

EVALUATION OF GENETIC DIVERSITY FOR COTTON LEAF CURL VIRUS (CLCUV), YIELD, GOT% AND FIBER TRAITS IN EXOTIC GERMPLASM OF *GOSSYPIUM HIRSUTUM* L.

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خلاصہ

سندھ کے علاقہ سکرنڈ کی آب و ہوا میں، پیٹرو وڈ وائرس، پیداوار اور ریشہ کی خصوصیات کے جینیاتی فرق تلاش کرنے کے لئے کپاس کی 151 غیر ملکی اقسام کا جائزہ لیا گیا۔ مزاحمت کے ممکنہ ذرائع کی تلاش کے لئے اعداد و شمار کے مختلف طریقہ کار یعنی بنیادی اعداد و شمار، باہمی ربط (Correlation)، اور بنیادی اجزا (Principal Components) کا جائزہ لیا گیا تاکہ ممکنہ ذرائع کو بریڈنگ پروگرام میں استعمال کرتے ہوئے مطلوبہ خصوصیات اور پیٹرو وڈ وائرس (CLCuV) کے خلاف مزاحمت رکھنے والی اقسام تیار کی جاسکیں۔ کپاس کی پیداوار کا شمار دارشاخوں، ٹینڈوں کی تعداد، ٹینڈوں کے وزن، چٹنی میں ریشہ کا تناسب، ریشہ کی لمبائی اور ریشہ کی یکسانیت (Uniformity index) کے ساتھ بڑا اہمیت ربا جبکہ غیر شمردار شاخوں (Monopodial Branches)، پودے کی اونچائی، چٹنی میں ٹینڈوں کی تعداد (Seed index) اور ریشہ کی نرمی (Micronaire Value) کے ساتھ منفی ربط (Negative correlation) مشاہدے میں آیا ہے۔ جینیاتی تغیر کو جانچنے کے لئے بنیادی اجزا (Principal Components) کا جائزہ لیا گیا۔ 13 بنیادی اجزا میں سے پانچ اجزا کی eigen value ایک سے زیادہ ہے، جس سے پتہ چلتا ہے کہ 67.5 فیصد تغیر ان اجزا کی وجہ سے اور باقی 32.5 فیصد تغیر بقیہ آٹھ اجزا کی وجہ سے ہے۔ سب سے زیادہ 22.2 فیصد تغیر PC1 کی وجہ سے جبکہ 14.8 فیصد PC2، 12.5 فیصد PC3، 9.2 فیصد PC4 اور 8.8 فیصد PC5 کی وجہ سے ہے۔ اس طرح بنیادی اجزا کا تجزیہ اس بات کی ضمانت دیتا ہے کہ مذکورہ خصوصیات میں تغیر موجود ہے اور ان اقسام کو ہم اپنے بریڈنگ پروگرام میں استعمال کر کے ہم اپنی اقسام میں مطلوبہ خصوصیات، پیٹرو وڈ وائرس کے خلاف مزاحمت، پیداوار اور وائرس کے اجزا اور ریشہ کے تناسب اور ریشہ کی دیگر خصوصیات کو بہتر بنا سکتے ہیں۔

Abstract

For the exploration of genetic diversity, 151 exotic cotton germplasm were evaluated for CLCuV, yield and fiber traits at the environmental conditions of central zone of Sakrand, Sindh. Basic statistical parameters, correlation and principal components were employed to explore the potential source for the utilization in breeding program to maintain the desired traits and develop CLCuV resistant/tolerant line. The significant positive association was observed among traits. Seed cotton yield was related positively significantly with traits sympodial branches, bolls plant⁻¹, boll weight, ginning outturn, staple length and uniformity index. Whereas the negative correlation was observed with number of monopodial branches, plant height, seed index, micronaire value and seed index. Principal components were employed to assess the genetic variability. Out of 13 PCs 5 components exhibited >1 Eigen value, which shows 67.5% variability, whereas the remaining 32.5% variability contributed by further 8 components. The PC1 contributed highest genetic variability (22.2%) followed by PC2 (14.8%), PC3 (12.5%), PC4 (9.2%) and PC5 (8.8%), respectively. The principal component analysis (PCA) authenticated the amount of variability among traits and the material which may be tested exploited in breeding program to maintain the desirable traits, CLCuV resistant/tolerant, yield, its components, GOT and fiber quality traits. For yield, its components, GOT, fiber traits and cotton leaf curl virus USG2554, USG2570, USG2807, USG2810, USG2813, USG2833 and USG2848 can be utilized in breeding program to maintain the desirable traits.

Introduction

The cotton is most important cash and fiber crop of Pakistan; it plays a vital role in the national economy. In addition to export fiber to the textile industry, also contributing 65 to 70% edible oil to the local industry and seed cake for the utilization as animal feed (Khan *et al.*, 2000; Khan, 2003 and Khan *et al.*, 2007). Cotton Leaf Curl Virus (CLCV) is one of the harsh diseases of the cotton crop; it appeared in the area of Punjab Pakistan

(Nelson *et al.*, 1998). The disease was characterized by downward or upward leaves curling. The veins of leaves are thickened on the bottom. In case of disease severity leaves become cup-shaped, a small leaf emerge on the bottom of leaves and plants growth stunted (Hussain *et al.* 1991, Brown, 2001)

Multivariate analytical and biometrical techniques are mostly utilized by plant breeders when dealing with massive amount of genotypes to exploit genetic variability. Among various biometrical techniques, a non-hierarchical analytical approach named principal component analysis (PCA) is usually utilized to evaluate the pattern of diversity in available germplasm (Khan *et al.*, 2015; Umer *et al.*, 2014). This is a very effective approach for determining which characteristics had positive contribution towards due important trait, and then these traits could be employed in the crop breeding program (Bilal *et al.*, 2015; Rehman *et al.*, 2015). As the improvement in wheat yield under drought is still a complicated task to achieve, therefore the main purpose of this study was to screen cotton genotypes with better grain yield and to identify reliable selection criteria for drought tolerant wheat genotypes. Keeping in view that scenario the present research was conducted to evaluate 151 exotic germplasm of *Gossypium hirsutum* for assessing genetic variability according to the traits wise by using principal component analysis (PCA).

Material and Methods

The present research was conducted during the year 2015-16. The 151 exotic cotton germplasm were imported from USA through a project named ICARDA Pak-US cotton productivity enhancement project for the evaluation of cotton leaf curl virus (CLCuV), yield and fiber traits at the environmental conditions of central zone of Sindh. To screen out the CLCuV disease resistant/highly tolerant accessions, late sowing in the month of June was done. Two rows of each genotype were planted with the space of 30 and 75cm plant to plant and row to row distance, respectively. The crop was grown under standard cultural practices. Cotton leaf curl virus (CLCuV) disease reaction was assessed according to disease rating scale (Table-1) suggested by Akhtar *et al.* (2010) and Farooq *et al.* (2011).

For the data collection of other agronomic, yield and fibre quality traits, 10 plants were selected from each genotype and tagged. Number of monopodial branches plant⁻¹, number of sympodial branches plant⁻¹, plant height (cm), bolls plant⁻¹, boll weight (g), seed index (g), GOT (%), seed cotton yield plant⁻¹ (g), staple length (mm), uniformity index (%), micronaire value and fiber strength (g tex⁻¹) were recorded. The data of basic statistics, correlation and principal component analysis (PCA) were analyzed by using statistical software Statistical Tool for Agricultural Research (STAR).

Table-1: Cotton Leaf Curl Virus (CLCuV) disease symptoms rating scale described by Akhtar *et al.* (2010) and Farooq *et al.* (2011).

Symptoms	Disease rating	Disease Index (%)	Disease reaction
No symptoms	0	0	Resistant
Thickening of only secondary and tertiary veins	1	0.1-10	Highly tolerant
Thickening of tertiary veins, secondary and primary veins	2	10-30	Tolerant
Vein thickening, leaf curl or enation or both	3	30-50	Susceptible
Stunting alone with vein thickening, leaf curl or enation	4	>50	Highly susceptible

Results and Discussion

The data of 151 exotic cotton germplasm were analyzed for basic statistics for various traits and presented in Table-2. A wide range of genetic diversity was observed among genotypes. The maximum coefficient of variance was observed in cotton leaf curl virus (74.53), because the range of disease severity was 0.0 to 100% according to the rating scale. The seed cotton yield CV% was observed (52.09), the range of seed cotton yield in genotypes was recorded 17.3 to 162.8 g. The considerable coefficient of variance was recorded for monopodial branches, boll plant⁻¹, boll weight, seed index, plant height, GOT%, micronaire value and sympodial branches

which were more than 10%. Similar results were reported by El-Kady *et al.* (2015), El-Mohsen and Amein (2016).

The phenotypic correlation is presented in Table-3. The strong association was observed between traits. The cotton leaf curl virus was non-significant correlated with all the traits studied. The association of seed cotton yield was observed significant positive with traits number of sympodial branches (0.152**), bolls plant⁻¹ (0.554**), boll weight (0.159**), ginning outturn (0.154**), staple length (0.341**) and uniformity index (0.318**). Whereas the negative correlation was observed with number of monopodial branches, plant height, seed index, micronaire value and seed index. The similar findings were observed by Vinodhana *et al.* (2013), Khan *et al.* (2017) and Baloch *et al.* (2015) that seed cotton yield was significantly positively association with bolls plant⁻¹, boll weight and sympodial branches.

The maintenance and exploitation of genetic resources could be made by separation of the total variance to its components. It gives the opportunity to utilize appropriate germplasm for the improvement of exact traits (Pecetti *et al.* 1996). The variability of characters depends on the value of eigen which is being calculated through principal components analysis. The maximum eigen value expresses the more variability and support to select the trait with positive loading factor. Principal components were analyzed to assess the genetic variability depicted in table-4. Out of 13 PCs 5 components exhibited >1 eigen value, which shows 67.5% variability, whereas the remaining 32.5% variability contributed by further 8 components. The PC1 contributed highest genetic variability (22.2%) followed by PC2 (14.8%), PC3 (12.5%), PC4 (9.2%) and PC5 (8.8%) respectively. The similar finds reported by Nazir *et al.* (2013), Saeed *et al.* (2014), Latif *et al.* (2015) and Khan *et al.* (2017) that PCs has the significant contribution towards the total variability for studying the various characters.

The PC1 shown maximum variability (22.2%) (Table-4) among traits in PC1 the maximum positive loading factor exhibited by staple length (0.490) followed by uniformity index (0.440), GOT (0.382), seed cotton yield (0.376), fiber strength (0.315), bolls plant⁻¹ (0.279), boll weight (0.195), CLCuV (0.061), monopodial branches (0.006) and seed index (0.004). Whereas sympodial branches (-0.184), micronaire value (-0.114) and plant height (-0.112) expressed negative loading factor. In PC2 the diversity of genotypes was observed for the traits plant height, boll weight, seed index, staple length, uniformity index, fiber strength and CLCuV revealed positive loading factor. Within PC3 monopodial branches, staple length, uniformity index and fiber strength had elucidated the positive effect. In PC4 bolls plant⁻¹, seed cotton yield and CLCuV contributed positive loading factor. The PC5 contributed (8.8%) variability, the traits which possess positive loading factors, monopodial branches, sympodial branches, plant height, bolls plant⁻¹, GOT, staple length, uniformity index, fiber strength and CLCuV. While the other traits explicated negative effects in PC5. Thus the principal component analysis (PCA) authenticated the amount of variability among traits and the material which will be tested that can be exploited in breeding program to maintain the desirable traits, CLCuV resistant/tolerant, yield, its components, GOT and fiber quality traits. These results are according with Nazir *et al.* (2013), Saeed *et al.* (2014), Latif *et al.* (2015), Shakeel *et al.* (2015), Javed *et al.* (2017) and Khan *et al.* (2017) who reported the highest eigenvalue in first five components with maximum variability in genotypes which were screened for yield, its components, fiber traits and cotton leaf curl virus through analyzing principle components.

Table-2: Basic statistics of various traits.

Plant Traits	Min.	Max.	Mean	CV%	SE
No. of Monopodial branches	0.0	10.7	3.2	51.88	0.1
No. of Sympodial branches	14.0	26.7	20.9	13.68	0.5
Plant Height (cm)	83.0	200.0	137.2	15.28	1.1
Bolls Plant ⁻¹	6.7	56.3	27.4	35.73	0.5
Boll Weight (g)	1.1	5.1	2.8	28.21	0.1
Seed Index (g)	5.5	12.4	9.2	15.54	1.1
GOT (%)	20.5	43.7	32.8	13.69	0.1
Seed Cotton Yield Plant ⁻¹ (g)	14.3	162.8	54.3	52.09	0.8
Staple Length (mm)	21.8	32.6	27.4	7.40	0.1
Uniformity Index (%)	79.0	89.5	84.6	2.42	0.2
Micronaire value	2.9	6.3	4.6	13.69	0.1
Fiber Strength (g tex ⁻¹)	22.1	35.7	27.6	8.37	0.5
CLCuV (%)	0.0	100.0	24.3	74.53	0.6

The 151 cotton germplasm were evaluated at the environmental condition of Sakrand for yield, its components, fiber traits and cotton leaf curl virus disease resistant/highly tolerant for utilization in hybridization breeding program. According to traits wise some elite germplasm were identified and presented in table-5. For yield, its components, GOT, fiber traits and cotton leaf curl virus USG2554, USG2570, USG2807, USG2810, USG2813, USG2833 and USG2848 can be utilized in breeding program to maintain the desirable traits.

Table-3: simple correlation coefficient of traits study of 151 exotic germplasm.

Traits	NOMB	NOSB	PH	BPP	BW	SI	GOT	SCY	SL	UI	MV	FS	CLCuV
NOMB	1												
NOSB	0.087 ns	1											
PH	-0.276 ns	0.215 **	1										
BPP	-0.059 ns	-0.037 ns	0.038 *	1									
BW	-0.215 **	-0.222 **	0.189 **	0.045 ns	1								
SI	-0.066 ns	0.048 ns	0.175 **	-0.44 ns	0.031 *	1							
GOT	0.152 ns	-0.138 *	-0.059 ns	0.206 **	0.088 ns	0.029 ns	1						
SCY	0.071 ns	0.152 **	-0.078 ns	0.554 **	0.159 **	-0.069 ns	0.451 **	1					
SL	0.046 ns	-0.129 *	-0.132 *	0.266 **	0.121 *	0.027 ns	0.435 **	0.341 **	1				
UI	-0.032 ns	-0.137 *	-0.160 ns	0.215 **	0.137 *	0.001 ns	0.364 ns	0.318 **	0.662 **	1			
MV	0.075 ns	0.189 **	0.183 *	-0.001 ns	0.046 ns	0.127 *	0.149 *	0.104 ns	-0.242 **	-0.075 ns	1		
FS	-0.019 ns	0.037 ns	-0.078 ns	-0.016 ns	0.240 **	-0.015 ns	0.251 **	0.073 ns	0.509 **	0.354 **	-0.323 **	1	
CLCuV	-0.302 ns	-0.087 ns	0.202 ns	0.118 ns	0.059 ns	-0.018 ns	0.113 ns	-0.079 ns	0.116 ns	-0.032 ns	-0.170 ns	0.025 ns	1

NOMB=Number of Monopodial Branches, NOSB=Number of Sympodial Branches, PH=Plant Height, BPP=Bolls per Plant, BW=Boll Weight, SI=Seed Index, GOT=Ginning outturn, SCY=Seed Cotton Yield, SL=Staple Length, UI=Uniformity Index, MV=Micronaire Value, FS=Fiber Strength, CLCuV=Cotton Leaf Curl Virus

Table-4: Principal component analysis of yield, fiber traits & CLCuV of 151 exotic germplasm.

Variables	PC1	PC2	PC3	PC4	PC5
Eigen value	2.884	1.927	1.622	1.195	1.139
Portion of Variance	22.200	14.800	12.500	9.200	8.800
Cumulative Portion (%)	22.200	37.000	49.500	58.700	67.500
Traits					
No. of Monopodial branches	0.006	-0.524	0.107	-0.186	0.002
No. of sympodial branches	-0.184	-0.123	-0.113	-0.269	0.717
Plant Height (cm)	-0.112	0.350	-0.364	-0.087	0.372
Bolls Plant ⁻¹	0.279	-0.082	-0.363	0.436	0.128
Boll Weight (g)	0.195	0.364	-0.098	-0.200	-0.299
Seed Index (g)	0.004	0.453	-0.114	-0.364	-0.198
GOT (%)	0.382	-0.139	-0.217	-0.106	0.038
Seed Cotton Yield Plant ⁻¹ (g)	0.376	-0.193	-0.370	0.139	-0.121
Staple Length (mm)	0.490	0.014	0.149	-0.082	0.209
Uniformity Index (%)	0.440	0.005	0.055	-0.236	0.040
Micronaire value	-0.114	-0.142	-0.575	-0.394	-0.095
Fiber Strength (g tex ⁻¹)	0.315	0.150	0.380	-0.256	0.257
CLCuV (%)	0.061	0.377	-0.045	0.454	0.251

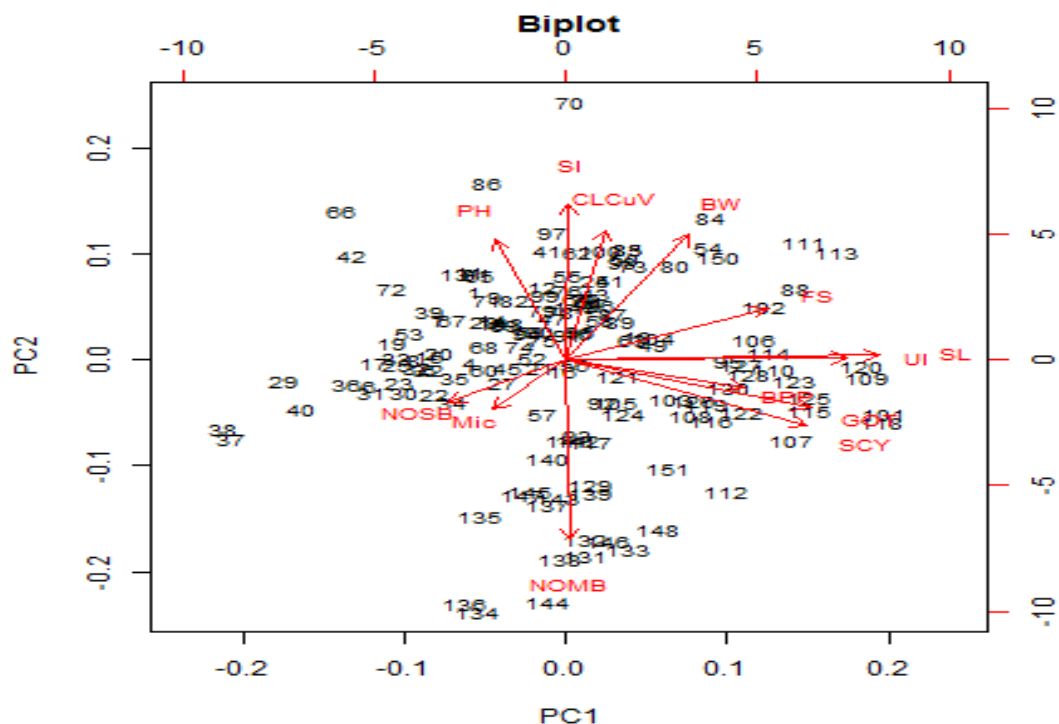


Fig-1. PCA of Biplot of 151 exotic cotton germplasm

Table-5: Potential germplasm for yield, its components, fiber traits and CLCuV.

Sr. No.	Traits	Potential Germplasm
1	Plant Height (cm)	USG2551,USG2570
2	Bolls Plant ⁻¹	USG2584, USG2892, USG2833
3	Boll Weight (g)	USG2526, USG2554, USG2566, USG2570
4	Seed Index (g)	USG2565, USG2570, USG2576, USG2584
5	GOT (%)	USG2848, USG2820, USG2827
6	Seed Cotton Yield Plant ⁻¹ (g)	USG2807, USG2809, USG2818, USG 2825
7	Staple Length (mm)	USG2810, USG2813, USG2554, USG2585
8	Uniformity Index (%)	USG2810, USG2815, USG2820, USG2850
9	Micronaire value	USG2566, USG2813, USG2833
10	Fiber Strength (g tex ⁻¹)	USG2802, USG2813
11	CLCuV resistant/highly tolerant	USG2554, USG2807, USG2833

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