Biological and Clinical Sciences Research Journal
eISSN: 2708-2261; pISSN: 2958-4728
www.bcsrj.com
DOI: https://doi.org/10.54112/bcsrj.v2022i1.197
Biol. Clin. Sci. Res. J., Volume, ***2022****: 197*
Original Research Article

GENETIC VARIABILITY STUDIES FOR WITHIN BOLL YIELD COMPONENTS IN COTTON (*GOSSYPIUM HIRSUTUM* L.)

NADEEM A, SHAKEEL A, IMTIAZ M, NASIR B, *KHALID MN, AMJAD I

Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, Pakistan
*Correspondence: noumankhalidpbg@gmail.com

(Received, 7th January 2022, Revised 22nd July 2022, Published 26th July 2022)

Abstract: *Cotton is a prominent fiber crop all across the world, including Pakistan. But the production of cotton is relatively low in Pakistan. As boll is the basic determinant for yield in cotton crops, the study on within-boll yield parameters was carried out using twenty exotic accessions of cotton to check their variability for within-boll yield components. The experiment was performed at the research area of the department of Plant Breeding and Genetics, University of Agriculture, Faisalabad. The genotypes were planted in three replications following a Randomized Complete Block Design (RCBD). At maturity, data were collected for different within-boll yield parameters. The analysis of variance showed significant results for nine out of eleven parameters studied. Principal component analysis revealed that genotype ZB-18015 showed maximum variation for all parameters because it was at a maximum distance from the origin, followed by genotypes ZB-18020, ZB-18019 and ZB-18018, respectively. Cluster analysis identified particular groups of genotypes that had maximum similarity with each other. In addition, the findings of the current study revealed the potential of different cotton accessions of cotton for the development of high yielding varieties. This information may be used to devise breeding strategies in the future to enhance cotton production and variety development.*

Keywords: PCA, correlation, boll yield, cotton

Introduction

Agriculture is the backbone of Pakistan's economy, contributing over 43% of the entire labor force (Razzaq et al., 2021). Cotton is one of the major crops that contribute significantly to the national economy by providing raw materials to different industries like the textile industry in the form of lint, crude oil to the oil industry, and seed cake to the poultry industry (Abbas, 2020). It is one of the world's oldest crops. Some evidence of its cultivation in Mohenjo Daro (Sindh, Pakistan) dates back to 5,000 years (Shuli et al., 2018). Cotton is the leading crop worldwide primarily due to its fiber. It also provides food to humans in the form of edible oil and feeds animals through its seedcake, which contains proteins (Bakhsh et al., 2005). It is cultivated on 2.52 million hectares in Pakistan with an output of 8.597 million bales (Ali et al., 2019). Pakistan ranks fifth concerning cotton production and third in terms of consumption globally. The share of cotton in GDP is 0.8%, accounting for 4.1% of the total value added in the agriculture sector (Khalid and Amjad 2018; Khalid and Amjad 2019; Shahzad et al., 2022). The world forecast of cotton production depicts that its production will decrease during 2023, according to the US department of agriculture. Globally, cotton production is expected to fall by 2.3%, and the area of its cultivation will also decrease in cotton-producing countries (Ali et al. 2014; Khalid et al., 2022; Raania & Zafar, 2009). In Pakistan, its per hectare production is 618 kg. When it is as compared to other leading cotton-producing countries like China (1720 kg) and the United States of America (916 kg), etc., it is still low, and it has the potential to improve a lot (Rehman et al., 2019). There are many pathways through which cotton production can be enhanced. One of them is the exploitation of variability within-boll yield components. To increase seed cotton yield, the increase in the number of bolls per unit area was crucial. Lint mass per seed and the number of seeds per boll proved to be the second and third most important parameters, respectively (Malik & Ahsan, 2016). The number of seeds per boll is positively linked with lint yield, as more seeds have more surface area and hence fetch more production (Iqbal et al., 2016). So, assessing germplasm with special concern to boll-related parameters will help to have

[Citation: Nadeem, A., Shakeel, A., Musab, I., Nasir, B., Khalid, M.N., Amjad, I. (2022). Genetic variability studies for within boll yield components in cotton (*Gossypium hirsutum* L.). *Biol. Clin. Sci. Res. J.,* **2022***: 197*. doi: https://doi.org/10.54112/bcsrj.v2022i1.197]

more insight and knowledge about these parameters (Abbas et al., 2016; Ali et al., 2013ab; Ali et al., 2016; Zafar et al. 2022; Puspito et al., 2015). Thus, the present study was conducted 1) to check the genetic variability among different cotton genotypes for boll-related parameters. 2) To find out the association among different within-boll parameters

Materials and methods

The germplasm consisting of 20 exotic genotypes of cotton was taken from the Department of Plant Breeding and Genetics Department, University of Agriculture Faisalabad. The experiment was carried out at the Department of Plant Breeding and Genetics experimental area. Twenty genotypes were field-planted using RCBD in three replications during the year 2019-20. P×P and R×R distances were kept at 30 & 75 cm, respectively. Seeds were planted manually on beds. All the recommended agronomic practices were implemented, like irrigation, weeding, pest control, fertilizers, etc.

Ten plants were planted in each line. Cotton descriptors were used for data collection. Data were obtained at maturity from five guarded plants for the number of bolls/plant (BPP), ginning out turn (GOT), average boll weight/plant (ABW), seed index (SI), number of seeds/boll (SPB), lint Index (LI), lint mass/boll (LMB), seed mass/boll (SMB), lint mass/seed (LMS), seed mass/seed (SMS) and seed cotton yield (SCY).

Statistical Analysis

Analysis of variance was calculated with the help of STATISTIX 8.1. PCA was performed with the help of XLSTAT. Cluster analysis was performed with the help of Minitab 17.

Results and discussion

The current research was performed to evaluate the differences within-boll yield parameters for variability and association among them. The experiment was set up using a three-replication randomized complete block design. Data related to the number of bolls per plant, ginning out turn, average boll weight, seed index, lint index, seed cotton yield, lint mass per seed and seed mass per seed showed significant results when analyzed through analysis of variance and indicated considerable variation among varieties for these parameters (Table 1).

Table 1: Analysis of variance for all attributes in twenty genotypes of *Gossypium hirsutum* L.

SOV	DF	BPP	GOT	BW	SI	SPB	LI	LMB	SMB	LMS	SMS	SCY
Replication	2	27.73	18.76	0.057	1.48	10.41	0.11	1.06	0.009	0.02	0.0001	168.54
Genotype	19	325.4*	79.25*	0.28*	1.93*	18.62	4.05*	4.02*	0.08	0.10*	0.0001*	2151.9*
Error	38	13.16	12.67	0.11	0.36	10.85	0.53	5.32	0.05	0.01	0.00003	118.50
Total	59											

number of bolls per plant (BPP), ginning out turn (GOT), boll weight per plant (BW), seed index (SI), number of seeds per boll (SPB), lint Index (LI), lint mass per boll (LMB), seed mass per boll (SMB), lint mass per seed (LMS), seed mass per seed (SMS) and seed cotton yield (SCY)

Principal component analysis (PCA)

Principal component analysis was used to identify the particular groups of genotypes that have required characters for yield in breeding. It is a tool that helps selection of parents to be used for a successful breeding program (Imran et al., 2012). The principal component analysis aims to reduce the number of observed variables to a manageable quantity. Components that account for less variance than those contributed by individual variables will not be able to achieve this effect. That’s why the components having eigenvalue < 1 are considered trivial and therefore ignored. Eigenvalues are considered quantitative assessments that point to how much a component represents the data. The higher the eigenvalues of a component, the more it represents the data (Zhi et al., 2016). There are three principal components which show more than one eigenvalue. PC 1 showed maximum variability of 54.96% with eigenvalue 6.046 in the germplasm (Table 2). The contribution of the number of bolls per plant, lint mass per seed, ginning out turn, lint index, seed cotton yield, seed mass per seed and lint mass per boll was more varied than other variables (Table 3). The results were considered by Kuai et al. (2015). PC 1 showed positive effects for all the parameters except for the number of seeds per boll (Table 3). PC 2 contributed about 27.80% to the total variability (Table 3) and was mainly due to average boll weight, number of seeds per boll, seed mass per boll, and lint mass per boll (Table 3). In this principal component, ginning out turn, seed mass per boll and lint mass per boll is showing positive effects while the number of bolls per plant, seed index, lint index, lint mass per seed, and seed mass per seed showed negative effects (Table 4). The findings were in consideration by Tang & Xiao, (2014). About 13.97% variability was present in PC 3 (Table 3). The parameters having major shares in variability were the number of bolls per plant, seed index, seed cotton yield, and seed mass per seed (Table 3). The parameters showing negative effects were average boll weight, seed index, lint index, lint mass per seed, seed mass per boll, and seed mass per seed (Table 3). On the other hand, ginning out turn number of bolls per plant, the number of seeds per boll, seed cotton yield, and lint mass per boll showed positive effects (Table 4).

[Citation: Nadeem, A., Shakeel, A., Musab, I., Nasir, B., Khalid, M.N., Amjad, I. (2022). Genetic variability studies for within boll yield components in cotton (*Gossypium hirsutum* L.). *Biol. Clin. Sci. Res. J.*, **2022**: *197*. doi: https://doi.org/10.54112/bcsrj.v2022i1.197]

A. Scree plot

Drawing a graph between eigenvalues and principal component numbers described the percentage variation associated with each PC. It showed that the first three principal components that had more than one eigenvalue explained 96.73 % variability, and after that, the line started to straighten (Figure 1).

B. Scatter plot

The scatter plot depicted that genotypes that were close together were considered to be similar when examined against 11 variables. Genotypes ZB-18015, ZB-18018, ZB-18019 and ZB-18020 were farther from each other and were different regarding distance between them. Genotypes 15 and 20 were farther away from the origin than other genotypes, which showed that they were more genetically diverse concerning 11 characters (Figure 2). While, genotypes ZB-18001, ZB-18003, ZB-18006, ZB-18008 and ZB-18010 etc. were close to each other and did not differ significantly concerning 11 parameters based on which we are comparing them. Many genotypes were close to the center of origin, which means that they were very similar to one another (Figure 2).

C. Principal component bi-plot

The principal component bi-plot presented the variables in a super-imposed form on the plot as vectors. The relative length of each variable represented the proportion of variability for each parameter. Number of seeds/bolls, seed mass/boll, ginning out turn, average boll weight, lint mass/boll and lint mass/seed showed more variation as compared to seed cotton yield, number of bolls/plant, and seed mass/seed which showed less variation as their vectors are smaller compared to other parameters (Figure 3).

Table 2: Eigenvalues of the correlation matrix, variability % and cumulative % explained by the principal components

	PC 1	**PC 2**	**PC 3**
Eigenvalue	6.046	3.058	1.537
Variability %	54.966	27.803	13.976
Cumulative %	54.966	82.768	96.745

Table 3: Contribution % of variables in total variability within principal components

Variables	**PC 1**	**PC 2**	**PC 3**
No. of bolls/plant (BPP)	6.227	2.708	32.453
Ginning out turn (GOT)	15.032	0.227	0.117
Average boll weight (ABW)	4.074	24.463	0.232
No. of seeds/ boll (SPB)	2.714	26.457	1.372
Seed index (SI)	10.699	1.460	17.404
Lint index (LI)	15.661	0.602	0.078
Seed cotton yield (SCY)	8.763	0.012	28.558
Lint mass/ seed (LMS)	15.661	0.602	0.078
Seed mass/ boll (SMB)	0.406	30.028	1.937
Lint mass/ boll (LMB)	10.064	11.984	0.369
Seed mass/ seed (SMS)	10.699	1.460	17.404

Table 4: Correlation between variables and principal components in 20 genotypes of *Gossypium hirsutum* L.

Variables	**PC 1**	**PC 2**	**PC 3**
No. of bolls/plant (BPP)	0.614	-0.288	0.706
Ginning out turn (GOT)	0.953	0.083	0.042
Average boll weight (ABW)	0.496	0.865	-0.060
No. of seeds/ boll (SPB)	-0.405	0.900	0.145
Seed index (SI)	0.804	-0.211	-0.517
Lint index (LI)	0.973	-0.136	-0.0
Seed cotton yield (SCY)	0.728	0.019	0.663
Lint mass/ seed (LMS)	0.973	-0.136	-0.035
Seed mass/ boll (SMB)	0.157	0.958	-0.173
Lint mass/ boll (LMB)	0.780	0.605	0.075
Seed mass/ seed (SMS)	0.804	-0.211	-0.517

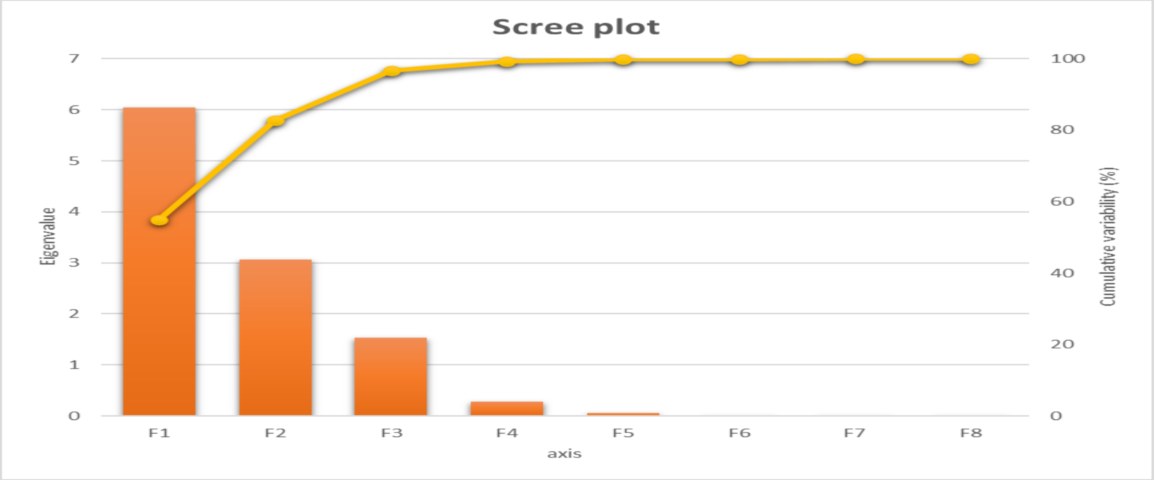

Figure 1: Scree plot of principal component analysis between eigenvalues and number of factors

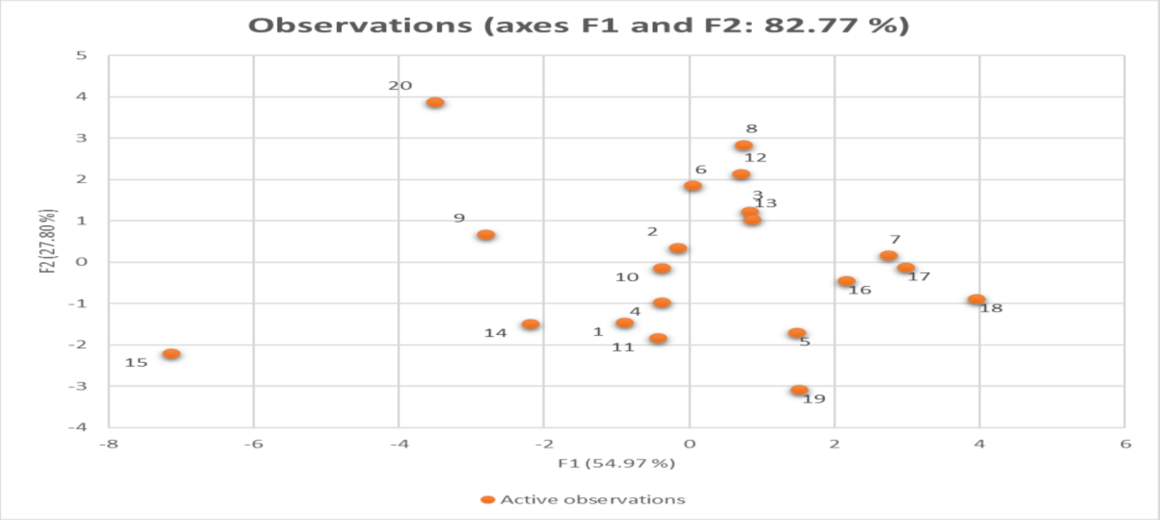

Figure 2: Two dimensional orientations of 20 *Gossypium hirsutum* L. genotypes on principal component axis 1 and 2

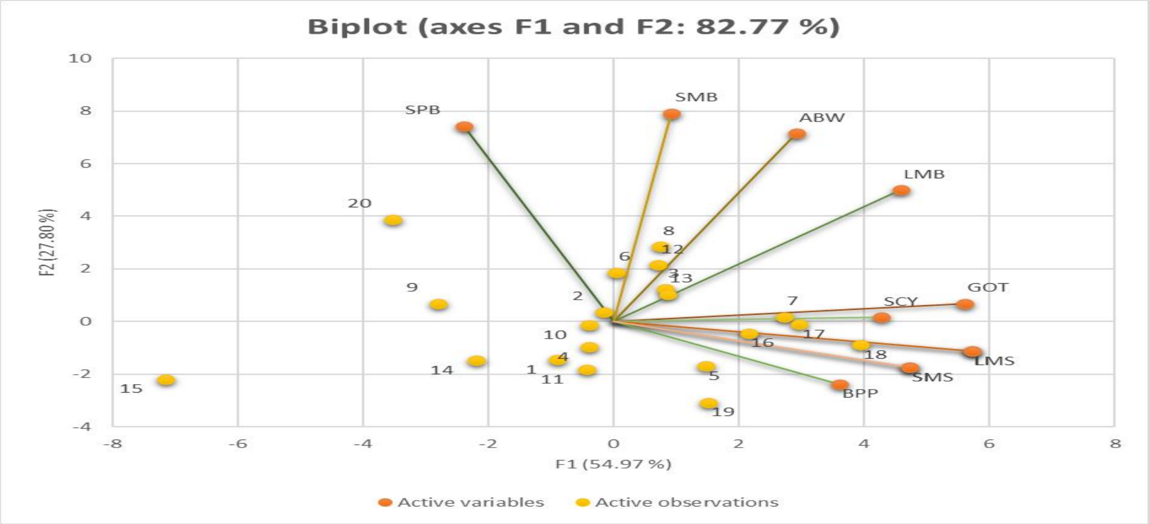

Figure 3: Principal component biplot of 20 *Gossypium hirsutum* L. genotypes, along with the parameters

[Citation: Nadeem, A., Shakeel, A., Musab, I., Nasir, B., Khalid, M.N., Amjad, I. (2022). Genetic variability studies for within boll yield components in cotton (*Gossypium hirsutum* L.). *Biol. Clin. Sci. Res. J.*, **2022***: 197*. doi: https://doi.org/10.54112/bcsrj.v2022i1.197]

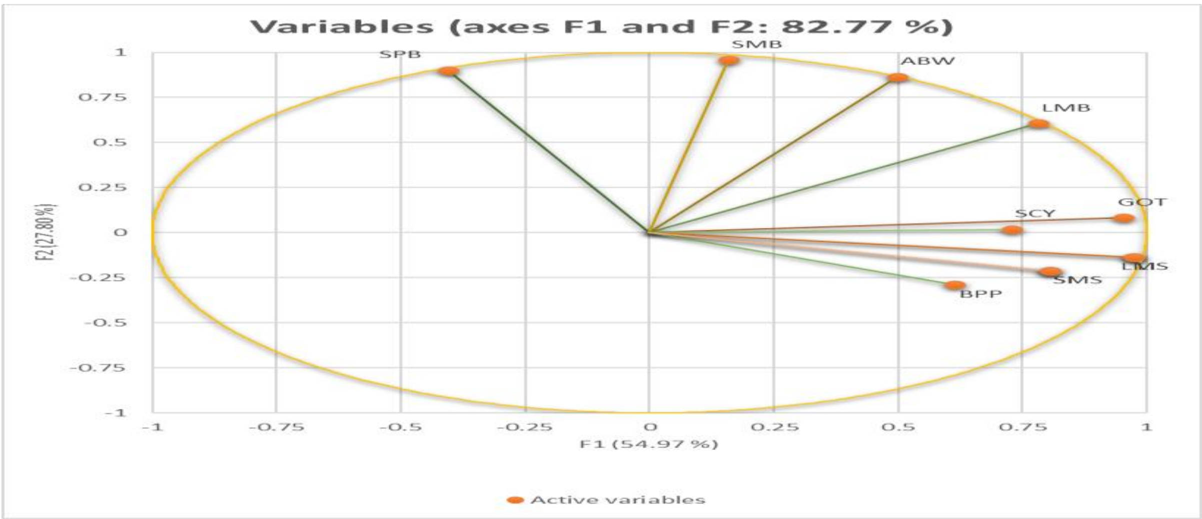

Figure 4: Principal component biplot graph showing the variability of different parameters

Cluster Analysis

Cluster analysis was performed to group the genotypes. In the current study, mean data of 20 exotic genotypes of *Gossypium hirsutum* L. were analyzed for clustering. The letters 1 to 20 represent the genotypes as illustrated in the dendrogram. Zafar et al. (2021) grouped 50 upland cotton genotypes through cluster analysis and characterized them according to Ward's method. They found three major clusters further subdivided into different sub-clusters, revealing similarities among different genotypes. Shakeel et al. (2015) assessed the interrelationship and repeatability of seven indices estimated from upland cotton (*Gossypium hirsutum* L.) genotypes and found different clusters of genotypes. Shabbir et al. (2016) evaluated the genotypes of cotton and found that cluster analysis identified groups of genotypes with more similarity.

Explanation

The dendrogram mainly consisted of two clusters then subdivided into two more clusters (Figure 5). The genotypes that joined together sooner were more similar to each other. For example, genotypes 3 and 6 were more similar to each other than other ones. If we number the four sub-clusters from left to right, then the first sub-cluster consists of seven genotypes (genotypes 1, 2, 10, 16, 13, 7, and 12), of which genotypes 2 and 10 were more similar to each other than others ones (Figure 5). Sub-cluster 2 consisted of only two genotypes (17 and 18). The third sub-cluster consisted of five genotypes of 3, 6, 5, 8, and 19, of which 3 and 6 were more similar (Figure 5). Similarly, the fourth sub-cluster consisted of six genotypes which are 4, 14, 9, 11, 15, and 20, out of which 4 and 14 were more similar to each other than other genotypes (Figure 5). Shakeel et al. (2020) revealed that cluster analysis distributes the genotypes with efficacy and identifies particular groups with maximum similarity using a dendrogram.

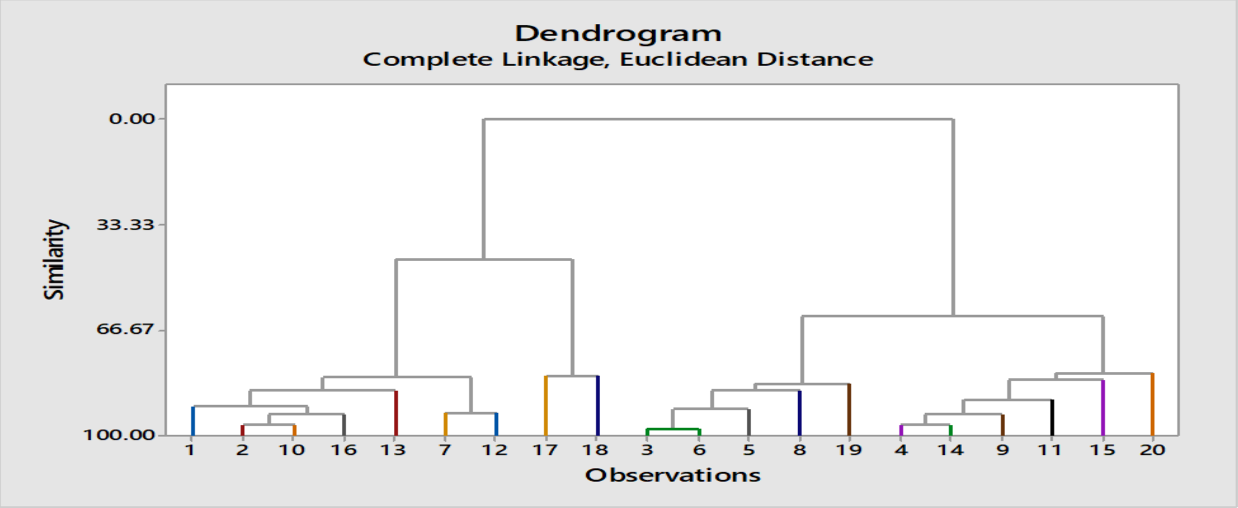

Figure 5: Dendrogram obtained by Ward's linkage cluster analysis

[Citation: Nadeem, A., Shakeel, A., Musab, I., Nasir, B., Khalid, M.N., Amjad, I. (2022). Genetic variability studies for within boll yield components in cotton (*Gossypium hirsutum* L.). *Biol. Clin. Sci. Res. J.*, **2022***: 197*. doi: https://doi.org/10.54112/bcsrj.v2022i1.197]

Conclusion

The current research was performed to evaluate the differences of within-boll yield parameters for variability and association among them. The genotypes ZB-18015, ZB-18020, ZB-18018 and ZB-18019 had maximum variability for all the traits examined. The correlation of different traits would help devise breeding strategies and behavior of the characters studied.

Conflict of interest

The authors declared the absence of a conflict of interest.

References

Abbas, S. (2020). Climate change and cotton production: an empirical investigation of Pakistan. *Environmental Science and Pollution Research* **27**, 29580-29588.

Abbas, H. G., Mahmood, A., & Ali, Q. (2016). Zero tillage: a potential technology to improve cotton yield. *Genetika*, **48**(2), 761-776.

Ali, M. A., Farooq, J., Batool, A., Zahoor, A., Azeem, F., Mahmood, A., & Jabran, K. (2019). Cotton production in Pakistan. *Cotton Production*, 249-276.

Ali, Q., Ahsan, M., & Ali, F. (2013b). Genetic advance, heritability, correlation, heterosis and heterobeltiosis for morphological traits of maize (Zea mays L). *Albanian Journal of Agricultural Sciences*, *12*(4), 689-698.

Ali, Q., Ahsan, M., Ali, F., Aslam, M., Khan, N. H., Munzoor, M., ... & Muhammad, S. (2013a). Heritability, heterosis and heterobeltiosis studies for morphological traits of maize (Zea mays L.) seedlings. *Advancements in Life sciences*, **1**(1).

Ali, Q., Ahsan, M., Kanwal, N., Ali, F., Ali, A., Ahmed, W., ... & Saleem, M. (2016). Screening for drought tolerance: comparison of maize hybrids under water deficit condition. *Advancements in Life Sciences*, *3*(2), 51-58.

Ali, Q., Ali, A., Ahsan, M., Nasir, I. A., Abbas, H. G., & Ashraf, M. A. (2014). Line× Tester analysis for morpho-physiol bogical traits of Zea mays L seedlings. *Advancements in Life sciences*, **1**(4), 242-253.

Bakhsh, K., Hassan, I., & Maqbool, A. (2005). Factors affecting cotton yield: a case study of Sargodha (Pakistan). *J. Agric. Soc. Sci* **1**, 332-334.

Imran, M., Shakeel, A., Azhar, F., Farooq, J., Saleem, M., Saeed, A., Nazeer, W., Riaz, M., Naeem, M., & Javaid, A. (2012). Combining ability analysis for within-boll yield components in upland cotton (Gossypium hirsutum L.). *Genetics and Molecular Research* **11**, 2790-2800.

Iqbal, M. A., Ping, Q., Abid, M., Kazmi, S. M. M., & Rizwan, M. (2016). Assessing risk perceptions and attitude among cotton farmers: A case of Punjab province, Pakistan. *International Journal of Disaster Risk Reduction* **16**, 68-74.

Khalid, M., & Amjad, I. (2018). Repercussions of waterlogging stress at morpho-physiological level on cotton and ways to lessen the damage to crop yields. *Bulletin of Biological and Allied Sciences Research*, *2018*(1), 16. https://doi.org/10.54112/bbasr.v2018i1.16

Khalid, M., & Amjad, I. (2019). combining ability and heterosis studies in upland cotton (*Gossypium hirsutum* L.). *Bulletin of Biological and Allied Sciences Research*, *2019*(1), 20. https://doi.org/10.54112/bbasr.v2019i1.20

Khalid, M., Hassan, U., Hanzala, M., Amjad, I., & Hassan, A. (2022). Current situation and prospects of cotton production in Pakistan. *Bulletin of Biological and Allied Sciences Research* **5**, 27-27.

Kuai, J., Zhou, Z., Wang, Y., Meng, Y., Chen, B., & Zhao, W. (2015). The effects of short-term waterlogging on the lint yield and yield components of cotton with respect to boll position. *European Journal of Agronomy* **67**, 61-74.

Malik, A., & Rasheed, M. (2022). An overview of breeding for drought stress tolerance in cotton. *Bulletin of Biological and Allied Sciences Research*, *2022*(1), 22. https://doi.org/10.54112/bbasr.v2022i1.22

Malik, T. H., & Ahsan, M. Z. (2016). Review of the cotton market in Pakistan and its future prospects. *OCL* **23**, D606.

Puspito, A. N., Rao, A. Q., Hafeez, M. N., Iqbal, M. S., Bajwa, K. S., Ali, Q., ... & Husnain, T. (2015). Transformation and evaluation of Cry1Ac+ Cry2A and GTGene in Gossypium hirsutum L. *Frontiers in plant science*, **6**, 943.

Raania, A., & Zafar, A. (2009). Development, adoption and performance of Bt cotton in Pakistan: a review. *Pakistan Journal of Agricultural Research* **22**, 73-85.

Razzaq, A., Zafar, M. M., Ali, A., Hafeez, A., Batool, W., Shi, Y., Gong, W., & Yuan, Y. (2021). Cotton germplasm improvement and progress in Pakistan. *Journal of Cotton Research* **4**, 1-14.

Rehman, A., Jingdong, L., Chandio, A. A., Hussain, I., Wagan, S. A., & Memon, Q. U. A. (2019). Economic perspectives of cotton crop in Pakistan: A time series analysis (1970–2015)(Part 1). *Journal of the Saudi Society of Agricultural Sciences* **18**, 49-54.

[Citation: Nadeem, A., Shakeel, A., Musab, I., Nasir, B., Khalid, M.N., Amjad, I. (2022). Genetic variability studies for within boll yield components in cotton (*Gossypium hirsutum* L.). *Biol. Clin. Sci. Res. J.,* **2022***: 197*. doi: https://doi.org/10.54112/bcsrj.v2022i1.197]

Shabbir, R. H., Bashir, Q. A., Shakeel, A., Khan, M. M., Farooq, J., Fiaz, S., Ijaz, B., & Noor, M. A. (2016). Genetic divergence assessment in upland cotton (Gossypium hirsutum L.) using various statistical tools. *J. Glob. Innov. Agric. Soc. Sci* **4**, 62-69.

Shahzad, K., Mubeen, I., Zhang, M., Zhang, X., Wu, J., & Xing, C. (2022). Progress and perspective on cotton breeding in Pakistan. *Journal of Cotton Research* **5**, 1-17.

Shakeel, A., Talib, I., Rashid, M., Saeed, A., Ziaf, K., & Saleem, M. F. (2015). Genetic diversity among upland cotton genotypes for quality and yield related traits. *Pakistan Journal of Agricultural Sciences* **52**, 73-77.

Shakeel, W., Ahmad, M., & Mahmood, N. (2020). Early Detection of Cercospora Cotton Plant Disease by Using Machine Learning Technique. 2020 30th International Conference on Computer Theory and Applications (ICCTA),

Shuli, F., Jarwar, A. H., Wang, X., Wang, L., & Ma, Q. (2018). Overview of the cotton in Pakistan and its future prospects. *Pakistan Journal of Agricultural Research* **31**, 396.

Tang, F., & Xiao, W. (2014). Genetic association of within-boll yield components and boll morphological traits with fibre properties in upland cotton (Gossypium hirsutum L.). *Plant Breeding* **133**, 521-529.

Zafar, M. M., Manan, A., Razzaq, A., Zulfqar, M., Saeed, A., Kashif, M., Khan, A. I., Sarfraz, Z., Mo, H., & Iqbal, M. S. (2021). Exploiting agronomic and biochemical traits to develop heat resilient cotton cultivars under climate change scenarios. *Agronomy* **11**, 1885.

Zafar, M. M., Mustafa, G., Shoukat, F., Idrees, A., Ali, A., Sharif, F., ... & Li, F. (2022). Heterologous expression of cry3Bb1 and cry3 genes for enhanced resistance against insect pests in cotton. *Scientific Reports*, **12**(1), 10878.

Zhi, X.-y., Han, Y.-c., Li, Y.-b., Wang, G.-p., Du, W.-l., Li, X.-x., Mao, S.-c., & Lu, F. (2016). Effects of plant density on cotton yield components and quality. *Journal of integrative agriculture* **15**, 1469-1479.

[Citation: Nadeem, A., Shakeel, A., Musab, I., Nasir, B., Khalid, M.N., Amjad, I. (2022). Genetic variability studies for within boll yield components in cotton (*Gossypium hirsutum* L.). *Biol. Clin. Sci. Res. J.*, **2022***: 197*. doi: https://doi.org/10.54112/bcsrj.v2022i1.197]