# Retraction Notice

Title of retracted article: **Study of Genetic Diversity in Germplasm of Upland Cotton (Gossypium hirsutum L.) in Pakistan**

Author(s): Irfan Talib, Saif Ali*, Muhammad Wajid Pervez, Muhammad Umair Hassan, Rashid Hussain, Khalid Rehman, Ramla Firdous, Sajid Hussain

* Corresponding author. Email: saifbhatti63@gmail.com

Journal: American Journal of Plant Sciences (AJPS)
Year: 2015
Volume: 6
Number: 13
Pages (from - to): 2161-2167
DOI (to PDF): http://dx.doi.org/10.4236/ajps.2015.613218
Paper ID at SCIRP: 2602140
Article page: http://www.scirp.org/Journal/PaperInformation.aspx?PaperID=59257

Retraction date: 2016/1/6

**Retraction initiative** (multiple responses allowed; mark with **X**):

☐ All authors
☐ Some of the authors:
☐ Editor with hints from
- ○ Journal owner (publisher)
- ○ Institution:
- ○ Reader:
- **X** Other:

Date initiative is launched: 2016/1/6

**Retraction type** (multiple responses allowed):

☐ Unreliable findings
- ○ Lab error ○ Inconsistent data ○ Analytical error ○ Biased interpretation
- ○ Other:

☐ Irreproducible results
☐ Failure to disclose a major competing interest likely to influence interpretations or recommendations
☐ Unethical research

☐ Fraud
- ○ Data fabrication ○ Fake publication ○ Other:

☐ Plagiarism ☐ Self plagiarism ☐ Overlap **X** Redundant publication *
☐ Copyright infringement ☐ Other legal concern:

☐ Editorial reasons
- ○ Handling error ○ Unreliable review(s) ○ Decision error ○ Other:

☐ Other:

**Results of publication** (only one response allowed):

☐ are still valid.
**X** were found to be overall invalid.

**Author's conduct** (only one response allowed):

**X** honest error
☐ academic misconduct
☐ none (not applicable in this case – e.g. in case of editorial reasons)

* Also called duplicate or repetitive publication. Definition: "Publishing or attempting to publish substantially the same work more than once."

**History**
Expression of Concern:
☐ yes, date:
☐ no

Correction:
☐ yes, date:
☐ no

**Comment:**

The paper has already been published in Pakistan Journal of Agricultural Sciences in March 2015 Pak. J. Agri. Sci., Vol. 52(1), 73-77; 201. ISSN (Print) 0552-9034, ISSN (Online) 2076-0906. http://www.pakjas.com.pk/papers/2391.pdf.

This article has been retracted to straighten the academic record. In making this decision the Editorial Board follows COPE's Retraction Guidelines. Aim is to promote the circulation of scientific research by offering an ideal research publication platform with due consideration of internationally accepted standards on publication ethics. The Editorial Board would like to extend its sincere apologies for any inconvenience this retraction may have caused.

Editor guiding this retraction: Prof. Sukumar Saha (EIC of AJPS)

**American Journal of Plant Sciences, 2015, 6, 2161-2167**
Published Online August 2015 in SciRes. http://www.scirp.org/journal/ajps
http://dx.doi.org/10.4236/ajps.2015.613218



# Study of Genetic Diversity in Germplasm of Upland Cotton (*Gossypium hirsutum* L.) in Pakistan

**Irfan Talib[1], Saif Ali[2*], Muhammad Wajid Pervez[1], Muhammad Umair Hassan[2], Rashid Hussain[3], Khalid Rehman[2], Ramla Firdous[3], Sajid Hussain[1]**

[1]Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad, Pakistan
[2]Department of Agronomy, University of Agriculture, Faisalabad, Pakistan
[3]Institute of Horticultural Sciences, University of Agriculture, Faisalabad, Pakistan
Email: saifbhatti63@gmail.com

Received 30 May 2015; accepted 23 August 2015; published 28 August 2015





## Abstract

**Cotton is an important cash crop of the region which provides raw material to textile industry. There are a lot of genetic variations responsible for yield traits. Successful breeding program depends on good knowledge about genetic variation of a crop. The present research was conducted to study the genetic divergence among different accessions of the upland cotton (*Gossypium hirsutum* L.). Therefore, 50 upland cotton genotypes were grown under field condition in Randomized Complete Block Design which was replicated twice in the research area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad in 2012. At maturity, data of different related parameters were recorded according to standard procedures. The results were analyzed by using Principle Components (PC) Analysis. The $PC_1$ have 23.8%, $PC_2$ showed 16.8%, $PC_3$ exhibited 12.3% and $PC_4$ exhibited 11.9% variability among the genotypes for the traits under study. Out of ten, four PCs exhibited more than 1 Eigen value. In $PC_1$ the genotypes possessed good yield and fiber traits whereas in $PC_2$ desired yield components were observed. Moreover, $PC_3$ exhibited both yield and fiber quality traits. Seed per boll and boll per plant showed the highest heritability 99% whereas boll size showed less heritability 70% as compared to other traits. Genetic advance for seed cotton yield was recorded as the highest 46.64 followed by seed per boll 16.37 and boll per plant 15.62 whereas boll size exhibited the lowest (0.33) genetic advance.**

## Keywords

***Gossypium hirsutum*, Germplasm, Genetic Diversity, Cotton, Upland**

**How to cite this paper:** Talib, I., Ali, S., Pervez, M.W., Hassan, M.U., Hussain, R., Rehman, K., Firdous, R. and Hussain, S. (2015) Study of Genetic Diversity in Germplasm of Upland Cotton (*Gossypium hirsutum* L.) in Pakistan. *American Journal of Plant Sciences*, **6**, 2161-2167. http://dx.doi.org/10.4236/ajps.2015.613218

## 1. Introduction

Four kinds of cotton are cultivated to supply worlds' textile fiber and are vital sources of oil and cottonseed meal [1]. Cultivated species include two diploids *G. herbaceum* and *G. arboreum*, and two New World tetraploids species, *G. hirsutum* and *G. barbadense*. Genetic diversity in cultivated cotton, though, is generally considered limited [2]-[5]. Coyle and Smith [6] studied evaluate traits for within-boll lint yield components among a group of cotton genotypes, which were diverse by date of release, type of release, originating program and fiber quality parameters. Within-boll yield components were determined by direct measurement or through calculations. Tatineni *et al.* [7] and Kumar *et al.* [8] studied genetic variation among cotton genotypes resulting from interspecific hybridization at the DNA level with the random amplified polymorphic DNA (RAPD) method. Pathak and Singh [9] used six populations of different cotton cultivars ($P_1$, $P_2$, $F_1$, $F_2$, $BC_1$ & $BC_2$). Even though the primitive upland cotton accessions contain extremely useful genetic variability for varietal improvement [10], breeders have been utilizing very closely related ancestors with few economic characters in their breeding programs with less gain in productivity. It included cross of five upland cotton cultivars (*G. hirsutum* L.) to evaluate genetic dominance bases for fiber traits. The results indicated the substantial potential for improving fiber properties. In this study, therefore Principal Component Analysis (PCA) and analysis of heritability were carried out; this may help in choosing parents for a successful breeding goal. Keeping all this in view the current study was conducted to access genetic diversity in germplasm of upland cotton (*G. hirsutum* L.) in Pakistan.

## 2. Materials and Methods

Regionally adapted 50 cotton genotypes (**Table 1**) were evaluated under field conditions during summer (2012). Delinted seeds of all genotypes were grown in a twice replicated randomized complete block design at the experimental area of the Department of Plant Breeding and Genetics, University of Agriculture, Faisalabad (UAF), Pakistan. Row to row and plant to plant distances were maintained 75 and 30 cm respectively. Recommended agronomic practices were followed throughout the crop growth and developmental period. Genotypes were evaluated for number of bolls per plant (NB), number of seed per boll (S/B), seed cotton yield (SCY), seed index (SI), lint index (LI), boll size (BS), ginning out turn (GOT) from five randomly selected plants from each replication. Fiber parameters including fiber length (FL), fiber fineness (FF), fiber uniformity (FU) and fiber elongation (FE) were measured by Spin lab HVI-900 from the Department of Fiber Technology, UAF. Standard descriptors for cotton were used to measure the traits at appropriate growth stages.

## 3. Data Analysis

Data were analyzed using PCA [11]. Two data matrixes (10 × 50) for combined 10 × 25 for 1st group and 10 ×

**Table 1.** Comparison of traits.

| Traits | Mean ± Standard Error | GV | PV | EV | GCV | ECV | PCV | $h^2$ (BS) | GA |
|---|---|---|---|---|---|---|---|---|---|
| **NB** | 23.38 ± 1.12 | 125.17 | 125.82 | 0.65 | 231.38 | 16.73 | 231.98 | 0.99 | 15.62 |
| **S/B** | 33.22 ± 0.60 | 2.03 | 2.04 | 1.12 | 203.71 | 18.37 | 204.54 | 0.99 | 16.37 |
| **BS** | 3.33 ± 0.031 | 0.082 | 0.12 | 0.035 | 8.55 | 1.02 | 18.64 | 0.7 | 0.33 |
| **SCY** | 77.27 ± 3.38 | 1134.74 | 1160.11 | 25.37 | 383.21 | 57.3 | 387.47 | 0.97 | 46.64 |
| **GOT** | 36.66 ± 0.46 | 21.05 | 22.98 | 1.93 | 75.77 | 22.99 | 95.98 | 0.91 | 6.14 |
| **LI** | 4.57 ± 0.11 | 1.12 | 1.16 | 0.04 | 49.65 | 9.7 | 50.59 | 0.96 | 1.49 |
| **SI** | 7.71 ± 0.12 | 1.41 | 1.47 | 0.06 | 42.87 | 8.95 | 43.8 | 0.95 | 1.63 |
| **FU** | 50.63 ± 0.41 | 17.56 | 17.33 | 0.19 | 58.56 | 6.1 | 58.68 | 0.98 | 5.8 |
| **FL** | 28.27 ± 0.22 | 4.6 | 4.9 | 0.26 | 40.72 | 9.9 | 41.86 | 0.94 | 2.9 |
| **FE** | 10.70 ± 0.17 | 3.19 | 3.24 | 0.05 | 54.64 | 6.58 | 55.08 | 0.98 | 2.5 |
| **FF** | 5.3 ± 0.065 | 0.41 | 0.45 | 0.04 | 27.91 | 8.7 | 29.26 | 0.9 | 0.85 |

NB = Number of Bolls per Plant; S/B = Number of Seed per Boll; BS = Boll Size; SCY = Seed Cotton Yield; GOT = Ginning Out Turn; LI = Lint Index; SI = Seed Index; FU = Fiber Uniformity; FL = Fiber Length; FE = Fiber Elongation; FF = Fiber Fineness.

25 for 2nd group were prepared for the analysis. The data matrices were standardized to make the variable traits unit less for computing PCA. The character loading was used to calculate the accession component scores. The first two components were extracted for a two dimensional ordinations of accessions (**Figure 1** and **Figure 2**).

## 4. Results and Discussion

To discern patterns of variation, PCA was performed on all variables simultaneously. Eigen values well representing the variation accounted for principal components and eigenvectors indicating the correlation among principal components and original data sets have been presented in **Table 2**. Out of 10, four PCs exhibited more than 1 Eigen value (**Table 2**). The $PC_1$ have 23.8%, $PC_2$ showed 16.8%, $PC_3$ exhibited 12.3% and $PC_4$ exhibited 11.9% variability among the genotypes for the traits under study. Fiber fineness, number of bolls per plant, seed cotton yield and ginning out turn were noted as the characteristics for variability. The first principal component exhibited positive effects for GOT, number of bolls per plant, seed cotton yield and fiber length and negative for fiber fineness. The second component has positive effect for GOT% but negative effects for fiber fineness, seed cotton yield and number of bolls, which showed variation among cotton genotypes for these traits. The third

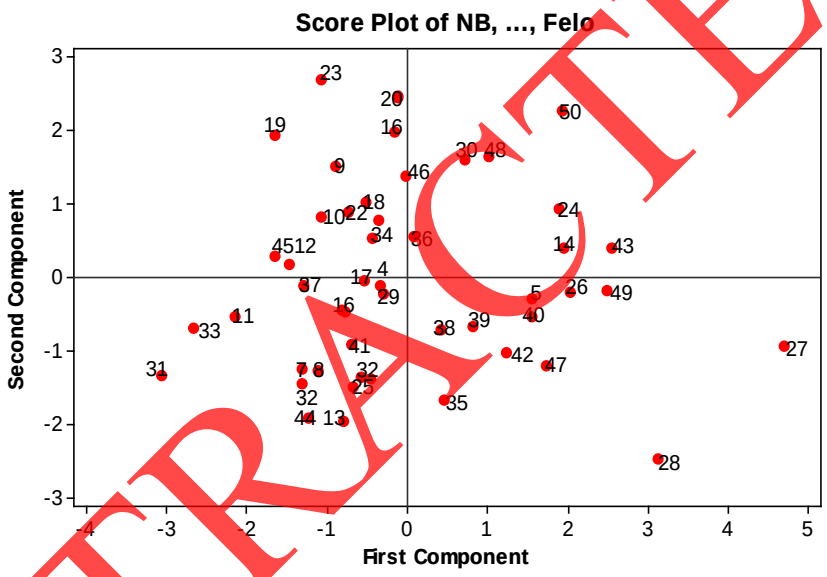


**Figure 1.** Two dimensional ordinations of 50 germplasm lines of cotton.

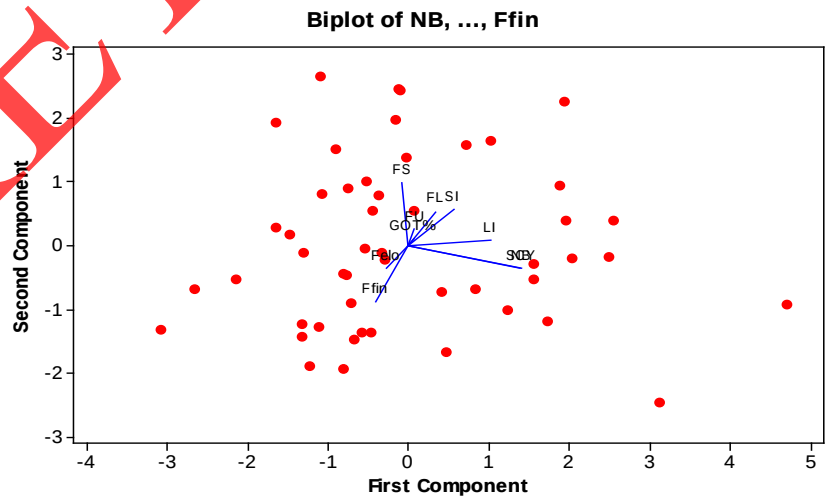


**Figure 2.** Principal component's biplot of 50 germplasm lines of cotton.

**Table 2.** Principal components (PCs) for twelve characters in 50 germplasm lines of cotton (5 - 10).

| | $PC_5$ | $PC_6$ | $PC_7$ | $PC_8$ | $PC_9$ | $PC_{10}$ |
|---|---|---|---|---|---|---|
| Eigenvalue | 0.9669 | 0.8444 | 0.6632 | 0.5301 | 0.4672 | 0.012 |
| Proportion | 0.097 | 0.084 | 0.066 | 0.053 | 0.047 | 0.001 |
| Cumulative | 0.748 | 0.833 | 0.899 | 0.952 | 0.999 | 1 |
| *Eigen vectors* | | | | | | |
| **Variables** | **$PC_5$** | **$PC_6$** | **$PC_7$** | **$PC_8$** | **$PC_9$** | **$PC_{10}$** |
| Number of bolls | −0.244 | −0.105 | 0 | 0.178 | 0.084 | −0.7 |
| Seed cotton yield | −0.224 | −0.066 | 0.005 | 0.15 | 0.07 | 0.713 |
| GOT% | 0.459 | 0.267 | 0.389 | 0.317 | −0.073 | −0.015 |
| Lint index | 0.401 | 0.126 | −0.01 | −0.371 | −0.628 | −0.027 |
| Seed index | 0.376 | 0.32 | −0.215 | 0.417 | 0.401 | 0.003 |
| Fiber uniformity | −0.1 | 0.222 | −0.322 | −0.279 | 0.323 | −0.024 |
| Fiber length | 0.344 | −0.598 | −0.401 | −0.211 | 0.131 | 0.014 |
| Fiber strength | −0.39 | −0.078 | −0.181 | 0.445 | −0.493 | 0.01 |
| Fiber elongation | 0.274 | −0.593 | 0.159 | 0.371 | 0.009 | 0.009 |
| Fiber fineness | 0.146 | 0.175 | −0.693 | 0.275 | −0.251 | −0.001 |

*PC = Principle component.

principal component exhibited positive effects for GOT, number of bolls per plant but negative effect for seed cotton yield. Among all the PCS: fiber fineness exhibited as the weighted average of the characters (**Table 2**). Among the genotypes in $PC_1$ are poor in fiber strength. Fiber elongation and fiber fineness were affected due to effect of rain. Number of bolls, seed cotton yield, lint index, seed index, GOT%, fiber strength and fiber have positive effects, these results are in the line of [12]. Yield parameters in $PC_1$ have positive effects. The traits exhibited low variability ranges from 1% to 36%. These results strengthen that the genotypes belong the same genus. In the $PC_2$ the genotypes are low in yield components i.e. number of bolls, seed cotton yield whereas Ginning out turn percentage is in desired direction. Genotypes belonging to $PC_2$ are erect type and must be given weight, fiber fineness and ginning out turn. This suggests that there will be more lint percentage (**Table 2**). $PC_3$ has variation for seed cotton yield and number of bolls per plant which are desired yield parameter, fiber fineness and fiber strength also in desired direction. All PCs exhibited low level of dissimilarity except 1st three PCs. From this study it is clear that a good hybridization breeding program can be initiated by the selection of genotypes from the $PC_1$ and $PC_2$ respectively.

## 4.1. Score Plot

A principle component scatter plot of the cotton accessions depicts that the accessions that are close together are perceived as being similar when rated on the 10 variables; accessions which are further apart are more different. Thus accessions 32 - 25, 29 - 4, 22 - 18, are very close to each other on both $PC_1$ and $PC_2$. The accessions 23, 31, 28, 27 and 50 are rather separated from other accessions. Thus accession 50 is opposite to 31 because one lies in positive region and second lies in negative region (**Figure 1**).

## 4.2. Biplot

A principal component biplot shows that variables wre super imposed on the plot as vectors; relative length of the vector represents the relative proportion of the variability in each variable represented. The variety which was far away from origin showed more variation and less similarity with other varieties. In $PC_1$ and $PC_2$ together number of bolls, seed cotton yield, GOT% and fiber uniformity are well represented in the plot but lint index, fiber strength and seed index have difference in $PC_1$ and $PC_2$ together. Number of bolls and seed cotton yield both are closely related to each other (**Figure 2**).

### 4.3. Analysis of Heritability

Genotypic and phenotypic variances, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and broad sense heritability ($h^2b$) of 17 yield and yield related traits of fifteen cotton genotypes are presented in **Table 1**. GCV ranged from 8.55 to 383.21 among all the traits which were studied. The highest value of GCV (383.21) was observed for seed cotton yield followed by number of bolls per plant (231.38) and the lowest GCV was found in fiber strength (1.82). PCV ranged from 387.47 to 231.98 among all the traits was studied. Number of bolls, seed per boll, seed cotton yield and ginning out turn showed more variation at phenotypic level. Zahid *et al.* [13] narrated similar types of findings while studying genetic variability for yield and its components in fourteen genotypes of upland cotton. Rana and Bhat [14] studied 59 cotton genotypes, 36% genetic diversity was detected. In 41 *G. hirsutum* cultivars, the average genetic resemblance was 74%. Percy *et al.* [15] examined the genetic deviation and heritability of agronomic and fiber traits among cotton genotypes. Genotype coefficients of variance (CV) were maximum for boll size and seed cotton yield. Most traits showed high broad sense heritability, ranging from 0.69 for lint yield to 0.97 for seed cotton yield. Heritability estimates in broad sense were relatively higher (more than 90%) for all the characters except boll size (0.70). High heritability estimates have been found to be useful in making selection of superior genotypes on the basis of phenotypic performance. Genetic advance value was the highest for seed cotton yield (46.64) preceded by seed per boll (16.37) and number of bolls (15.62), which showed that due to high heritability value and genetic advance, the trait which could be further improved was seed cotton yield, number of bolls, seed per boll and GOT.

### 4.4. Ward's Linkage Cluster Analysis

The letters 1 - 50 correspond to the genotypes as exhibited in the dendrogram (**Figure 3**). Two major clusters, *i.e.*, I and II, are formed by using the Wards linkage. May *et al.* [3] reported that cluster analysis identified groups of cotton cultivars that were more closely related. Menezes-Sobrinho *et al.* [16] conducted a study to characterize 89 garlic germplasm of Brazil and found 13 clusters. Similarly [17] also evaluated 65 garlic accessions and found six clusters on the basis of morphological characters. In the current study cluster-I consisted of two sub clusters *i.e*, ia and ib respectively. Sub cluster ia is further portioned into ic and id, sub cluster ic consisted of 15 genotypes whereas sub-cluster id exhibited 12 genotypes and sub cluster ib consisted of 5 genotypes, whereas Cluster-II is partitioned into two sub-clusters iia, iib. Sub-cluster iia is composed of 11 cotton genotypes whereas sub-cluster iib consists of 6 genotypes.

Accessions DPL-6 and QUALANDARI showed 92.02% similarity in sub-cluster iia. Whereas genotypes COKER-307 and FH-113 showed 87.15% similarity whereas BH-160 75.34% level of similarity with both COKER-307 and FH-113 in sub cluster ib. Similarly in sub cluster ia FH-87 and LRA-5166 showed 86.68% and with other varieties *i.e*. STONEVILLE, VH-61, VH-141 showed 61.82% similarity (**Figure 3**). Rana and Bhat

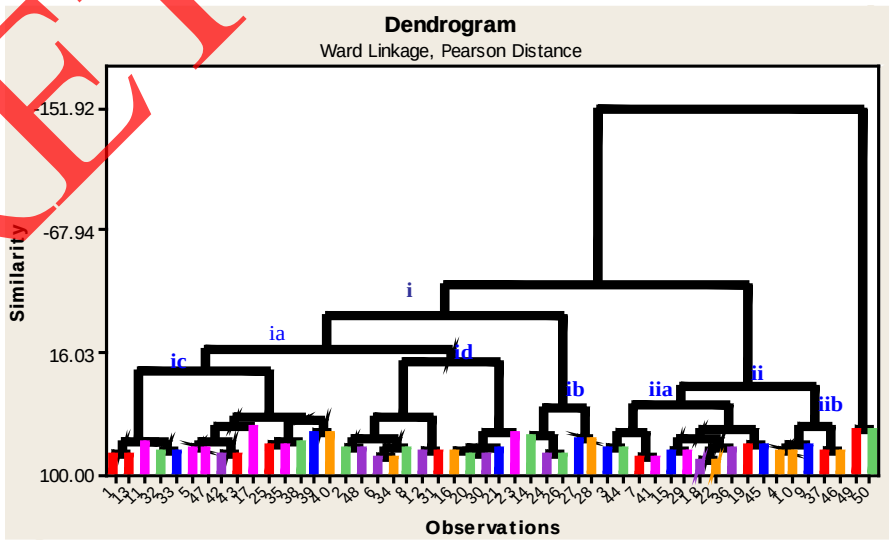


**Figure 3.** Dendrogram of 50 genotypes of *G. hirsutum* L.

[14] observed that average genetic similarity was 74% in 41 *G. hirsutum* cultivars. Aliyu *et al.* [18] reported that cluster analysis had the singular efficacy and ability to identify crop accessions with the highest level of similarity using dendrogram. Ghafoor *et al.* [19] showed multivariate analyses to be a valid system to deal with germplasm collection. Pillay and Myers [1] and Abdukarimov *et al.* [5] reported that cotton had low genetic diversity. Agronomical traits are expected to provide a general representation of variety relationship according to their growing environment.

## 5. Conclusion

The whole discussion can be concluded that variety performance of cotton germplasm did not necessarily depend on the geographical origin or even pedigree relationship. Varieties that display high phenotypic similarity need not be genetically similar because the environment can manipulate phenotypic expression.

## References


[1] Pillay, M. and Myers, G.O. (1999) Genetic Diversity in Cotton Assessed by Variation in Ribosomal RNA Genes and AFLP Markers. *Crop Science*, **39**, 1881-1886. http://dx.doi.org/10.2135/cropsci1999.3961881x

[2] Van Esbroeck, G. and Bowman, D.T. (1998) Cotton Germplasm Diversity and Its Importance to Cultivar Development. *The Journal of Cotton Science*, **2**, 121-129.

[3] May, O.L., Bowman, D.T. and Calhoun, D.S. (1995) Genetic Diversity of US Upland Cotton Cultivars Released between 1980 and 1990. *Crop Science*, **35**, 1570-1574. http://dx.doi.org/10.2135/cropsci1995.0011183X003500060009x

[4] McCarty, J.C., Jenkins, J.N. and Wu, J.X. (2005) Primitive Accession Derived Germplasm by Cultivar Crosses as Sources for Cotton Improvement. *Crop Science*, **44**, 1231-1235. http://dx.doi.org/10.2135/cropsci2004.1231

[5] Abdukarimov, A.S., Djataev, S. and Abdukarimov, I. (2003) Cotton Research in Uzbekistan: Elite Varieties and Future Cotton Breeding. *Proceedings of World Cotton Research Conference*, Cape Town, 27 September 2004, 5-15.

[6] Coyle, G.G. and Smith, C.W. (1997) Combining Ability for Within-Boll Yield Components in Cotton (*Gossypium Hirsutum* L.). *Crop Science*, **37**, 1118-1122. http://dx.doi.org/10.2135/cropsci1997.0011183X003700040014x

[7] Tatineni, V., Cantrell, R.G. and Davis, D.D. (1996) Genetic Diversity in Elite Cotton Germplasm Determined by Morphological Characteristics and RAPDs. *Crop Science*, **36**, 186-192. http://dx.doi.org/10.2135/cropsci1996.0011183X003600010033x

[8] Kumar, P., Singh, K., Vikal, Y., Randhawa, L.S. and Chahal, G.S. (2003) Genetic Diversity Studies of Elite Cotton Germplasm Lines Using RAPD Markers and Morphological Characteristics. *Indian Journal of Genetics and Plant Breeding*, **63**, 5-10.

[9] Pathak, R.S. and Singh, R.B. (1975) Genetic Analysis of the Duplicate Loci, Cluster and Short Branch in (*Gossypium hirsutum* L). *Theoretical and Applied Genetics*, **46**, 281-287.

[10] Meredith, W.R. (1990) Yield and Fiber-Quality Potential for Second-Generation Hybrids. *Crop Science*, **30**, 1045-1048. http://dx.doi.org/10.2135/cropsci1990.0011183X003000050018x

[11] Ogunbayo, S.A., Ojo, D.K., Gwei, R.G., Oyelakin, O.O. and Sanni, K.A. (2005) Phylogenetic Diversity and Relationship among 40 Rice Accessions Using Morphlogical and RAPDs Techniques. *African Journal of Biotechnology*, **4**, 1234-1244.

[12] Chen, Z.F., Zhang, Z.W. and Wang, Z.Y.L.Y.F. (1991) Study on the Correlation between the Earliness of Upland Cotton and Its Yield and Fibre Quality. *China Cotton*, **5**, 16-17.

[13] Zahid, M.A., Akhter, M., Sabar, M., Manzoor, Z. and Awan T. (2006) Correlation and Path Analysis Studies of Yield and Economic Traits in Upland Cotton. *Asian Journal of Plant Sciences*, **5**, 643-645. http://dx.doi.org/10.3923/ajps.2006.643.645

[14] Rana, M.K. and Bhat, K.V. (2005) Assessment of Genetic Diversity in Upland Cotton (*Gossypium hirsutum* L.) Breeding Lines by Using Amplified Fragment Length Polymorphism (AFLP). *Genetic Resources and Crop Evolution*, **52**, 989-997. http://dx.doi.org/10.1007/s10722-003-6113-6

[15] Percy, R.G., Cantrell, R.G. and Zhang, J. (2003) Genetic Variation for Agronomic and Fiber Properties in an Introgressed Recombinant Inbred Population of Cotton. *Crop Science*, **43**, 515-518.

[16] Menezes-Sobrino, J.A., Decharcher, J.M. and Arago, F.A.S. (1999) Morphoilogical Characterization of Garlic Germplasm by Multivariate Analysis of Principal Component and Canonic Variables. *Horticultura Brasileira*, **17**, 96-101.

[17] Lallemand, J., Messian, C.M., Briand, F. and Etoh, E. (1997) Delimitation of Varietal Groups in Garlic (*Allium sativum* L.) by Morphological, Physiological and Biochemical Characters. *Acta Horticulturae*, **433**,123-129.

[18] Aliyu, B.N., Fawal, Q. and Kohel, R.J. (2000) Inheritance of Pubescence in Crosses between *V. unguiculata* and *V. rhomboidea*. *Nigerian Journal of Genetics*, **15**, 9-14.

[19] Ghafoor, A., Sharif, A., Ahmad, Z., Zahid, M.A. and Rabbani, M.A. (2001) Genetic Diversity in Black Gram (*Vigna mungo* L.). *Field Crops Research*, **69**, 183-190. http://dx.doi.org/10.1016/S0378-4290(00)00141-6