	0	0	0	0
Orgosta 644	32.5	28	84.6	5.1	0.89	28.1	4.2	36.2	31.4	86.4	4.1	0.85	32.4	5.87
IS 10	35.5	29.4	82.4	5.4	0.9	25.1	3.6	37.2	29.7	85.3	4.3	0.86	36.4	5.67
Samon	35.9	29.5	84.6	5	0.89	25.9	4	37.5	33.2	86.1	3.9	0.85	42.4	6.57
Ujchi 2 Uzbek	33.6	34.6	81.7	4.2	0.87	34.3	5	36.6	28.8	84.5	4.6	0.87	29.6	5.47
108F	36.7	27.8	82.5	4.3	0.87	28.3	4.6	38	29.9	85.8	3.7	0.85	32.2	5.47
Acala 3080	38.3	29.8	83.1	5.5	0.91	28.7	4.1	37.8	33.4	85.7	4	0.86	38.5	5.17

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
Acala S.J. 2	38	29.1	83.6	4.7	0.89	34.1	3.6	36.3	31	86.1	4.8	0.88	34.6	4.87
Coker 413/68	35.4	27.4	83.9	4.4	0.87	28.3	5.6	36.7	29.5	84.5	4.1	0.85	32.1	6.27
DPL 15/21	37.7	26.6	80.5	4.1	0.87	21.2	4	38.3	27.6	85	4.4	0.86	29.2	5.47
DPL529	38.4	29	80.6	4.5	0.88	34.9	4.1	37.9	30.4	82.7	4.2	0.86	29.7	5.74
DPL 90	40.6	28.8	81.7	5.3	0.89	32.7	4.8	36.8	28.9	82.5	5	0.87	26.9	6.44
Ege-69	35.2	29.9	81.3	4.5	0.87	32.7	5.3	36.3	28.8	79.2	5.2	0.88	28.4	5.64
Extreme Okra	32.9	24.5	78.3	5	0.89	26.9	4.5	33.6	26.1	80.8	4.7	0.87	23.8	5.74
Eksi-91	40.3	27.6	81.5	5.2	0.9	30.6	4.1	35	30.2	81	3.7	0.85	27.5	5.64
Gossypollfree86	39.9	28.3	82.5	4.7	0.88	29	4	37.3	28.1	83.8	3.7	0.85	25.2	5.44
H-88029	31.8	27.7	82.7	5	0.89	29.6	4.7	35.6	28.5	84.1	4.9	0.84	29.9	5.14
Hint Ç.9	30.2	27.2	82	5.1	0.89	27.1	3.8	33.4	29.5	81.9	5	0.88	27.8	5.64
HYC-76/59	37.1	28.7	80.6	5.1	0.89	31.5	4.5	37.1	28.9	80	4.4	0.85	28.4	7.74
IS 4	34.4	28.3	83.4	5.6	0.9	34.1	5	34.7	29.5	82.9	5	0.88	29.3	5.84
IS 8	36.6	31.3	83.1	5.1	0.9	39.8	4.1	36.1	32.5	83.4	4.7	0.87	32.9	5.34
Kurak-1	36	28.1	81	4.4	0.87	29.7	4.9	38	29.2	81.8	3.7	0.83	29	7.04
Lockette	38	28.3	83.3	5	0.89	33.1	4.7	36.8	30.2	79	4.5	0.86	28.4	6.04
Nazilli 87	35.9	29.6	84.9	5.3	0.9	33.2	4.1	34.3	29.6	81.4	5	0.88	32	5.84
Özbek 142	43.6	28	78.7	6.1	0.91	29.5	4.6	45.2	30.5	83.1	5.6	0.89	31.9	5.74
Visalia Elmer	37.3	29.7	83.3	4.7	0.88	38.4	4.3	38.6	29.7	83.3	4.7	0.88	37.3	5.34
Sealand 542	34.5	30.7	83.1	4.8	0.88	34.6	4.5	35.2	30.5	83.8	4.5	0.86	31	5.94
Siokra 133	35.1	32.8	83.5	4.2	0.87	33.7	4.6	37	32.2	79	4.5	0.83	30.4	5.24
STN. K311	39.8	31.5	85.4	4.3	0.87	37.1	4.7	36.4	30.4	82.4	4.9	0.87	31.5	6.64
Stonville 506	34.5	29.4	84.5	5.4	0.89	33.5	5.3	36.5	28.2	81.9	4.7	0.87	29.5	6.14
YB141	29.5	24.3	81.8	4.3	0.86	28.3	5.6	32.3	24.1	77.1	4.6	0.81	25.5	4.84
Acala 44	38.7	27.2	81.3	4.4	0.87	29.9	4.2	35	29.3	81.3	4.2	0.86	24.4	5.24
Acala Royale	39.9	29.5	84.8	5.2	0.9	38.3	4.3	39.2	27.7	81.9	4.3	0.86	30.8	5.24
Acala1517-99	37.2	30.6	84.4	4.9	0.89	38.4	4.7	33.5	32.2	84.4	4.4	0.86	32.7	5.74

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
Acala Prema	38.2	29.5	84.3	4.3	0.87	35.9	4.8	39.5	28.6	81.6	4.7	0.87	27.6	5.84
Acala1517-95	37.4	28.8	82.8	5.2	0.89	30.4	4.5	35.9	30.1	78.8	4	0.85	27.2	6.04
Stoneville 132	40	28.1	83.1	4.7	0.88	28.7	4.9	38.1	28	81.9	4.6	0.86	27.4	7.04
YB149	40.9	29.4	83.4	4.8	0.89	34.4	3.8	37.7	31	83.6	4.1	0.86	30.6	5.34
YB150	38.1	31.2	83	4.1	0.86	35.7	5.2	36.6	29.4	81.7	4	0.85	27.1	5.94
YB151	21.6	29.4	82.4	4.7	0.88	31.4	4.4	25.8	29.2	82.7	5	0.84	31.9	4.84
YB152	36.9	29.4	82.5	3.4	0.85	37.8	4.6	34.1	29	81.8	4.2	0.85	24.7	5.74
YB1535	38.4	28.2	82.9	4.6	0.88	31.3	4.4	34.1	29.2	82.2	4.6	0.87	27.7	5.74
YB154	32.4	29.4	82.7	4.6	0.83	28	7	34.2	31.3	81.7	3.8	0.84	29.3	6.64
YB155	36.9	28.7	84.6	5	0.88	33.5	5.3	35.4	29	83.3	4.5	0.86	24.8	6.54
YB156	43	27.1	80.4	4.9	0.89	30.7	3.8	38.7	29.9	82.7	4.5	0.86	27.6	6.64
YB157	35.1	27.2	80.5	6.2	0.92	32.8	4.7	37.2	29.5	82.1	5.6	0.89	28.6	5.54
YB158	32.4	29.4	82.4	5.4	0.9	31.9	4.8	37.2	31.1	82.6	4.3	0.85	30.2	6.74
YB159	37	26.9	81.5	5.1	0.89	30.7	5.4	39.7	30.4	84.2	4.2	0.85	31.1	7.04
YB160	37.2	29.4	83.3	5.2	0.9	34.6	3.6	38.3	30.6	82.4	4.7	0.87	27.4	5.34
YB161	4.3	26.8	82.8	5.6	0.9	32.9	5.5	3.9	29.5	82.9	4.8	0.87	30.2	6.24
Gosspollfree	37.9	31.7	84.5	4.9	0.89	41.2	5	36.8	29.6	83.1	4.4	0.85	25.2	6.64
PI 528420	34.4	23	79.4	3.7	0.85	25.9	6.1	38.2	21	85.8	3.7	0.85	30.8	5.04
NP-ozbek 100	40.9	28.4	85.9	4.3	0.87	38.8	5.7	37.1	29.1	84.6	3.9	0.84	31.2	7.14
TX 0175-2	29.8	27.8	82.3	5	0.89	29.9	4.8	34.2	29.8	83.2	3.6	0.83	31.6	7.54
Özbek 105	38.7	26	82	5.3	0.9	31	4.8	39.3	27.5	82	3.9	0.84	28.7	5.84
TX 0175-1	34.1	24	82.2	5.5	0.9	31.4	5.2	34.4	27.6	84.1	4.5	0.86	29.7	6.44
TX 0061-2	35.9	28.6	83.3	5	0.9	34.1	4	40	30.4	84.1	4	0.86	36.5	5.14
Nazilli 07	9.7	27.1	81.8	4.7	0.88	29	5.6	11.3	28.6	81.9	4.1	0.85	27.1	6.34
Sezener 76	38.4	29.8	83	4.8	0.89	39.8	4.4	39.4	29.6	85.1	4.6	0.86	35.7	6.94
TX 0060-2	34.8	28.5	82.4	4.7	0.88	35.3	5	36.1	28.6	84.2	4.2	0.85	29.7	6.74
TX 0091-1	31.1	30	82.4	4.3	0.87	31.1	4.8	34.5	30	84.7	4.2	0.84	27.9	7.44

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
İpek 607	34.7	26.8	78.8	5.2	0.89	32	5.6	38.6	24	82.4	5.4	0.87	25.9	7.84
PI 528426	4.3	0	0	0	0	0	4.7	3.9	0	0	0	0	0	0
NP EGE 2009	37.5	30	84	5.1	0.89	34.8	5	39.5	30.7	86.7	5.1	0.83	35.7	6.04
PI 173332	37.6	30	83.8	3.8	0.87	31.4	4.1	41.2	29.3	82.4	4.2	0.8	32.3	5.14
PI 529128	34.4	29.9	81.2	4.4	0.88	35.9	4.8	38.6	27.9	80.3	4.1	0.84	27.2	6.74
STN498	40	28.2	83.7	4.9	0.89	31.3	4	43.1	29.1	84.8	5.1	0.87	33.4	6.34
TX 0091-2	35.8	27.1	83.8	5.5	0.9	33	4.9	38.7	26.6	86.3	5.4	0.81	33.7	5.84
GAİA	40	28.8	84.2	4.8	0.89	33.9	4.6	42.8	29.8	82.4	4.7	0.85	31.2	5.44
PI 165325	37.5	28.1	84.5	4.7	0.89	34.9	4.8	39.3	27	84.1	4.6	0.85	27.6	7.04
ZN243	31.8	26.8	81.3	4.9	0.89	28.7	4.7	34.8	27.8	84.5	4.4	0.85	32.2	7.14
PI 528429	9.7	22.6	84.6	5	0.88	32.9	5.9	11.3	24.47	85.9	4.7	0.86	31.7	7.5
PI 528450	27.2	21.2	81.5	5.2	0.89	36.1	5.7	31	24	75.5	4.3	0.84	31.1	7.94
PI 528525	38.3	27.4	83.3	4.6	0.88	30.7	5	37.2	26	82.7	3.6	0.83	28.2	7.24
GAPEAM1	36.3	31	83.5	4.6	0.88	33.3	5	35.6	27.7	84.2	4	0.84	26.9	7.34
PI 529869	34.3	27.9	82.9	4.8	0.89	36.5	4.1	36.5	31.2	85.4	4.1	0.84	30.3	7.84
Spears3(967)	34.4	32.1	78.4	4.2	0.88	32.5	3.8	38.3	35.5	83.9	3.4	0.84	34.2	5.34
YB193	40	28.3	82.1	5.5	0.9	37	5.1	38.3	27.4	81.3	3.8	0.83	27.9	7.14
YB194	37.2	26	81.3	5.2	0.9	37.7	4.9	41.8	27.8	85.6	4.1	0.85	30.4	6.34
YB195	37.9	27.7	83.9	5.1	0.89	33.3	4.7	36	31.3	82.3	4.6	0.86	28	6.14
YB196	37.8	26.7	80.9	5.5	0.9	32.4	5.4	35.7	27.9	83	4.6	0.85	29.5	7.14
YB198	37.3	28.4	80.1	4.1	0.87	27.8	4.7	36.1	30.5	86.4	4.2	0.85	29.4	6.04
TX0175-1	30.2	26.5	83.4	6	0.91	30	5.4	34	28.5	85	4.8	0.9	32.3	5.84
TX 0175-2	34.4	27.5	84.8	4.8	0.89	31.9	4.8	38.4	30.4	85.7	5	0.9	29	6.24
528875	33.6	34.1	80.5	3.9	0.88	33	3.8	36.8	33.1	84.9	4.1	0.88	30.2	5.34
Acala wild 1517	35.9	28.9	85.3	4.9	0.89	31.5	5	38	30.8	87.2	3.5	0.86	35.7	6.44
Ugur	41.2	26.8	83.8	5	0.89	29.3	5.1	36.1	30.1	86.3	4.3	0.88	32.2	5.94
Acala 1517-99	39.03	24.5	81	5.8	0.87	31.7	6.78	38.7	33.6	86.5	3.4	0.84	37.1	6.35

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
TX 0091-2	37.5	25.1	84.4	6.0	0.92	32.8	4.4	39.6	25	80.3	5.7	0.89	32.7	4.24
YB214	32.8	22.4	82.3	4.6	0.87	24.3	5.7	34.1	28.4	83.5	3.4	0.86	30.6	6.54
YB215	27.9	24.3	80.0	4.0	0.85	29.3	6.9	30	25.5	82.7	3.1	0.84	27.6	7.54
YB216	24.9	21.7	79.3	4.2	0.86	21.4	6.0	34.5	24.7	83.1	3.7	0.86	23.8	6.74
PI 163722	38.1	28.7	82.8	4.8	0.88	30.8	5.5	40.5	28.6	84.9	4.3	0.88	29.1	5.84
PI 163615	28.1	28.8	84.1	4.4	0.87	31.8	5.4	33	31	86.2	4.4	0.89	35.2	5.74
163615	33.9	24.9	81.6	4.5	0.89	27.4	3.7	38.3	26.5	84.1	3.6	0.87	30.4	5.44
YB225	35.5	24.5	77.8	4.8	0.88	26.0	5.7	37.4	22.6	81.8	4.8	0.88	22.2	7.04
Krem	32.7	22.6	79.5	4.6	0.88	24.6	5.2	34	27.2	82.9	5.1	0.9	29.6	6.64
Acala 1517 D	32.8	33.2	85.0	4.4	0.89	36.9	3.0	36.5	33.1	85.2	3.9	0.88	36.5	4.44
ADN 123	39.3	27.1	83.5	3.5	0.85	28.6	5.8	41.7	26.8	83.8	4.3	0.88	27	6.24
Sealand 1	34.4	34.4	85.9	3.9	0.88	38	3.6	35.7	36.9	88.5	3.2	0.87	39.5	4.54
TMN 170	43.6	28.7	84.9	4.8	0.89	36.6	5.5	41.8	30.4	87.6	4.2	0.87	38.1	7.74
TM-1	34	27.8	84.7	4.3	0.87	30.4	5.9	37.2	29.9	86.3	3.2	0.85	31.9	6.24
Coker 312	38.7	29.1	83.1	4.9	0.89	28.5	5.0	37.5	31.3	85.7	4.1	0.88	34.7	5.34
Sicala 3/2	34.3	27.5	84.9	5.0	0.90	34.3	4.6	36.8	30.1	88.7	4.3	0.89	32.1	5.24
Tamcot H 0 95	38.4	27.1	83.5	3.8	0.87	30.1	4.6	39.8	29.3	84.1	3.8	0.87	31.7	6.34
Gossy. Nazilli	39.8	28.9	83.3	4.9	0.89	29.3	4.5	39.9	29.2	87.1	4.7	0.85	33.4	4.24
Cooker 100 Ahıl	40.0	28.6	84.0	4.6	0.88	27.5	5.1	37.8	29.7	86.1	4.6	0.89	27.4	5.34
Naz. 954	42.5	27.5	84.4	5.3	0.90	29.3	5.2	40.3	30.1	86.2	4.5	0.88	31.2	6.94
Paymaster 404	40.0	27.1	85.1	4.5	0.89	34	4.4	36.7	28	86	3.9	0.88	31.3	5.54
GSN 12	39.6	28.4	84.3	4.5	0.88	32	4.7	39.1	28.9	85.1	3.9	0.88	29.6	4.94
HT1	40.1	30.0	85.0	4.1	0.87	33.2	4.5	40.1	29.9	86.3	4.1	0.88	34.3	5.24
Naz 143	38.6	28.8	84.6	4.6	0.89	35.1	4.5	39.1	29.4	85	5.2	0.89	31.3	5.64
Emand 542	35.8	29.1	81.0	4.8	0.89	28.2	4.6	37.9	30.7	84.3	4.6	0.85	32.1	4.34
Flora	39.6	36	79.6	5.3	0.89	36.6	5.4	39.1	33.7	87.1	4.8	0.90	34.7	4.14
Napa	41.0	28.2	83.6	4.7	0.88	33.1	5.3	36.7	31	87.8	4.4	0.89	33.9	5.94

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
YB247	43.4	29.0	83.6	5.2	0.9	34.1	5.2	39.7	29.9	87.2	4.9	0.9	34.6	5.94
DP 493	39.9	28.3	84.6	4.0	0.87	29.9	4.8	41.2	29.1	85.5	4.6	0.89	32.5	5.54
H- 23	39.8	29.1	84.3	5.2	0.90	39.1	4.7	37.8	28.7	86.0	4.4	0.89	34.3	4.94
GSN 22	41.3	31.3	82.4	4.0	0.82	29.2	6.2	39.8	31.1	84.9	3.7	0.87	30.9	5.54
YB251	37.3	31.5	86.0	3.9	0.87	35.7	4	38.6	30.1	84.5	4.4	0.88	30.7	6.04
Cooker 100 A 2	36	28.7	85.6	4.4	0.87	29.2	5.1	39.3	30.1	87.3	4.4	0.84	31	5.54
Cabu CS 2-1-8-3	38.2	29.8	83.3	4.8	0.88	29.4	4.7	39.6	31.2	84.7	4.8	0.9	29.8	5.74
Menderes 2005	34.9	31.9	88.1	3.9	0.86	42.3	5.4	34.3	32.1	86.3	3.3	0.85	36.7	6.74
S-9	36.1	29.9	86.1	4.3	0.86	31.7	5.4	36.9	30.4	83.2	4.3	0.88	26.2	5.64
H-10	38.4	28.2	85.5	4.9	0.89	33.0	4.4	36.5	30.4	83.7	4.3	0.88	28.6	5.44
DP 5111	37.3	28.4	83.5	5.0	0.89	32.0	4.8	38.4	30.4	85.6	4.6	0.88	29.2	7.14
SG 96	37	29.6	85.1	4.8	0.89	33.6	4.2	41.2	30	84.9	3.9	0.87	30.1	5.84
Adana 98	37.6	30.4	85.7	3.3	0.84	32.3	5.7	36.6	31.6	85.2	3.7	0.87	35.9	6.34
Cun S-2	37.0	27.0	82.0	2.7	0.83	29.0	5.1	37.0	28.4	84.3	3.1	0.86	24.6	5.34
Tamcot SP 21-9	36.5	28.2	83.1	4.4	0.87	25.3	5.3	38.6	28.7	83.9	3.8	0.86	29.3	6.44
Siokra L 22	38.3	29.4	83	3.6	0.85	33.6	4.6	40.1	30.7	81.9	4.0	0.88	25.9	4.64
Coskun-1	37.9	30.5	86.4	4.0	0.85	30.9	6.7	42.3	32.0	85.2	4.6	0.89	34	5.34
DKG 658	37.0	29.2	83.8	4.5	0.87	30.4	4.5	36.4	32.7	86.9	4.3	0.89	29.1	5.14
Naz M 39	38.5	28.2	87.6	5.0	0.88	33.0	5.8	40.8	27.4	83.3	4.9	0.89	30.3	7.04
DP 396	39.1	29.2	86.9	5.0	0.88	36.2	5.3	40.2	28.2	84.8	4.9	0.89	29.4	6.44
DP419	39.5	29.6	84.7	4.0	0.85	33.5	6.7	39.2	30.1	86.5	4.1	0.86	34.5	7.94
Primera	40.8	29.0	86.5	5.0	0.87	30.5	6.3	40.3	29.4	86.1	5.2	0.89	31.5	7.54
Veret	37.3	30.7	84.6	4.3	0.88	37.4	4.0	35.1	32.2	86.0	4.2	0.89	33.3	4.84
BA 525	38.2	29	83.5	4.7	0.88	31.3	4.8	42.1	30.3	85.6	5.1	0.90	31.6	5.44
DP 5690	35.0	29.7	83.9	5.1	0.88	32.2	5.5	38.9	29.6	85.3	4.4	0.89	33.9	5.64
SJU 86	40.4	31.7	86.1	4.5	0.88	35.9	4.2	38.1	32.6	87.2	4.1	0.87	35.3	7.24
Blightmaster	33.8	30.6	84	4.7	0.88	33	4.9	37.2	32.3	86.4	3.8	0.88	36	5.24

Table 4.9. Continue

Genotype	GOT %	FL	UI	FF	MAT	STR	FE	GOT %	FL	UI	FF	MAT	STR	FE
Sicala 33	42.3	28.2	84.6	4.2	0.87	29.1	4.7	41.6	30.7	83.5	3.8	0.87	33	5.84
HT2	35.9	30.1	85.2	4.2	0.87	36.7	5.0	36.2	32.5	84.8	3.8	0.87	34.4	6.64
Dicle 2002	37	29.3	86.9	5.0	0.89	31.6	4.5	37.4	27.5	83.5	3.6	0.87	25.4	5.14
Semu 55/6	34.6	28.1	84.4	4.4	0.87	27.9	5.1	39.2	30.2	86.1	3.8	0.86	31.3	7.54
Tropical 225	37.7	30.7	84.2	4.6	0.87	29.4	5.2	35.8	32.9	87.2	3.4	0.86	32.4	6.44
STV 373	38.4	29.6	85.3	4.3	0.87	30.1	5.3	39.4	31.5	86.2	3.6	0.86	30.4	7.24
Naz 84	37.5	29.9	85	4.0	0.86	31.5	4.8	36.4	31.7	86.4	4.0	0.87	30.1	6.44
4 SB	40.0	29.9	84.5	4.8	0.88	31.1	5.2	40.1	29.8	83.6	4.0	0.87	26.9	6.64
İdeal	37.5	29.2	85.2	3.7	0.85	39.9	5.3	39.2	31.0	85.5	3.9	0.87	29.6	6.24
Vurcano	36.3	29.7	85.4	4.1	0.86	29.1	5.5	37.4	30.2	85.6	4.8	0.88	30.2	7.74
STV 478	42.8	28.3	83.6	4.8	0.88	31.9	5.4	40.8	29.9	84.9	4.6	0.88	32.7	7.64
SG 1001	33.6	31.1	85.0	4.4	0.87	35.1	4.5	36.5	31.7	86.9	4.3	0.88	33.2	7.04
Barut 2005	39.4	27.6	84.4	4.2	0.87	28.8	5.3	40.6	27.8	83.6	4.6	0.87	25.0	6.7
Nazilli 303	38.8	27.7	84.6	4.6	0.89	30.5	4.5	39.8	28.3	82.3	4.6	0.87	28.3	6.5
Siokra 1/4	38.6	30.0	86.1	4.8	0.89	34.7	5.2	38.2	30.1	86.1	4.9	0.87	33.1	7.0
YB289	40.2	28.8	83.6	4.5	0.88	32.5	5.3	39.4	29.0	85.0	4.5	0.86	31.4	7.6
STV 474	40.3	28.5	83.0	4.7	0.89	32.6	4.9	41.2	28.8	84.1	4.9	0.87	27.4	7.2
Fantom	36.1	27.5	85.3	4.7	0.89	35.9	5.0	36.8	27.4	81.4	4.1	0.85	27.0	7.3
Famosa	37.9	28.5	83.4	5.5	0.91	34.4	4.6	37.8	28.2	83.9	5.5	0.89	29.2	6.4
TMK 122	41.8	30.5	85.6	5.7	0.9	32.0	6.2	41.2	28.1	84.9	4.5	0.85	27.0	8.1
ADN 710	40.6	28.0	84.4	4.1	0.87	29.4	4.5	39.0	30.4	85.3	4.6	0.87	33.0	6.1
TMN 16	39.6	30.6	85.0	4.5	0.88	30.8	4.8	40.9	29.7	85.2	4.6	0.86	30.0	7.3
TMS 108/2	41.4	29.6	85.3	4.9	0.89	36.5	5.0	42.3	28.8	84.3	5.3	0.89	30.8	6.5
ADN 712	38.9	28.2	84.1	3.3	0.85	33.1	5.6	40.4	27.3	84.3	4.4	0.86	30.7	7.6
TMN 199	40.2	29.9	86.1	5.4	0.91	37.1	4.5	41.0	26.9	82.7	5.3	0.88	22.3	6.8
BEREN	38.2	28.4	82.5	4.2	0.87	30.7	4.5	39.8	30.4	84.5	3.5	0.84	31.4	6.5
Sarı Gelin	38.3	23.1	81.6	4.5	0.87	22.2	5.1	41.3	24.8	79.9	3.8	0.84	21.1	6.9

Table 4.9. Continue

Genotype	**GOT %**	**FL**	**UI**	**FF**	**MAT**	**STR**	**FE**	**GOT %**	**FL**	**UI**	**FF**	**MAT**	**STR**	**FE**
Nihal	39.6	27.5	82.5	4.1	0.87	28.6	4.7	37.2	26.4	81.1	4.1	0.85	27.8	6.9
Gelincik	38.1	23.2	82.4	4.9	0.88	22.9	5.7	39.8	22.8	80.8	4.5	0.86	20.9	7
TMN 18	38.7	31.2	87.2	4.2	0.87	34.4	5.2	37.9	29.5	83.8	4.5	0.86	28.1	7.1
ADN 413	40.1	28.3	85.4	4.5	0.88	34.1	5.0	39.7	27.2	82.7	4.2	0.85	28.1	7.4
Ozaltın 112	38.7	31.5	82.8	4.1	0.87	31.0	5.2	38.3	31.1	83	3.8	0.84	32.0	7.1
Ozaltın 404	32.7	31.6	85	4.0	0.88	34.8	3.8	36.8	31.2	84.2	4.2	0.87	33.4	4.6
Lodos	39.5	29.2	84.6	4.7	0.88	35.4	5.4	41.7	26.2	82.1	5.3	0.89	26.6	5.5
Flash	37.3	28.7	85.4	4.1	0.88	36.5	4.2	37.1	29.5	83.8	4.8	0.88	35.4	6.5
Carisma	39.6	29.6	83.9	4.5	0.87	30.9	5.7	40.8	29.3	83.5	4.8	0.86	30.5	8.1
Aksel	37.8	29.5	84.9	4.3	0.88	38.4	4.4	37.5	29.7	84.7	4.8	0.87	34.6	6.6
BA 440	44.6	26.6	82.9	5.1	0.89	34.4	5.7	44.4	27.4	84	4.6	0.86	35.3	8
BA 811	41.2	28.4	83.3	4.9	0.88	35.3	5.8	44.2	28.1	83	4.4	0.86	30.3	6.7
Lydia	39.1	28.4	85	4.2	0.87	37.4	5.0	44.0	28.2	80.8	4.6	0.88	37.7	5.6
PG 2018	41.2	27.5	82.7	4.7	0.89	33.5	4.3	42.8	25.0	82.4	5.2	0.89	26.0	5.7
Julia	39.6	28.5	82.7	4.3	0.88	35.1	3.8	39.3	29.2	83.3	4.4	0.87	31.2	5.7
Claudia	42.6	29.9	84.4	4.9	0.89	33.9	5.1	42.0	31.1	83.9	4.3	0.87	28.8	5.6
Carla	46.2	29.4	84.1	4.3	0.88	34.9	4.6	40.4	29.7	84	4.1	0.86	28.5	6.1
Candia	42.7	29.9	85.4	4.6	0.88	37.8	5.3	41.9	30.6	86.6	4.2	0.85	32.5	7.6
Gloria	39.3	29.2	85.3	4.4	0.88	40.5	4.5	43.1	29.6	82.7	4.3	0.86	32.6	6.2
Means	37.0	28.3	83.3	4.7	0.88	31.9	4.9	37.5	29.0	83.6	4.3	0.86	30.28	6.2
BA119	40.9	28.4	84.5	4.9	0.89	33.5	5.6	40.8	28.3	84.2	4.0	0.85	29.9	7.03
STV468	41.4	28.2	85/0	5.1	0.88	31.9	5.6	41.2	28.3	84.8	4.4	0.85	30.3	7.33
TEX	41.2	29.1	84.2	4.8	0.88	34.0	5.0	41.3	30.8	84.5	4.2	0.86	32.1	5.96

GOT (%): Ginning outturn; FL: Fiber length (mm); UIN: Uniformity Index (%); FF: Fiber fineness (µg $inch^{-1}$); STR: Strength (g tex^{-1}); MAT: Maturity (ratio); FE: Fiber elongation (%).

4.1.3.3.6. Strength (g tex^{-1})

Mean values ranged from 21.6 g tex^{-1} to 44.6 g tex^{-1} as compared to checks GW-TEX, BA119 and STV468 had 33.6 g tex^{-1}, 31.6 g tex^{-1} & 31.1 g tex^{-1} , respectively (Table 4.9). Delcerro had highest strength 44.6 g tex^{-1} followed by Menderes 2005 with 39.5 g tex^{-1} while Seri Gelin had the lowest 21.6 g tex^{-1}. The phenotypic data of germplasm was divided into different groups according to cotton standards (Cotton incorporated). The categorization of genotypes showed diversity of fiber strength as very strong included 67.0% genotypes while 21.8% genotypes of total collection had more strength g tex^{-1} as compared to superior check GW-Tex with 33.1 g tex^{-1} (Figure 4.33). Asymetrical distribution was found in genotypes using means (Figure 4.34).

Strength is of vital importance from industry perspectives as it is directly involved for yarn firmness. If the fiber is having greater strength, then it can resist the power during spinning and will result in quality yarn. Moreover, it has been observed that strength had high heritability and the environment had no effect on the genotypes which confirmed the presence of more influence of genetical effects. Our observations are in accordance to Zeng et al., 2011; Karademir et al., 2010; Ilci et al., 2014) who observed same pattern for fiber strength among genotypes.

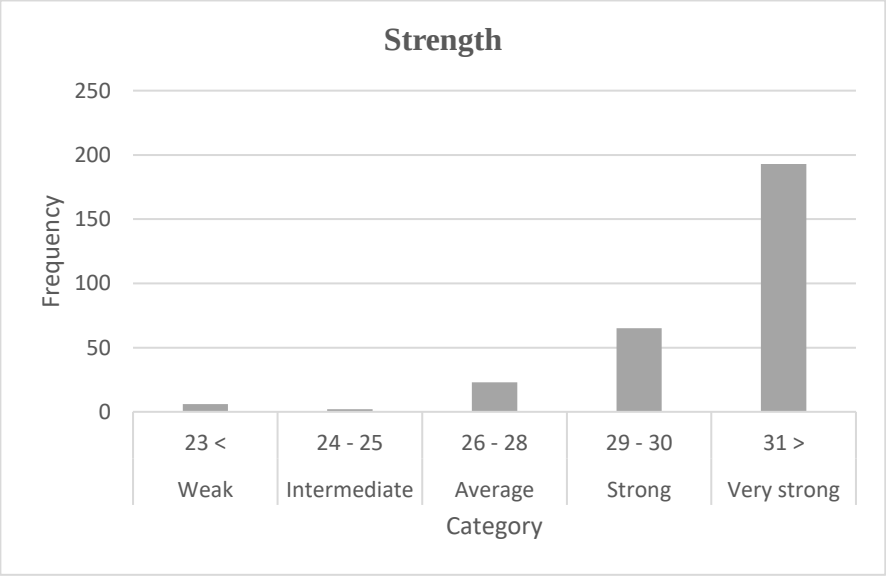

Figure 4.33. Combined strength classification

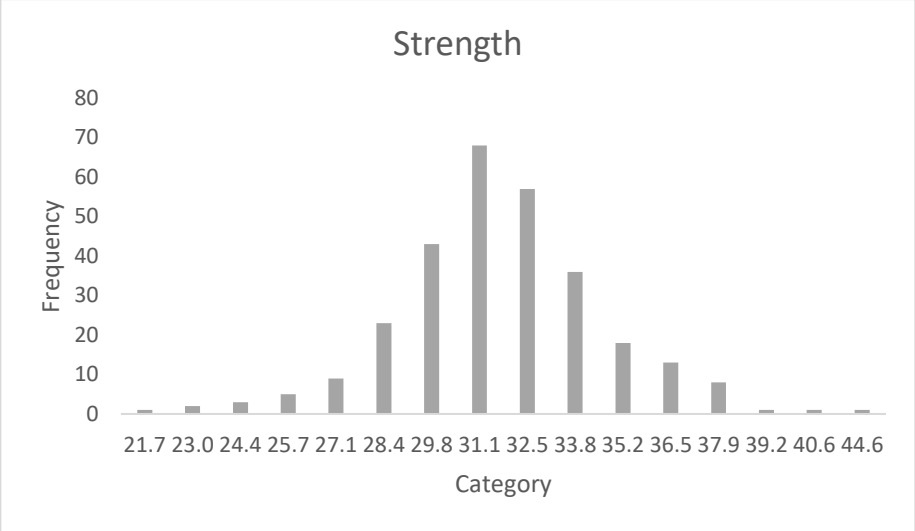

Figure 4.34. Strength frquency distribution

4.1.3.3.7. Elongation (%)

The genotypes varied from 3.7% to 7.7% on mean basis as compared to checks 5.4%, 6.3% and 6.4% GW-Tex, BA119 and STV468 respectively while NSCH-777 had maximum 7.8% fiber elongation (Table 4.9). Frequency curves of this trait exhibited normal distribution. It is the property of substance that whenever force is applied then its texture is changed but cotton is having unique feature. Elongation regulates the power to split fiber and is involved in the production of garments with more flexibility and to resist load and should restore its texture. From processing perspectives "work-to-break" is an essential feature as both strength and elongation are associated with firmness. Cotton Incorporated (2012) assigned five different groups to fiber elongation designated as very low to very high ranged from less than 5% to more than 7.6% (Figure 4.35). Frequency curves were developed using means and wider variation found in genotypes (Figure 4.36).

It has been revealed that elongation contribute a lot to yarn manufacturing and different values for this trait has been determined. Fiber elongation found to be moderately high heritable (53.8%) which showed the presence of additive effects which was same to findings of Dahiya et al., 2014; Ahsan et al., 2015; Saho et al., 2016 who also observed same variation for elongation. The genotypes with more elongation have more valuable fabrics as there is no deformity; so present variation will be a good source for fiber quality improvement. Our findings are in accordance to Zulkadir and Bolek, (2014) who observed wide variation among germplasm entries.

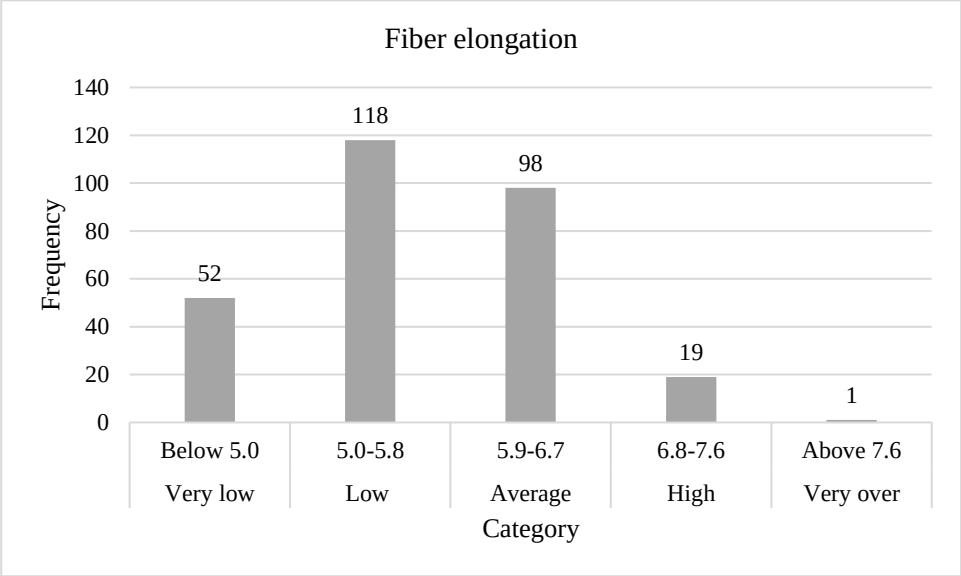

Figure 4.35. Combined elongation classification

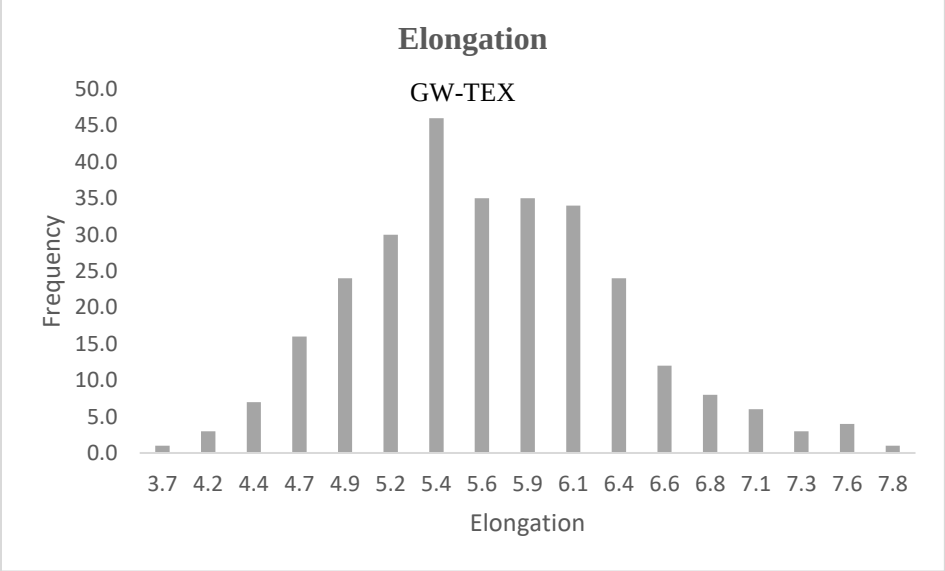

Figure 4.36. Elongation frequency distribution

Heritability estimates should be used with care for any breeding purpose as these are highly affected by the climatic conditions (Falconer and Mackey, 1996). Paterson et al. (2003) showed that fiber quality contributing parameters can be analyzed using QTL analysis as being highly heritable. As most of the parameters in the current studies are highly heritable like ginning outturn, micronaire, strength and length with 64.9, 91.2, 65.18 and 49.7 respectively (Table 4.8) so it is concluded that germplasm can be used for broadening

of genetic base for fiber quality improvement. Our results in accordance to (Qin et al., 2015; Shao et al., 2016).

4.1.4. Combined correlation

The means were pooled of both locations and association among different fiber traits were determined via Pearson correlation coefficient (Table 4.10). Ginning out turn showed positive and significant associations with fiber length and uniformity index. While positive non-significant association observed between GOT and fineness, strength and elongation. Fiber length had highly significant positive correlation with strength (0.457) and uniformity index (0.253) but negative among micronaire (-0.361) and maturity with non-significance while negative significant with elongation. Uniformity index highly significantly (0.206) associated with strength and elongation while negatively non-significant related to maturity. Fiber fineness showed highly significant negative relation (-0.140) with elongation while non-significant indirect with strength and significant positive with maturity ratio. Maturity ratio related positively and significantly with strength (0.099) and negative with elongation with highly significance (-0.466). Fiber elongation was found negatively related to strength with significance (-0.212).

Table 4.10. Correlation for fiber quality traits

	GOT	FL	UI	FF	MAT	SR	FE
GOT	1						
FL	0.091*	1					
UI	0.120**	0.253**	1				
FF	0.008	-0.194**	0.005	1			
MAT	-0.013	-0.061	-0.045	0.502**	1		
SR	0.064	0.457**	0.220**	-0.063	0.099*	1	
FE	0.048	-0.1104*	*0.103	-0.140**	-0.466**	-0.212**	1

GOT: Ginning outturn (%); FL: Fiber length (mm); UI: Uniformity Index (%); FF: Fiber fineness (µg $inch^{-1}$); STR: strength (g tex^{-1}); MT: Maturity (ratio); FE: Fiber elongation (%).

The crop scientists should be aware about the impact of ginning out turn on yield when strategy is made for boosting yield using this parameter for selection. The goal of germplasm studies was to select genotypes with good ginning outturn and essential fiber traits. It has been reported that refinement of GOT% has direct association with uniformity and fiber length (Zeng et al., 2009). Zulkadir and Bolek, 2014 also found positive association among ginning outturn and micronaire. Zeng and Meredith, (2009); Liu et al. (2011)

witnessed that GOT is diretcly related to fiber strength and fineness with significance and same relation found in current study but non-significance. This kind of behavior might be due to inclusion of genes with more than on effects (Meredith, 1984; Smith and Coyle, 1997). While uniformity was found to be positively related with GOT% and it is an agreement to (Wang et al., 2013). Meredith, 1977; Meredith and Bridge, 1971 has revealed that yield components and fiber traits can be refined using proper breeding measures. The crop scientists should screen all characters together as using recurrent selection, ginning outturn increased, micronaire and lint production boosted (Miller and Rawlings, 1967). There was highly significant positive association among fiber length and strength while inverse relation found with micronaire. Our observations are same to Abdurakhmonov et al., (2008) who also found same association in a germplasm screening of world collection among between fiber length to strength and elongation. In addition, uniformity index was significantly and positively correlated to fiber strength which was like to (Abdurakhmonov et al., 2008). Uniformity had positive association and significant relation with elongation which is according to (Karademir et al., 2010). Kardemir et al., (2010); Zulkadir and Bolek (2014) had reported negative with non-significance association of micronaire with strength and our observations are also similar. Shiva et al. (2017) observed negative association among micronaire and elongation as in this study. As far as association of strength and elongation; it was negative and highly significant which was like to (Percy et al., 2006). Morover, maturity is a valuable trait from fiber perspectives as it determines the diameter secondary wall thinking. As it has been reported earlier by Zeng et al., (2009) that maturity ratio is directly related with strength and indirectly to elongation; we also found same relationship. It was shown from association analysis that strength and elongation are indirectly associated with each other. Association analysis involve linkage disequilibrium and multiple effects of gene. The effect of gene remains among the permanent populations and will not be disturbed which result in stable association. Earlier opposite association has been reported among ginning outturn and fiber length and micronaire while direct association between ginning outturn and strength and micronaire (Ulloa et al., 2006; Percy et al., 2006). As a result, cotton breeders have a big task to refine fiber quality without compromising yield.

4.1.5. Conclusion

The success of any breeding program depends upon extent of genetic variation and the approach utilized for determining such diversity. Likewise, variation was observed in a

global germplasm of upland cotton. The variability on standard deviation basis; varied from 0.01-4.22 being high for ginning outturn followed by fiber strength, length, with values of 4.22, 2.91 and 1.92 respectively. Moreover, about same pattern was found for these traits at each location also while coefficient of variability fluctuated from 1.5-12.4% on combined basis. Fiber elongation had maximum 12.4% while minimum (1.5%) for maturity ratio.

Analysis of variance revealed highly significance among genotypes for all traits at different locations, while interactions among genotype and location were highly significant for ginning outturn and micronaire. Genotypes had wider variability for fiber traits as ginning outturn ranged from 4.1 to 46.1%, fiber length (21.9 to 35.6mm), uniformity index (78.4 to 87.2%), micronaire (2.8 to 5.9 µg $inch^{-1}$), maturity ratio (0.8 to 0.9), strength (21.6 to 44.6 $gtex^{-1}$) and elongation (3.7 to 7.7%).

Morover genotypes were categorized according to fiber traits. Fiber length had five categories but most of genotypes were classified in long-staple; 51% of genotypes included in high uniformity index; 69.2% genotypes had medium micronaire; almost all genotypes were mature, 67% genotypes had very strong strength and 47.6% had fiber elongation in low category. The variation among traits based on multi-environmental trials showed that considerable amount of variation is prevailing in the genepool which can be used for ascertaining whether these are due to variants or from hybridization with superior parents and acquisition of QTLs.

Association analysis showed considerable relation among fiber quality traits. Fiber length was positively and significantly related with strength (r=0.457**) and uniformity (r=0.253**) while negatively correlated with micronaire (0.194**). Uniformity index was positively associated with strength (r=0.220**) and micronaire significanlty with maturity ratio (r=0.502**). Morover strength found to have negative association with elongation (r=-0.212) and maturity also found to be negatively associated with elongation (r=-0.466**).

Phenotypic screening showed that considerable variation is present among germplasm entries for refinement of trait in upland cotton.

It was concluded that some genotypes can be used as potential parents in variety development like AB80, BA440, Carla for increasing lint percentage; YB-230, Flora, SPEARS3(67) and PI528875 for fiber length; Delcerro, Menderes for fiber strength and NSCH-777 for increasing fiber elongation. As a whole Acala Maxa, Nazilli342, Acala

Prema, NP Ozbek100, YB242, GSN22, STV373, Flash, Julia, Claudia, Candia had multiple desired fiber traits.

4.2. Association mapping using genotyping by sequencing

Molecular breeding is on fast track due to availability of enormous robust markers. Thanks to advances in sequencing, it is has become feasible to transfer traits of interest in the genotypes in a short time which contribute to increase efficiency of variety development. Highly saturated map and higher variation for intended character is achieved via linkage disequilibrium mapping in contrast to family-based mapping (Yu and Buckler, 2006). LD mapping utilizes primitive reproducibility prevailing in germplasm collections while genetic mapping involves designed populations like F_2, BC or RIL. Genotyping by sequencing (GBS) is a reliable high-throughput procedure for the analyzing genetic variation at the whole-genome level using association mapping. We describe the investigation of SNPs detected in a germplasm panel of 90 genotypes of global level using Illumnia GBS platform.

4.2.1.1. DNA isolation

4.2.1.1.1. Leaves grinding and DNA extraction

DNA extracted from fresh leaves of association panel each entry stored at -80^{0}C according to (Zhang & Stewart, 2000). The samples were cleaned, screened via electrophorasis under UV light, quantified using spectrophoto meter on 260/280 wave lentgh for genomic DNA. DNA samples were diluted to 50µl.

4.2.1.2. Sequencing of libraries

4.2.1.2.1. Processing raw sequences from illumnia

The samples sequenced in Illumina Hiseq2000 by BGI were used in Trait Analysis by Association, Evolution and Linkage (TASSEL) v.5.2 for association analysis.

4.2.1.2.2. Filtering of SNPs

GBS analysis was performed according to Bejing Genomic Institute protocol (http://www.bioinformatics.bgi.cnoorg/projects/fastqc/). As a whole the platform produced 10135 SNPs; after filtering at 0.05 MAF resulted in high quality 4730 SNPS.

4.2.1.2.3. Genotyping for association mapping

The goal was to evolve informative SNPs in an association panel of upland cotton germplasm with diverse collections. 10135 SNPs develpoed from GBS were used for filteration in TASSEL v.5.2 (Maize genetics) with MAF <0.05. Finally 4730 SNPs were selected for further analysis. As association mapping is highly influenced by frequency of markers, number of individuals in a population and heredity pattern of the required trait. Therefore, marker frequency is of vital value for ascertaining scarce mutations in the genome. GBS provides a way for genotyping using enormous SNPs i.e about higher than a million (Elshire et al., 2011) and fine mapping in the genome. Poland et al., (2012); Huang et al., (2014) showed that numerous SNPs are produced with GBS but with more percentage of missing values. Moreover, it has been studied that such data can evolve spurious SNPs Arnold et al., (2013) and it should be solved. Accordingly, SNPs were determined after deleting missing data. The number of SNPs were higher with alignment and it was in accordance to Islam et al., (2015) and also similar to (Torkamaneh et al., 2016). Further, association among marker and trait is affected by number of genotypes in the mapping population.

4.2.1.2.4. Population structure

The knowledge about members of the population and their evolutionary relationship plays an important part for association analysis (Pritchard et al., 2002; Yu et al., 2006; Zhao et al., 2007). Differences between alleles matters a lot in population organization for elaborating the genetic variants which is highly influenced by topographical origin and admixtures. Bayesian cluster (model-based) program STRUCTURE (v.2.3.4); Pritchard et al., (2000) used for the assessment of population stratification in upland cotton and to determine groups of accessions based on SNP markers distributed among all loci of *G. hirsutum*. Structure matrix (Q) for populations were calculated using K=2-10 with burn-in-time of 1000-10000 permutations. Germplasm entries showed wider variation based on K-means using ADMIXTURE model in STRUCTURE.

The population was differentiated into definite clusters (K=6). As a whole, the ADMIXTURE analysis with STRUCTURE produced distinct differentiation among upland cotton and greater genetic differences with considerable homoplasy or recombination among the alleles. It was found that geographic conditions have been involved in gene transfer Zhao

et al., (2014); Nie et al., (2016). Abdurakhmonov et al. (2009) differentiated genotypes of upland cotton into precise groups according to their place of origin utilizing Structure like Latin America, Australia and Uzbekistan. Population structure is normally characterized regarding extent of allele, density and difference of alleles at specific gene or locus. Within a population, reproducibility occurs due to presence of different alleles and their density. In our study, high heterozygosity was observed among germplasm collections of *G. hirsutum*.

4.2.1.2.5. Kinship

Heredity pattern and compound organization are usually observed in germplasm collections. Recombination and mutations are associated for the development of relative proportion of alleles in these individuals. Moreover, phenotypic character variation may be involved for the disparity between populations. Likewise, coefficient of kinship matrix (K) was determined. Morover, negative values were assumed as 0 according to (Mei et al., 2013). The kinship ranged from 0 to 1 (Figure 4.37). Kinship coefficient found 69.0% near to 0 but association inside the entries found to fluctuate as 11.1% kinship for 0.01 to 0.02. 16.1% had value of 0.02 to 1.0 while 3.2% showed varied degree of kinship coefficient.

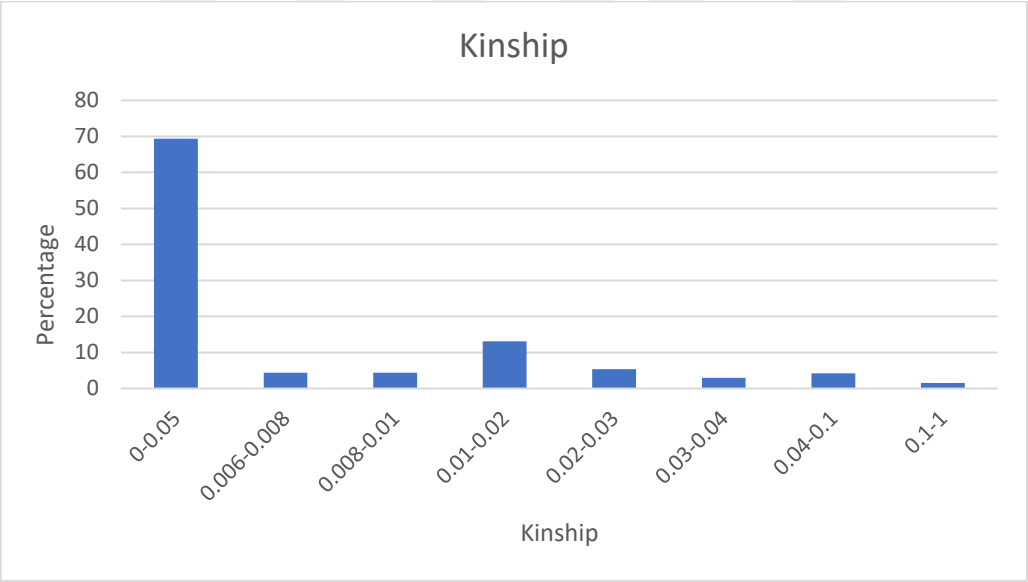

Figure 4.37. Kinship coefficient in germplasm

It showed that same parents have been used in the development of cultivars owing to their promising characters. The pattern of kinship is similar to the findings of Mei et al., (2013) who found 83% kinship value near to zero and 4.5% had varying percentage. It was also shown from the results that 47.3% kinship value was near to zero without considering

the substracted values which is in accordance to Abdurakhmonov et al., (2008) who argued that the germplasm collection are found to be derived from closely reltives. Iqbal et al., (2001) also speculated that most of the genotypes has been developed from the parents which had similar gentic make-up. The pattern of population stratification showed that it will be helpful to analyze material for marker-trait associations.

4.2.1.2.6. Linkage disequilibrium and LD decay

TASSEL 5.2.2 was used for the determination of linkage disequilibrium on the basis of coefficient of determination or marker R_{seq}. As a whole 259561 comparisons were observed in an association panel through screening of 4730 SNPs, only 3.7 and 9.3% found highly significant at $P<0.001$ and $P<0.01$. While 18.5% at $r^2 \geq 0.1$ and 14.8% on $r^2 \geq 0.2$. This showed that 14.8% markers found in 6-8cM and 18.5% in the genetic map distance of 10cM. Abdurakhmonov et al., (2009) found that LD decay lies in the range of 50 cM among the microsatellites but Witt and Buckler, (2003) reported that at $r^2>0.1$ it diminishes within map distance of 25 cM. This showed that linkage is involved in the major part of LD. Pairwise LD blocks were developed using r^2 values which showed considerable LD between markers. These markers will be helpful for ascertaining quantitaive traits (Figure 4.38).

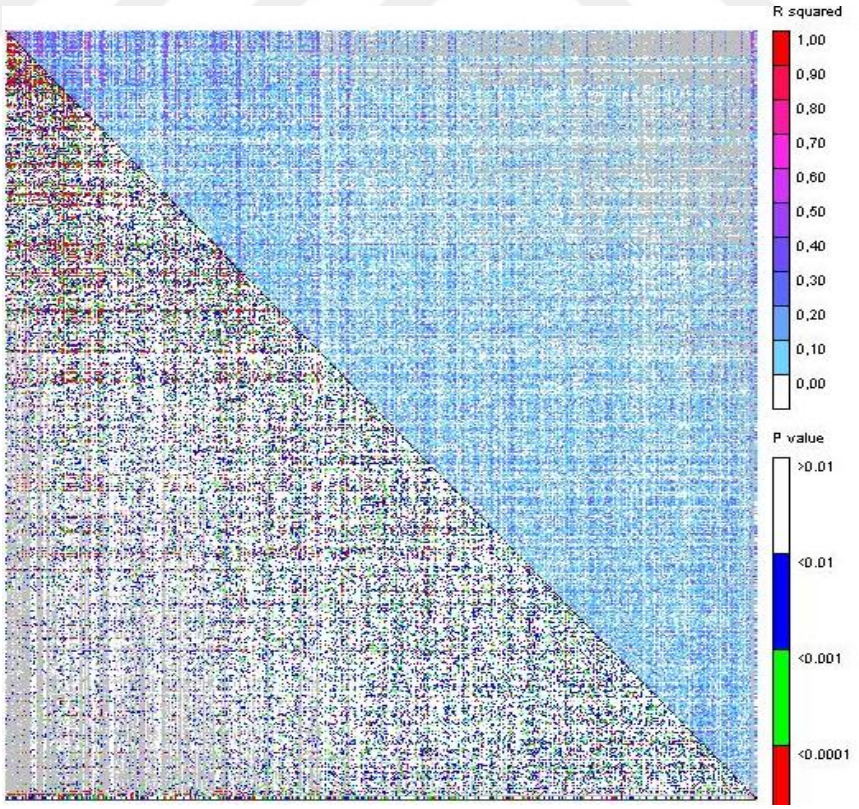

Figure 4.38. LD decay in germplasm

"r^2" values were plotted on Y-axis while markers on X-axis for observing LD pattern among chromosomes. D' will =1.0 when there is no reproducibility between markers, but r^2 based on gene frequency of both markers. As the length among couple of SNPs raised, the power and extent of LD decreased drastically, which confirmed classic genetic variants (Figure 4.39).

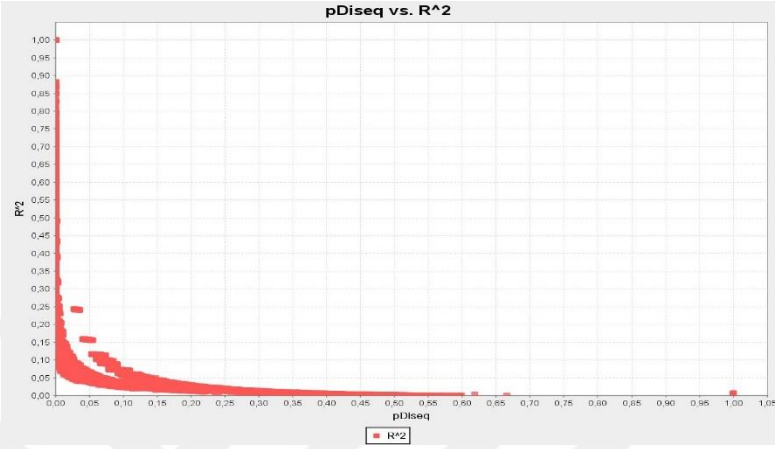

Figure 4.39. LD Scatter diagram. Below r^2 = 0.1 LD decay is determined.

Nonrandom association of alleles at different loci is the backbone of association mapping (Flint-Garcia et al., 2003). Several association were observed on the basis pairwise LD in every locus particularly in locus Chr. 19 (Figure 4.39) with more SNPs for fiber traits. Chr19 had SNPs connected to multiple traits fiber length, uniformity, strength. It has been reported that LD decay vary according to crop species. Owing to which it is assumed that allelic variation within every combined-loci is the influence of LD. The extra QTLs related to traits found due to the powerful LD extent among the genetic variants.

For the execution of association mapping it is compulsory to calculate LD. 14.8% SNPs showed significance at r^2>0.2. Variation in LD have been described in number of species containing cotton (Adurakhmonov et al., 2008, 2009; Saeed et al., 2014; Iqbal and Rahman, 2017). Due to intense selection intensity for maximizing the required traits which forced the addition of genes in the germplasm entries; developed condensed LD.

4.2.1.2.7. Association analysis

Different models were used for determining marker-trait associations General Linear Model ((GLM); The naive model, and Mixed Linear Model (MLM) (Q+K). The models were compared and the most appropriate model was selected for association analysis.

4.2.1.2.8. GLM using TASSEL

As majority of the accessions had very low kinship coefficient; in order to overcome this association analysis was peformed. Graut and Long, (2003), found that not only false association are produced but extent and pattern of genetic variation is affected due to organization of population and kinship values. For overcoming statistical type I problems, TASSEL executed GLM model according to Bradbury et al. (2007) using population matrix "Q" for overcoming false marker-trait pairwise differentiation in GLM. 5% minor allele frequency was used to obtain reliable associations. The association analysis conducted using least mean squares among germplasm entries with 4730 SNPs. As a whole 33111 associations were found; out of which 1.2, 2.4 and 5.6% were highly significant at $p \leq 0.001$, $p \leq 0.01$ and $p \leq 0.05$ respectively. Spurious associations were observed as expected and quantile-quantile curves found for fiber quality traits (Figure 4.40).

The observations were analyzed with the findings of (Abdurakhmonov et al., 2008; Mei et al. 2013). 332 marker-trait associations found to be moderately-strong to very strong. Highly valuable SNPs related to different fiber traits shown in (Table 4.11).

We used "r^2" as a parameter for determining association in-contrast to coefficient of LD (D') as it is more suitable for analysis in population and is affected by permanant alteration of DNA sequence and reproduciability in the germplasm collections. Morover, SNPs were identified using probability i.e -log10(Pvalue)$\geq$3.0 as Manhutton plots and 93 SNPs found to be related with fiber length (Figure 4.41) including the most significant A9218, A8810, A9003, A9664, A9279, A7094, A8519, A8065, A8007, A9388, A8449, A8792, A8153 and eight SNPs were observed for fiber length without any location on genome. While chromosome 19 had seven SNPs with very good probaility like A7094 with probability of 0.00001 and "r^2" 0.1745 and A9388 had 0.000001 and 0.2508 respectively. These very high significant SNPs were identified according using -log10(P-value) as described by (Islam et al., 2016). They assumed that SNPs selected using high probaility will be highly authentic as such QTLs can be detected in a very short distance among the loci during association mapping at whole genome. These association were very useful and observed in MLM.

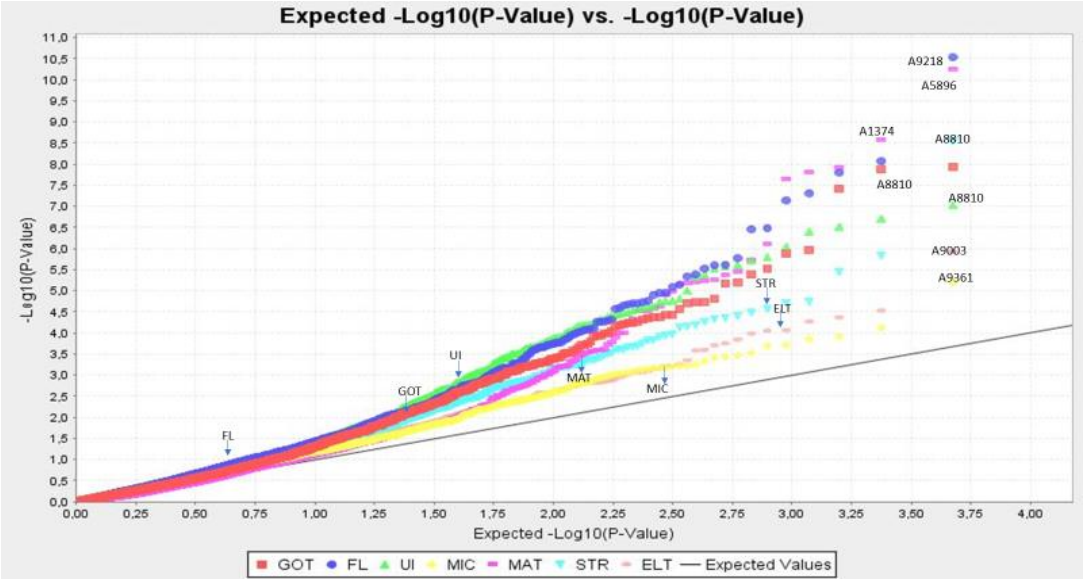

Figure 4.40. Q-Q Plots for fiber traits using GLM

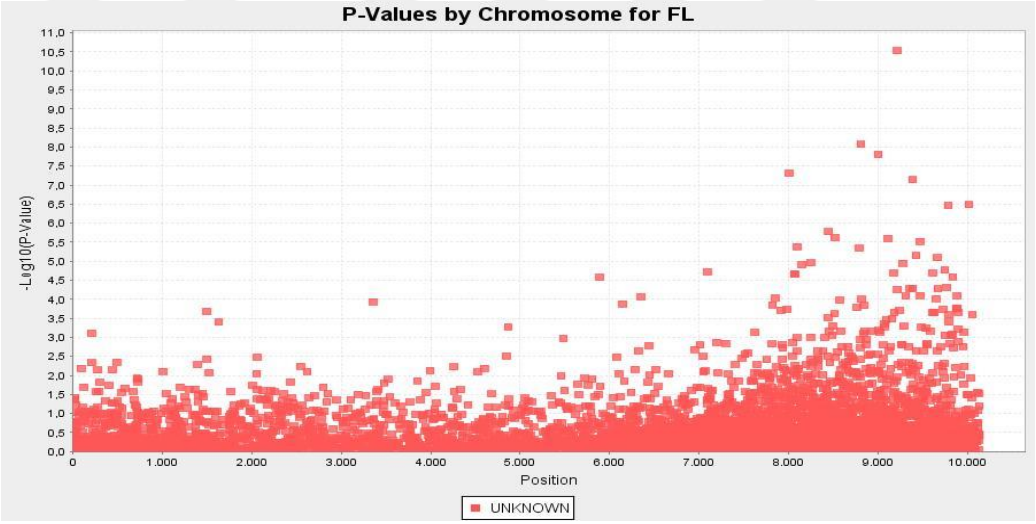

Figure 4.41. Manhutton Plot for fiber length in GLM

There were 78 significant SNPs having -log10(P-value) greater than 3 (Figure 4.42) but the most significant at 0.0001 included A8810, A8098, A9078, A8850 with probability 0.00000013, 0.000006, 0.00001, and "r^2" of 0.349, 0.2479, 0.1766 and 0.175 respectively found for ginning outturn in GLM. It was also found that chromosome 19 had more desirable SNPs A8810, A8850, A9279, A9220 than other ones.

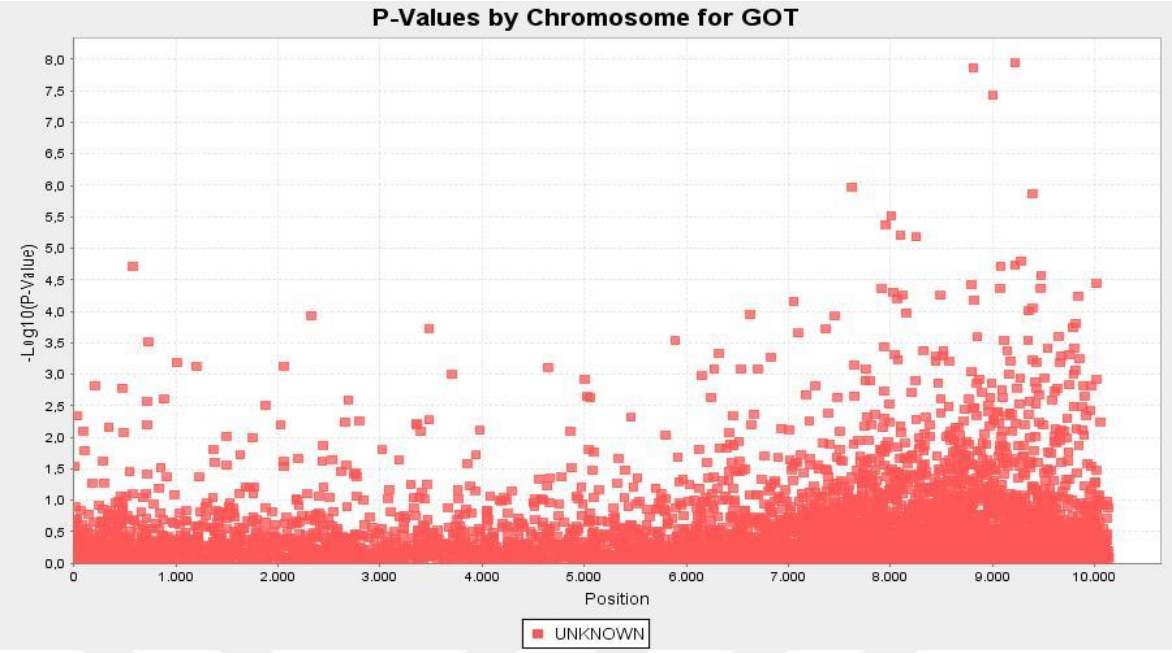

Figure 4.42. Manhutton Plot for Ginning outturn in GLM

A large number of SNPs for uniformity observed from GLM. The -log10 values ranged from 3.026 to 7.03. The highly significant markers include A9218, A9361, A8007, A8792, A6148, A9879, A8250 with -log10 values of 7.03, 6.522, 5.727, 5.790, 6.033, 5.376, 5.327 respectively (Figure 4.43). There were large number of associations but the verified markers are shown in Table (Table 4.11).

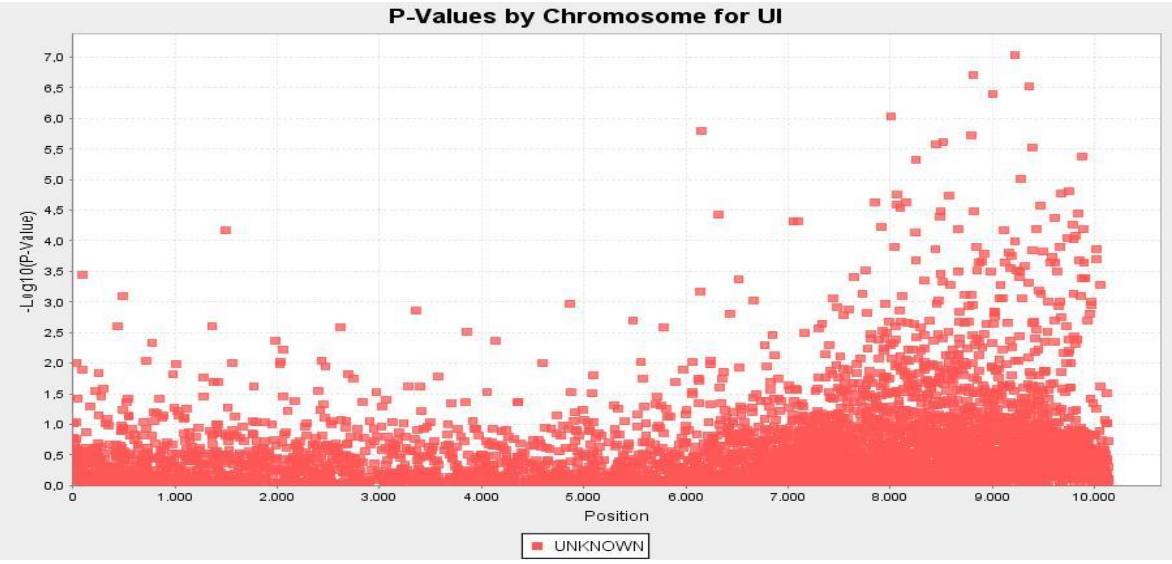

Figure 4.43. Manhutton plot for unifomity in GLM

As expected number of marker-trait association found for micronaire (Figure 4.44). The -log10 value varied from 3.016 to 5.205. A8573, A6860 found to highly informative

markers with 0.0001 and 0.0009 probability and "r^2" 0.1577 and 0.195 respectively. The other significant SNPs include A6739, A8320 (Table 4.11).

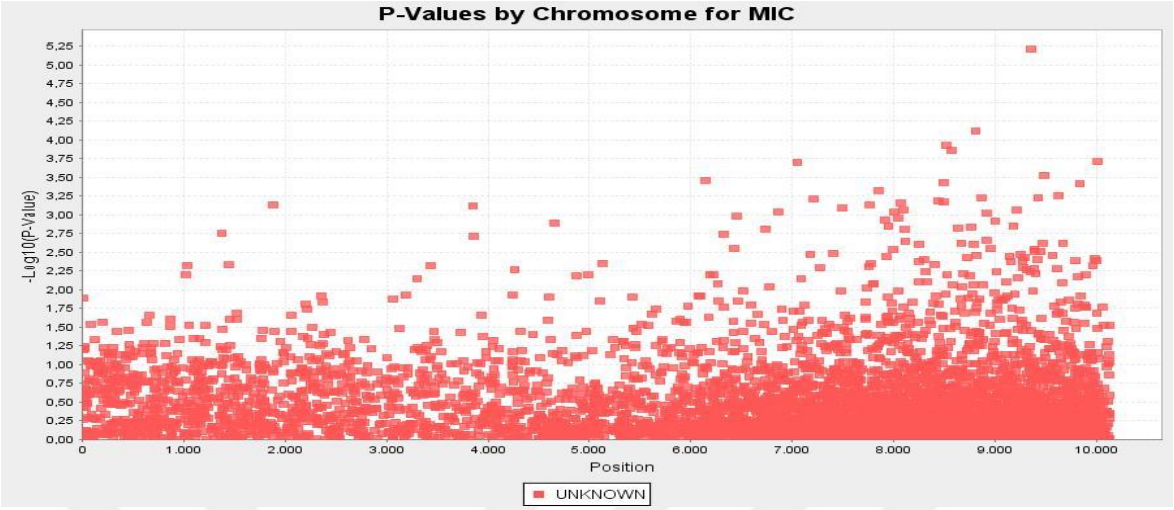

Figure 4.44. Manhutton plot for micronaire in GLM

Highly significant SNPs associated with maturity found on chromosome 8, 9, 15, 21, 22 with -log10(p-value) varied from 3.216 to 10.261. A5896 had probability of 5.4E+9 with "r^2" of 0.244 can be novel marker as no position was found (Figure 4.45).

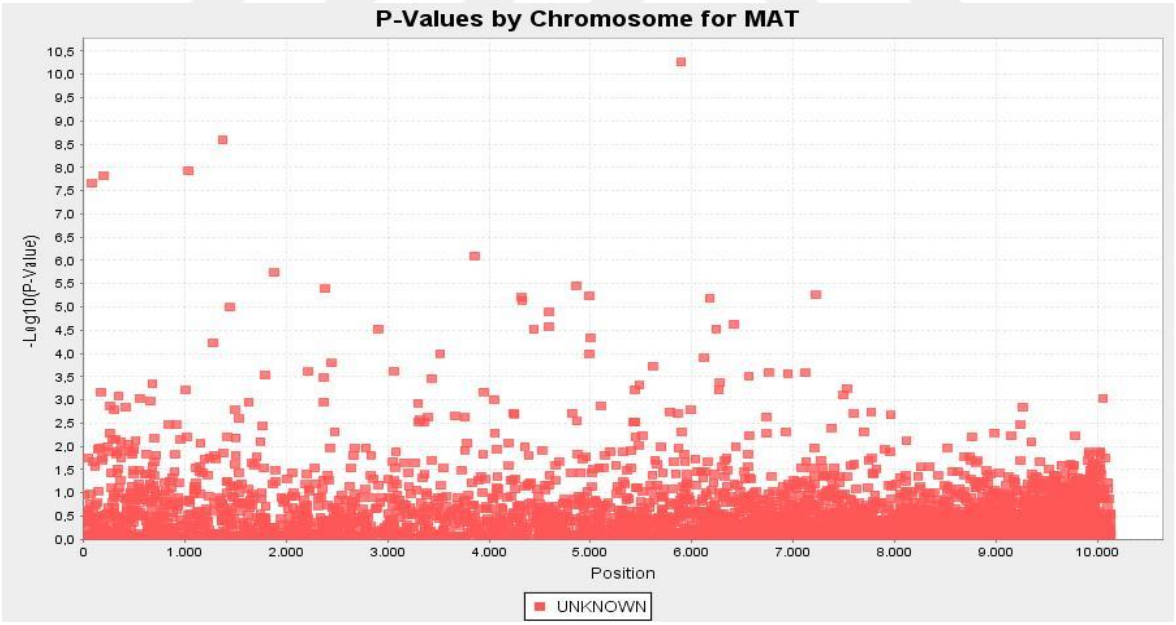

Figure 4.45. Manhutton plot for maturity in GLM

42 significant (P<0.01) SNPs produced in association analysis using GLM. The most significant SNPs include A8810 and A9279 with probability of 0.0000000029, 0.000019

with "r^2" 0.2883 and 0.201 respectivley while -log10(P-value) 8.537, 4.705 alternatively (Figure 4.46).

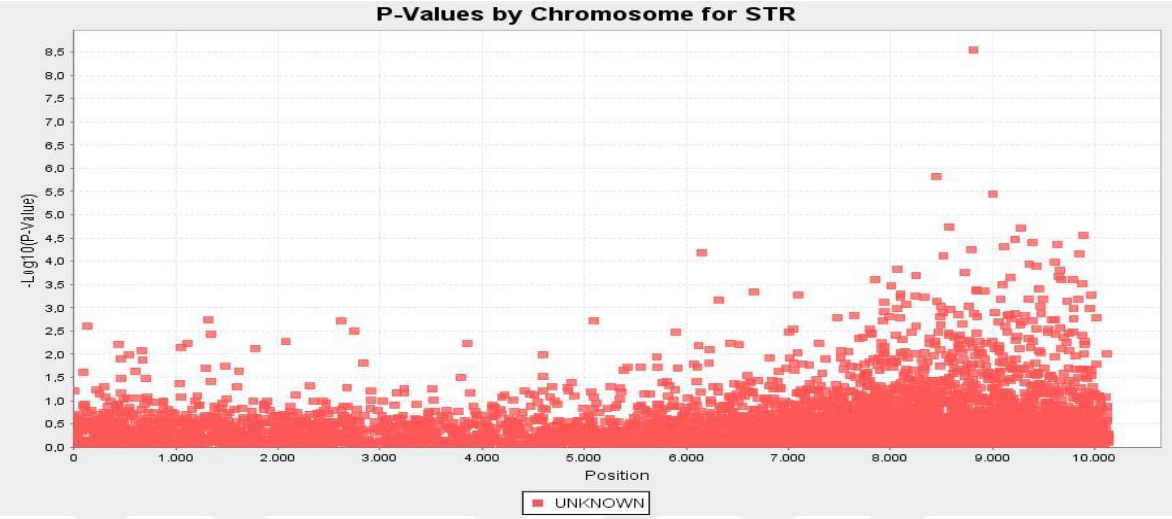

Figure 4.46. Manhutton plot for strength in GLM

A9003, A9840, A9078 were the highly significant SNPs found on Chromosome 20, 9, 17 for fiber elongation (Figure 4.47). The probability and "r^2" were found 0.000001, 0.00004, 0.0001 and 0.214, 0.172, 0.134 respectively. QTLs validation will be confirmed by MLM as Islam et al., (2016) reported that these QTLs were found on Chr-12 and Chr-25 qFE-Chr-12 and qFE-Chr-25.

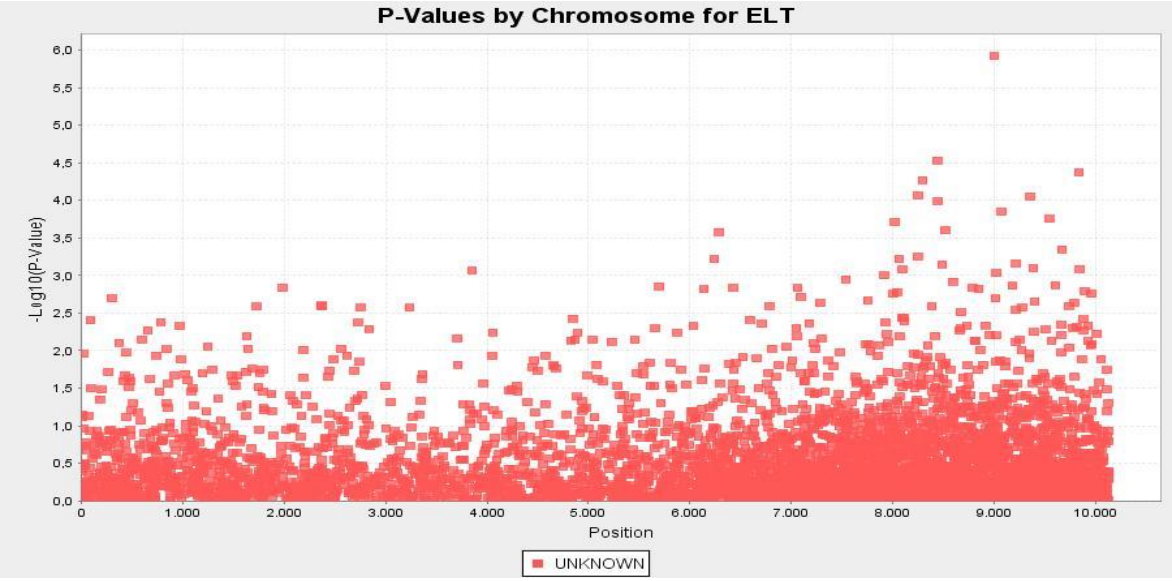

Figure 4.47. Manhutton plot for strength in GLM

It was found that marker probability values are lower in GLM for majority of the markers than MLM which is in accordance to (Yu et al. 2001; Iqbal and Rahman, 2017). It was observed that the some of the SNPs were common for different traits like A8810 was associated with fiber strength, uniformity index and ginning outturn. It has been reported in literature that reliable association mapping can be accomplished with limited amount of markers as compared to the ones required mostly with medium-significance of LD blocks (Abdurakhmonov et al., 2008). It was revealed from germplasm population stratification that it was derived from different ecological areas as population was partitioned into six groups showing the value of relatedness and organization of individuals. Different procedures has been developed for observing such relationship like structure-based association (Pritchard et al. 2000), regression analysis (Setakis et al. 2006) and model based association involving kinship and population matrix (Braudbury et al., 2000). As false associations are common in population based model so these were compared using mixed linear model.

Table 4.11. Significant associations of SNP loci with fiber traits identified by GLM

Trait	**Marker**	**Position**	**Marker Probab.**	**R^2**	**-LOG10 (P-VALUE)**	**Effect**
FL	A9428	1	0,0000071	0,2551	5.147	1,38E-14
FL	A9472	5	0,0000029	0,2306	5.524	1,40E-14
FL	A9218	8	2.00E-11	0,41133	10.528	3.95E-14
FL	A9840	9	0,000025	0,23816	4.768	-3,47E-13
FL	A8938	9	0,000687	0,15248	3.163	4,89E-13
FL	A8250	11	0,000011	0,2003	4.954	2,64E-13
FL	A9003	12	1,5E-08	0,30593	7.807	3.32E-13
FL	A8453	12	0,00068	0,15184		4,00E-14
FL	A10019	14	0,000036	0,18598	4.436	-1,11E-13
FL	A9474	14	0,0000797	0,18391		-5,13E-14
FL	A8388	15	0,00232	0,12177		4,23E-14
FL	A9664	16	0,0000081	0,22256	5.089	-1,82E-12
FL	A7297	18	0,00143	0,12694		8,63E-14
FL	A9279	19	0,0000112	0,2337	4.998	6,96E-13
FL	A8810	19	8.00E-09	0,30593	8.069	3.79E-13
FL	A7094	19	0,000019	0,17458	4.719	2,96E-14
FL	A9220	19	0,000055	0,15555	4,253	6,71E-14
FL	A8573	19	0,000105	0,1943	3.975	2,58E-14
FL	A7814	19	0,0015	0,10899		-3,97E-13
FL	A8065	21	0,000021	0,2072		-1,26E-13
FL	A8768	21	0,000165	0,17447	3.782	-2,64E-13
FL	A9631	21	0,000218	0,14795	Mar.66	-2,75E-13
FL	A8519	22	0,0000024	0,29589	5.619	4,09E-13
FL	A8070	22	0,0000222	0,20007	4.654	3,84E-14

Table 4.11. Continue

Trait	Marker	Position	Marker Probab.	R^2	-LOG10 (P-value)	Effect
FL	A8819	22	0,0000991	0,17056	4.004	-1,90E-15
FL	A9361	23	0,0000527	0,16846	4.294	-9,00E-13
FL	A9888	23	0,0000810	0,17638		-2,65E-13
FL	A8007	23	0,0000030	0,21588	5.519	1,97E-14
FL	A8751	26	0,0000913	0,10737		-5,21E-14
FL	A9158	26	0,0003267	0,15226	3,486	6,37E-14
FL	A9075	26	0,0005202	0,14386		-1,44E-13
FL	A7986	11	0,0001857	0,13704	3.731	-3,24E-14
FL	A8850	11	0,0006926	0,1558		2,40E-14
FL	A9388	NA	0,0000013	0,25089	5.867	-6,05E-13
FL	A8449	NA	0,0000016	0,29589	5.775	5,44E-14
FL	A8792	NA	0,0000045	0,23816	5.344	-2,22E-14
FL	A8153	NA	0,0000123	0,22812	4, 908	-8,47E-14
FL	A9177	NA	0,000029	0,23037	4.693	6,29E-14
FL	A8845	NA	0,000146	0,14961	3.834	-1,05E-13
FL	A9715	NA	0,000191	0,19711	3.717	
FL	A8871	NA	0,001140	0,09377		-8,92E-15
GOT	A9078	6	0,000019	0,17666	Nis.72	-4,68E-14
GOT	A9349	13	0,000099	0,19859	4.002	-7,05E-13
GOT	A9474	14	0,000027	0,1954	4.565	-5,50E-14
GOT	A8250	15	0,000006	0,23854	5.577	5,21E-13
GOT	A9347	18	0,000289	0,14825	3.539	-7,89E-13
GOT	A8810	19	1,354E-08	0,34902	7.868	-2,95E-13
GOT	A8850	19	0,0002565	0,17599	3.591	-2,91E-14
GOT	A9279	19	0,0000158	0,20908	4.Ağu	4,15E-13
GOT	A9220	19	0,0000184	0,18823	4.733	2,37E-14
GOT	A7365	12	0,0001922	0,26757	3.653	-1,31E-13
GOT	A9796	NA	0,0003841	0,13797	3.416	1,81E-13
MIC	A6739	2	0,00573	0,08667		3.20E-15
MIC	A8320	6	0,00573	0,08667		6,44E-14
MIC	A8573	19	0,0001401	0,15776	3.853	2,32E-14
MIC	A6267	21	0,00831	0,08179		8,31E-16
MIC	A6860	26	0,0009232	0,19503	3.035	-2,24E-15
MIC	A6739	2	0,00155	0,12172		3,20E+15
UI	A9145	2	0,00215	0,16322		4,89E-12
UI	A8810	19	1,946E-07	0,34377	6.711	-3,71E-12
UI	A8819	22	0,0000331	0,2688	Nis.48	2,77E-15
MAT	A5896	XM_01682182.1	5,4E-11	0,244	10,261	4,56E-15
MAT	A7223	8	0,0000055	0.15705	5.257	-1,07E+16
MAT	A5424	9	0,00299	0,10219		7,55E-15
MAT	A6418	15	0,0000237	0,15432	4.625	1,50E-15
MAT	A6267	21	0,0006084	0,12189	3.216	3,58E-15

Table 4.11. Continue

Trait	Marker	Position	Marker Probab.	R^2	-LOG10 (P-value)	Effect
MAT	A3301	22	0,0011800	0,11123		-1,31E-12
MAT	A5859	22	0,0019900	0,10257		-3,94E-16
MAT	A1278	NA	0,0000598	0,16721	4.223	1,07E-15
STR	A7935	9	0,0012300	0,13057		3,24E-15
STR	A8810	19	0,00000000290620	0,28837	8.537	-3,56E-13
STR	A9279	19	0,00001970900	0,20101	4.705	-4,01E-13
ELT	A9840	9	0,000042552	0,17259	4.371	-1,90E+05
ELT	A8490	12	0,000711450	0,15042		-6,12E+04
ELT	A8024	13	0,000194740	0,17281	3.711	-7,82E+03
ELT	A9078	17	0,000142010	0,13448	3.848	-7,79E+04
ELT	A9003	20	0,000001211	0,21443	5.917	-1,27E+04
ELT	A6428	25	0,001450000	0,15692		-7,86E+04
ELT	A8449	NA	0,000102280	0,19341	3.99	-1,41E+04

Fl: Fiber length; GOT: Ginning outturn; U. I: Uniformity index; MIC: Micronaire; MAT: Maturity; STR: strength; ELT: Elongation; R^2, Marker Rseq; -log10(P-value), Threshold level

Spurious associations can be induced among phenotype and marker due to statistical errors. Yu et al. (2006) assumed that such marker-trait relations are more authentic with combined analysis of population pattern and kinship matrix (Yu et al., 2006). Mixed linear models can utilize kinship measures where population pattern neglected. The strength of QTL detection is enhanced, spurious associations are diminished, and efficiency of model is improved with the addition of kinship in the association analysis.

4.2.1.2.9. MLM using TASSEL

Mixed linear model used to overcome false associations. The naive model showed that magnitude based on R^2 for fiber trait varied from (0.081 to 0.413). Mixed linear model (MLM) was performed for association analysis among fiber quality traits (FL, GOT%, UI, MIC, MAT, STR and FE) using SNPs. Population relatedness and Q-matrix (Q+K) were included (Yu et al., 2006) for the execution of MLM in TASSEL. Marker-trait associations were observed in association panel and it was shown that 95 SNPs found to be highly valueable as compared to GLM model. This is due to the incorporation kinship matrix which allows to overcome false genetic variants. It was found that 15.7% of the SNPs were found in more than than one trait. 60.0% of total related to fiber length, 13.7% to GOT (%), 10.5% to maturity, 7.4% for elongation and 3.1% each were associated with strength, uniformity and 2.2% to micronaire. It was found that 86.4%of the markers observed in MLM were also present in GLM.

As probaility is used to select the most desirable genetic varaiants. In contrast to Zhao et al., 2014 who used 0.05 probability; 0.01 and 0.001were used for identification of associations and as a result most reliable loci were identified.

Moreover, SNPs were screened at -log(p)≥3.0 according to (Mei et al. 2013; Iqbal and Rahman, 2017) for observing the most reliable ones. Moreover, Q-Q plots showed that SNPs can be useful as for each trait (Figure 4.48) which were constructed using arranged noticed p-values and drwan with expected values from χ^2- distribution for every SNP (Ehret, 2011).

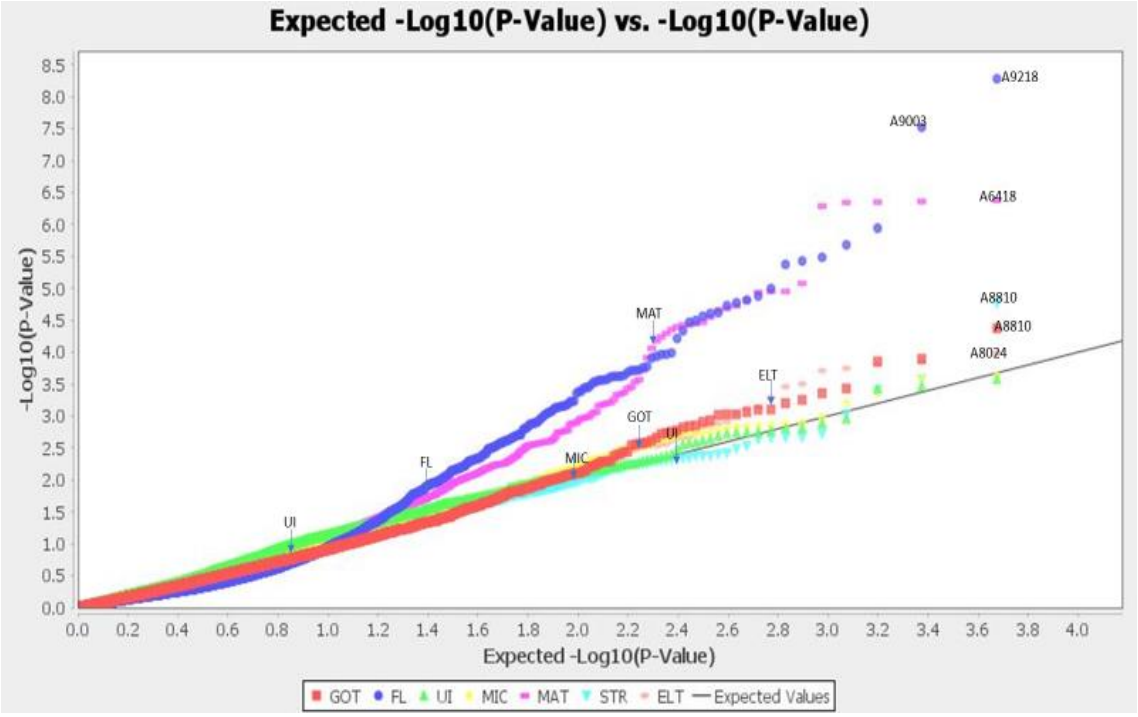

Figure 4.48. Q-Q plot for fiber traits using MLM

Manhutton plots were developed using -log10 (P value) in order to detect genetic variants. QTLs were observed for each trait and the loci connected to trait greater than 3 were designated as major QTLs according to (Mei et al., 2013; Iqbal and Rahman, 2017).

It is a matter of great concern how to relate the genetic varaiants with the morphological traits in whole genome studies as huge amount of SNPs are used for association analysis. Manhutton plots are the one way to asses this association using appropriate p-value by plotting the expected -log10 (P-value) to the thresh hold level for the association. It has reported that occassional polymorphism among genetic variants tend to push highly significant SNPs top of the plot which looks like Manhutton (Ehret, 2011). Similar observations were observed in current study and the QTLs were designated as major

ones which were found on the top like SNPA8098 and SNPA9003 with 8.09 and 7.292 for fiber length. It is assumed that Manhutton plots are useful for ascertaining QTLs.

As Q-Q plots are developed using values of genetic variants from distribution and if the noticed and expected values are realted then all values are found in the center. Eitherway the values are different then the scattered lines partitioned from each other from the base and statistically significant loci move towards vertical bar. Many loci were observed in Q-Q plots for traits which deviated from the centter which can be induced due to different pattern of population.

Totally 57 SNPs were observed using mixed linear model for fiber length using 0.001 probability (Table 4.12). These were distributed to chromosomes 1, 4, 5, 8, 9, 11,12,13, 14, 15, 16, 18, 19, 21, 22, 23, 25, 26 in upland cotton while eight markers had no location on the genome but SNPA8449, SNPA9388 had very low probability i.e 0.000003, 0.000001 with r^2 0.2196 and 0.17875. It was also found that chromosome 19 had highest number of markers which include A8810, A9279, A7094, A9220, A8573, A7814, A8299. While 10 major QTLs designated as qFL-Chr-5, qFL-Chr-9, qFL-Chr-11, qFL-Chr-14, qFL15, qFL-Chr-19 and qFL-Chr-19 (Figure 4.49). The results were compared with earlier findings and it was observed that majority of the SNPs are in accordance to (Zhao et al., 2011; Xu et al., 2016; Islam et al., Sun et al., 2017). There were QTLs with very high LOD like A9218 with -log10(p-value) of 8.09 with high "R^2" value of 0.32; A9003 had 7.292 and "R^2" of 0.25; A8519 with a threshold of 5.394, qFL-Chr14-1 with maker probability of 0.0000042 and 0.1686 "r^2". Such QTLs can be more powerful as Hunag et al., (2017) used LOD>4.0 and observed QTLs for fiber and agronomic traits.

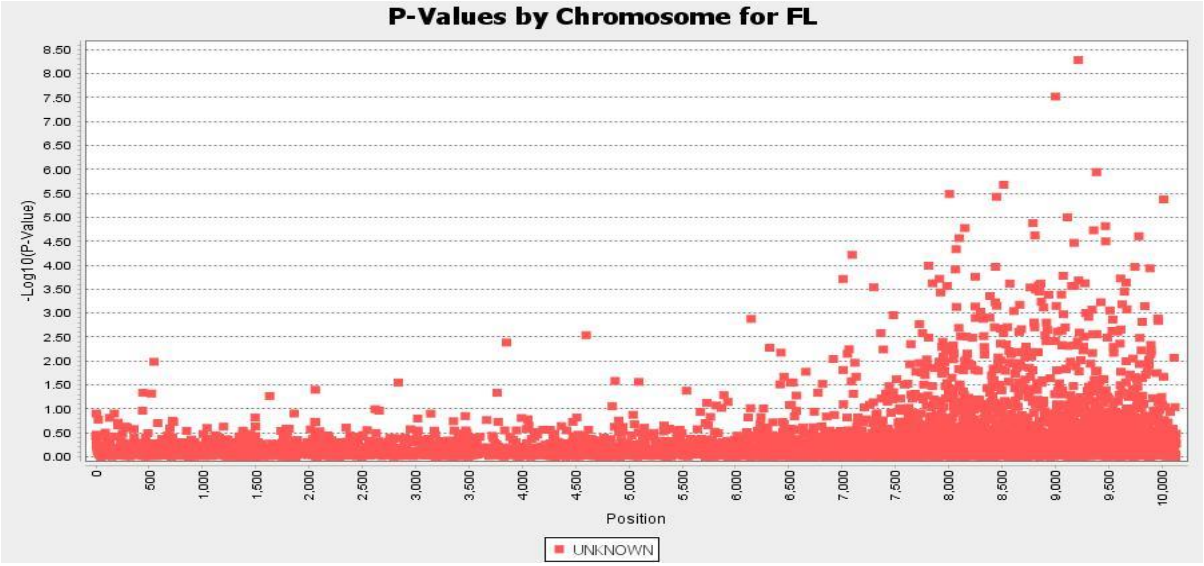

Figure 4.49. Manhutton plot for fiber length using MLM

Association based of linkage diseuilibrium is an efficient way to observe traits of interest Such mapping is affected by population stratification, genetic drift, recombination. The genetic pattern of trait under consideration and type of marker also plays a significant role. Association studies in cotton are less owing to allopolyploid nature of cotton. Association analysis for fiber quality traits conducted using robust SNPs which resulted in valuable associations. Stich et al., (2005) revealed that relatedness results in linkage disequilibrium among homologues and non-homologues. The observations in this study showed that relatedness among populations should be considered to overcome spurious associations. SNPs markers are on top priority for execution of genome-wide analysis (Remington et al., 2001; Hulse-kemp et al., 2015; Zhao et al., 2016).

Table 4.12. Significant associations of SNP loci with fiber traits identified by MLM

Trait	Marker	Chromosome	Marker Probability	R^2	-LOG10(P-Value)	Effect
FL	A9428	1	0,0005	0,09	3.123	-8,37E+04
FL	A9010	1	0.0007	0.0998	3.051	-7,22E+04
FL	A8893	4	0.0007	0.11501	3.011	-8,37E+04
FL	A9472	5	0.000015	0.14814	4.685	-1,04E+05
FL	A8098	5	0.000027	0.15853	4.484	-1,35E+05
FL	A9218	8	0.000000005	0.32279	8.09	-1,65E+05
FL	A9649	8	0.00035	0.093	3.401	-6,30E+04
FL	A9840	9	0.00071	0.08819	3.054	-7,82E+03
FL	A8938	9	0.00041	0.10745	3.205	1.316.153
FL	A8865	9	0.00024	0.12639	3.517	1.103.195
FL	A8437	9	0.00059	0.11089	3.101	1.042.999
FL	A8250	11	0.00017	0.13623	3.66	-1,29E+05
FL	A9003	12	0.00000003	0.25061	7.292	-1,90E+05
FL	A8453	13	0.000702	0.09676	2.992	101.818
FL	A8251	13	0.00072	0.11599	3.076	-9,06E+03
FL	A10019	14	0.0000042	0.16864	5.168	-8,91E+04
FL	A9474	14	0.0000318	0.1244	4.382	-1,01E+05
FL	A8388	15	0.00044	0.10269	3.163	-8,26E+04
FL	A8250	15	0.000017	0.13623	3.66	-1.29E+05
FL	A9664	16	0.000232	0.09917	3.522	-8,29E+04
FL	A7297	18	0.00028	0.14499	3.469	-1,01E+05
FL	A8810	19	0.000024	0.14877	4.58	-1,27E+05
FL	A9279	19	0.00023	0.12286	3.559	-1,24E+05
FL	A7094	19	0.00006	0.18394	4.087	2.099.811
FL	A9220	19	0.0002	0.10509	3.599	-1,01E+05
FL	A8573	19	0.000241	0.11043	3.443	-1,07E+05
FL	A7814	19	0.000102	0.1431	3.905	-1,06E+05
FL	A8299	19	0.00094	0.09102	2.981	-1,04E+05
FL	A8065	21	0.00012	0.13016	3.812	-1,22E+05
FL	A8768	21	0.0002	0.11289	3.415	-8,60E+04
FL	A9631	21	0.00065	0.09181	3.07	-7,52E+04
FL	A7927	21	0.00036	0.13082	3.274	1.136.879
FL	A8519	22	0.000002	0.20888	5.394	-1,75E+05
FL	A8070	22	0.000046	0.15816	4.225	-1,36E+04
FL	A8819	22	0.00032	0.12092	3.413	-1,35E+05
FL	A9361	23	0.00001	0.13965	4.534	-1,28E+05
FL	A9888	23	0.00011	0.09735	3.809	-8,77E+04
FL	A8007	25	0.000003	0.18475	5.354	-1,52E+05

Table 4.12. Continue

Trait	Marker	Chromsome	Marker Probability	R^2	-LOG10(P-Value)	Effect
FL		25	0.00073	0.10059	3.061	-8,70E+04
FL	A7851	26	0.00023	0.14644	3.559	-1,27E+05
FL	A9158	26	0.00027	0.10945	3.387	-9,11E+04
FL	A9075	26	0.00016	0.10589	3.513	-7,64E+04
FL	A7986	11	0.00027	0.12402	3.428	-7,94E+04
FL	A8850	11	0.00035	0.11493	3.387	-1,13E+05
FL	A9388	NA	0.0000011	0.17875	5.619	-1,11E+05
FL	A8449	NA	0.0000037	0.21967	5.181	-1,41E+04
FL	A8792	NA	0.000013	0.19023	4.695	-1,26E+05
FL	A8153	NA	0.00001	0.16858	4.462	-1,22E+05
FL	A9177	NA	0.00003	0.1353	4.243	-1,01E+05
FL	A8845	NA	0.0002	0.10227	3.521	-9,73E+04
FL	A7915	NA	0.0001	0.14127	3.563	-1,05E+05
FL	A8871	NA	0.0005	0.09479	3.146	-8,34E+04
FL	A9613	XM_016882891	0.0001	0.10397	3.598	-9,65E+03
GOT	A8098	5	0.00043	0.08844	3,491	-1,27E+05
GOT	A9349	13	0.00012	0.09638	3,274	-1,11E+05
GOT	A9474	14	0.00004	0.09747	4,353	-1,12E+05
GOT	A8250	15	0.0008	0.07887	3,137	-1,67E+05
GOT	A9230	16	0.0009	0.07081	3,224	-8,08E+04
GOT	A9078	17	0.0007	0.06543	3,314	-1,15E+05
GOT	A9347	18	0.00055	0.06612	3,016	-5,13E+04
GOT	A8810	19	0.00013	0.11434	3,945	-1,69E+05
GOT	A8850	19	0.00062	0.07959	3,642	-1,21E+05
GOT	A9279	19	0.0007	0.07562	3,323	-1,29E+05
GOT	A7365	12	0.0003	0.10557	3,303	-9,72E+04
UI	A9145	2	0.0003	0.07586	3,428	-4,81E+03
UI	A8810	19	0.0002	0.09903	3,579	-3,11E+05
UI	A8819	22	0.0003	0.10227	3,446	-2,96E+05
MIC	A8573	19	0.0002	0.12293	3.103	-2,02E+04
MIC	A6860	26	0.00042	0.13389	3.758	156.143
MAT	A7223	8	0.00005	0.16989	4.239	115.713
MAT	A5424	9	0.001	0.10394	3.959	-8,38E+03
MAT	A6418	15	0.00001	0.16205	4.935	0.99453
MAT	A6267	21	0.0001	0.11823	3.715	0.88524
MAT	A3301	22	0.0006	0.11325	3.201	-5,87E+03
MAT	A5859	22	0.0009	0.10649	3.021	0.69939
MAT	A1278	NA	0.00003	0.16948	4.468	-1,24E+04
MAT	A3064	NA	0.00042	0.10004	3.37	-1,68E+04

Table 4.12. Continue

Trait	Marker	Chromosome	Marker Probability	R^2	-LOG10(PValue)	Effect
MAT	A3668	NA	0.00029	0.08073	3.535	-1,76E+04
MAT	A7498	XM_016871575	0.00066	0.11144	3.176	138.854
STR	A8155	16	0.00093	0.08631	3.029	332.365
STR	A8810	19	0.00001	0.14114	4.747	-1,89E+05
STR	A9279	19	0.00039	0.08809	3.508	-1,40E+05
ELT	A9840	9	0.00017	0.06969	3.539	-7,82E+03
ELT	A8490	12	0.00034	0.06908	3.296	-1,27E+04
ELT	A8024	13	0.00014	0.09572	3.591	-6,12E+04
ELT	A9078	17	0.00019	0.06172	3.487	-7,79E+04
ELT	A9003	20	0.0001	0.08174	3.868	-1,90E+05
ELT	A6428	25	0.00052	0.0781	3.163	-7,86E+04

FL: Fiber length; GOT: Ginning outturn; UI: Uniformity index; MIC: micronaire; MAT: maturity; STR: Fiber strength; FE: Fiber elongation; R^2, Marker R_{seq}; -log10(P-value), Threshold level;

It was observed that 12 SNPs found to be associated with ginning outturn which lies on Chromosome 5, 13, 14,15, 16, 18, 19 (Figure 4.50). Among these markers SNPA8810 and SNPA9279 was common with probability of 0.0001, 0.00007 and r^2 0.11434, 0.07562 respectively. The same number of SNPs found in both models. Nine SNPs related to GOT were observed in other fiber traits also which showed that lint yield can be increased using GOT % as a parameter using association mapping which is accordance to Iqbal and Rahman, (2017). Lehner, (2011) assumed that a single point within a gene can execute multiple functions which is the effect of pleiotropy. It is assumed that "A8810" is a genetic variant which has been developed from protein ligase KEG which can be used to study the evolutionary as MGHES-51 an expressed sequence tag was used (Wang et al., 2007). Wang et al., (2015) screened RIL population and detected 19 QTLs on 7-chromosomes and 18 microsatellites were associated GOT (%). While Zhang et al., (2013) mapped lint percentage traits on separate points of the same chromosomes (1, 2, 10, 14, 16, 17, 18, 19, 22, 23, 24, 25 and 26. Our findings are also in accordance to Nie et al., (2016); Huang et al., (2017) who found SNPs for GOT at different loci with association with multiple fiber traits. Li et al., (2016) found qLP on Chr5, 14, 17 which confirms the reliability of such SNPs for improving ginning outturn as this will ultimaltely leads to fiber yield and will be a source of food security at the global level.

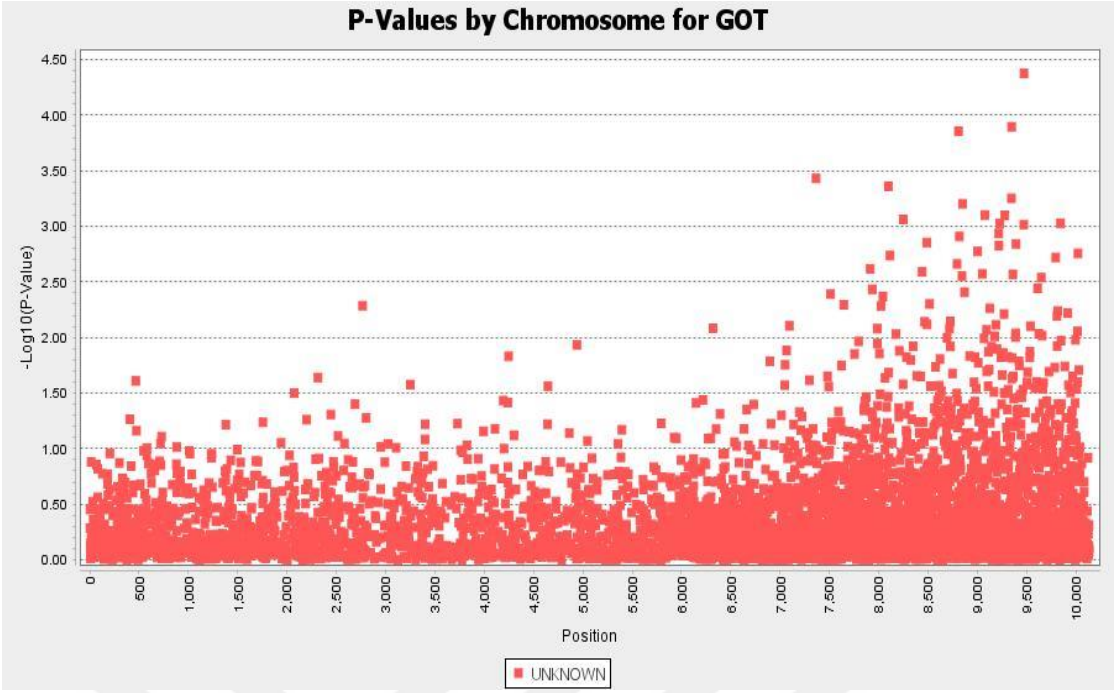

Figure 4.50. Manhutton plot for ginning outturn using MLM

MLM produced three marker-trait associations for fiber uniformity which include A8810 located on chromosome 19, A8819 on chromosome 22 and A9145 on chromosome 2 (Figure 4.51) with marker probability of 0.0002. 0.0003, 0.0003 respectively while r^2 was 0.09903, 0.102, 0.0758. GLM and MLM jointly showed associations among these markers. One major QTL "qUI-Chr-19 was observed in a common marker A8810. Sun et al., (2012) tagged uniformity markers at separate locations on chromosome (7, 13, 14, 16, 25) while same pattern was also observed by (Zhang et al. 2013; Islam et al., 2016). Likewise in our study this differential location may be produced due to germplasm entries developed from different methods of breeding like 3-way crosses or composite parents. SNPs were mapped in a mapping population for fiber uniformity on Chr-01, Chr5, Chr-09 and Chr-19 (Li et al., 2016). In our observations major QTL for uniformity was mapped on qUIChr-19. Iqbal and Rahman, (2017) also found unformity markers at different chromosomes in a golbal germplasm collection.

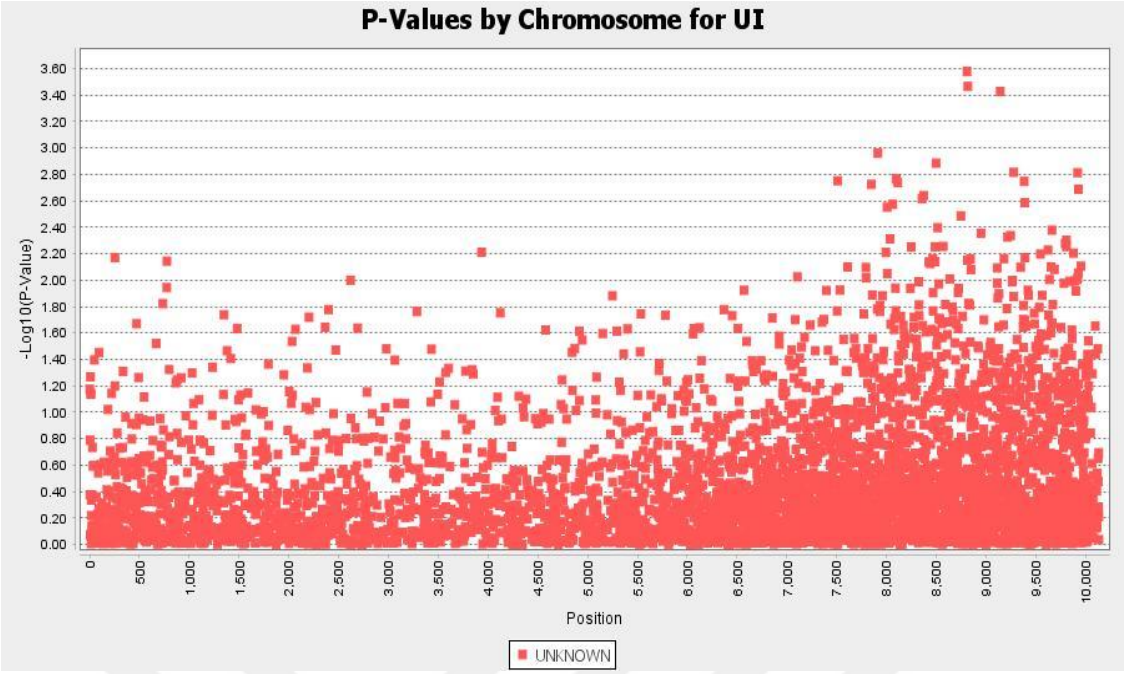

Figure 4.51. Manhutton plot for uniformity using MLM

2 marker-trait associations were for micronaire; first found on chromosome 19 and second on chromosome 26 (Figure 4.52) with marker probability of 0.0002 and 0.0004 using MLM while 6 associations were found in GLM. Moreover, two QTLs i.e qMIC-Chr-19 and qMIC-Chr-26 were observed. The allele effect was found to be positive in A6860. Huang et al., (2017) found QTLs which were found on Chr-19 and Chr-26. While Sun et al., (2012) also observed qMIC-Chr-19 and our results are also similar as one major QTL found on same chromosome. While Shen et al., (2005) micronaire QTL located on chromosome 26. As phenotypically there is a positive association among micronaire and maturity (Table 4.12) so it is speculated that such QTLs can be used for breeding as it will be useful for improving fiber as allele effect was positive for qMIC-Chr-26.

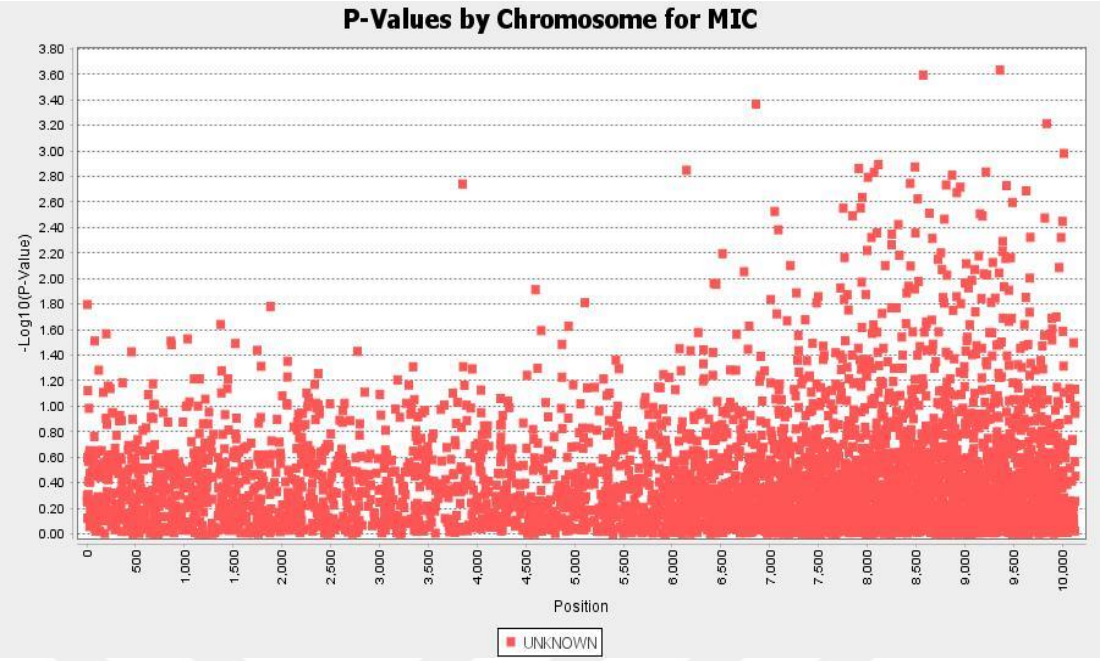

Figure 4.52. Manhutton plot for micronaire using MLM

For maturity, 10 significant SNPs i.e A7223, A5424, A6418, A6227, A3301, A5859, were observed on chromosomes 8, 9, 15, 21, 22 while A7498 found in NCBI XM_016871575 and A1278, A3064, A3668 without genomic location (Figure 4.53). Among these markers A6418 had probability 0.00001 with r^2= 0.162; A7223 with probability of 0.000057 and r^2= 0.169 and A1278 had 0.00003 marker probability. One major QTL qMAT-Chr-21 was found which had positive allele effect. Such QTL will be a source for fiber improvement using SNPs. Sun et al., (2017) observed SNPs for fiber maturity on Chr19 and same results were found in current studies as A8573 was found Chr19. It is expected from the allele effect that QTLs are of higher value for breeders as positive effect was observed. Shappley et al., (1998) argued that the traits which have highly correlated each other; show same pattern during mixed linear model analysis. Likewise, the correlation between fiber maturity and strength that revealed positive impact in majority of the associations in maturity.

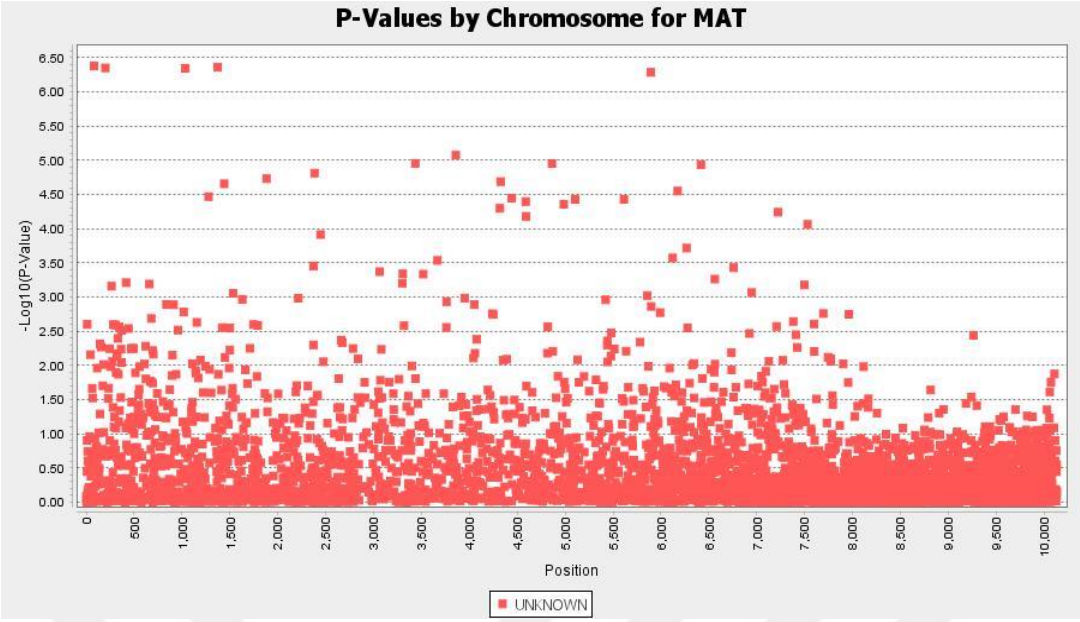

Figure 4.53. Manhutton plot for maturity using MLM

A common SNP A8810 observed for fiber strength in MLM and it was also verified in GLM using LOD >3 and had marker probability 0.000016 with "r^2" value of 0.1411 and was found on chromosome 19 in MLM while had 2.9E-03 and r^2 0f 0.288 in GLM. The second common marker A9279 for fiber strength also present on same locus (Figure 4.54) with 0.00039 and 0.088 marker probability and "r^2" respectively in MLM and 0.000019, 0.201 probability and "r^2" alternatively in GLM. A major QTL was found on A8810 designated as qFS-Chr-19.

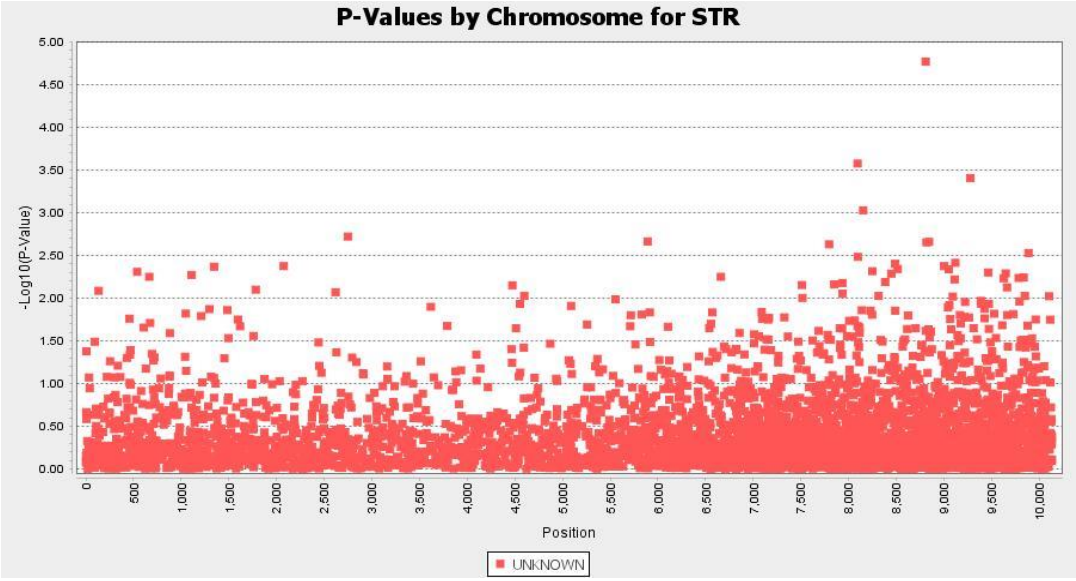

Figure 4.54. Manhutton plot for fiber stregth strength using MLM

The allele effect among markers was positive in one marker while negative in the other. Three markers were found for fiber length with highly valuable significance. Sun et al., (2017) found chromosome 19 to be associated with fiber strength as they screened the germplasm for fiber traits. 2 common SNPs were located on chromosome 19 and qFS-Chr-19 was valuable for marker assisted selection to refine fiber strength being a highly desirable trait in fiber quality. In another study, Ni et al., (2016) observed QTLs on chromosome 5, 14, 19, 20 for fiber strength using SNPs while varying chromosome positions for fiber strength were reported (Wang et al. 2006). The different mapping populations may be the factors which created such alterations. Nonetheless, these QTLs can be used for determining breeding resources.

Chromosome 9, 12, 13, 17, 20, 25 had SNPs (A9840, A8490, A8024, A9078, A9003, A6428) related to fiber elongation (FE) while no locus found for A8449 (Figure 4.55). The significance of these markers was 0.00017, 0.00013, 0.00014, 0.00019, 0.0001, 0.00052, 0.0007 with r^2 0.069, 0.069, 0.095, 0.061, 0.081, 0.078 and 0.062 respectively. These markers were also found in GLM. Seven major QTLs qFE-Chr-9, qFE-Chr-12, qFE-13, qFE-Chr-17, qFE-Chr-20, qFE-Chr-25 were detected. Li et al., (2016) found QTLs connected to fiber elongation on Chr11, Chr16, Chr17, Chr18, Chr20, Chr24 using SNPs. Islam et al., (2016) found SNPs related to fiber elongation on Chr5, Chr6, Chr12, Chr17, Chr23, Chr24. QTLs related to fiber elongation for SNPs were observed on Chr10, Chr12, Chr13, Chr16, Chr17 and Chr18 showing that loci vary for elongation. It is expected that the qFE-Chr-17 and qFE-Chr-20 can be useful for fiber quality.

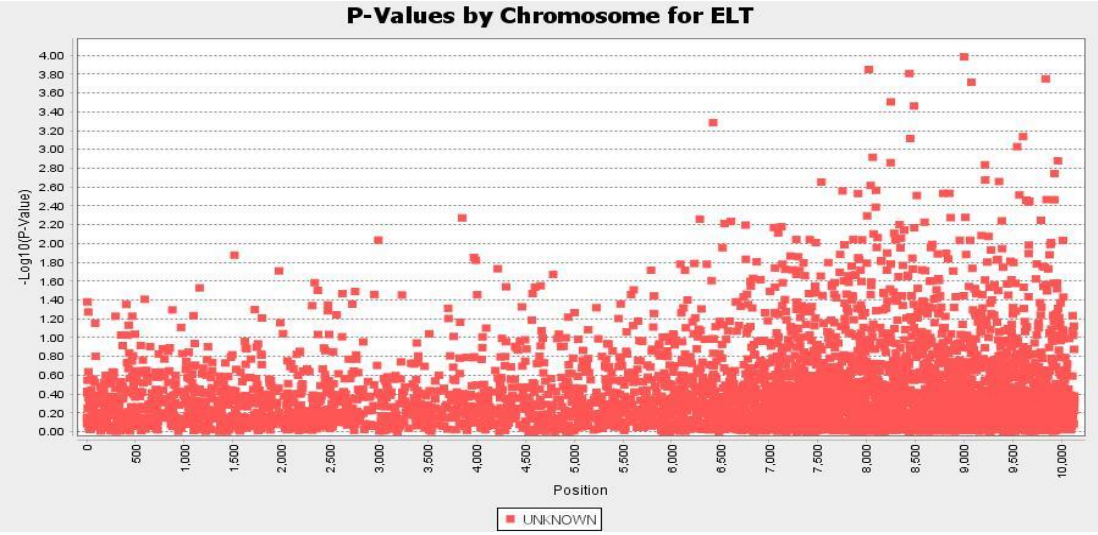

Figure 4.55. Manhutton plot for fiber elongation using MLM

It was observed from the results that there is significant association among the phenotypic characters caused by a gene with more than one effect. 32 multiple QTLs were found in 15 SNPs like qFL-chr19-1, qFl-Chr19-2, qFL-Chr19-3. qFL-Chr19-4, qGOT-Chr-19-5, qGOT-Chr-19-6, qGOT-Chr-19-7, qGOT-Chr-19-8, qUI-Chr19-9, qChr-19-10, qFSChr-19-11, qFSChr-19-12. Likewise, qFL-Chr15-1, qGOT-Chr15-2 and qFL-Chr-14-1, qFL-Chr14-2. Li et al., (2016) found that Chr-19 has qFL, qUI, qFS validating findings in current studies. Huang et al., (2017) found multiple QTLs for morphological traits and quality traits as the four loci were determined which control growth period, yield components and fiber traits. Our findings also found some loci which were connected to multiple traits.

The efficiency of QTLs is largely effected by the ecological conditions. It was found that in most of the detected QTLs the phenotypic variation was less and these found to have minor and additive effects. There was absorbing association observed as qFL-Chr18 had positive effect for fiber length while negative was found for strength on same marker. Genome wide association is a reliable tool for QTL analysis which is in accordance to (Huang et al., 2017).

Association mapping is an efficient way to map QTLs for fiber traits in cotton. Number of major QTLs detected for all traits except uniformity, micronaire and strength; it was assumed that traits are highly influenced by the environment which resulted in less mapping. Moreover, it was also observed that most of the observed QTLs had less phenotypic variation as depicted by "R^2" which showed that the pattern of minor and additive. Finely saturated mapping at GWAS can induce efficient mapping but it all depends upon on LD decay. In future study will planned to observe LD decay at less distance so that QTLs of high information can be detected.

Due to ever increasing competition with synthetic fiber; vigilant endeavours should be planned for improving fiber quality without undermining lint production. Likewise, various strategies are being applied but polygenic nature of related traits is main hindrance. The outcome of current findings can be utilized for devising any future approach for advancement of quality. It was found that these promising genotypes in the germplasm like AB-80 with high ginning outturn, Delcerro for fiber length and YB198 can serve as rich source for fiber length. As these are the major traits which contribute directly towards fiber quality.

The global germplasm evaluation can serve as a corner stone for association mapping studies for selection of parents in cultivars development. QTLs has been detected related to fiber traits using genotyping by sequencing. Owing to developments in omics studies for tagging QTLs for agronomic and fiber traits based on linkage disequilibrium. There are some QTLs which have been confirmed in upland cotton with family-based mapping and association mapping. But novel markers like A8810 can be used for tagging QTLs for fiber via high-throughput technologies globally.

5. CONCLUSION AND RECOMENDATIONS

The success of any breeding program depends upon extent of genetic variation and the approach utilized for determining such diversity. Likewise, variation was observed in a global germplasm of upland cotton. The variability on standard deviation basis; varied from 0.01-4.22 being high for ginning outturn followed by fiber strength, fiber length, with values of 4.22, 2.91 and 1.92 respectively. Moreover, about same pattern was found for these traits at each location also while coefficient of variability fluctuated from 1.5-12.4% on combined basis. Fiber elongation had maximum 12.4% while minimum (1.5%) for maturity ratio.

Analysis of variance revealed highly significance among genotypes for all traits at different locations, while interactions among genotype and location were highly significant for ginning outturn and micronaire. Genotypes had wider variability for fiber traits as ginning outturn ranged from 4.1 to 46.1%, fiber length (0 to 35.6mm), fiber uniformity index (78.4 to 87.2%), fiber fineness (2.8 to 5.9 μg $inch^{-1}$), maturity ratio (0.8 to 0.9), fiber strength (21.6 to 44.6 g tex^{-1}) and fiber elongation (3.7 to 7.7%).

Morover genotypes were categorized according to fiber traits. Fiber length had five categories but most of genotypes were classified in long-staple; 51% of genotypes included in high uniformity index; 69.2% genotypes had medium fiber fineness; almost all genotypes were mature, 67% genotypes had very strong strength and 47.6% had fiber elongation in low category. The variation among traits based on multi-environmental trials showed that considerable amount of variation is prevailing in the genepool which can be used for ascertaining whether these are due to variants or from hybridization with superior parents and acquisition of QTLs.

Association analysis showed considerable relation among fiber quality traits. Fiber length was positively and significantly related with fiber strength ($r=0.457^{**}$) and uniformity ($r=0.253^{**}$) while negatively correlated with fiber fineness (0.194^{**}). Uniformity index was positively associated with fiber strength ($r=0.220^{**}$) and fiber fineness significanlty with maturity ratio (r=0.502**). Morover strength found to have negative association with fiber elongation (r=-0.212) and maturity also found to be negatively associated with elongation ($r=-0.466^{**}$).

Phenotypic screening showed that considerable variation is present among germplasm entries for refinement of trait in upland cotton.

It was concluded that some genotypes can be used as potential parents in variety development like AB80, BA440, Carla for increasing lint percentage; YB-230, Flora, SPEARS3(67) and PI528875 for fiber length; Delcerro, Menderes for fiber strength and NSCH-777 for increasing fiber elongation. As a whole Acala Maxa, Nazilli342, Acala Prema, NP Ozbek100, YB242, GSN22, STV373, Flash, Julia, Claudia, Candia had multiple desired fiber traits.

Association mapping was conducted using 4730 SNPs among association panel for determing marker-trait association for fiber quality. The population was differentiated into definite clusters (K=6) using ADMIXTURE model with STRUCTURE produced distinct differentiation among upland cotton and greater genetic differences with considerable recombination among the alleles. The kinship ranged from (0 to 1). Kinship coefficient found 69.0% near to 0 but association inside the entries found to fluctuate 11.1% for 0.01 to 0.02. 16.1% had relatedness value of 0.02 to 1.0 while 3.2% showed varied degree of kinship coefficient. 259561 comparisons were observed through screening of 3930 SNPs, only 3.7 and 9.3% found highly significant at $P<0.001$ and $P<0.01$. While 18.5% at $r^2 \geq 0.1$ and 14.8% on $r^2 \geq 0.2$. This showed that 14.8% markers found in 6-8cM and 18.5% in the genetic map distance of 10cM.

33111 associations were found; out of which 1.2, 2.4% were highly significant at $p<0.001$, $p<0.01$ respectively in general linear model. Spurious associations were observed as expected and quantile-quantile curves found for fiber quality traits. Moreover, SNPs were screened using high probability i.e. $-\log10(Pvalue) \geq 3.0$ using Manhutton plots and number of markers found to be related with different traits like A9218 for fiber length, A9003 for strength. It was observed that SNPA8810 was common for different traits like fiber length, fiber strength, fiber uniformity index and ginning outturn.

The Q+K model selected for association analysis among genotypes using variation on combined basis. Marker-trait associations were observed in association panel and it was shown that 93 SNPs found to be highly valueable as compared to GLM model. This is due to the incorporation kinship matrix which allows to overcome false genetic variants. It was found that 15.7% of the SNPs were found in more than than one trait. 60% of total related to fiber length, 13.7% to GOT (%), 10.5% to maturity, 7.4% for elongation and 3.1% each were associated for fiber strength, uniformity and 2.2% to micronaire. It was found that 86.4%of the markers observed in MLM were also present in GLM.

Totally 57 SNPs were observed using mixed linear model for fiber length using 0.001 probability. These were distributed to chromosomes 1, 4, 5, 8, 9, 11,12,13, 14, 15, 16, 18, 19, 21, 22,23, 25, 26 upland cotton while eight markers had no location on the genome but SNPA8449, SNPA9388 had very low probability i.e 0.000003, 0.000001 with r^2 0.2196 and 0.17875. QTLs connected to these markers will be of good source as were also detected in GLM with very low probability.

It was observed from the results that there is significant association among the phenotypic characters caused by a gene with more than one effect. 32 multiple QTLs were found in 15 SNPs like qFL-chr19-1, qFl-Chr19-2, qFL-Chr19-3. qFL-Chr19-4, qGOT-Chr-19-5, qGOT-Chr-19-6, qGOT-Chr-19-7, qGOT-Chr-19-8, qUI-Chr19-9, qChr-19-10, qFSChr-19-11, qFSChr-19-12. Likewise, qFL-Chr15-1, qGOT-Chr15-2 and qFL-Chr-14-1, qFL-Chr14-2. It was also found that chromosome 19 had highest number of markers which include A8810, A9279, A7094, A9220, A8573, A7814, A8299. While 12QTLs were found on chromosome 19 i.e qFL-chr19-1, qFl-Chr19-2, qFL-Chr19-3. qFL-Chr19-4, qGOT-Chr-19-5, qGOT-Chr-19-6, qGOT-Chr-19-7, qGOT-Chr-19-8, qUI-Chr19-9, qChr-19-10, qFSChr-19-11, qFS-Chr-19-12.

Association mapping is an efficient way to map QTLs for fiber traits in cotton. Number of major QTLs detected for all traits except uniformity, micronaire and strength; it was assumed that traits are highly influenced by the environment which resulted in less mapping. Moreover, it was also observed that most of the observed QTLs had less phenotypic variation as depicted by R^2 which showed that the pattern of minor and additive. Finely saturated mapping at GWAS can induce efficient mapping but it all depends upon on LD decay. In future study will planned to observe LD decay at less distance so that QTLs of high information can be detected.

Due to ever increasing competition with synthetic fiber; vigilant endeavours should be planned for improving fiber quality without undermining lint production. Likewise, various strategies are being applied but polygenic nature of related traits is main hindrance. The outcome of current findings can be utilized for devising any future approach for advancement of quality. It was found that these promising genotypes in the germplasm like AB-80 with high ginning outturn, Delcerro for fiber strength and YB230 can serve as rich source for fiber length. As these are the major traits which contribute directly towards fiber quality. The global germplasm evaluation can serve as a corner stone for association

mapping studies for selection of parents in cultivars development. QTLs has been detected related to fiber traits using genotyping by sequencing. Owing to developments in omics studies for tagging QTLs for agronomic and fiber traits based on linkage disequilibrium. There are some QTLs which have been confirmed in upland cotton with family-based mapping and association mapping. But novel markers like A8810 can be used for tagging QTLs for fiber via high-throughput technologies globally.

REFERENCES

Abdurakhmonov, I.Y., Buriev, Z.T., Saha, S., Pepper, A.E., Musaev, J.A., Almatov, A., Shermatov, S.E., Kushanov, F.N., Mavlonov, G.T., Reddy, U.K., Yu, J.Z., Jenkins., J.N., Kohel, R.J., Abdukarimov, A. 2007. Microsatellite Markers Associated with Lint Percentage Trait in Cotton, *Gossypium hirsutum*. *Euphytica,* 156(1-2): 141-156.

Abdurakhmonov, I.Y. 2007. Exploiting genetic diversity. In: Ethridge D (ed) Plenary presentations and papers. Proceedings of World Cotton Research Conference-4. Lubbock, TX, USA, 10-14 Sept 2007 p. 2153.

Abdurakhmonov, I.Y., Kohel, R.J., Yu, J.Z., Pepper, A.E., Abdullaev, A.A., Kushanov, F.N., Salakhutdinov, I.B., Buriev, Z.T., Saha, S., Scheffler, B.E., Jenkins, J.N., Abdukarimov, A. 2008. Molecular diversity and association mapping of fiber quality in exotic *G. hirsutum* L. germplasm. *Genomics,* 92: 478-487.

Abdurakhmonov, I. Y. Saha, S., Jenkins, J.N., Buriev, Z.T., Shermatov, S.E., Scheffler, B.E., Pepper, A.E., Yu, J.Z., Kohel, R.J., Abdukarimov A. 2009. Linkage disequilibrium based association mapping of fiber quality traits in *G. hirsutum* L. variety germplasm. *Genetic*a, 136, 401–417.

Agrama, H.A., Eizenga, G.C., Yan, W. 2007. Association mapping of yield and its components in rice cultivars. *Mol Breed*.;19:341–356.

Ahmad, Q.K., Khan, I.A., Zubair, M., Tariq, M. 1997. Inheritance of lint yield quality characters in cotton. *The Pak. Cotton*., 41: 6-11.

Ahsan, M.Z., Majidano, M.S., Bhutto, H., Soomro, A.W., Panhwar, F.H., Channa, A.R., Sial, K.B. 2015. Genetic variability, coefficient of variance, heritability and genetic advance of some *Gossypium hirsutum* L. accessions. *J. Agric. Sci*., 7(2): 147-151.

Akhtar, K.P., Khan, M.K.R., Ahmad, M., Sarwar, N., Ditta, A. 2010. Partial resistance of a cotton mutant to cotton leaf curl burewala virus. *Spanish J. Agr. Res*., 8: 1098-1104.

Akiscan, Y. 2012. Determination of Genetic Improvement on Fiber Quality Traits in Some Cotton Cultivars Released between 1980 and 2009 in Turkey. *Süleyman Demirel Üniversitesi Ziraat Fakültesi Dergisi*, 7(2):32-40.

Akiscan, Y.1., Gencer, O. 2015. Diallel analysis for fiber quality properties of cotton (*Gossypium Hirsutum* L.). *Genetics and Plant Physiolo*., 4 (3-4): 209–212.

Ali, M.A., Khan, I.A., Awan, S.I., Ali, S., Niaz, S. 2008. Genetics of fiber quality traits in cotton (*Gossypium hirsutum*). *Aus. J. of Crop Sci*., 2: 10-17.

Ali, M.A., Khan, I.A., Nawab, N.N. 2009. Estimation of genetic divergence and linkage for fiber quality traits in cotton. *J. Agri. Res*., 47(3): 229-236.

Al-Joibouru, H.A., Miller, P.A., Robinson, H.F. 1958. Genotypic and environmental covariances in an upland cotton cross of interspecific origin. *Agron. J*., 50: 633-636.

Anonymous, 2016. Turkish Statistical Institute, Plant Production Statistical. http://www.tuik.gov.tr.

Anonymous. 2017. Turkish Statistical Institute, Plant Production Statistical. http://www.tuik.gov.tr. (in Turkish)

Anthony, W.S. 1999. Postharvest management of fiber quality. In: Cotton Fibers Developmental Biology, Quality Improvement and Textile Processing. Basra, A.S. (Ed.) The Haworth Press, Binghamton NY, pp. 293-333.

Asif, M., J. I. Mirza., Zafar, Y. 2008. Genetic analysis for fiber quality traits of some cotton genotypes. *Pak. J. Bot*., 40(3): 1209-1215

Atwell, S., Huang, Y.S., Vilhjalmsson, B.J., Willems, G., Horton, M. et al. 2010. Genome-wide association study of 107 phenotypes in *Arabidopsis thaliana* inbred lines. Nature, 465 (7298): 627-631.

Augado, A., Santos, a., Gamane, B., Garcia, M.C., Romero, F. 2010. Gene effects for cotton-fiber traits in cotton plant (*Gossypium hirsutum* L.) under verticillium conditions. *Field Crops Research*, 116: 209-221.

Azhar FM, Naveed M., Ali A. 2004. Correlation analysis of seed cotton yield with fiber characteristics in *Gossypium hirsutum* L. *IJAB*. 1560–8530/2004/06–4–656–658

Badigannavar, A.M. 2010. Genetic linkage mapping and marker traits associations in diploid and association genetics for quantitative traits in tetraploid cottons. Ph. D Thesis submitted to Louisana State University USA.

Baloch, M.J., Kumar, C., Jatoi, W.A., Rind, I.H. 2014. Phenotypic correlation and regression analysis of yield and fibre traits in upland cotton (*Gossypium hirsutum* L.). *Pak. J. Agri. Engg. Vet. Sci*., 30(2): 135-146.

Bardak, A., Bolek, Y. 2012. Genetic diversity of diploid and tetraploid cottons determined by SSR and ISSR markers. *Turkish J. of Field Crops*., 17(2): 139-144.

Bardak, A., Bolek, Y. 2016. Inheritance of fuzz and lint fiber initiation of cotton (*G. hirsutum* L.). *Tukish J. of Agri. Forestry*., 40: 606-612.

Basal, H., Turgut, I. 2005. Genetic analysis of yield components and fiber strength in upland cotton (*Gossypium hirsutum* L.). *AJPS*., 4: 293-298.

Basal, H., Unay, A., Canavar, O., Yavaş, I. 2009. Combining ability for fiber quality parameters and within-boll yield component in intraspesific and interspesific cotton populations. *Span J. Agric. Res*., 7(2): 364-374.

Basara, A.S., Malik, C.P. 1984. Development of cotton fiber. *Inter Rev. Cyto*., 65-113.

Bassett, D.M., Hyer, A.H. 1985. Acala cotton in California: 60 years of varietal improvement. Proc. Beltwide Cotton Prod. Research Conf: 76.

Baxevanos, D., Ioannis, T.T., Christos, G. 2013. Repeatability and stability analysis for fiber traits in upland cotton (*Gossypium hirsutum* L.). *AJCS*., 7(10):1423-142

Bayles, M.B., Verhalen, L.M., Johnson, W.M., Barnes, B.R. 2005. Trends over time among cotton cultivars released by the Oklahoma Agricultural Experiment Station. *Crop Sci*., 45: 966-980.

Behery, H.M. 1993. Short-fiber content and uniformity index in cotton. p. 40. International Cotton Advisory Committee review article on cotton production research No. 4, CAB Int., Wallingford, UK.

Berlin, J.D. 1986. The outer epidermis of the cottonseed. In: Mauney, I.R., Srewart I.M. (Ed.), *Cotton physiology*. The cotton foundation reference book series. Memphis, TN: The Cotton Foundation, : 375-414.

Blenda, A., Fang, D.D., Rami, J.F., Garsmeur, O., Feng, L., Lacape, A. 2012, High density consensus genetic map of tetraploid cotton that integrates multiple component maps through molecular marker redundancy. *J. Genetics*, 91(3): 22-25.

Blenda, A., Fang, D.D., Rami, J.F., Garsmeur, O., Luo, F., Lacape, J.M. 2012. A high-density consensus genetic map of tetraploid cotton that integrates multiple component maps through marker redundancy check. *PLoS ONE*, 7: e45739.

Bolek, Y. 2003. Status of Genome Mapping and Use in Cotton Improvement, *KSÜ Fen ve Mühendislik Dergisi*, 6(2):72-79.

Bolek, Y., El-Zik, K.M., Pepper, A.E., Bell, A.A., Magill, C.W., Thaxton, P.M., Reddy, O.K. 2005. Mapping of *Verticillium* wilt resistance genes in cotton. *Plant Science*,168: 1581–1590.

Bolek, Y., Cokkızgın, H., Bardak, A. 2014. Genetic Analysis of Fiber Traits in Cotton. *KSU J. Nat. Sc*i., 17(1).

Bolek, Y., Hayat K., Bardak, A., Azhar, M.T. 2016. Molecular breeding of cotton.: Adurakhmonov, I.Y. Cotton Research. Intech Publishers, in Cotton Research, ed I. Y. Abdurakhmonov (InTech): 123-166.

Bourland, F.M., Hogan, R., Jones, D.C., Barnes, E. 2010. Development and utility of Q-score for characterizing cotton fiber quality. *J. Cotton Sci*. 14: 53-63.

Braden, C.A. 2005. Inheritance of cotton fiber length and distribution, Texas A and M Univ., Ph.D Diss. Abstr.

Bradow, J.W., Davidonis, H.D. 2000. Quantification of fiber quality and the cotton production-processing interface: A physiologist perspective. *The J. of Cotton sci*., 4: 34-64.

Breseghello, F., Sorrells, M.E. 2006. Association mapping of kernel size and milling quality in wheat (*Triticum aestivum* L.) cultivars. *Genetics*, 172: 1165-1177.

Bridge, R.R., Meredith, W.R., Chism, J.F. 1971. Comparative performance of obsolete varieties and current varieties of upland cotton. *Crop Sci*., 11: 29-32.

Bridge, R.R., Meredith, W.R. Jr. 1983. Comparative performance of obsolete and current cotton cultivars. *Crop Sci*., 23:949-952.

Brubaker, C.L., Bourland, F.M., Wendel, J.E. 1999. The origin and Domestication of cotton, in cotton, Smith, C.W., Cothren, J.T. editors, pp. 3-64. John Wiley & sons, new york, ny.

Burr B, Burr FA, Thompson KH, Albertson MC, Stuber CW. Gene mapping with recombinant inbreds in maize. *Genetics*, 1988, 118: 519-526.

Burstin, J., Marget, P., Huart, M., Moessner, A., Mangin, B., Duchene, C., Desprez, B., Munier-Jolain, N., Duc, G. 2007. Developmental genes have pleiotropic effects on plant morphology and source capacity, eventually impacting on seed protein content and productivity in pea. *Plant Physiol.* 144: 768–781

Cai, C., Ye, W., Zhang, T., Guo, W. 2014. Association analysis of fiber quality traits and exploration of elite alleles in upland cotton cultivars/accessions (*G. hirsutum* L.). *J. of Integ. Plant Bio*., 56: 51-62.

Campbell, B.T., Myers, G.O. 2015. Quantitative genetics. In: D.D. Fang and R.G. Percy, editors, Cotton. CSSA, Madison, WI. 187–204.

Campbell, B.T., Greene, J., Jones, D.C. 2016. Genetic variation for agronomic and fiber quality traits in a population derived from high-quality cotton germplasm. *Crop Sci.* 56:1689-1697.

Chee P., Draye, X., Jiang, C.X., Decaanini L., Delmonte, T.A. Bredjauer, R., Smith, C.W., Paterson, A.H. 2005. Molecular dissection of interspecific variation between *Gossypium hirsutum* and *Gossypium barbadense* (cotton) by a backcrossself approach: I. Fiber elongation. *Theor. Appl. Genet*. 111: 757-763.

Chen, Z., Scheffler, B., Dennis, E., Triplett B., Zhang, T., Guo, W., Chen, X., Stelly, D.D., Rabinowicz, P.D., Christopher. D.T., Arioli, T., Brubaker, C., Cantrell, R.G., Lacape, M.R., Ulloa, M., Chee, P., Gingle, A.R., Haigler, C.H., Percy, R., Saha, S., Wilkins, T., Wright, R.J., Deynze, A.V., Zhu, Y., Yu, X., Abdurakhmonov, I., Katageri, I., Kumar, P.A., Rahman, M., Zafar, Y., Yu, Y.Z., Kohel, R.J., Wendel, J.F., Paterson, A.H. 2007. Towards sequencing of (*Gossypium*) genomes. *Plant Physiol*., 145: 1303-1310.

Chulmann, A.H. 2007. Molecular markers to assess genetic diversity, *Euphytica*, 158(3): 313-321

Clement J.D., Constable, G.A., Stiller, W.N., Liu, S.M. 2012. Negative associations still exist between yield and fibre quality in cotton breeding programs in Australia and USA. *Field Crops Research*, 128. 1-7.

Collard, B.C., Mackill, D.J. 2008. Marker-assisted selection: an approach for precision plant breeding in the twenty-first century. *Philo. Trans. Of the Royal Soc. Of Lon*., 363: 557-572.

Collins, F.S., Brooks, L.D., Chakravarti, A. 1998. A DNA polymorphism discovery resource.

Constable, G.A., Llewellyn, D.J., Walford., Clement, J.D. 2015. Cotton breeding for fiber quality improvement.

Copur, O. 2006. Determination of yield and yield components of some cotton cultivars in semi-arid conditions. *Pak. J. of Bio. Sci*., 9(14): 2572-2578.

Cotton Incorporated. 2013. Fiber processing information. Available at http://www.cottoninc.com/product/Textile-Research/Fiber-Processing/ (verified 26 August 2013. Cotton Inc., Cary, NC.

Culp, T.W., Green, C.C. 1992. Performance of obsolete and current cultivars and Pee Dee germplasm lines of cotton. *Crop Sci*., 32: 35-41.

Culp, T.W., Harrell, D.C. 1973. Breeding mehods for improving yield and fiber quality of upland cotton (*Gossypium hirsutum* L.). *Crop Sci*., 13: 686-689.

Damp J.E., Pearsall, D.M. Early cotton from coastal Ecuador. *Econ. Bot*., 1994; 48:163-5.

Davey, J.W., Hohenlohe, P.A., Etter, P.D., Boone, J.Q., Catchen, J.M., Blaxter, M.L. 2011. Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nat. Rev. Genet*. 12: 499-510.

Delmer, P.D., Amor, Y. 1995. Cellulose biosynthesis. *The Plant Cell*, 7: 987-1000.

Desalegn, Z.N. Ratanadilok, N., Kaveeta, R. 2009. Correlation and heritability for yield and fiber quality parameters of Ethiopian cotton (*Gossypium hirsutum* L.) estimated from 15 (diallel) Crosses. *Kasetsart J. Nat Sci*., 43:1-11.

Deussen, H. 1992. Improved cotton fiber properties: The textile industry's key to success in global competition. p. 43–63. In C.R. Benedict (ed.) Cotton fiber cellulose: Structure, function, and utilization conference, Savannah, GA. Oct. 28–31, 1992. Natl. Cotton Counc. Am., Memphis, TN.

Deynze V., Stoffel, K., Lee, M., Wilkins, T.A., Kozik, A., Cantrell, R.G., Yu, Y.Z., Kohel, R.J., Stelly, D. 2009. Sampling nucleotide diversity in cotton. *BMC Plant Biology*, 9(8):125.

Dhivya, R., Amalabalu, P., Pushpa, R., Kavithaman, D. 2014. Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). *Afr. J. Plant Sci*., 8(1): 1-5.

Dutt, Y., Wang, X.D., Zhu, Y.G., Li, Y.Y. 2004. Breeding for high yield and fiber quality in coloured cotton. *Plant Breeding*, 123:145-151.

Ehret, G.B. 2010. Genome-wide association studies: contribution of genomics to understanding blood pressure and essential hypertention. Curr. Hypertens. Rep., 12(1):17-25.

Elci, E., Akiscan, Y., Akgol, L. 2014. Genetic diversity of Turkish commercial cotton varieties revealed by molecular markers and fiber quality traits. *Turk. J. Bot*., 38: 1274-1286.

Elshire, R.J., Glaubitz, J.C., Sun, Q., Poland, J.A., Kawamoto, K., Buckler, E.S., Mitchell, S.E. 2011. A robust, simple genotyping-by- sequencing (GBS) approach for high diversity species. *PLoS ONE*, 6: e19379.

Endrizzi, J.E., Turcotte, E.L., Kohel, R.J. 1985. Genetics, cytology and evolution of *Gossypium*. *Advances in Genetics*, 23: 271-235.

Falconer, D.S., Mackey, T.F.C. 1996.Introduction to Quantitative Genetics". Third Edition. Longman, 106: 384-396. London, pp: 65-92.

Fang, D.D., Jenkins, J.J., Deng, D.D., McCarty, J.C., Li, P., Wu, J. 2014. Quantitative trait loci analysis of fiber quality using a random-mated recombinant inbred line population in upland cotton (*Gossypium hirsutum* L.). *BMC Genomics*, 15-397.

Federer W. T. 1956. Augmented (or hoonuiaku) designs. Hawaii. *Plant. Rec*. 55, 191–208

Felkner, G.S. 2001. Fiber quality and new spinning technologies. p.5–7. In Proc. Beltwide Cotton Conf., Anaheim, CA. 9-13 Jan. 2001. Natl. Cotton Counc. Am., Memphis, TN.

Feuillet, C., Leach, J.E., Rogers, J., Schnable, P.S., Eversole, K. 2011. Crop genome sequencing: lessons and rationales. *Trends Plant Sci*., 16: 77-88.

Flint-Garcia, S.A., Thornsberry, J.M., Buckler, E.S. 2003. Structure of linkage disequilibrium in plants. *Annual Review of Plant Bio*., 54: 357-374.

Fryxell, P.A. 1979. The Natural History of the Cotton Tribe. Texas A&M University Press, College Station, TX, USA

Fryxell, P.A. 1992. A revised taxonomic interpretation of *Gossypium* L. (*Malvaceae*). *Rheeda*, 2(2): 108-165.

Gallagher, J.P., Gover, C.E., Rex, K., Moran, M., Wendel, J.F. 2017. A new species of cotton from Wake Atoll. *Gossypium stephensii* (Malvaceae). *Systematic Botany*, 42:115-123.

Gaut, B.S. Long, A.D. 2003. The lowdown on linkage disequilibrium. *Plant Cell*, 15:1502-1506.

Gilbert, M.K., Kim, H.J., Tang, Y., Naoumkina, M., Fang, D.D. 2014 Comparative transcriptome analysis of short fiber mutants Ligon-lintless 1 and 2 reveals common mechanisms pertinent to fiber elongation in cotton (*Gossypium hirsutum* L.). *PLoS One*, 9: e95554.

Gilio, T.A.S., Araujo, D.V.D., Krause, w., Rosa, R.H.H., Ascari, J.P. 2017. Genetic divergence among cotton genotypes grown in the main season and off season. *Rev. Caatinga, Mossoro*, 30(2): 377-390

Gore, M.A., Fang, D.D., Poland, J.A., Zhang, J., Percy, R.G., Cantrell, R.G., Thyseen, G., Lipka, A.E. 2014. Linkage map construction and quantitative trait analysis of agronomic and quality traits in cotton, *The Plant Genome*, 7(1): 1-10.

Gould, S. J., Johnston, R.F. 1972. Geographic variation. *Annu. Rev. Ecol. Syst*. 3: 457–498

Grover, C.E., Gallagher, J.P., Jareczek, J.J., Page, J.T., Judall, J.A., Wendel, J.F. 2015. Re-evaluating the phylogeny of allopolyploid *Gossypium* L. *Mol. Phylognet. Evol*., 92: 45-52.

Guang, C., Xiong- Ming, D. 2006. Genetic diversity of source germplasm of upland cotton in China as determined by SSR marker analysis. *Acta. Genetic Sinca*, 33: 733-745.

Gulati, A.N., Turner AJ. 1929. A note on the early history of cotton. *J. Text. Inst*., Trans.

Guo, W., Cai, C., Wang, C., Han, Z., Song, X., Wang, K., Niu, X., Wang, C., Lu, K., Shi, B., Zhang, T. 2007. A microsatellite-based gene-riched linkage map of reveals genome structure, function, and evolution in *Gossypium*. *Genetics*, 176: 527-541.

Gupta, P.K., Varseny, R.K., Sharma, P.C., Ramesh, B. 1999. Molecular markers and their application in bwheat breeding. *Plant Breed*. 118:369-390.

Gupta, P.K., Roy, J.K., Prasad, M., 2001. Single nucleotide polymorphisms: a new paradigm molecular marker technology and DNA polymorphism detection with empahais on their use in plants. *Curr. Sci*., 80:524:535.

Haigler, C.H., Zhang, D., Wilkerson, C.G. 2005. Biotechnological improvement of cotton fiber. *Phsioyl. Plant*., 124: 285-294.

Hale, A. L., Farnham M. W., Nzaramba M. N., Kimbeng, C.A. 2007. Heterosis for horticultural traits in broccoli. *Theoretical and Applied Genetics*, 115: 351-360.

Hallauer, A.R., Miranda, J.B. 1981. Quantitave genetics in maize breeding. Iowa State University Press.

Han, Z.G., Guo, W.Z., Song, X.L., Zhang, T.Z. 2004. Genetic mapping of EST-derived microsatellites from the diploid *Gossypium arboreum* in allotetraploid cotton. *Molecular Genetics and Genomics*, 272: 308-327.

Hanson, W.D. 1963. Heritability, pp. 125-139 in Statistical Genetics and Plant Breeding, edited by W. D. Hanson and H. F. Robinson. Pub. 982, National Academy of Science-National Research Council, Washington, DC

Harper, A.L., Trick, M., Higgins, J., Fraser, F., Clissold, L., Wells, R., Hattori, C., Werner, P., Bancroft I. 2012. Associative transcriptomics of traits in the polyploid crop species *Brassica napus*. *Nature Biorechnol*. 30: 798-802.

Hauge, S.S., Smith, C.W., Berger, G., Clemet, J., Jones, D.C. 2011. Variation in an extra-long staple upland x medium staple upland cotton F_2 population. *J. of Cotton Sci*. 15(3):265-270.

He, D.H., Lin, Z.X., Zhang, X.L., Nie, Y.C., Guo, X.P., Feng, C.D., Stewart, Mc.D.J. 2005. Mapping QTLs contributing to yield and analysis of genetic effects in tetraploid cotton. *Euphytica*, 144(1-2):141-149

Helentjaris, T., Slocum, M., Wright, S., Schaefer, A., Nienhuis, J. 1986. Construction of genetic linkage maps in maize and tomato using restriction fragment length polymorphisms, *Theoretical and Applied Genetics*, 72(6):761-769

Holsinger, K.E., Lewis, P.O. 2003. Hickory: a package for analysis of population genetic data V1.0. Storrs, CT: Department of Ecology and Evolutionary Biology, University of Connecticut.

Holsinger, K.E., Lewis, P.O., Dey, D.K. 2002. Bayesian analysis of population structure with dominant marker data. *Mol. Ecol*., 111157– 1164.

Hu, X.P., Hsieh, Y.L. 1997. Breaking elongation distributions of single fibres. *Journal of Materials Science*. 32: 3905

Huang, Y.F., Poland. J.A., Wight, C.P., Jackson, E.W., Tinker, N.A. 2014. Using genotyping-bysequencing (GBS) for genomic discovery in cultivated oat. *PLoS One*, 9: e102448

Huang, C., Nie, X., Shen, C., Yu, C., Li, W., Zhao, W., Zhang. X., Lin, Z. 2017. Population structure and genetic basis of the agronomic traits of upland cotton in China revealed by a genomewide association study using high-density SNPs. *Plant biotechnology J*., 1-13.

Hulse-Kemp, A.M, Lemm, J., Plieske, J., Ashrafi, H., Buyyarapu, R., Fang, D.D., Frelichowski, J., Giband, M., Hague, S., Hinze, L.L., Kochan, K.J., Riggs, P.K., Scheffler, J., Udall, J., Ulloa, M., Wang, S.S., Zhu, Q.H., Bag, S.K., Bhardwaj, A., Burke, J., Byers, R.L., Claverie, M., Gore, M.A., Harker, D.B., Islam, M.S., Jenkins, J.N., Jones, D.C., Lacape, J.M., Llewellyn, D., Percy, R., Pepper, A., Poland, J.A., Mohan. R.K., Sawant. S.V., Singh. S.K., Spriggs. A., Taylor. J.M., Wang. F., Yourstone. S.M., Zheng. X., Lawley. C.T., Ganal. M.W., Deynze. V.A., Wilson, I.W., Stelly, D.M. 2015. Development of a 63K SNP array for cotton and high-density mapping of intraspecific and interspecific populations of *Gossypium* spp. *G3* (Bethesda), 5: 1187-1209.

Hussain, S., Nawab, N.N., Ali, M.A., Hussain, A., Nawaz, M.A., Malik, T.A. 2010. Evaluation of performance, genetic divergence and character association of some polygenic traits in upland cotton. *J. Agric. Soc. Sci*., 6: 79-82.

Hwang, E.U., Song, O., Jia, G., Specht, J.E., Hyten, D.L., Costa, J., Cregan, P.B. 2014. A genome-wide association study of seed protein and oil content in soybean. *BMC Genomics*, 15:1

Imran, M., Kamaran, S., Khan, T.M., Muneer, M.T., Rashid, M.A., Munir, A.Z., Azhar, F.M. 2016. Genetic analysis of fiber quality parameter under water Stress in upland Cotton. (*Gossypium hirsutum* L.). *Journal of Agriculture and Environmental Sciences*, 5(1): 134-139.

Indest, M.O. 2015. Factors affecting within-plant variation of cotton fiber quality and yield". LSU Doctoral Dissertations. 1091.

International cotton advisory committee. 2017. http://www.icac.org

Iqbal, M., Khan, R.S.A., Hayat, K., Khan, N.I. 2005. Genetic variation and combining ability for yield and fiber traits among F_1 hybrid population. *J. Bio. Sci*., 5: 713-716.

Iqbal, M.A., Rahman, M. 2017. Identification of marker-trait associations for lint traits in cotton. *Front Plant Sci*., 8: 86.

Iqbal, M.J., Aziz, N., Saeed, N. A., Zafar, Y. 1997. Genetic diversity evaluation of some elite cotton varieties by RAPD analysis. *Theor. Appl.Genet*., 94: 139-144.

Iqbal, M.J., Aziz, N., Saeed, N.A., Zafa, Y., Malik, K.A. 2001. Genetic diversity evaluation of some elite cotton cultivars by RAPD analysis. *Theo. Applied Gene*., 94:139-144.

Islam, A., Gregory, N., Thyssen, Johnie, N., Jenkins, J.J., Linghe, Zeng., Christopher, D., Delhom., McCarty, J.C., Dewayne, D., Deng., Hinchliffe, D.J., Jones, DC., Fang, D.D. 2016a. A MAGIC population-based genome-wide association study reveals functional association of GhRBB1_A07 gene with superior fiber quality in cotton. *BMC Genomics*, 17:903.

Islam, M., Zeng, L., Thyseen, G., Delhom, C., Kim, H., Li, P., Fang, D.D. 2016b. Mapping by sequencing in cotton (*Gossypium hirsutum*) line MD52ne identified genes for fiber strength and its related quality attributes. *Theor. Appl. Genet*., 129: 1071-1086.

Islam, M.S., Thyssen, G.N., Jenkins, J.N., Fang, D.D. 2015. Detection, validation, and application of genotyping-by-Sequencing based single nucleotide polymorphisms in upland cotton. *The Plant Genome*, 8:1-10.

Jacobson, T., Smith, G. 2001. Cotton Renaissance: a study in market innovation. New York: Cambridge Univeristy press.

Jamshed, M., Fei, J., Gong, J., Palanga, K.K., Shi, Y., Li, J., Shang, H., Liu, A., Chen, T., Zhang, Z., Cai, J., Ge, Q., Liu, Z., Lu, Q., Deng, X., Tan, Y., Rashid, H., Sarfraz, Z., Hassan, M., Gong, W., Yuan, Y. 2016. Identification of stable quantitative trait loci (QTLs) for fiber quality traits across multiple environments in *Gossypium hirsutum* recombinant inbred line population. *BMC Genomics*, 17, 197.

Jenkins, J.N., McCarty, J.C., J. Wu., Gutierrez, O.A. 2009. Genetic variance components and genetic effects among eleven diverse upland cotton lines and their F_2 hybrids. *Euphytica*, 167:397-408.

Jiang, C.X., Chee, P.W., Draye, X., Morrell, P.L., Smith, C.W., Paterson, A.H. 2000. Multi-locus interactions restrict gene introgression in interspecific populations of polyploid *Gossypium* (cotton). *Evolution.*, 54: 798-814.

Johnson, H.W., Robinson, H.F. Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agron. J*., 47: 314-318.

Joshi C.P., Nguyen H.T. 1993. RAPD (random amplified polymorphic DNA) analysis based inter varietal genetic relationships among hexaploid wheats, *Plant Science*, 93(1): 95-103.

Joy, K., Smith, C.W., Hequet, E., Hague, S., Thaxton, P.S., Souder, C. 2010. Fiber properties and mini-spun yarn performance of extra-long staple upland cotton. *J. Cotton Sci*. 14: 82–90.

Kalivas, A., Xanthopoulos, F., Kehagia, Tsaftaris, A.S. 2011. Agronomic characterization, genetic diversity and association analysis of cotton cultivars using simple sequence repeat molecular markers. *Genet Mol Res*. 10: 208-217.

Kantartzi, S.K., Stewart, J.M. 2008. Association analysis of fibre traits in Gossypium arboreum accessions. *Plant Breeding*, 127: 173-179.

Karademir, C., Karademir, E., Gencer, O. 2011. Yield and fiber quality of F_1 and F_2 generations of cotton (*Gossypium hirsutum* L.) under drought stress conditions. *Bulgarian Journal of Agricultural Science*, 17(6): 795-805.

Karademir, E., Karademir, C., Ekinci, R., Gencer, O. 2010. Relationship between yield, fiber length and other fiber-related traits in advanced cotton strains. *Not. Bot. Hort. Agro bot*., 38 (3):111-116.

Karademir, C., Karademir, E., Ekinci, R., Berekatoglu, K. 2011. Yield and fiber quality properties of cotton (*Gossypium hirsutum* L.) under water stress and non-stress conditions. *African Journal of Biotechnology*, 10(59): 12575-12583.

Kaushik, S.K., Kapoor, C.J. 2010. Component analysis of upland cotton (*Gossypium hirsutum* L.) in different environments. *IUP Journal of Genetics & Evolution*; 56: 49-56.

Kerby, T.A., Hugie, W.V. 2006. Yield and quality improvement of significant D&PL varieties during the last 25 years. In Proc. Beltwide Cotton Conf. San Antonio, TX 3-6 Jan 2006 National Cotton Council Memphis, TN. pp: 858-865.

Khan, F.U.Z., Rehman, S.U., Abid, M.A., Malik, W., Hanif, C.M., Bilal, M., Qanmber, Latif, G.A., Ashraf, J., Farhan, U. 2015. Exploitation of germplasm for plant yield improvement in cotton (*Gossypium hirsutum* L). J. *Green Physiology Genetics & Genomics*, 1(1): 1-10.

Khan, N.U., Marwat, K.B., Hassan, G., Farhatullah., Batool, S., Makhdoom, K., Ahmad, W., Khan, H.U. 2010. Genetic variation and heritability for cotton seed, fiber and oil traits in *Gossypium hirsutum* L. *Pak. J. of Bot*. 42(1): 615-625.

King R.C., Stansfield, W.D. 1990. A dictionary of genetics, Oxford University Press, New York, pp.188

Koebner, R.M.D., Summers R.W. 2003, 21st century wheat breeding: plot selection or plate detection? *Trends in Biotechnology*, 21(2): 59-63

Kohel, R.J., Yu, J., Park, Y.H., Lazo, G.R. 2001, Molecular mapping and characterization of traits controlling fiber quality in cotton. *Euphytica*, 121(2): 163-172.

Koli, G.P., Patil, D.V., Bagade, A.B. 2014. Comparative study for fiber quality parameters in cotton (*Gossypium sp*. L.). Int. J. Curr. Microbiol. *App. Sci*., 3(11): 628-632

Kruglyak, L. 2008. The road to genome-wide association studies. *Nat. Rev. Genet*., 9: 314-318.

Kumar, L.S. 1999. DNA markers in plant improvement: an overview, *Biotechnology Advances*, 17(2): 143-182.

Kumar, S.K., Nidagundi, J.M., Hosamani, A.C. 2017. Association analysis for seed cotton yield and fiber quality improvement in intra specific crosses of cotton (*Gossypim hirsutum* L.), *Int. J. Pure App. Biosci*., 5(2): 282-284

Kumar, P., Gupta, V.K., Misra, A.K., Modi, D.R., Pandey, B.K. 2009. Potential of molecular markers in plant biotechnology. *Plant Omics Journal*, 2: 141-162.

Kumpatla, S.P., Buyyarapu, R., Abdurakhmonov, I.Y., Mammadov, J.A. 2012. In: Abdurakhmonov I.Y., (ed.), Genomics-Assisted Plant Breeding in the 21st Century: Technological Advances and Progress, Plant Breeding, In Tech, Croatia, 131-184.

Kuraparthy, V., Bowman, D.T. 2013. Gains in breeding upland cotton for fiber quality. *J. Cotton Sci.*,

Lacape, J.M., Nguyen, T.B., Courtois, B., Belot, J.L., Giband, M., Gourlot, J.P., Gawryziak, G., Roques, S., Hau, B. 2005. QTL analysis of cotton fiber quality using multiple *G. hirsutum* × *G. barbadense* backcross generations. *Crop Sci*., 45:123–140.

Lacape, J.M., Claverie, M., Vidal, R.O., Carazzole, M.F., Guimaraes, P., Goncalo, A., Pereira, D., Ruiz, M., Pre, M., Llewellyn, D., Al-Ghazi, Y., Jacobs, J., Dereeper, A., Huguet, S., Giband, M., Lanaud, C. 2012. Deep sequencing reveals differences in the transcriptional landscapes of fiber from two cultivates species of cotton. *PLoS One*, 7(11): e48855.

Lacape, J.M., Dessauw, D., Rajab, M., Noyer, J.L., Hau, B. 2007. Microsatellite diversity in tetraploid Gossypium germplasm: assembling a highly informative genotyping set of SSRs. *Molecular Breeding*, 19:45-58.

Lacape, J.M., Llewellyn, D., Jacobs, J., Arioli, T., Becker, D., Calhoun, S., Al-Ghazi, Y., Liu, S., Palai, O., Georges, S., Giband, M., De-Assunção, H., Barroso, P.A., Claverie, M., Gawryziak, G., Jean, J., Vialle, M., Viot, C. 2010. Meta-analysis of cotton fiber quality QTLs across diverse environments in a *Gossypium hirsutum x Gossypium barbadense* RIL population. *BMC Plant Bio*., 10: 132-156.

Lande, R., Thomson, R. 1990. Efficiency of marker assisted selection in the improvement of quantitative traits. *Genetics*, 124:743-756.

Li, G., Quiros, C.F. 2001. Sequence-related amplified polymorphism (SRAP), a new marker system based on a simple PCR reaction: Its application to mapping and gene tagging in *Brassica*. *Theor. Appl. Genet*., 103:455-461.

Li, C., Dong, Y., Zhao, T., Li, L., Li, C., Yu. E., Mei, L., Daud, M.K., He, Q., Chen, J., Zhu, S. 2016. Genome-wide SNP linkage mapping and QTL analysis for fiber quality and yield traits in the upland cotton recombinant inbred lines population. *Front. Plant Sci*., 7: 1356.

Li, C., Zhang, J., Hu, G., Fu, Y., Wang, Q. 2016b. Association mapping and favorable allele mining for node of first fruiting/sympodial branch and its height in Upland cotton (*Gossypium hirsutum* L.). *Euphytica*, 210:57-88

Li, F., Fan. G., Wang, K., Sun, F., Yuan, Y., Guoli. Song., Qin, Li., Zhiying, Ma., Cairui, Lu., Zou, C., Chen, W., Liang, X., Shang, H., Liu, W., Shim C., Xiao, G., Goum C., Ye1, W., Xu. X., Zhang, X., Wei1, H., Li, Z., Zhang, G., Wang, J., Liu, K., Kohel, R.J., Percy, R.J., Yu, J.Z., Zhu, Y., Wang, J., Yu, S. 2014. Genome sequence of the cultivated *Gossypium arboreum*. *Nat. Genet*., 46:567-572.

Liu, G.Z., Mei, H.X., Wang, S., Li, X.H., Zhu, X.F., Zhang, T.Z. 2015. Association mapping of seed oil and protein contents in upland cotton. *Euphytica*, 205:637–645.

Liu, J., Yang, H., Hsieh, Y.L. 2005. Distribution of single fiber tensile properties of four cotton genotypes. *Textile Res. J*., 75:117-122.

Liu, S., Llewellyn, D.J., Stiller, W.N., Jacobs, J., Lacape, J.M., Constable, G.A. 2011. Heritability and predicted selection response of yield components and fibre properties in an interspecific derived line of cotton. *Euphytica*, 178: 309-320.

Liu, S., Saha, S., Stelly, D., Burr, B., Cantrell, R.S. 2000. Chromosomal assignment of microsatellite loci in cotton. *J. Hered*., 91: 326-332.

Lu, Y., Jessica C., Percy, R.G., Hughs, S.E., Shuxun, Y., Zhang, J. 2009. DNA polymorphisms of genes involved in fiber development in a selected set of cultivated tetraploid cotton. *Crop Sci*. 49:1695-1704.

Mackay, I., Powell, W. 2007. Methods for linkage disequilibrium mapping in crops. Trends plant sci., *Trends Plant Sci*., 12: 57-63.

Mackill, D.J., Nguyen, H.T., Zhang, J. 1999. Use of molecular markers in plant improvement programs for rainfed lowland rice. *Field Crops Res*., 64, 177–185.

Mahalingam, G., Thiyagu, K., Nadarajan, N. 2010. Estimation of Genetic Parameters for Yield and Fibre Quality Traits in Inter-Specific Crosses of Cotton (*Gossypium* spp.). WCRC-5 Proceedings Mumbai. Nov. 7-11, 2011.

Maughan, P.J., Yourstone, S.M., Jellen, E.N., Udall, J.A. 2009. SNP discovery via genome reduction, barcoding and 454-pyrosequencing in amaranth. *Plant Genome*, 2: 260-270.

May, O.L. 2000. Genetic variation for fiber quality. p. 183–229. In A.S. Basra(ed.) Cotton Fibers-Developmental biology, quality improvement, and textile processing. *Food Products* Press, New York.

May, O.L., Jividen, G.M. 1999. Genetic modification of cotton fiber properties as measured by single- and high-volume instruments. *Crop Sci*., 39:328-333.

May, O.L., Green, CC. 1994. Genetic-variation for fiber properties in elite Pee-Dee cotton populations. *Crop Sci*., 34:684-690.

May, O.L., R.A. Taylor. 1998. Breeding cottons with higher yarn tenacity. *Textile Res. J*. 68:302-307.

McCarty, J.C., Percy, R.G. 2001. Genes from exotic germplasm and their use in cultivar improvement in Gossypium hirsutum L. and G. barbadense L. pp. 65-80. In Jonkins J.J., Saha S. (ed.) Genetic improvement of cotton-emerging technologies. Sci. Publ. Enfield, NH.

McCarty, J.C.Jr., Jenkins, J.N., Tang, B., Watson, C.E. 1996. Genetic analysis of primitive cotton germplasm accessions. *Crop Sci*., 36: 581-585.

McCouch, S.R., Zhao, K., Wright, M., Tung, C.W., Ebana, K., Thomson, M., Reynolds, A., Wang, D., DeClerck, G., Ali, M.L., McClung, A., Eizenga, G., Bustamanteet, C. 2010. Development of genome-wide SNP assays for rice. *Breed Sci*., 60, 524-535.

McCreight, D.J. 1992. Cotton quality requirements for producing world-class textiles. p. 1197–1199. In Proc. Beltwide Cotton Conf., Nashville, TN. 6–10 Jan. 1992. Natl. Cotton Counc. Am., Memphis, TN.

Mei, H., Zhu, X., Zhang, T. 2013. Favorable QTL alleles for yield and its components identified by association mapping in Chinese upland cotton cultivars. *PLoS One*, 8: e82193.

Mei, M., Syed, N.H., Gao, W., Thaxton, P.M., Smith, C.W. Stelly, D.M., Chen, Z.N. 2004. Genetic mapping and QTL analysis of fiber-related traits in cotton (Gossypium). *Theor. Appl. Genet*. 108:280-291.

Meredith, W.R. 1992. RFLP association with varietal origin and heterosis. p. 607. In: D. Herber (ed.) Proc. Beltwide Cotton Prod. Res. Conf., Nashville, TN., Jan. 1992. Natl. Cotton Council Am., Memphis, TN., pp.6-10.

Meredith, W.R., 1984. Quantitative genetics. In: Cotton, Kohel, R.J. and Lewis, C.F. (eds). Agron. Monogr. 24:131-150 ASA, CSSA, and SSSA, Madison, WI.

Meredith, W.R.Jr., Culp, T.W., Robert, K.Q., Ruppenicker, G.F., Anthony, W.S., Williford, J.R. 1991. Determining future cotton variety fiber quality objectives. *Textile Res.* J., 61(16):715-720.

Meredith, W.R.Jr. 1977. Backcross breeding to increase fiber strength of cotton. *Crop Sci*. 17: 172-175.

Meredith, W.R.Jr. 2002. Factors that contribute to lack of genetic progress. Proc. Beltwide Cotton Conf. Atlanta, GA 8-13 Jan 2002. National Cotton Coun. Am, Memphis, TN. Pp: 528-532.

Meredith, W.R.Jr., Bridge, R.R. 1971. Breakup of linkage blocks in cotton, *Gossypium hirsutum* L. Crop Sci., 11: 695-698.

Meredith, W.R.Jr., Bridge, R.R. 1972. Heterosis and gene action in cotton, *Gossypium hirsutm* L. *Crop Sci*., 12:304-310.

Meredith, W.R.Jr., Heitholt, J.J., Pettigrew, W.T., Rayburn, S.T. 1997. Comparsion of obsolete and modern cultivars at two nitrogen levels. *Crop Sci*., 37: 1453-1457.

Meritt, B.T. 2014. Transgressive segregation for fiber properties of three populations in cotton. Thesis submitted for MSc. Texas A&M.

Miller, P.A., Rawlings, J.O. 1967. Selection for increased lint yield and correlated responses in upland cotton, *Gossypium hirsutum* L. *Crop Sci*. 7: 637-640

Mingbaoa, L., Xiang-mo, G., Yong-Shana, Z., Jina-boy, Y. 2016. Genetic effects on yield and fiber quality traits of 16 chromosome substitution lines in upland cotton. *J. Agric. Sci*., 7(11): 1290-1297.

Mohan, M., Nair, S., Bhagwatt, A., Karisma, T., Yano, M., Bhatia, C.R., Sasaki, T. 1997. Genome mapping, molecular markers and marker assisted selection in crop plants. *Mol. Breed*., 3: 87-103.

Murray, J.C., Verhalen, L.M. 1970. Genotype by environment interaction study of cotton in Oklahoma. *Crop Sci*., 10:197–199.

Nagaraj, B., Katageri, I.S. 2011. Genetic diversity studies in recombinant lines from interspecific cross of *G. hirsutum* x *G. barbadense*. *Karnataka J. Agric. Sci*., 24 (3):268 - 272.

Naoumkina, M.G., Thyssen, G., Fang, D.D., Hinchliffe, D.J., Florane, C., Yeater, M.K., Page, J.T., Udall, J,A. 2014. The Li2 mutation results in reduced subgenome expression bias in elongation fibers of allotetraploid cotton (*Gossypium hirsutum* L). *PLoS One*, e90830.

Nei, M., Li, W.H. 1979 Mathematical model for studying genetic variations in terms of restriction endonucleases. Proceedings of National Academy of Sciences, USA 76, 5369-5373.

Nei, M. 1972. Genetic distances between populations. *American Naturalist*, 106, 283–292.

Nei, M. 1978. Estimation of average heterozygosity and genetic distance from a small number of individuals. *Genetics*, 89, 583–590.

Nguyen, T.B., Giband, M., Brottier, P., Risterucci, A.M., Lacape, J.M. 2004. Wide coverage of the tetraploid cotton genome using newly developed microsatellite markers. *Theo. and App, Gene*. 109:167-175.

Nie X., Huang, C., You, C., Li, W., Zhao, W., Shen, C., Zhang, B., Wang, H., Yan, Z., Dai, B., Wang, M., Zhang, X., Lin, Z. 2016. Genome-wide SSR-based association mapping for fiber quality in nation-wide upland cotton inbreed cultivars in China. *BMC Genomics,* 17:1-16.

Nie, X., Tu, J., Wang, B., Zhou, X., Lin, Z. 2015. A BIL population derived from *G. hirsutum* and *G. barbadense* provides a resource for cotton genetics and breeding. *PLoS One,* 10: e0141064.

Nordborg, M., Borevitz, J.O., Bergelson, J., Berry, C.C., Chory J., Hagenblad, J., Kreitman, M., Maloof, J.N., Noyes, T., Oefner, P.J., Stahl, E.A., Weigel, D. 2002. The extent of linkage disequlibrium in *Arabdopsis thaliana*. *Nature Genetics,* 30: 190-193.

Nordborg, M., Tavare, S. 2002. Linkage disequilibrium: what history had to tell us. *Trend Genet*., 18: 83-90.

Nyquist, W.E. 1991. Estimation of heritability and prediction of selection response in plant populations. *Crit. Rev. Plant Sci*. 10: 235–322

Osman, C. 2006. Determination of yield and yield components of some cotton cultivars in semi-arid conditions. *Pak. J. of Bio. Sci*., 9(14): 2572-2578.

Paterson, A., Lander, E., Hewitt, J., Peterson, S., Lincoln, S.E., Tanksely, S.D. 1988 Resolution of quantitative traits into Mendelian factors by using a complete linkage map of restriction length polymorphisms. *Nature,* 335: 721-726.

Paterson, A.H., sarangi, Y., Menz, M., Jiang, C.X., wright, R.J. 2003. QTL analysis of genotype x environment interactions affecting cotton fiber quality. *Theor. Appl. Genet*., 106: 384-396.

Paterson, A.H., Tanksely, S.D., Sorells, S.E. 1991. DNA markers in plant improvement. *Advances in Agronomy*, 46: 39-90.

Paterson, A.H., Wendel, J.F., Gundlach, H., Guo, H., Jenkins, J., Jin, D., Danny Llewellyn, D., Showmaker, K.C., Shu, S., Udall, J., Yoo, M., Byers, R., Chen, W., Faigenboim, A.D., Duke, M.V., Gong, L., Grimwood, J., Grover, C., Grupp, K., Hu, G., Lee, T., Li, J., Lin, L., Liu, T., Marler, B.S., Page, J.T., Roberts, A.W., Romanel, E., Sanders, W.S., Szadkowski, E., Tan, X., Tang, H., Xu, C., Wang, J., Wang, Z., Zhang, D., Zhang, L., Ashrafi, H., Bedon, F., Bowers, J.E., Brubaker, C.R., Chee, P.W., Das, S., Gingle, A.R., Haigler, C.H., Harker, D., Hoffmann, L.V., Hovav, R., Jones, D.C., Lemke, C., Mansoor, S., Rahman, M., Rainville, L.N., Rambani, A., Reddy, U.K., Rong, J.K., Saranga, Y., Scheffler, B.E., Scheffler, J., Stelly, D.M., Triplett, B.A., Deynze, AV., Vaslin, M.F.S., Waghmare, V.N., Walford, S.A., Wright, R.J., Zaki, E.A., Zhang, T., Dennis, E.S., Mayer, K.F.X., Peterson, D.G., Rokhsar, D.S., Wang, X., Schmutz, J. 2012. Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibers. *Nature,* 492: 423-427.

Paudel, D.R., Hequet, D.F., Abidi, N. 2013. Evaluation of cotton fiber maturity measurements. *Industrial Crops and Products*, 45:435-44.

Peleg, Z., Fahima, T., Abbo, S., Krugman, T., Saranga, Y. 2008. Genetic structure of wild emmer wheat populations as reflected by transcribed versus anonymous SSR markers. *Genome*, 51: 187-195.

Percival, A.E. 1987. The national collection of *Gossypium* germplasm. *Southern Cooperative Series Bulletin*, 321.

Percy, R.G., Cantrell, R.G., Zhang, J. 2006. Genetic variation for agronomic and fiber properties in an introgressed recombinant inbred population of cotton. *Crop Sci*., 46: 1311-1317.

Poehlman, J.M. 1986. Breeding Field Crops. 3rd Eds. Van Nostrand Reinhold, New York, USA. pp. 724.

Poehlman, J.M., Sleper, D.A. 1995. Breeding Cotton. Breeding Field Crops Fourth Edition, Iowa State University Press/Ames, SB 185.7, 369-387.

Poland, J.A., Brown, P.J., Sorrells, M.E., Jannink, J.L. 2012. Development of high-density genetic maps for barley and wheat using a novel two-enzyme genotyping-by-sequencing approach. *PLoS One*, 7:32253

Poland, J.A., Rife, T.W. 2012. Genotyping-by-sequencing for plant breeding and genetics. *Plant Genome*, 5: 92-102.

Pritchard, J.K., Przeworski, M. 2001. Linkage disequilibrium in humans: models and data. *Am J. Hum Genet*., 69:1-14.

Pritchard, J.K., Stephens, M., Donnelly, P. 2000. Inference of population structure using multilocus genotype data. *Genetics*, 155, 945–959.

Pritchard, J.K., Stephens, M., Rosenberg, N.A., Donnelly, P. 2000. Association mapping in structured populations. *American Journal of Human Genetics*, 67, 170–181.

Qin, H., Chen, M., Yi, X., Bie, S., Zhang, C., Zhang, Y., Lan, J., Meng, Y., Yuan. Y., Jiao, C. 2015. Identification of associated SSR markers for yield component and fiber quality traits based on frame map and upland cotton collections. *PLoS One*, 10(1): 1-16.

Rafalaski, A. 2002. Applications of SNPs in crop plants. *Curr. Opin. Plant Bio*., 5(2):94-100.

Rahman, M., Asif, M., Ullah, I., Malik, K.A., Zafar, Y. 2005. Overview of cotton genomic studies in Pakistan, Plant and Animal Genome Conference XIII, San Diego, USA

Rahman, H., Murtaza, N., Shah, M.K.N. 2007. Study of cotton fiber traits inheritance under different temperature regimes. *J. Agron. Crop Sci*. 193:45-54.

Rahman, M., Rahmat, Z., Mahmood, A., Abdullah, K., Zafar, Y. 2014. "Cotton Germplasm of Pakistan," in World Cotton Germplasm Resources, ed I. Y. Abdurakhmonov (Rijeka: InTech), 137-166.

Rahman, M., Ullah, I., Ashraf, M., Stewart JM, Zafar Y. 2008. Genotypic variation for drought tolerance in cotton. *Agron. Sustain Dev*., 28:439-447.

Reddy, V.R., Baker, D.N., Reddy, K.R. 1991. Temperature effect on growth and development of cotton during the fruiting period. *Agron. J*., 83: 211-217

Reiisch, A.J., Dong, J.M., Brubaker, C.L., Stelly, D.M., Wendel, J.F., Paterson, A.H. 1994. A detailed RFLP map of cotton, *Gossypium hirsutum* x *Gossypium barbadense*: chromosome organization and evolution in a disomic polyploid genome. *Genetics*, 138: 829-847.

Roesti, M., Moser, D., Berner, D. 2013 Recombination in the three-spine stickleback genome-patterns and consequences. *Mol. Ecol*., 22: 3014–3027.

Rogers, J.S. 1972. Measures of genetic similarity and genetic distance. Studies in genetics. VII. Univ. Texas Publ. 7213,145-153.

Rong, J.K., Abbey, C., Bowers J.E., Brubaker, C.L., Chang, C., Chee, P.W., Delmonte, T.A., Ding, X., Garza. J.J., Marler, B.S., Park, C.H., Pierce, G.J., Rainey, K.M., Rastogi, V.K., Schulze, S.R., Trolinder, N.L., Wendel, J.F., Wilkins, T.A., Williams-Coplin, T.D., Wing. R.A., Wright, R.J., Zhao, X., Zhu, L., Paterson, A.H. 2004. A 3347-locus genetic recombination map of sequence-tagged sites reveals types of genome organization, transmission and evolution of cotton *Gossypium*. *Genetics*, 166: 389-417.

Rong, J., Feltus, F.A., Waghmare, V.N., Pierce, G.J., Chee, P.W., Draye, X., et al. 2007. Meta-analysis of polyplois cotton QTL shows unequal distributions of sub-genomes to a complex network of genes and gene clustered implicated in lint fiber development. *Genetics*, 176: 2577-2588.

Roychowhury, R., Taoutaou, A., Khalid, R.K., Mohamed R.A.G., Jagatpati, T. 2014. Crop improvement in the ear of climate change, In: Roychowhury (eds.), I.K International Publication Ltd.

Rungis, D., Llewellyn, D., Dennis, E.S., Lyon, B.R. 2005. Simple sequence repeat (SSR) markers reveal low levels of polymorphism (*Gossypium hirsutum* L.) cultivars. *Aus. J. Agri. Res*. 56: 301-307.

Ryser, U. 1985. Cell wall biosynthesis in differentiating cotton fibers. *Eur. J. Cell Bio*. 39: 236-256.

Saeed, A., Sarwar, G., Khan, A.M., Mahmood, K., Siddiqui, G.M., Munir, S., Akhtar, L.H. 2015. Response of cotton varieties to CLCuV under district vehari conditions. *International Journal of Innovative and Applied Research*, .3(1): 23- 31.

Saeed, F., Farooq, J., Mahmood, A., Hussain, T., Riaz, M., Ahmad, S. 2014. Genetic diversity in upland cotton for cotton leaf curl virus disease, earliness and fiber quality. *Pak. J. Agric. Res*. 27, 226-236.

Saeed, M., Wangzhen, G., Tianzhen, Z. 2014. Association mapping for salinity tolerance in cotton (*Gossypium hirsutum* L.) germplasm from US and diverse regions of China. *Aust. J. Crop Sci*. 8, 338-346.

Said, J.I., Lin, Z., Zhang, X., Song, M., Zhang, J.A. comprehensive meta QTL analysis for fiber quality, yield, yield related and morphological traits, drought tolerance, and disease resistance in tetraploid cotton. *BMC Genomics,* 2013, 14:776.

Saleem, M.F., Bilal, M.F., Awais, M., Shahid, M.Q., Anjum. S.A. 2010. Effect of nitrogen on seed cotton yield and fiber qualities of cotton (*Gossypium hirsutum* l.) cultivars. *The Journal of Animal & Plant Sciences*, 20(1): 23-27.

Sambamurthy, J. S. V., Reddy, D. M. and Reddy, K. H. G., 1985, genetic variability correlation and path analysis in cotton (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv*., 20: 133-138.

Schnable, P.S., Liu, S., Wu, W. 2013. Genotyping by next-generation sequencing. U.S. Patent Appl. No. 13/739,874.

Seelanan, T., Schnable, A., Wendel, J.F. 1997. Congruence and consensus in cotton tribe (Malvaceae). *Sys. Bot*. 22: 259-290.

Sezener, V., Bozbek, T., Unay, A., Yavas, I. 2006. Evaluation of cotton yield trials under Mediterranean conditions in Turkey. *Asian J. of Plant Sci*. 5(4): 686-689.

Sezener, V., Kabakci y., Y I., Aydin U. 2006. A clustering study on selection of parents in cotton breeding. *Asian J. of Plant Sci*. 5(6):1031-1034.

Shang, L., Liang, Q., Wang, Xiaocui, Y., Kunbo, W., Abdugheni, W., Lingling, A., Cai, M., Hua, J. 2015. Identification of stable QTLs controlling fiber traits properties in multi-environment using recombinant inbred lines in Upland cotton (*Gossypium hirsutum* L.). *Euphytica*, 205: 877.

Shanti M.L., George M.L.C., Cruz C.M.V., Bernardo, M.A., Nelson, R.J., Leung, H., Banos, L., Reddy, J.N., Sridhar R. 2001. Identification of resistance genes effective against rice bacterial blight pathogen in eastern India, *Plant Disease*, 85(5): 506-512

Shao, D., Wang, T., Zhang, H., Zhu, J., Feiyu, T. 2016. Variation, heritability and association of yield, fiber and morphological traits in a near long staple upland cotton population. *Pak. J. Bot*. 48(5): 1945-1949.

Shappley, Z.W., Jenkins, J.N., Zhu, J., McCarty, J.C. 1998. Quantitative trait loci associated with agronomic and fiber traits of upland cotton. *J. Cotton Sci*., 4:153-163.

Shen, X., Cow, Z., Singh, R., Lubbers, E.L., Smith, C.W., Paterson, A.H., Chew, P.W. 2011. Efficacy QFL-chr1 a quantitative trait locus for fiber length on cotton (Gossypium sp.). *Crop Sci*., 51:2005-2010.

Shen, X.L., Guo, W.Z., Zhu, X.F., Yuan, Y.L., Yu, J.Z., Kohel, R.J., Zhang, T.Z. 2005. Molecular mapping of QTL for fiber qualities in three diverse lines in upland cotton using SSR markers. *Mol. Breed*. 15:169-181.

Singh, P. 2004. Cotton Breeding. 2nd edition. Kalyani Publishers, New Delhi, India.

Slatkin, M. 2008. Linkage disequilibrium-understanding the evolution past and mapping the medical future. *Nat. Rev. Genet*. 9: 477-485.

Small, R.I., Ryburn, J.A., Cronn, R.C., Seelanan, T., Wendel, J.F. 1998. The tortoise and the hare: chossing between noncoding plastome and nuclear Adh sequences for phylogenetic reconstruction in a recently diverged plant group. *Am. J. Bot*., 85: 1301-1315.

Smith, C.W., Coyle, G.G. 1997. Association of fiber quality parameters and within-boll yield components in upland cotton. *Crop Sci*., 37:1775-1779.

Somers, D.J., Banks, T., Depauw, R., Fox, S., Clarke, J., Pozniak, C. McCartney, C. 2007. Genome-wide linkage disequilibrium analysis in bread wheat and durum wheat. *Genome*, 50:557-567.

Sonah, H., Bastien, M., Iquira, E., Tardivel, A., Legare, G., Boyle, B., Normandeau, E., Laroche, J., Larose, S., Jean, M., Belzileet, F. 2013. An improved genotyping by sequencing (GBS) approach offering increased versatility and efficiency of SNP discovery and genotyping. *PLoS ONE*, 8(1): 1-9.

Song, M., Fang, S., Pang, C., Wei, H., Liu, J., Yu, S. 2015. Genetic analysis of fiber quality traits in short season cotton (*Gossypium hirsutum* L). Euphytica, 202:97-108.

Spindel, J., Wright, M., Chen, C., Cobb, J., Gage, J., Harrington, S., Lorieux, M., Ahmadi, N., McCouchet, S. 2013. Bridging the genotyping gap: Using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. *Theor. Appl. Genet*., 126:2699-2716.

Hague, S.S., Smith, C.W., Berger, G., Clement, J., Jones, D.C. 2011. Variation in an Extra-Long Staple Upland X Medium Staple Upland Cotton F_2 Population. The Journal of Cotton Science 15:265-270.

Stewart J. McD. 1995. Potential for crop improvement with exotic germplasms and genetic engineering. In challenging the Future, World Cotton Research Conference, Brisbance Australia 14-17 February 1994. Constable CA and Forester NW (Eds.) CSIRO, Melbourne. pp.313-332.

Stewart, J. McD. 1986. Integrated events in the flower and fruit. pp. 261-300. In: Manuey, J. R. and J. McD. Stewart (Eds.). *Cotton phsyiology*. The Cotton Foundation, Memphis, TN.

Stuber, C.W., Polacco, M., Senior, M.L. 1999. Synergy of empirical breeding, marker-assisted selection, and genomics to increase crop yield potential. *Crop Science*, 39(6): 1571-1583.

Sugars J.E., Slosser, M.N., Parajulee, D.L., Hendrix, T.J., Henneberry, Pinchak, W.E. Cotton Aphid (Homoptera: *Aphididae*) Abundance in Relation to Cotton Leaf. Environmental Entomology, Volume 33, Issue 3, 1 June 2004, Pages 690–699,

Suh, M.W., Cui, X., Sasser, P.E. 1993. Interpretation of HVI bundle tensile properties through single fiber test results- effects of fiber slack. Proc. Beltwide Cotton Conference. 1101-1104.

Suh, M.W., Cui, X., Sasser, P.E. 1994. New understanding on HVI tensile data based in Mantis single fiber test results. Proc. Beltwide Cotton Conference. 1400-1403.

Sun, F., Zhang, J.H., Wang, S.F., Gong, W., Shi, Y., Liu, A., Li, J., Gong, J., Shang, S., Yuanet, Y. 2012. QTL mapping for fiber quality traits across multiple generations and environments in upland cotton. *Molecular Breeding*, 30, 569-582.

Sun, Z., Wang, X., Liu, Z., Gu, Q., Zhang, Y., Li, Z., Ke, H., Yang, J., Wu, J., Wu, L., Zhang, G., Zhang, C., Ma, Z. 2017. Genome-wide association study discovered genetic variation and candidate genes of fibre quality traits in *Gossypium hirsutum* L. *Plant Biotechnology Journal*, 1-15.

Swamy, M.L., Gopinath, M., Murthy, K.G.K. 2013. Line × Tester analysis for yield and yield attributes in upland cotton (*Gossypium hirsutum* L.). *Helix*. 5: 378-382

Tang, B., Jenkins, J.N., Watson, C.E., McCarty, J.C., Green, R.G. 1996. Evaluation of genetic variances, heritability, and correlations for yield and fiber traits among cotton F2 hybrid populations. *Euphytica*, 91: 315-322.

Tankley, S.D., Hewitt, J. 1988. Use of molecular markers in breeding for soluble solids in tomato- a re-examination. *Theor. And App. Genet*. 75: 811-823.

Tanksley, S.D. 1983. Molecular markers in plant breeding. *Plant Mol Biol Rep*., 1:3–8

TASSEL. 2016. User manual, trait analysis by association, evolution and linkage. www.maizegenetics.net/tassel

Thibodeauxa D., James K., Herman, S., McAlisterd, D., Cui, X. Measuring the Short Fiber Content of Cotton. *WCRC-4*. Wednesday, September 12, 2007 - 1:30 PM.

Thomas, W. 2003, Prospects for molecular breeding of barley. *Annals of Applied Biology*, 142(1): 1-12

Thornsberry, J.M., Goodman, M.M., Doebley, J., Kresovich, S., Nielson, D., Buckler, E.S. 2001. $Dwarf_8$ polymorphisms associate with variation in flowering time. *Nature Genet*., 28: 286-289.

Timmerman-Vaughan, D.A., Tomooka, N., Kaga, A., Singh, R.J., Jauhar, P.P. Azuki, B. 2004. Genetic resources, chromosome engineering, and crop improvement: Grain legumes. Boca Raton, FLCRC Press. 341-353.

Tiwari, S.C., Wilkins, T.A. 1995. Cotton (*Gossypium hirsutum* L.) seed trichomes expand via diffuse growing mechanism. *Canadian Journal of Botany*, 73: 746-757.

Tuberosa, R., Salvi, S., Sanguineti, M.C., Maccaferri, M., Giuliani, S., Landi, P. 2003. Searching for quantitative trait loci controlling root traits in maize: a critical appraisal. *Developments in Plant and Soil Science*, 101: 35-54.

Ulloa, M., Meredith, W.R. Jr. 2000. Genetic linkage map and QTL analysis of agronomic and fiber quality traits in an intraspecific population. *J. Cotton Sci*., 4: 161-170.

Ulloa, M., Robert, B., Hutmacher, R., Michael, D., Wright, S.D. 2006. Breeding for fusarium wilt race 4 resistance in cotton under field and greenhouse conditions. *The Journal of Cotton Science* 10:114-127.

Ulloa, M., Saha, S., Jenkins, J.N., Meredith, W.R.Jr., McCarty, J.C. Jr., Stelly, D.M. 2005. Chromosomal assignment of RFLP linkage groups harboring important QTLs on an intraspecific cotton (*Gossypium hirsutum* L.) joinmap. J. Here., 96(2): 132-144.

United State Department of Agriculture (USDA). http//www.usda.gov.

Usman, K., Ayatullah., Khan, N., Khan, S. 2016. Genotype-by-sowing date interaction effects on cotton yield and quality in irrigated condition of Dera Ismail Khan. *Pak. J. Bot*., 48(5): 1933-1944.

Uster Technologies. 2010. Website: http://www.uster.com/fileadmin/customer/Knowledge/Textile_Know_How/Yarn_testing/U_Lab Systems_Description_of_al_quality.pdf.

Vos, P., Hogers, R., Bleeker, M., Reijans, M., Van, D.L.T., Hornes, M., Friters, A., Pot, J., Paleman, J., Kuiper, M., Zabeau, M. 1995. AFLP: a new technique for DNA fingerprinting, *Nucleic Acids Research*, 23(21): 4407- 4414

Wang, H.M., Lin, Z.X., Zhang, X.L., Chen, W., Guo, X.P., Nie, Y.C., Li, Y.H. 2008. Mapping and quantitative trait loci analysis of verticilium wilt resistance genes in cotton. *J Integr Plant Biol*., 50(2): 174-182.

Wang, B., Guo, W., Zhu, X., Wu, Y., Huang, N., Zhang, T. 2006. QTL mapping of fiber quality in an elite hybrid derived-RIL population of upland cotton. *Euphytica,* 152: 367–378.

Wang, J., Guo, W.Z., Zhang. T.Z. 2007. QTL mapping for fiber quality properties in cotton cultivar yumian 1. *Acta Agron Sin*, 33:1915-1921

Wang, P., Zhu, Y., Song, X., Cao, Z., Ding, Y., Liu, B., Zhu, X., Wang, S., Guo, W., Zhang, T. 2012. Inheritance of long staple fiber quality traits of *Gossypium barbadense* in *G. hirsutum* background using CSILs. *Theor Appl Genet*., 124(8):1415-1428.

Wang, H., Huang, C., Guo, H., Li, X., Zhao, W., Dai, B., Yan, Z., Lin, Z. 2015. Mapping for fiber and yield traits in upland cotton under multiple environments. *PLoS ONE*, 10(6): 1-14.

Wang, K., Wang, Z., Li, F., Ye, W., Wang, J., Song, G., Yue, G., Cong, L., Shang, H., Zhu, Z., Zou, C., Li, Q., Yuan, Y., Lu, C., Wei, H., Gou, C., Zheng, Z., Yin, Y., Zhang, X., Liu, K., Wang, B., Song, C., Shi, N., Kohel, R.J., Percy, R.J., Yu, Z.Y., Zhu, Y., Wang, J., Yu, S. 2012. The draft genome of diploid cotton *Gossypium raimondii* Ulbrich. *Nat. Genet*., 44: 1098-1103.

Wang, X., Yu, Y., Sang, J., Wu, Q., Zhang, X., Lin, Z. 2013. Intraspecific linkage map construction and QTL mapping of yield and fiber quality of *Gossypium barbadense*. *Aust. J. Cop Sci*., 7:1252–1261

Weiss, K.M., Clark, A.G. 2002. Linkage disequilibrium and mapping of human traits. *Trend Genet*., 18: 19-24.

Welsh J., McClelland, M. 1990. Finger printing genomes using PCR with arbitrary primers, *Nucleic Acids Research*, 18(24): 7213-7218.

Wendel, J.F., Albert, V.A. 1992. Phylogenetics of the cotton genus (*Gossypium* L.): Characterestate weighted parsimony analysis of chloroplast DNA restriction site data and its systematic and biogeographic implications. *Syst. Bot*., 17: 115-143.

Wendel, J.F., Cronn, R.C. 2003. Polypolidy and the evolutionary history of cotton. *Advances in Agronomy*, 78: 139-186.

Wu, C.C., Jian, G.L., Wang, A.L., Liu, F., Zhang, X.L., Song, S.L., Song, Li, S.H., Chen, C.H., Wang, C.Y., Zhang, X.Z., Wang, K.B. 2010. Primary detection of QTL for verticillium wilt resistance in cotton. *Mol Plant Breeding*, 8(4): 680-686.

Xiao, J., Fang, D.D., Bhatti, M., Hendrix, B., Cantrell, R. 2010. A SNP haplotype associated with a gene resistant to Xanthomonas axonopodis pv. malvacearum in upland cotton (*Gossypium hirsutum* L.). *Mol. Breeding*., 25:593-602.

Xiao, J., Wu, K., David, D.F., Stelly, D.M., Yu, J., Roy, G.C. 2009. New SSR markers for use in cotton (*Gossypium* spp.) improvement. *J. Cotton Sci*., 13: 75-157.

Yan, J. B., Kandianis, C.B., Harjes, C.E., Bai, L., Kim, E.H., Yang, X.H., Skinner, D.J., Fu, Z., Mitchill, S., Li, Q., Fernandez, M.G.S., Zaharieva, M., Babu, R., Fu, Y., Palcious, N., Li, J., DellaPena, D., Brutnel, D., Bucler, E.S., Warburton, W.L., Rocheford, T. 2010. Rare genetic variation at Zea mayscrtRB1 increases beta-carotene in maize grain. *Nat. Genet*., 42:322-327.

Yang, L., Liu, H., Cao, M., Li, P., Wang, J., Chen, G. 2009. The inheritance of cotton yield and fiber quality characters. *Cotton Sci*., 21(3): 179-183.

Yang, X.H., Yan, J.B., Zheng, Y.P., Yu, J.M., Li, J.S. 2007. Reviews of association analysis for quantitative traits in plants. *Acta Agron Sin*., 33(4):523-30.

Yaqoob, M., Fiaz, S., Ijaz, B. 2016. Correlation analysis for yield and fiber quality traits in upland cotton. *Communications in Plant Sciences*, 6(3-4): 55-60.

Yingzhi, L., Curtissa, J., Percy, R.G., Hughsc, S.E., Shuxun, Y., Zhang J. 2008. DNA polymorphisms of genes involved in fiber development in a selected set of cultivated tetraploid cotton. *Crop Sci*., 49(5):1695-1704.

Ynturi, P., Jenkins, J.N., McCarty, J.C., Gutierrez, O.A., Saha, S. 2006. Association of rootknot nematode resistance genes with simple sequence repeat markers on two chromosomes in cotton. *Crop Science*, 46: 2670–2674.

Young, C.J.L. 2013. Comparative genomics of *Gossypium* spp. Through GBS and candidate genes-delving into the controlling factors behind photoperiodic flowering. Thesis submitted for Ph. D Texas A&M.

Yu, J., Zhang, K., Li, S., Yu, S., Zhai, M., Wu, M., Li, X., Fan, S., Song, M., Yang, D., Li, Y., Zhang, J. 2013. Mapping quantitative trait loci for lint yield and fiber quality across environments in a *Gossypium hirsutum* × *Gossypium barbadense* backcross inbred line population. *Theor. and App. Genet.*, 126: 275–287.

Yu, J., Buckler, E.S. 2006. Genetic association mapping and genome organization of maize. *Current Opinion in Biotechnology*, 17, 155-160

Yu, J., Pressoir, G., Briggs, W.H., Vroh, I., Yamasaki, B.M., Doebley, J.F., McMullen, M.D., Gaut, B.S., Nielsen, D.M., Holland, J.B., Kresovich, S., Buckler, E.S. 2006. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. *Nature Genetics*, 38, 203–208.

Yu, J.Z., Fang, D.D., Kohel, R.J., Ulloa, M., Hinze, L.L., Percy, R.G., Zhang, J., Chee, P., Scheffler, B.E, Jones, D.C. 2012. Development of a core set of SSR markers for the characterization of *Gossypium* germplasm. *Euphytica*, 187: 203-213.

Zeng, L., Meredith, W.R.Jr. 2009. Associations among lint yield, yield components, and fiber properties in an introgressed population of cotton. *Crop Sci*., 49: 1647-1654.

Zeng, L., Meredith, W.R.Jr., Gutiérrez, O.A., Boykin, D.L. 2009. Identification of associations between SSR markers and fiber traits in an exotic germplasm derived from multiple crosses among *Gossypium* tetraploid species. *Theor. Appl Genet*. 119:93–103.

Zeng, L., Meredith, W.R.Jr., Boykin, D.L. 2011. Germplasm potential for continuing improvement of fiber quality in upland cotton: combining ability for lint yield and fiber quality. *Crop Sci*., 51(1): 60-68.

Zeng, L., Meredith, W.R.Jr., Boykin, D.L. 2011. Germplasm potential for continuing improvement of fiber quality in upland cotton: combing ability for lint yield and fiber quality. *Crop Sci*. 51:60-68.

Zeng, L., Wu, J. 2012. Germplasm for genetic improvement of lint yield in Upland cotton: genetic analysis of lint yield with yield components. *Euphytica*, 187: 247-261.

Zeng, L., Meredith, W.R.Jr., Campbell, B.T., Dever, J.K., Zhang, J., Glass, K.M., Jones, A.S., Myers, G.O., Bourland, F.M. 2014. Breeding and genetics. Genotype-by-environment

interaction effects on lint yield of cotton cultivars across major regions in the U.S. cotton belt. *J. Cotton. Sci*., 18:75-84.

Zeng, Z.B. 1994. Precision mapping of quantitative trait loci. *Genetics*, 136:999–1009.

Zeng, Z.B., Weir, B.S. 1996. Statistical methods for mapping Quantitative Trait Loci. *Acta Agronomica Sinica*., 22: 535-549.

Zhang, B.L., Yang, Y.W., Chen, T.Z., Yu, W.G., Liu, T.L., Li, H., Fan, X., Ren, Y., Shen, D., Liu, L., Dou, D., Chang, Y. 2012. Island cotton GbVe1 gene encoding a receptor-like protein confers resistance to defoliating and non-defoliating isolates of *Verticilium dahliae*. *PLoS One*, 7(12): 1-10.

Zhang, T., Qian, N., Zhu, X., Chen, H., Wang, S., Mei, H., Zhang, Y. 2013. Variations and transmission of QTL alleles for yield and fiber qualities in upland cotton cultivars developed in china. *PLoS One*, 8(2): 1-12.

Zhang, T., Hu, Y., Jiang, W., Fang, L., Guan, X., Chen, Zhang, J.J., Saski, C.A., Scheffler, B.E., Stelly, D.M., Hulse-Kemp, A.M., Wan, Q., Liu, B., Liu, C., Wang, S., Pan, M., Wang, Y., Wang, D., Ye, W., Chang, L., Zhang, W., Song, Q., Kirkbride, R.C., Chen, X., Dennis, E., Llewellyn, D.J., Petersonm D.G., Thaxton, P., Jones, D.C., Wang, Q., Xu, X., Zhang, H., Wu, H., Zhou, L., Mei, Z., Chen, S., Tian, Y., Xiang, D., Li, X., Ding, J., Zuo, Q., Tao, L., Liu, Y., Li, J., Lin, Y., Hui, Y., Cao, Z., Cai, C., Zhu, X., Jiang, Z., Zhou, B., Guo, W., Li, W., Chen, F. 2015. Sequencing of allotetraploid cotton (*Gossypium hirsutum* L. acc. TM-1) provides a resource for fiber improvement. *Nat. Biotechnol*., 33: 531-537.

Zhao, X.P., Lin, Y.R., Paterson, A.H. 1994. Characterization and genetic mapping of DNA microsatellites from cotton. Plant genome II conference. Town & Country Conference Center, San Diego, January 1994

Zhnag, J., Stewart, J. McD. 2000. Economical and Rapid Method for Extracting Cotton Genomic DNA. *The Journal of Cotton S*cience, 4:193-201

Zhu, C., Gore, M., Buckler, E., Yu, J. 2008. Status and prospects of association mapping in plants. *The Plant Genome*, 1(1): 5-20.

Zulkadir, G., Bolek, Y. 2014. Polymorphism of the genes related to cotton fiber elongation. *Nevşehir Bilim ve Teknoloji Dergisi*., 3(1) 79-98

Zumba, J.X., Myers, G.O. 2008. Evaluation of the USDA shafter cotton (Gossypium spp.) collection for agronomic and fiber traits. The Journal of Cotton Science, 12:73–80

CURRICULUM VITAE

Particulars

Name, surname : Khezir Hayat Bhatti

Country : Pakistan

Date of Birth/Location : 28.06.1980/MULTAN

Martial Status : Married

Telefone : 05455766496

Fax :

Email : khezirso@gmail.com

Education

Degree	University	Graduation Date
Ph. D	KSÜ / Graduate School of Natural & Applied Sciences	2018
Postgraduate	U. A. F / University of Agriculture Faisalabab	2004
Graudate	U. A. F / University of Agriculture Faisalabab	2002
College	Govt. College Bosan Road Multan	1998

Foreign Language

English, Turkish

Articles

SCI, SSCI, AHCI indekslerine giren dergilerde yayınlanan makaleler

Bolek, Y., **Hayat, K**., Bardak, A., Azhar, M.T. 2016. Molecular Breeding of Cotton. *InTech Publishers,* Croatia.

Anjum, Z. I., **Hayat, K.,** Celik, S., Azhar, T. M., Shehzad, U., Ashraf, F., Tariq M., Mehmood, H.T., Azam, M. 2015. Development of cotton leaf curl virus tolerance varieties through interspecific hybridization. *African J. of Agri. Res*. Vol. 10(13): 1612-1627.

Diğer dergilerde yayınlanan makaleler

Celik, S., Bardak, A., Erdogan, O., Parlak, D., Ucar, R., Tekerek, H., Sever, A., **Hayat, K**.**B**. 2017. Determination of the Response of Some Cotton Varieties to Verticillium Wilt Disease Caused by *Verticillium dahliae* Kleb. Turkish Journal of Agriculture-Food Science and Technology, 5(12): 1488-1492.

Bolek, Y., Tekerek, **H., Hayat**, K., Bardak, A. 2016. Screening of Cotton Genotypes for Protein Content, Oil and Fatty Acid Composition. *Journal of Agricultural Science*; Vol. 8(5):107-121.

Bolek, Y., **Hayat, K.,** Bardak, A., Azhar M.T. 2016. Insight in the Utilization of Marker Assisted Selection in Cotton (A Review). *Molecular Plant Breeding*, 2016, Vol.7, No.10.

Anjum, Z.I., Azhar, M.T., Hayat, K., Ashraf, F., Shahzad, U., Azam, M. 2014. Development of high yielding and CLCuV resistant ulpand cotton variety "CIM-608". *Pak. J. Phytopathol*., Vol. 26 (01). 23-32.

Hakemli konferans/sempozyumların bildiri kitaplarında yer alan yayınlar

Hayat, K., Bardak, A., Ikinci, R., Bolek, Y. 2016. Molecular Tagging of QTLs for fiber quality in cotton by using SNPs. *World Cotton Research Conference*-6 May 2nd-6th, 2016 Goiana-Goias, Brazil.

Hayat, H., Bardak, A., Tekerek, H., Parlak, D., Celik, S., Sever, A. 2017. Genetic Mapping and Quantitative Trait Locus Analysis of Fiber Quality Traits Using a Multi-Parent Composite Population in Upland Cotton (*Gossypium hirsutum* L.). *International*

Conference on Agriculture, Forest, Food Sciences and Technologies (ICAFOF 2017 Cappadocia / Turkey.

Bardak, A., Fidan, M.S., Dağğeçen, E., Tekerek, H., Celik, S., Parlak, D., **Hayat, K**. 2017. Identification of markers related to gossypol contents in cotton using association mapping. *12th International Field Crops Conference on Agriculture, Forest, Food Sciences and Technologies* 12-15th September 2017 Kahramanmaras/Turkey.

Tekerek, H., Bardak, A., **Hayat, K.,** Done Parlak, Alican Sever, Sadettin Celik, Oktay Erdogan. 2017. Quantitative Trait Analysis for Verticilium Wilt Resistance in Recombinant Inbred Line of Cotton. *12th International Field Crops Conference on Agriculture, Forest, Food Sciences and Technologies* (ICAFOF 2017 Cappadocia / Turkey.

Parlak, D., Bardak, A., Guvercin, R.S., Celik, S., Tekerek, H., Sever, A., **Hayat, K.,** Daggecen, E.C. 2017. The Assessment of Earliness Related Morphological Characters in Cotton Germplasm. *12th International Field Crops Conference on Agriculture, Forest, Food Sciences and Technologies* (ICAFOF 2017 Cappadocia / Turkey.

Master Thesis:

Hayat, K. 2004. Assesment of Heat Tolerance in *Lysopersicon esculentum* L. University of Agriculture Faisalalabad. Prof. Dr. Rao Asif Ali.

APPENDIES

Appendix-I. Means for fiber quality traits in Kahramanmaras

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
11180-Glandless	35.7	28.1	81.4	5.4	0.9	34.3	5
152-F	37.1	28	83.8	5.3	0.9	32.2	4.9
153-F	42.3	27.6	82.7	5.4	0.89	28.9	6.5
2421-A	36.1	30.1	84.7	4.8	0.9	34.4	4.1
308 (CAMPO)	41.8	27.8	82.3	5.4	0.9	30.7	5.2
4SP	38.6	30.3	83.5	4.9	0.89	33.3	5.6
919 (LİDER)	43.1	27.3	83.5	4.9	0.9	31.1	4
93 FF 01	41.6	27.8	79	4.9	0.89	31.4	5.2
YB10	40.7	29	83.8	4.9	0.9	34.2	3.7
Acala-172	38.3	32.4	81	4.5	0.88	33.4	4.7
Acala-552	38.9	25.1	79.6	5.4	0.9	30.9	5.2
AK-4	32.2	25.7	84.2	5.2	0.9	30.9	4.5
Aktas-3	36.6	24.4	81.4	5.3	0.91	33.5	3.9
Albania-6172	37.7	27.1	81.3	5.4	0.91	28.6	3.4
Aleppo 1	36.1	27.6	81.8	4.2	0.88	29.2	4.1
Aleppo 40	41.1	27.3	82.5	5.9	0.92	31.1	4.7
Aydın-110	35.3	32.2	78	4.4	0.89	38.1	3.7
Azerbaycan 3038	33.6	27	81	4.4	0.88	33.2	5
Beli Izvor-432	36	27.5	83.2	5.4	0.91	32.3	3.5
Belserroms-30	36.5	31.6	84.1	5.1	0.9	34.3	4
BSC-4	39.2	27.3	83.4	5	0.89	32.5	4.8
CA-228	40.5	28.6	83.4	4.6	0.89	32.6	3.7
Carmen	39.4	29.6	83	4.7	0.89	35.5	4.1
Caskot BR-1	39	27.7	82.3	4.5	0.88	33	5
Corina	39.9	29.8	85.2	4.9	0.88	34.1	5.8
Crincle Leaf	40	27.8	76	3.5	0.86	22.5	4.3
Cırpan 603	32.7	27.8	85.5	5	0.89	37.5	5
Cukurova-1518	36.9	28.6	80.7	4.3	0.88	33.9	4
Cun S-1	36.3	25	83.1	5.3	0.9	30.8	5
Delcerro	34	31.3	83.6	4.6	0.9	49.1	3.9
Delta Opal	35.3	31.2	83.5	4.5	0.88	33.4	4.6
DP-388	37.4	28	82.1	5.1	0.89	31.6	5.1
DPL-20	39	26.9	83.3	5.4	0.91	35.3	4.6
DPL-50	33.6	27.2	83.2	5.6	0.91	33.4	4.8
DPL-5409	38.5	29.8	82.4	4.5	0.89	32.7	3.4
DPL-5614	36.4	29.5	80.8	4.9	0.89	33.9	4.9

Appendix-I. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
AB-80	47.6	29.7	84.6	5.3	0.89	32.4	5.3
Europa-1752	33.3	30.4	85.1	4.7	0.88	34.4	4.9
Fibermax 819	38.8	29.4	86.5	4.9	0.88	32	5.3
Fibermax 832	38.5	29.9	83	4.3	0.87	36.6	5.1
Fibermax 958	40.5	28.4	83.9	5.2	0.9	33.4	4.3
Garant	34.9	28.7	84	5.3	0.89	28.4	5.5
Gedera-5	40.5	29	84.2	4.4	0.87	32.1	6.1
Golda	36.7	28.3	85.2	5.8	0.9	30.7	5.3
Gurbeyms34/1	36	29	85.6	4.6	0.88	33.5	5.2
IS-2	37.1	27.9	83	5.4	0.89	30.4	6
Kahinath	37.4	28.8	84	5.9	0.91	33.6	5.3
Lachata	39.2	31	85.6	5.3	0.89	32.9	5.4
Maras92	37.6	29.9	82.9	5	0.89	34.9	4.7
Marcel leaf	35.6	25.5	81.9	5	0.88	27.1	5.7
McNair-235-612	38.2	29.3	84.3	5.2	0.89	34.8	5.3
MC Namara	35.5	28.1	84.6	5.6	0.9	32.7	5.3
NAKBC1-14/2	41.2	27.8	81.7	4.6	0.88	31.7	4.9
NATA	37.8	31.4	85.8	4.9	0.89	35.9	4.3
Nazilli 342	40.4	30.9	85.7	5	0.89	33.4	4.9
Nazilli 84S	38.2	29.4	82.7	4.8	0.88	32.3	5.2
Nazilli M-503	38.3	28.6	82.9	5.4	0.9	31.7	5.2
Nazilli (93-7)	37.2	28.3	84.5	5.4	0.9	31	4.7
Nectar free	40.3	29.6	83.7	5	0.89	33.6	4.7
Nieves	35.9	27.4	85	5.5	0.9	35.3	5.2
NSCH-777	30.7	28.3	85.2	4.9	0.88	27	7.7
Okra 201	34.4	27.5	82.4	4.8	0.88	30.8	6
Okra 204	36.7	26.1	82.7	4.9	0.89	30.2	4.8
Okra-frego	39.4	27	82.4	5.5	0.9	33	4.8
P.D. 0648	37.7	28	83.3	5	0.89	34.9	4.8
Paymaster 2379	37.5	28.5	84.1	5.7	0.9	38.7	6
Paymaster 330	35.2	27.8	83.3	5.4	0.9	33.2	5.3
R-5 (STG-6)	38.9	27.9	81.5	4.1	0.86	40.2	6.4
RKNR 261	38.1	27.9	85.5	4.6	0.87	31.1	6.1
SAHEL 1	36.6	27.3	86.1	6.1	0.91	32.8	5.1
SAYAR-314	37.7	31.1	85.6	5.5	0.89	29.9	6.4
Semer. Uzbek	36.6	27.3	84.6	5	0.88	31.7	6.1
Semu SS7G	38.7	26.7	80.5	5.2	0.88	27.6	6.3

Appendix-I. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
SG 404	37.5	27.8	82.9	4.8	0.88	26.5	4.7
SG 501	40.4	28.6	84.4	5.1	0.89	27.4	5
Sindos 80	38.7	28.5	82.6	4.8	0.88	27.1	5.6
Siocra	39.1	30.7	84.8	4.9	0.89	24.8	4.7
Sivon	43.7	29.5	82.4	5.2	0.89	31.8	5.1
Sphinx V	36.6	28.4	82.5	4.3	0.87	24.7	4.7
STG 14	38.4	29.2	81.1	4.7	0.83	28.4	7.8
Stn 8a	40.1	26.6	82	4.5	0.87	22.4	5.3
Stoneville-453	40.2	27.7	80.9	5	0.88	22.9	6.1
Suregrow 125	41.8	27.7	83.8	5.8	0.9	23.5	5.6
Sahin 2000	38.1	29.2	84.1	5.2	0.89	25.5	5.5
Tamcot CABCS	40.5	29.1	82.1	3.9	0.86	29.4	5.4
Tamcot Luxor	40.8	26.3	83.4	4.3	0.87	27.8	4.8
Tamcot Pyramid	37.3	29.4	84.2	4.8	0.88	30.9	5.5
Tamcot SP 37-N	38.2	28.5	82.1	3.8	0.86	24.7	4.8
Tamcot Sphinx	37.1	30.2	85.5	4.8	0.88	32.5	5.3
Taskend-6	35.6	28.6	84.3	4.3	0.87	25.3	4.2
YB101	41.4	30	84.9	4.8	0.89	31.7	4.3
TKY-9409	36.6	28.5	84.4	5.4	0.9	28.4	4.3
Togo	38.1	30.1	80.6	4.5	0.81	27.6	6.1
Veramine	37.1	32	86.2	5	0.89	32.2	4.1
Zeta 2	29.9	21.1	81.8	5.7	0.9	23.1	5.3
YB106	25.4	25.2	80	4.2	0.86	20.3	5
Kurak 2	38.5	28.1	81.9	5	0.88	24.4	5.1
NGF-63	37.4	30.7	85.1	4.7	0.88	29.5	4.7
Naked	5.33	0	0	0	0	0	0
Orgosta 644	32.5	28	84.6	5.1	0.89	28.1	4.2
IS 10	35.5	29.4	82.4	5.4	0.9	25.1	3.6
Samon	35.9	29.5	84.6	5	0.89	25.9	4
Ujchi 2 Uzbek	33.6	34.6	81.7	4.2	0.87	34.3	5
108F	36.7	27.8	82.5	4.3	0.87	28.3	4.6
Acala 3080	38.3	29.8	83.1	5.5	0.91	28.7	4.1
Acala S.J. 2	38	29.1	83.6	4.7	0.89	34.1	3.6
Coker 413/68	35.4	27.4	83.9	4.4	0.87	28.3	5.6
DPL 15/21	37.7	26.6	80.5	4.1	0.87	21.2	4
DPL529	38.4	29	80.6	4.5	0.88	34.9	4.1
DPL 90	40.6	28.8	81.7	5.3	0.89	32.7	4.8
Ege-69	35.2	29.9	81.3	4.5	0.87	32.7	5.3

Appendix-I. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
Extreme Okra	32.9	24.5	78.3	5	0.89	26.9	4.5
Eksi-91	40.3	27.6	81.5	5.2	0.9	30.6	4.1
Gossypollfree86	39.9	28.3	82.5	4.7	0.88	29	4
H-88029	31.8	27.7	82.7	5	0.89	29.6	4.7
Hint Ç.9	30.2	27.2	82	5.1	0.89	27.1	3.8
HYC-76/59	37.1	28.7	80.6	5.1	0.89	31.5	4.5
IS 4	34.4	28.3	83.4	5.6	0.9	34.1	5
IS 8	36.6	31.3	83.1	5.1	0.9	39.8	4.1
Kurak-1	36	28.1	81	4.4	0.87	29.7	4.9
Lockette	38	28.3	83.3	5	0.89	33.1	4.7
Nazilli 87	35.9	29.6	84.9	5.3	0.9	33.2	4.1
Özbek 142	43.6	28	78.7	6.1	0.91	29.5	4.6
Visalia Elmer	37.3	29.7	83.3	4.7	0.88	38.4	4.3
Sealand 542	34.5	30.7	83.1	4.8	0.88	34.6	4.5
Siokra 133	35.1	32.8	83.5	4.2	0.87	33.7	4.6
STN. K311	39.8	31.5	85.4	4.3	0.87	37.1	4.7
Stonville 506	34.5	29.4	84.5	5.4	0.89	33.5	5.3
YB141	29.5	24.3	81.8	4.3	0.86	28.3	5.6
Acala 44	38.7	27.2	81.3	4.4	0.87	29.9	4.2
Acala Royale	39.9	29.5	84.8	5.2	0.9	38.3	4.3
Acala1517-99	37.2	30.6	84.4	4.9	0.89	38.4	4.7
Acala Prema	38.2	29.5	84.3	4.3	0.87	35.9	4.8
Acala1517-95	37.4	28.8	82.8	5.2	0.89	30.4	4.5
Stoneville 132	40	28.1	83.1	4.7	0.88	28.7	4.9
YB149	40.9	29.4	83.4	4.8	0.89	34.4	3.8
YB150	38.1	31.2	83	4.1	0.86	35.7	5.2
YB151	21.6	29.4	82.4	4.7	0.88	31.4	4.4
YB152	36.9	29.4	82.5	3.4	0.85	37.8	4.6
YB1535	38.4	28.2	82.9	4.6	0.88	31.3	4.4
YB154	32.4	29.4	82.7	4.6	0.83	28	7
YB155	36.9	28.7	84.6	5	0.88	33.5	5.3
YB156	43	27.1	80.4	4.9	0.89	30.7	3.8
YB157	35.1	27.2	80.5	6.2	0.92	32.8	4.7
YB158	32.4	29.4	82.4	5.4	0.9	31.9	4.8
YB159	37	26.9	81.5	5.1	0.89	30.7	5.4
YB160	37.2	29.4	83.3	5.2	0.9	34.6	3.6
YB161	4.3	26.8	82.8	5.6	0.9	32.9	5.5
Gosspollfree	37.9	31.7	84.5	4.9	0.89	41.2	5

Appendix-I. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
PI 528420	34.4	23	79.4	3.7	0.85	25.9	6.1
NP-ozbek 100	40.9	28.4	85.9	4.3	0.87	38.8	5.7
TX 0175-2	29.8	27.8	82.3	5	0.89	29.9	4.8
Ozbek 105	38.7	26	82	5.3	0.9	31	4.8
TX 0175-1	34.1	24	82.2	5.5	0.9	31.4	5.2
TX 0061-2	35.9	28.6	83.3	5	0.9	34.1	4
Nazilli 07	9.7	27.1	81.8	4.7	0.88	29	5.6
Sezener 76	38.4	29.8	83	4.8	0.89	39.8	4.4
TX 0060-2	34.8	28.5	82.4	4.7	0.88	35.3	5
TX 0091-1	31.1	30	82.4	4.3	0.87	31.1	4.8
İpek 607	34.7	26.8	78.8	5.2	0.89	32	5.6
PI 528426	4.3	0	0	0	0	0	4.7
NP EGE 2009	37.5	30	84	5.1	0.89	34.8	5
PI 173332	37.6	30	83.8	3.8	0.87	31.4	4.1
PI 529128	34.4	29.9	81.2	4.4	0.88	35.9	4.8
STN498	40	28.2	83.7	4.9	0.89	31.3	4
TX 0091-2	35.8	27.1	83.8	5.5	0.9	33	4.9
GAİA	40	28.8	84.2	4.8	0.89	33.9	4.6
PI 165325	37.5	28.1	84.5	4.7	0.89	34.9	4.8
ZN243	31.8	26.8	81.3	4.9	0.89	28.7	4.7
PI 528429	9.7	22.6	84.6	5	0.88	32.9	5.9
PI 528450	27.2	21.2	81.5	5.2	0.89	36.1	5.7
PI 528525	38.3	27.4	83.3	4.6	0.88	30.7	5
GAPEAM1	36.3	31	83.5	4.6	0.88	33.3	5
PI 529869	34.3	27.9	82.9	4.8	0.89	36.5	4.1
Spears3(967)	34.4	32.1	78.4	4.2	0.88	32.5	3.8
YB193	40	28.3	82.1	5.5	0.9	37	5.1
YB194	37.2	26	81.3	5.2	0.9	37.7	4.9
YB195	37.9	27.7	83.9	5.1	0.89	33.3	4.7
YB196	37.8	26.7	80.9	5.5	0.9	32.4	5.4
YB198	37.3	28.4	80.1	4.1	0.87	27.8	4.7
TX0175-1	30.2	26.5	83.4	6	0.91	30	5.4
TX 0175-2	34.4	27.5	84.8	4.8	0.89	31.9	4.8
528875	33.6	34.1	80.5	3.9	0.88	33	3.8
Acala wild 1517	35.9	28.9	85.3	4.9	0.89	31.5	5
Ugur	41.2	26.8	83.8	5	0.89	29.3	5.1
Acala 1517-99	39.03	24.53	81	5.8	0.87	31.7	6.78

Appendix-I. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
TX 0091-2	37.5	25.1	84.4	6	0.92	32.8	4.4
YB214	32.8	22.4	82.3	4.6	0.87	24.3	5.7
YB215	27.9	24.3	80	4	0.85	29.3	6.9
YB216	24.9	21.7	79.3	4.2	0.86	21.4	6
PI 163722	38.1	28.7	82.8	4.8	0.88	30.8	5.5
PI 163615	28.1	28.8	84.1	4.4	0.87	31.8	5.4
163615	33.9	24.9	81.6	4.5	0.89	27.4	3.7
YB225	35.5	24.5	77.8	4.8	0.88	26	5.7
Krem	32.7	22.6	79.5	4.6	0.88	24.6	5.2
Acala 1517 D	32.8	33.2	85	4.4	0.89	36.9	3
ADN 123	39.3	27.1	83.5	3.5	0.85	28.6	5.8
Sealand 1	34.4	34.4	85.9	3.9	0.88	38	3.6
TMN 170	43.6	28.7	84.9	4.8	0.89	36.6	5.5
TM-1	34	27.8	84.7	4.3	0.87	30.4	5.9
Coker 312	38.7	29.1	83.1	4.9	0.89	28.5	5
Sicala 3/2	34.3	27.5	84.9	5	0.9	34.3	4.6
Tamcot H 0 95	38.4	27.1	83.5	3.8	0.87	30.1	4.6
Gossy. Nazilli	39.8	28.9	83.3	4.9	0.89	29.3	4.5
Cooker 100 Ahıl	40	28.6	84	4.6	0.88	27.5	5.1
Naz. 954	42.5	27.5	84.4	5.3	0.9	29.3	5.2
Paymaster 404	40	27.1	85.1	4.5	0.89	34	4.4
GSN 12	39.6	28.4	84.3	4.5	0.88	32	4.7
HT1	40.1	30	85	4.1	0.87	33.2	4.5
Naz 143	38.6	28.8	84.6	4.6	0.89	35.1	4.5
Emand 542	35.8	29.1	81	4.8	0.89	28.2	4.6
Flora	39.6	36	79.6	5.3	0.89	36.6	5.4
Napa	41	28.2	83.6	4.7	0.88	33.1	5.3
YB247	43.4	29	83.6	5.2	0.9	34.1	5.2
DP 493	39.9	28.3	84.6	4	0.87	29.9	4.8
H- 23	39.8	29.1	84.3	5.2	0.9	39.1	4.7
GSN 22	41.3	31.3	82.4	4	0.82	29.2	6.2
YB251	37.3	31.5	86	3.9	0.87	35.7	4
Cooker 100 A 2	36	28.7	85.6	4.4	0.87	29.2	5.1
Cabu CS 2-1-8-3	38.2	29.8	83.3	4.8	0.88	29.4	4.7
Menderes 2005	34.9	31.9	88.1	3.9	0.86	42.3	5.4
S-9	36.1	29.9	86.1	4.3	0.86	31.7	5.4
H-10	38.4	28.2	85.5	4.9	0.89	33	4.4

Appendix-I. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
DP 5111	37.3	28.4	83.5	5	0.89	32	4.8
SG 96	37	29.6	85.1	4.8	0.89	33.6	4.2
Adana 98	37.6	30.4	85.7	3.3	0.84	32.3	5.7
Cun S-2	37	27	82	2.7	0.83	29	5.1
Tamcot SP 21-9	36.5	28.2	83.1	4.4	0.87	25.3	5.3
Siokra L 22	38.3	29.4	83	3.6	0.85	33.6	4.6
Coskun-1	37.9	30.5	86.4	4	0.85	30.9	6.7
DKG 658	37	29.2	83.8	4.5	0.87	30.4	4.5
Naz M 39	38.5	28.2	87.6	5	0.88	33	5.8
DP 396	39.1	29.2	86.9	5	0.88	36.2	5.3
DP419	39.5	29.6	84.7	4	0.85	33.5	6.7
Primera	40.8	29	86.5	5	0.87	30.5	6.3
Veret	37.3	30.7	84.6	4.3	0.88	37.4	4
BA 525	38.2	29	83.5	4.7	0.88	31.3	4.8
DP 5690	35	29.7	83.9	5.1	0.88	32.2	5.5
SJU 86	40.4	31.7	86.1	4.5	0.88	35.9	4.2
Blightmaster	33.8	30.6	84	4.7	0.88	33	4.9
Sicala 33	42.3	28.2	84.6	4.2	0.87	29.1	4.7
HT2	35.9	30.1	85.2	4.2	0.87	36.7	5
Dicle 2002	37	29.3	86.9	5	0.89	31.6	4.5
Semu 55/6	34.6	28.1	84.4	4.4	0.87	27.9	5.1
Tropical 225	37.7	30.7	84.2	4.6	0.87	29.4	5.2
STV 373	38.4	29.6	85.3	4.3	0.87	30.1	5.3
Naz 84	37.5	29.9	85	4	0.86	31.5	4.8
4 SB	40	29.9	84.5	4.8	0.88	31.1	5.2
İdeal	37.5	29.2	85.2	3.7	0.85	39.9	5.3
Vurcano	36.3	29.7	85.4	4.1	0.86	29.1	5.5
STV 478	42.8	28.3	83.6	4.8	0.88	31.9	5.4
SG 1001	33.6	31.1	85	4.4	0.87	35.1	4.5
Barut 2005	39.4	27.6	84.4	4.2	0.87	28.8	5.3
Nazilli 303	38.8	27.7	84.6	4.6	0.89	30.5	4.5
Siokra 1/4	38.6	30	86.1	4.8	0.89	34.7	5.2
YB289	40.2	28.8	83.6	4.5	0.88	32.5	5.3
STV 474	40.3	28.5	83	4.7	0.89	32.6	4.9
Fantom	36.1	27.5	85.3	4.7	0.89	35.9	5
Famosa	37.9	28.5	83.4	5.5	0.91	34.4	4.6
TMK 122	41.8	30.5	85.6	5.7	0.9	32	6.2

Appendix-I. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
ADN 710	40.6	28	84.4	4.1	0.87	29.4	4.5
TMN 16	39.6	30.6	85	4.5	0.88	30.8	4.8
TMS 108/2	41.4	29.6	85.3	4.9	0.89	36.5	5
ADN 712	38.9	28.2	84.1	3.3	0.85	33.1	5.6
TMN 199	40.2	29.9	86.1	5.4	0.91	37.1	4.5
Beren	38.2	28.4	82.5	4.2	0.87	30.7	4.5
Sarı Gelin	38.3	23.1	81.6	4.5	0.87	22.2	5.1
Nihal	39.6	27.5	82.5	4.1	0.87	28.6	4.7
Gelincik	38.1	23.2	82.4	4.9	0.88	22.9	5.7
TMN 18	38.7	31.2	87.2	4.2	0.87	34.4	5.2
ADN 413	40.1	28.3	85.4	4.5	0.88	34.1	5
Ozaltın 112	38.7	31.5	82.8	4.1	0.87	31	5.2
Ozaltın 404	32.7	31.6	85	4	0.88	34.8	3.8
Lodos	39.5	29.2	84.6	4.7	0.88	35.4	5.4
Flash	37.3	28.7	85.4	4.1	0.88	36.5	4.2
Carisma	39.6	29.6	83.9	4.5	0.87	30.9	5.7
Aksel	37.8	29.5	84.9	4.3	0.88	38.4	4.4
BA 440	44.6	26.6	82.9	5.1	0.89	34.4	5.7
BA 811	41.2	28.4	83.3	4.9	0.88	35.3	5.8
Lydia	39.1	28.4	85	4.2	0.87	37.4	5
PG 2018	41.2	27.5	82.7	4.7	0.89	33.5	4.3
Julia	39.6	28.5	82.7	4.3	0.88	35.1	3.8
Claudia	42.6	29.9	84.4	4.9	0.89	33.9	5.1
Carla	46.2	29.4	84.1	4.3	0.88	34.9	4.6
Candia	42.7	29.9	85.4	4.6	0.88	37.8	5.3
Gloria	39.3	29.2	85.3	4.4	0.88	40.5	4.5
Means	37	28.3	83.3	4.7	0.88	31.9	4.9
BA119	40.9	28.4	84.5	4.9	0.89	33.5	5.6
STV468	41.4	28.2	85	5.1	0.88	31.9	5.6
TEX	41.2	29.1	84.2	4.8	0.88	34	5

GOT (%): Ginning outturn; UHML: Fiber length (mm); UIN: Uniformity Index (%); MIC: Micronaire (µg inch-1); STR: Strength (g tex-1); MT: Maturity (ratio); ET: Elongation (%).

Appendix-II. Means for fiber quality traits in Diyarbakir

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
11180-Glandless	38.5	28.3	85.3	4.8	0.86	29.7	7.77
152-F	39.7	30	85	4.7	0.87	31.3	7.27
153-F	38.5	28.5	82.2	4.4	0.86	26.1	7.37
2421-A	38.7	27.5	81.9	4.2	0.86	31.2	6.47
308 (CAMPO)	39.2	26.5	85.4	4.8	0.86	28.1	7.77
4SP	37.9	29.1	83	4.5	0.86	28.7	6.57
919 (LİDER)	40.7	28.2	85.1	4.4	0.87	31	6.07
93 FF 01	38.5	26.5	81.4	4.4	0.87	24.9	5.97
YB10	39.3	27.8	81.8	4.7	0.86	29.5	5.07
Acala-172	40.1	30.7	82.9	4.6	0.84	29.8	5.87
Acala-552	35.8	24.7	82.8	5	0.88	24.4	6.27
AK-4	34.1	23.5	82	5.1	0.84	27.3	5.57
Aktas-3	39.9	24	83.7	5.2	0.87	28.9	4.97
Albania-6172	38.1	27.3	83.9	4.3	0.87	28.9	5.47
Aleppo 1	35.2	26.1	82.9	4.1	0.85	23	6.67
Aleppo 40	37.8	27.5	84.3	5.1	0.87	26.8	6.97
Aydın-110	35.5	29.2	81.8	3.5	0.85	27.9	5.27
Azerbaycan 3038	36.7	28.5	83.8	4	0.86	30.2	5.67
Beli İzvor-432	37.4	26.1	84.4	3.6	0.85	27.9	5.57
Belserroms-30	38.3	28.9	84.3	3.9	0.86	30	5.67
BSC-4	41.4	26.1	82.6	4.5	0.87	28.3	5.71
CA-228	40.4	30.2	83.9	3.6	0.85	32.8	5.07
Carmen	38.1	26	83	4.2	0.86	24.3	5.67
Caskot BR-1	39.1	26.4	82.4	4.3	0.86	24.7	6.77
Corina	38.1	28.6	82.6	4.6	0.86	26.8	7.77
Crincle Leaf	36	29	82.5	3.9	0.85	25.9	6.17
Cırpan 603	37.9	28.4	82.8	5.1	0.89	34.6	5.37
Cukurova-1518	38.8	27.4	81.8	4.4	0.86	25.9	5.95
Cun S-1	38.6	26.3	83.1	4.8	0.88	28.4	5.67
Delcerro	37	32.2	84.1	4.6	0.88	40.2	5.57
Delta Opal	35.9	30.8	82.8	4.1	0.86	29.2	5.83
DP-388	37.2	26	82.7	4.6	0.87	27.3	6.07
DPL-20	36.6	27.4	85.1	4.4	0.86	32.9	6.77
DPL-50	35.9	23.8	81.6	4.6	0.87	26.9	5.47
DPL-5409	34.7	29.3	83.6	3.9	0.85	30.9	6.06
DPL-5614	37.4	28.8	84.9	4.1	0.85	32.5	6.97

Appendix-II. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
AB-80	44.6	27.8	82.2	3.7	0.84	25.9	6.3
Europa-1752	36.8	31.7	84	4.7	0.88	30.5	4.9
Fibermax 819	38.1	28.7	83.5	4.1	0.86	29.5	5.6
Fibermax 832	36.8	31	83.8	3.9	0.86	30.5	5.6
Fibermax 958	40.2	29.6	84.9	4.8	0.88	30.8	5.6
Garant	35	29.2	84.2	4.8	0.87	30	6.4
Gedera-5	37.3	27.8	81.8	4.1	0.85	28.9	6.6
Golda	37	29.5	80.2	4.5	0.86	30.9	7.1
Gurbeyms34/1	37.2	27.1	82	4.6	0.86	26.5	7.6
IS-2	39.5	28.8	83.2	4.7	0.87	30.4	6.4
Kahinath	39.1	27.5	79.8	5.6	0.87	30.4	4.4
Lachata	42	30.2	83.3	4.8	0.87	28.5	6.3
Maras92	39.2	29.9	84.2	4.4	0.87	31.3	5.8
Marcel leaf	39.1	27.1	80.2	4.8	0.87	26.9	6.4
McNair-235-612	37.2	29	82.1	3.8	0.85	28.3	6.1
MC Namara	35.2	26.8	81.6	4.9	0.88	24.9	5.7
NAKBC1-14/2	40.8	28.7	81.3	5.1	0.87	26.9	6.7
NATA	36.2	30	83.8	3.8	0.85	33	5.7
Nazilli 342	38.2	30.1	84.6	3.6	0.85	27.6	5.6
Nazilli 84S	38.6	29.9	83.4	3.5	0.84	31	6.7
Nazilli M-503	37.3	28.8	82.6	4.7	0.88	26.3	5.2
Nazilli (93-7)	40.9	30.5	83.5	4.5	0.87	31.4	5.7
Nectar free	39.1	29	84.2	4	0.86	28.2	5.4
Nieves	37.8	27.1	84.4	4.3	0.86	28.5	6.4
NSCH-777	35.2	26.7	82	4.6	0.85	27.3	7.9
Okra 201	36.5	28.4	82.5	4.2	0.87	25.9	4.7
Okra 204	37.5	28.1	83.1	5.4	0.88	29.5	6.9
Okra-frego	35.2	28.4	84.3	5.1	0.88	31.3	6.2
P.D. 0648	37.2	29.4	85.4	3.7	0.85	30.7	5.2
Paymaster 2379	37.8	28.4	83.8	4.9	0.87	31.8	7.4
Paymaster 330	39.1	26.8	83	5.2	0.88	29.4	6.9
R-5 (STG-6)	40.1	28.9	83.5	5.1	0.88	32.2	6.8
RKNR 261	38.1	27.4	83	3.7	0.83	27.3	7.7
SAHEL 1	38.2	27.4	83.8	4.6	0.87	33.4	5.9
SAYAR-314	39.8	30.9	86.2	3.9	0.84	29.6	8.4
Semer. Uzbek	39.5	27	82.1	3.8	0.84	30.1	8.1
Semu SS7G	36.9	26.6	82.1	4.4	0.85	28.6	7.57

Appendix-II. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
SG 404	38.3	30	85.9	3.7	0.84	32.5	6.27
SG 501	38.9	30.1	85.2	4.1	0.85	33.5	6.27
Sindos 80	36.4	29.3	83.9	3.8	0.85	37.5	6.27
Siocra	41.3	31.9	83.4	3.2	0.83	32.6	5.77
Sivon	39.4	29.2	85.1	3.8	0.85	28.5	4.87
Sphinx V	36.9	29.4	83.3	3.1	0.83	28.4	5.87
STG 14	38.6	29.2	85.2	4.3	0.85	32.3	7.07
Stn 8a	37.7	28.6	84	3.8	0.84	28.6	6.47
Stoneville-453	38.6	27.8	81.6	4.2	0.85	26.2	6.17
Suregrow 125	37.3	27.5	84.6	5	0.88	28.8	5.57
Sahin 2000	37.2	30.7	85.2	4.3	0.83	29.9	9.27
Tamcot CABCS	38.6	28.8	84.1	3.7	0.84	32.3	6.67
Tamcot Luxor	42.7	27.4	80.9	3.9	0.82	31.6	5.37
Tamcot Pyramid	37.8	30.8	85	4.2	0.85	33.1	6.77
Tamcot SP 37-N	40.5	28.1	85.1	3.8	0.81	32.6	5.17
Tamcot Sphinx	41.1	28.4	84.5	4.6	0.86	36	6.37
Taskend-6	37.6	29.8	84.5	3.8	0.84	28.8	6.37
YB101	40.1	32.6	88.4	4.4	0.86	35.3	6.37
TKY-9409	36.2	30.6	85.9	4.7	0.87	34.1	5.37
Togo	37.4	29.9	85.1	4.1	0.85	32.1	5.67
Veramine	34.5	30.9	85.4	4.1	0.86	33	5.27
Zeta 2	34.4	23.8	80.7	4.4	0.85	29.9	7.07
YB106	36	26.6	80.2	3.3	0.83	27.5	6.57
Kurak 2	38.8	27.4	81.2	4	0.85	26.4	5.97
NGF-63	37	31.1	82.8	3.2	0.83	32.5	5.77
Naked	3.9	0	0	0	0	0	0
Orgosta 644	36.2	31.4	86.4	4.1	0.85	32.4	5.87
IS 10	37.2	29.7	85.3	4.3	0.86	36.4	5.67
Samon	37.5	33.2	86.1	3.9	0.85	42.4	6.57
Ujchi 2 Uzbek	36.6	28.8	84.5	4.6	0.87	29.6	5.47
108F	38	29.9	85.8	3.7	0.85	32.2	5.47
Acala 3080	37.8	33.4	85.7	4	0.86	38.5	5.17
Acala S.J. 2	36.3	31	86.1	4.8	0.88	34.6	4.87
Coker 413/68	36.7	29.5	84.5	4.1	0.85	32.1	6.27
DPL 15/21	38.3	27.6	85	4.4	0.86	29.2	5.47
DPL529	37.9	30.4	82.7	4.2	0.86	29.7	5.74
DPL 90	36.8	28.9	82.5	5	0.87	26.9	6.44

Appendix-II. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
Ege-69	36.3	28.8	79.2	5.2	0.88	28.4	5.64
Extreme Okra	33.6	26.1	80.8	4.7	0.87	23.8	5.74
Eksi-91	35	30.2	81	3.7	0.85	27.5	5.64
Gossypollfree86	37.3	28.1	83.8	3.7	0.85	25.2	5.44
H-88029	35.6	28.5	84.1	4.9	0.84	29.9	5.14
Hint Ç.9	33.4	29.5	81.9	5	0.88	27.8	5.64
HYC-76/59	37.1	28.9	80	4.4	0.85	28.4	7.74
IS 4	34.7	29.5	82.9	5	0.88	29.3	5.84
IS 8	36.1	32.5	83.4	4.7	0.87	32.9	5.34
Kurak-1	38	29.2	81.8	3.7	0.83	29	7.04
Lockette	36.8	30.2	79	4.5	0.86	28.4	6.04
Nazilli 87	34.3	29.6	81.4	5	0.88	32	5.84
Özbek 142	45.2	30.5	83.1	5.6	0.89	31.9	5.74
Visalia Elmer	38.6	29.7	83.3	4.7	0.88	37.3	5.34
Sealand 542	35.2	30.5	83.8	4.5	0.86	31	5.94
Siokra 133	37	32.2	79	4.5	0.83	30.4	5.24
STN. K311	36.4	30.4	82.4	4.9	0.87	31.5	6.64
Stonville 506	36.5	28.2	81.9	4.7	0.87	29.5	6.14
YB141	32.3	24.1	77.1	4.6	0.81	25.5	4.84
Acala 44	35	29.3	81.3	4.2	0.86	24.4	5.24
Acala Royale	39.2	27.7	81.9	4.3	0.86	30.8	5.24
Acala1517-99	33.5	32.2	84.4	4.4	0.86	32.7	5.74
Acala Prema	39.5	28.6	81.6	4.7	0.87	27.6	5.84
Acala1517-95	35.9	30.1	78.8	4	0.85	27.2	6.04
Stoneville 132	38.1	28	81.9	4.6	0.86	27.4	7.04
YB149	37.7	31	83.6	4.1	0.86	30.6	5.34
YB150	36.6	29.4	81.7	4	0.85	27.1	5.94
YB151	25.8	29.2	82.7	5	0.84	31.9	4.84
YB152	34.1	29	81.8	4.2	0.85	24.7	5.74
YB1535	34.1	29.2	82.2	4.6	0.87	27.7	5.74
YB154	34.2	31.3	81.7	3.8	0.84	29.3	6.64
YB155	35.4	29	83.3	4.5	0.86	24.8	6.54
YB156	38.7	29.9	82.7	4.5	0.86	27.6	6.64
YB157	37.2	29.5	82.1	5.6	0.89	28.6	5.54
YB158	37.2	31.1	82.6	4.3	0.85	30.2	6.74
YB159	39.7	30.4	84.2	4.2	0.85	31.1	7.04
YB160	38.3	30.6	82.4	4.7	0.87	27.4	5.34

Appendix-II. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
YB161	3.9	29.5	82.9	4.8	0.87	30.2	6.24
Gosspollfree	36.8	29.6	83.1	4.4	0.85	25.2	6.64
PI 528420	38.2	21	85.8	3.7	0.85	30.8	5.04
NP-ozbek 100	37.1	29.1	84.6	3.9	0.84	31.2	7.14
TX 0175-2	34.2	29.8	83.2	3.6	0.83	31.6	7.54
Özbek 105	39.3	27.5	82	3.9	0.84	28.7	5.84
TX 0175-1	34.4	27.6	84.1	4.5	0.86	29.7	6.44
TX 0061-2	40	30.4	84.1	4	0.86	36.5	5.14
Nazilli 07	11.3	28.6	81.9	4.1	0.85	27.1	6.34
Sezener 76	39.4	29.6	85.1	4.6	0.86	35.7	6.94
TX 0060-2	36.1	28.6	84.2	4.2	0.85	29.7	6.74
TX 0091-1	34.5	30	84.7	4.2	0.84	27.9	7.44
İpek 607	38.6	24	82.4	5.4	0.87	25.9	7.84
PI 528426	3.9	0	0	0	0	0	0
NP EGE 2009	39.5	30.7	86.7	5.1	0.83	35.7	6.04
PI 173332	41.2	29.3	82.4	4.2	0.8	32.3	5.14
PI 529128	38.6	27.9	80.3	4.1	0.84	27.2	6.74
STN498	43.1	29.1	84.8	5.1	0.87	33.4	6.34
TX 0091-2	38.7	26.6	86.3	5.4	0.81	33.7	5.84
GAİA	42.8	29.8	82.4	4.7	0.85	31.2	5.44
PI 165325	39.3	27	84.1	4.6	0.85	27.6	7.04
ZN243	34.8	27.8	84.5	4.4	0.85	32.2	7.14
PI 528429	11.3	24.47	85.9	4.7	0.86	31.7	7.5
PI 528450	31	24	75.5	4.3	0.84	31.1	7.94
PI 528525	37.2	26	82.7	3.6	0.83	28.2	7.24
GAPEAM1	35.6	27.7	84.2	4	0.84	26.9	7.34
PI 529869	36.5	31.2	85.4	4.1	0.84	30.3	7.84
Spears3(967)	38.3	35.5	83.9	3.4	0.84	34.2	5.34
YB193	38.3	27.4	81.3	3.8	0.83	27.9	7.14
YB194	41.8	27.8	85.6	4.1	0.85	30.4	6.34
YB195	36	31.3	82.3	4.6	0.86	28	6.14
YB196	35.7	27.9	83	4.6	0.85	29.5	7.14
YB198	36.1	30.5	86.4	4.2	0.85	29.4	6.04
TX0175-1	34	28.5	85	4.8	0.9	32.3	5.84
TX 0175-2	38.4	30.4	85.7	5	0.9	29	6.24
528875	36.8	33.1	84.9	4.1	0.88	30.2	5.34
Acala wild 1517	38	30.8	87.2	3.5	0.86	35.7	6.44

Appendix-II. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
Ugur	36.1	30.1	86.3	4.3	0.88	32.2	5.94
Acala 1517-99	38.7	33.6	86.5	3.4	0.84	37.1	6.35
TX 0091-2	39.6	25	80.3	5.7	0.89	32.7	4.24
YB214	34.1	28.4	83.5	3.4	0.86	30.6	6.54
YB215	30	25.5	82.7	3.1	0.84	27.6	7.54
YB216	34.5	24.7	83.1	3.7	0.86	23.8	6.74
PI 163722	40.5	28.6	84.9	4.3	0.88	29.1	5.84
PI 163615	33	31	86.2	4.4	0.89	35.2	5.74
163615	38.3	26.5	84.1	3.6	0.87	30.4	5.44
YB225	37.4	22.6	81.8	4.8	0.88	22.2	7.04
Krem	34	27.2	82.9	5.1	0.9	29.6	6.64
Acala 1517 D	36.5	33.1	85.2	3.9	0.88	36.5	4.44
ADN 123	41.7	26.8	83.8	4.3	0.88	27	6.24
Sealand 1	35.7	36.9	88.5	3.2	0.87	39.5	4.54
TMN 170	41.8	30.4	87.6	4.2	0.87	38.1	7.74
TM-1	37.2	29.9	86.3	3.2	0.85	31.9	6.24
Coker 312	37.5	31.3	85.7	4.1	0.88	34.7	5.34
Sicala 3/2	36.8	30.1	88.7	4.3	0.89	32.1	5.24
Tamcot H 0 95	39.8	29.3	84.1	3.8	0.87	31.7	6.34
Gossy. Nazilli	39.9	29.2	87.1	4.7	0.85	33.4	4.24
Cooker 100 Ahıl	37.8	29.7	86.1	4.6	0.89	27.4	5.34
Naz. 954	40.3	30.1	86.2	4.5	0.88	31.2	6.94
Paymaster 404	36.7	28	86	3.9	0.88	31.3	5.54
GSN 12	39.1	28.9	85.1	3.9	0.88	29.6	4.94
HT1	40.1	29.9	86.3	4.1	0.88	34.3	5.24
Naz 143	39.1	29.4	85	5.2	0.89	31.3	5.64
Emand 542	37.9	30.7	84.3	4.6	0.85	32.1	4.34
Flora	39.1	33.7	87.1	4.8	0.905	34.7	4.14
Napa	36.7	31	87.8	4.4	0.89	33.9	5.94
YB247	39.7	29.9	87.2	4.9	0.9	34.6	5.94
DP 493	41.2	29.1	85.5	4.6	0.89	32.5	5.54
H- 23	37.8	28.7	86	4.4	0.89	34.3	4.94
GSN 22	39.8	31.1	84.9	3.7	0.87	30.9	5.54
YB251	38.6	30.1	84.5	4.4	0.88	30.7	6.04
Cooker 100 A 2	39.3	30.1	87.3	4.4	0.84	31	5.54
Cabu CS 2-1-8-3	39.6	31.2	84.7	4.8	0.9	29.8	5.74
Menderes 2005	34.3	32.1	86.3	3.3	0.85	36.7	6.74

Appendix-II. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
S-9	36.9	30.4	83.2	4.3	0.88	26.2	5.64
H-10	36.5	30.4	83.7	4.3	0.88	28.6	5.44
DP 5111	38.4	30.4	85.6	4.6	0.88	29.2	7.14
SG 96	41.2	30	84.9	3.9	0.87	30.1	5.84
Adana 98	36.6	31.6	85.2	3.7	0.87	35.9	6.34
Cun S-2	37	28.4	84.3	3.1	0.86	24.6	5.34
Tamcot SP 21-9	38.6	28.7	83.9	3.8	0.86	29.3	6.44
Siokra L 22	40.1	30.7	81.9	4	0.88	25.9	4.64
Coskun-1	42.3	32	85.2	4.6	0.89	34	5.34
DKG 658	36.4	32.7	86.9	4.3	0.89	29.1	5.14
Naz M 39	40.8	27.4	83.3	4.9	0.89	30.3	7.04
DP 396	40.2	28.2	84.8	4.9	0.89	29.4	6.44
DP419	39.2	30.1	86.5	4.1	0.86	34.5	7.94
Primera	40.3	29.4	86.1	5.2	0.89	31.5	7.54
Veret	35.1	32.2	86	4.2	0.89	33.3	4.84
BA 525	42.1	30.3	85.6	5.1	0.9	31.6	5.44
DP 5690	38.9	29.6	85.3	4.4	0.89	33.9	5.64
SJU 86	38.1	32.6	87.2	4.1	0.87	35.3	7.24
Blightmaster	37.2	32.3	86.4	3.8	0.88	36	5.24
Sicala 33	41.6	30.7	83.5	3.8	0.87	33	5.84
HT2	36.2	32.5	84.8	3.8	0.87	34.4	6.64
Dicle 2002	37.4	27.5	83.5	3.6	0.87	25.4	5.14
Semu 55/6	39.2	30.2	86.1	3.8	0.86	31.3	7.54
Tropical 225	35.8	32.9	87.2	3.4	0.86	32.4	6.44
STV 373	39.4	31.5	86.2	3.6	0.86	30.4	7.24
Naz 84	36.4	31.7	86.4	4	0.87	30.1	6.44
4 SB	40.1	29.8	83.6	4	0.87	26.9	6.64
İdeal	39.2	31	85.5	3.9	0.87	29.6	6.24
Vurcano	37.4	30.2	85.6	4.8	0.88	30.2	7.74
STV 478	40.8	29.9	84.9	4.6	0.88	32.7	7.64
SG 1001	36.5	31.7	86.9	4.3	0.88	33.2	7.04
Barut 2005	40.6	27.8	83.6	4.6	0.87	25	6.7
Nazilli 303	39.8	28.3	82.3	4.6	0.87	28.3	6.5
Siokra 1/4	38.2	30.1	86.1	4.9	0.87	33.1	7
YB289	39.4	29	85	4.5	0.86	31.4	7.6
STV 474	41.2	28.8	84.1	4.9	0.87	27.4	7.2
Fantom	36.8	27.4	81.4	4.1	0.85	27	7.3

Appendix-II. Continue

Genotype	GOT %	SL	UI	FF	MAT	STR	ELT
Famosa	37.8	28.2	83.9	5.5	0.89	29.2	6.4
TMK 122	41.2	28.1	84.9	4.5	0.85	27	8.1
ADN 710	39	30.4	85.3	4.6	0.87	33	6.1
TMN 16	40.9	29.7	85.2	4.6	0.86	30	7.3
TMS 108/2	42.3	28.8	84.3	5.3	0.89	30.8	6.5
ADN 712	40.4	27.3	84.3	4.4	0.86	30.7	7.6
TMN 199	41	26.9	82.7	5.3	0.88	22.3	6.8
BEREN	39.8	30.4	84.5	3.5	0.84	31.4	6.5
Sarı Gelin	41.3	24.8	79.9	3.8	0.84	21.1	6.9
Nihal	37.2	26.4	81.1	4.1	0.85	27.8	6.9
Gelincik	39.8	22.8	80.8	4.5	0.86	20.9	7
TMN 18	37.9	29.5	83.8	4.5	0.86	28.1	7.1
ADN 413	39.7	27.2	82.7	4.2	0.85	28.1	7.4
Ozaltın 112	38.3	31.1	83	3.8	0.84	32	7.1
Ozaltın 404	36.8	31.2	84.2	4.2	0.87	33.4	4.6
Lodos	41.7	26.2	82.1	5.3	0.89	26.6	5.5
Flash	37.1	29.5	83.8	4.8	0.88	35.4	6.5
Carisma	40.8	29.3	83.5	4.8	0.86	30.5	8.1
Aksel	37.5	29.7	84.7	4.8	0.87	34.6	6.6
BA 440	44.4	27.4	84	4.6	0.86	35.3	8
BA 811	44.2	28.1	83	4.4	0.86	30.3	6.7
Lydia	44	28.2	80.8	4.6	0.88	37.7	5.6
PG 2018	42.8	25	82.4	5.2	0.89	26	5.7
Julia	39.3	29.2	83.3	4.4	0.87	31.2	5.7
Claudia	42	31.1	83.9	4.3	0.87	28.8	5.6
Carla	40.4	29.7	84	4.1	0.86	28.5	6.1
Candia	41.9	30.6	86.6	4.2	0.85	32.5	7.6
Gloria	43.1	29.6	82.7	4.3	0.86	32.6	6.2
Means	37.5	29	83.6	4.3	0.86	30.28	6.2
BA119	40.8	28.3	84.2	4	0.85	29.9	7.03
STV468	41.2	28.3	84.8	4.4	0.85	30.3	7.33
TEX	41.3	30.8	84.5	4.2	0.86	32.1	5.96

GOT (%): Ginning outturn; UHML: Fiber length (mm); UIN: Uniformity Index (%); MIC: Micronaire (µg inch-1); STR: Strength (g tex-1); MT: Maturity (ratio); ET: Elongation (%).

Appendix-III. Sequences for Common SNPs General linear model and Mixed Linear Model

Marker	CON-SEQUENCE
A9218	CAGCTTTTGAAGAGCATGGAACTCACAACAGTATCAAGAACAACGAMATTGGAGTATAAGTAAGCAATTAAGACCACTTCTA
A8810	CAGCATTGTGGAGATGCTCACTGGTATTGTTCCTTGGCATGGGAAATCAGCTGATGAAATTYATGACCTGGTTGTCAGAAAA
A9003	CAGCATATGCACGGTTGAAAGCTAACTCAGATTCYACTGTCACAGCAAAGCAATGTGAGATGATGCCCTTCATCTGAGACAT
A8007	CAGCTACTCTTGTTGGTCTTCAAAGCATTCCAGGGCTTCTTATCCTTTATGGAGGGTCRGTGAAGAAGAAATGGGCAGTAAA
A9388	CAGCCCATATCYAGCATTGAGCACATAAGAAAAGACATTGATTGCAACATAAATAGACATACTCACAGGGAATGTGCATGTA
A10019	CAGCTTGATTACCTGGACAGAAGTTGAAGGRTCAAGAAAAAGCTGAACCAAAGGAATCACGATAGTTTCATTCATAAAATAA
A8449	CAGCATGTGGAAGGCATTTATTTTCCCAACAAACTCCAACACCGATTGCAATCAAAATGYTTTCTTAAAAAAATGGATATTT
A8519	CAGCAGTAATTTTAAGTAGTATCAGATTTCTCRGTAATAACAAAGAGAAACCACAAAAGGGATACCATTATGAGCAACAACC
A9472	CAGCACAAATGCACCAAAATGGTGAGAGGGCTAATCACAATCAACAGTCAGCTTATCCGAGTGAAAGCAAAGGGGATGATYA
A8098	CAGCTGGTGTAAGTGGGACGGTCATCTCGTTATGGCCTAATCCAACAAGGCAAACCYTGCCACCGGCTCGAGTGGCACTCAA
A8792	CAGCAAACCAACAGTACATAACTGAAAACAAGGACAAAAAAAGCTTTGTACTTCCGAGAAACCTTTGTACTWACGCCATGAT
A9428	CAGCAATGTTGTAGTTCAAGGAATWACAATCCTCGCACCGGTAACTTCTCCAAACACTGATGGGATCAATCCAGGTGGGAAA
A9664	CAGCTCAAATTGGGTGTGGATGAGAGTTATACTTTGTTTATAACAAAGACTGGAGGGAAGTCTAYTGCTTGGGAGGCTATAA
A8250	CAGCAACCCAGTCCCAGGAGTTCTTTAGAACTCTTCAAMGATATTATAGCAATGCATATATGGATGCACAGAAACAAGATGC
A9279	CAGCCTATCCTTTCATGAGTTCAGCTGTGAATCCAAGGAGAAAAGCACTTGCRCTCTATCCTGTTTTTCTTATGTATGTATC
A8153	CAGCTGGTCGMGTATTTGGAATGCCCATCTCCCTCCTAAAGTGAAAGATTTTGTGTGGCGTTGTTTAAAGAATTTTATCCCG
A9748	CAGCTTGCAAGCTCTTGAAAAGGAGGTGCAGTCCCACCTGCATTTTYGCACCCTATTTCCGGTCCGACGAGCCGAAGAAATT
A7094	CAGCCTCTGCGACCGGCACCAAACGGGATTAGCTCGAAGTTGCGTCCGCGGAGATCGATGTCRCTTCCAATGAATCTCTCCG
A9177	CAGCTATCATAAAAGGAAGGGTGAAGACAGTAATGTAAATAAAAAGAAATTATAWGATTCCATAAAAGAGCTTCAATAATTC

Appendix-III. Continue

Marker	CON-SEQUENCE
A9613	CAGCCGCTTGCAATGTGACATGATCACCCCACTCRCCACTCCTGGCATCATTCATAGATGGTATTAACATTGCTATTCTTTT
A8065	CAGCCGGCGTCCTTCGGCTATATGTTGGCGCACGCCGTAACCGTCTTGYAAGCAATGGCCAAGTTCACGCAGGGCGTCCACG
A8070	CAGCCGCCAGGTCCAAACCAGCTTGCARTTCATCCCCCACCCTGTTGTTCTCTTGTTTCATGTTCAATATTTCGCCTTGGAA
A9840	CAGCTGTTGTGCMATTCCCATCTCCAATTTCCATGTTATCATGCTCATCTGGTGCATTGTTCAAAGAAAACGTTTGAGTTAA
A9361	CAGCAGGCAAGCAAGAGCTTGCTTACTGGCTTTGTTCAAGTAATCATCGTTGCTTAYAAAAACCGAAATCTGACATTTCCAC
A9672	CAGCCAGTTACATTAAACAAGCAAAAGACSATCAAGATTTCAATCATGGCATTGTATTTAGGGGATGTCAATAGTGTTGTTC
A9220	CAGCAGAGTCCGAGAGGAAATGGGTCCGCTTCAGCTGATTTGGATTATGTTGKTTCGCCCATGCGCCATCGTCTAGAGTTTG
A9474	CAGCTGGTCTTCAGTCTCWTCAGCTGACCCGTCTTCACAACCAACCTCAGGAACAAGAGGGTTCAAATCCCATACTTTTCCC
A9888	CAGCTAACTGTTACACTCAAAGAAACAATGAGGCCTGATTCATCTAATCTCTGCCCTAATAACMAAAATCTCAAATCTTTTT
A8751	CAGCACGAGGTAGCGCTGGATCAGTCACTCTCTTTGTTGAGATACTGAACAAGTAAATKCCTGCAAACCCTGATTGCGATGA
A9649	CAGCTCTTACATGGCTCGTCAAATTCCTTGGAGAAAACCCAGCAGTTTTGGAACAGCTTCGAGTAAAACRCTTATTCGATCT
A8819	CAGCAGAATCAACTCCAATAGCCAAGCTCGATTGCCAAGACAGATGTGGGAACGTYAGTATCCCATATCCATTTGGTACAAC
A8573	CAGCCCACTGAGTTACATAACCGGYACTTAGCGCCCTCCACCACTGGTCATCTCGGACTTGAACTATGTCCTTGAAGATCAC
A8845	CAGCCATTTGTGGCCCTAATTGAGGCCTTAAAATATACAAAWGCTTCGTTCTAATATAATGTCATTGATATGCCTCTAGGTG
A8768	CAGCCTCCGAGGACWCTTCATTGATGCATAGACTAGAAAGGTCTATATTTTCTAGCTCAACTTGACCTGCATACTGTGGATA
A7986	CAGCATCTCTCCATAGAGCCATTCCTGTTGATGAGGGGAAATTAGTTAGATACCAAAAGATTGAATGCATGGTTTGCCTTMT
A9715	CAGCCTTTATTTTATTCAGGTTGGTCTTATTCCCATCTTTTAATGATTACAGGAATATAMAAGTTGAATTATGACTTCTAAG
A9631	CAGCAGGAGGGAAYTATACAAATCTTAACAAAATGAAATGGTAGCAACTATGTAGCTTGTGAGGCGGACTGTTCATCCTTCT
A9183	CAGCTCTGGTWAATGGTGAAGGTGGTTCGGACATGGATATTTTGAGCTCTTTGATCACATCTTTGCTCAGAGGTTGTGCTGA
A9158	CAGCGGAAGCATCCAAATGTCATGGAGATACCAAGAATAGTCTCCCACTCTTTGAACATCAACCGCCATRTAATTAACAATT
A9075	CAGCCAAACTGGTTCATCATTGGTCAAAATTGCATGAAAGGCACACCTTTTTGCAACCAAGTTCCCGTGGTTTCGGTGGCRT
A9010	CAGCATACCTAGAAGCYGGAGTAGCAACCAACGCATTTATCAACGTAGGAGTTAGAGGGGATCCTTTCATCAACGACGACCA

Appendix-III. Continue

Marker	CON-SEQUENCE
A8938	CAGCTGAGAAGTTTGGRAACAAGTTTTCGTATTGCTTGGTTGATCATCTGAGCCCAAGTGACCTCGTTAACTTCCTTGTTTT
A8453	CAGCTGGGGTTGGAACTGGCTGGAGAGATGGATGGCTGTACGTCCATGGGAGAATCGTTTTCTCGACATTAATCTTCRGGAT
A8850	CAGCTCCATGAACAACTTGAGGTATGCTACTGGTAACTAAGCATTTATTTGTTTCKGTCACAAACTATGCAGGTTAACTCAA
A8251	CAGCAAGAATGCGTTGAAATGGGCTGTGGATAACGTTATCCGGAAAGGGGATCATCTTATMCTTGTTGCCGTTCGACCTGAA
A8871	CAGCAAACAAAGTAAGCACAGTATCCGAATTTGGAATTCATTGTTTTCCAGGTTGGGATATAGAAAACAAAAGARAAAGGTA
A7297	CAGCCATTTGTAATGAACTATTTTGAACAGCATTCTTGAAGAAGAAAAATGTTAGTTTTAGATTCYCCAGTAACTCTTTGAT
A7814	CAGCTGTTCAACTGCTTGATTGACAGAAAACAACRAAGAACGCCATTTTTGTAAAGCTGAAATACCATTCACTGCCAATATA
A8865	CAGCATAAAAGCTCAAAAATTGATGAAGTTGGTGCAATTAAAGTAGCAGGCTGAAAGGKTGGCTCTCTAGTTCATATTGTCT
A7927	CAGCTAAAGAGGGAGCTGAGGTCTTAATTCCTGTGACTCCTACAGACTTKAAAACTGCAAATGATAGAACAAGAATCATAGA
A7012	CAGCAGTAAGATCCTCATCYTTCTCTAATTTCATTTGTTGTGCCAAACCCAAACCAATGCATTTGAATGGGGAACCAGAGCC
A9058	CAGCAAGAATGGKTCTGCCCATGATTTGGGACAGCAGATGCCTGATTTGCATGTGGTCAGAAACCTCAATGCTTGCAGTCCT
A8388	CAGCGGCTCTTGCCATTATCATGAGGTRCAGACTTGTATCCCAAGAGATCTTTATTTTCTAAACGAGATCTTAGATTTGGAG
A8893	CAGCTAACAATGCATATTCATGGTGGTGGGCTAGTCATATCARAACAAAGCAGTCTAAATGGATGGATCAAAACCTTCAAGG
A8437	CAGCTGACATATTTCCAGGACTACCTTGCAAAAGCTGGCTGAGTAAACAAAATAAGGARGAAAAAGAATGAGAGACTCAGTC
A8669	CAGCCAAGTAGCGTGCAAGATCAGCCCAGTATTTAGTGGAGCCGAGCTCTATGTCGAAGTCTATACCATTCAACACGGCRCT
A8073	CAGCTGAACAGTTTGAGATATATCAGAGTCTTGTACCTGAAGAATTTCCGCAGAGARGGTTCCTTGATGATGTTGTACTGGA
A8299	CAGCTGGGTTTGGTTGGTCTTGGGGTCCTCTCAGTTGGCTCATTCCAAGTGAAATATTCCCCATTAAAATCCGRTCCACGGG
A9474	CAGCTGGTCTTCAGTCTCWTCAGCTGACCCGTCTTCACAACCAACCTCAGGAACAAGAGGGTTCAAATCCCATACTTTTCCC
A9349	CAGCATAAGAGACGARGAATCAATGCTAACCCCAAAGAGAAGATTGTTCTGTGGATCAGTTGCATTGTGGTAAGCAGAATAC
A8810	CAGCATTGTGGAGATGCTCACTGGTATTGTTCCTTGGCATGGGAAATCAGCTGATGAAATTYATGACCTGGTTGTCAGAAAA
A7365	CAGCAAGAGTGAGGAATTTTCTTGTGTGTGCATGTATGCATATCATTGKCTGGTTTTGTGTATTAACTTGATTGTTTTCTTC
A8098	CAGCTGGTGTAAGTGGGACGGTCATCTCGTTATGGCCTAATCCAACAAGGCAAACCYTGCCACCGGCTCGAGTGGCACTCAA

Appendix-III. Continue

Marker	CON-SEQUENCE
A9347	CAGCTTCTATTTGTACAAGTACTGAGTCTTGTATGCTTGAATTTGACCAAGGATGTGCAGGTAATGTAATAGAAAWTTTTCA
A8850	CAGCTCCATGAACAACTTGAGGTATGCTACTGGTAACTAAGCATTTATTTGTTTCKGTCACAAACTATGCAGGTTAACTCAA
A9078	CAGCAGTTGGCATCTCTCTCTGGCRATAAACTATCATCTTCTGCACATGGAATATCAGAAGAACATGCTGATGAGTTACGAA
A9279	CAGCCTATCCTTTCATGAGTTCAGCTGTGAATCCAAGGAGAAAAGCACTTGCRCTCTATCCTGTTTTTCTTATGTATGTATC
A8250	CAGCAACCCAGTCCCAGGAGTTCTTTAGAACTCTTCAAMGATATTATAGCAATGCATATATGGATGCACAGAAACAAGATGC
A9230	CAGCAATCTTYGCTCCACTAGGCATCCAGTCCAGAATAGACCCCATTAATTCCTTTGGTTCAGAGGAAGCATGTACAGCTCC
A9220	CAGCAGAGTCCGAGAGGAAATGGGTCCGCTTCAGCTGATTTGGATTATGTTGKTTCGCCCATGCGCCATCGTCTAGAGTTTG
A9796	CAGCTCTTGTGCAATTGAGGTAYAAGTTCTCACTTTGAATAAGTTTCTTGGTTGAAGAACTATGGATGCAAGAGTGTAAGTG
A8810	CAGCATTGTGGAGATGCTCACTGGTATTGTTCCTTGGCATGGGAAATCAGCTGATGAAATTYATGACCTGGTTGTCAGAAAA
A8819	CAGCAGAATCAACTCCAATAGCCAAGCTCGATTGCCAAGACAGATGTGGGAACGTYAGTATCCCATATCCATTTGGTACAAC
A9145	CAGCTCACGGTTYTTGTACCTCTTATCTTGAAGAACCTTCTTTATAGCAACAGTTTCACCCGTCTCCAAGCACTTTGCCTTT
A8573	CAGCCCACTGAGTTACATAACCGGYACTTAGCGCCCTCCACCACTGGTCATCTCGGACTTGAACTATGTCCTTGAAGATCAC
A6860	CAGCTTTTCAGCTGTTGCARGACATGTCGCCTTACGTTAAATTTGGTCACTTCACGGCCAATCAAGCCATCCTGGAAGCAGT
A8320	CAGCTGTGTGGTTCCTATAGCCACTAACAAACTCCCCCACTCGTYGTTTTCCCCTCCGGCAACCCTTTCCTTCCCACCTCAC
A7213	CTGCTCGAAAAAGTGGGTTCACAGCAGTTCCTGTCATCCATGGAAGGCTGGCAGTMGTAACAATGGCAACATGCCTTTTCCC
A6739	CTGCTGAATTTGAATGGGAGAAAGGAGAAGAAATGGAAGTTGTTACASGAGGAAGGGGCAATCTGTGGCTTTGTTGTTTTCC
A6267	CTGCAATTCCATTATTGGCCCGGAAACAAGGTCTSGTGACTGTCACGTGTGATCCGAAGAATTTGGAGCATATTTTGAAGAT
A7223	CAGCTTGTAGTTATGTACCTCTTCCAAAGTTCTAGACCAAAGAGATTTCTTTTTCAAACTCCTTACAARCTTTCTTTGTTGT
A6418	CTGCTTATTACGAAACGAAGAMGGATTGGTGTGATTTGTGGTCACAATGTATATGCGGTTTTGAAGAGTGAGATGATTCCCC
A1278	CAGCTCCAAATCTTGTAAGTAGTTTGATTGCTGTTTGAGAACGGCTTCTTTTGMATGTGGGTAAATTTTAGTTTCTTTTAAA
A3064	CAGCTTCCAAACTTTACAATACCATCATAATATTGACTTGTGGTGGTACMAAATTGCATCTAGATAATTTTGTATTAAAAAG
A6267	CTGCAATTCCATTATTGGCCCGGAAACAAGGTCTSGTGACTGTCACGTGTGATCCGAAGAATTTGGAGCATATTTTGAAGAT

Appendix-III. Continue

Marker	CON-SEQUENCE
A7498	CAGCTCGAGGCATCAAGTGTGAATGACCTCTCAGGTGTTTCAATGAGTAAAGTRTTTTCACAGCTGTTGAAATCTGAAGGCA
A3301	CAGCAGGAAATCTCCAAATTCCAAGAGAAATTTGTGTATCTGGAGGTCAAGATRGAATCCCGACTAAAGGAGCTTCGAACGG
A5859	CTGCCTCTTCGGCTGTTTCGAATGTCCCAAGCCAAACCCTTCTTTTCCTATCACAAATTATATTGAMATCAGCATCCACTAC
A3668	CAGCAGGCTCAGCTTCAGGAAATGGTTACTATRTGGACTTACAGGCAAATCAGGTTGCTTGTCTCTGAGGTGGAATAATGAA
A5424	CAGCCGCCATTCCTTTCCAAAATATCAGACCAGATCAGCTGTTGATCAGATCGAGGCCCACCTTTGGAAAACACAACCCCCY
A8810	CAGCATTGTGGAGATGCTCACTGGTATTGTTCCTTGGCATGGGAAATCAGCTGATGAAATTYATGACCTGGTTGTCAGAAAA
A9279	CAGCCTATCCTTTCATGAGTTCAGCTGTGAATCCAAGGAGAAAAGCACTTGCRCTCTATCCTGTTTTTCTTATGTATGTATC
A7935	CAGCTCCTTCTGTTTAGGTGCCACTGCATCTCTATTCCGAYCCTCCACAATCTGTTGTAGTTCTTCCATCCCGATTTCAAGC
A8155	CAGCACAGATATGAGCATGAGCAACATTCTCRACATAGGTAAAGTCAGACATATTTCCACCACTTCCTGTAATGAACTGAAA
A9003	CAGCATATGCACGGTTGAAAGCTAACTCAGATTCYACTGTCACAGCAAAGCAATGTGAGATGATGCCCTTCATCTGAGACAT
A8024	CAGCCTCAACTCTGCYGGATGATTAAGGACTAAATCCTTGATTCCCATTAATGCATCTTCAAGGAGAAGAAAACTCATATAA
A9840	CAGCTGTTGTGCMATTCCCATCTCCAATTTCCATGTTATCATGCTCATCTGGTGCATTGTTCAAAGAAAACGTTTGAGTTAA
A9078	CAGCAGTTGGCATCTCTCTCTGGCRATAAACTATCATCTTCTGCACATGGAATATCAGAAGAACATGCTGATGAGTTACGAA
A8490	CAGCGTGAAGGAATTAGACCCAATTCTGTAACAACTGCATGTATTCTCTCTGTTTGTGSTCACTTGTCAGTTAGGATTCTGT
A6428	CAGCGATTCTTTAGCACCATCTAGCTCTGAAGTAATWGTTCGCACAGACTCCAGATCGGAAGCCTTTGCACTTTCCATCTGT
A8449	CAGCATGTGGAAGGCATTTATTTTCCCAACAAACTCCAACACCGATTGCAATCAAAATGYTTTCTTAAAAAAATGGATATTT