

ESTIMATION OF GENETIC EFFECTS CONTROLLING DIFFERENT PLANT TRAITS IN COTTON (*GOSSYPIUM HIRSUTUM* L.) UNDER CLCuV EPIDEMIC CONDITION

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ABSTRACT. Nine cotton genotypes, comprised of four non Bt males (CIM-1100, CIM-506, FH-942 and FH-900), five Bt female genotypes (FH-113, FH-114, MNH-886, AA-703 and IR-3701) and their 20 crosses were screened in order to evaluate their response to Cotton leaf curl virus symptoms through epidemiology in the field and greenhouse. The 20 crosses among their nine parents were sown in two replications under randomized complete block design, during 2013 and 2014. The mean squares were significant for all traits indicating that both additive and non-additive genes control the characters, but non-additive genes were

more important because, variance of dominant genes were higher than additive genes. In our test, FH-900 showed the best performance against CLCuV, number of lobes per boll and seed yield. The CIM-1100 genotype performed well in boll weight, fiber strength and fiber fineness, whereas CIM-506 was good for plant height, number of sympodial branches and ginning. Maximum boll number, seed index and fiber length were shown by FH-942. Among lines, MNH886, FH-113, IR-3701 and FH-114 exhibited the best general combination for many traits. Hence, parents were preferred for hybridization program to

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improve the majority of characters. Hybrids FH-113 × FH-942, MNH-886 × CIM-1100, MNH-886 × FH-942, IR-3701 × CIM-506, AA-703 × CIM-1100, FH-114 × FH-942, FH-114 × CIM-1100 and MNH-886 × FH-900 was best in specific combinations for different traits, especially against CLCuV. The results indicated that to increase resistance against CLCuV, hybrids should be exploited to develop CLCuV resistance.

Keywords: *Gossypium hirsutum*; cotton leaf curl virus (CLCuV); genetic effects; general and specific combing ability; North Carolina Design II.

INTRODUCTION

Agriculture is the backbone of Pakistan economy and has always given importance to major crops to boost up their productivity. Among major crops, the importance of *Gossypium hirsutum* is evident from the fact that it is the world's leading fiber producing specie (Dutt *et al.*, 2004). Pakistan ranked 4th in world cotton production after China, USA and India (Akhtar, 2005). Cotton is an essential source of foreign exchange earnings in total agriculture output is about 8.6% and 1.8% contribution in gross domestic production (GDP). It provides more than 90% of the raw material to the textile industry (Pakistan Economic Survey, 2012-13). The average production of cotton has increased in Pakistan, but yield of cotton is still low as compared to many other countries. It is considered a major cash crop among the farmers in Pakistan and is known as "White Gold". Millions of people and brings about 60% through export products (Iqbal *et al.*, 2005). The cotton's

contribution is getting their livelihood from cotton farming, ginning and textile industry. Cotton not only produce fiber, it also provides edible oil and seed cake for animals.

Cotton is a summer crop with sown in May-June. The late sown is affected by many biotic and abiotic factors, such as high temperature on August, sucking insects and Cotton leaf curl virus. Many important plant diseases show up due to biotic stresses, i.e viruses are responsible for deteriorating quality and yield decrease. Cotton leaf curl virus disease (CLCuD) is an epidemic disease transmitted by white fly (*Bemisia tabaci* Genn), being considered a major threat to the production of cotton in Pakistan (Ahmad *et al.*, 2010). A loss around 2.3 million bales affected by CLCuV was reported in Pakistan (Pakistan Economic Survey, 2012-13). Besides affecting the seed cotton yield, it also stunted growth of plant; deteriorate fiber quality, decrease boll weight, seed weight and the number of monopodia land sympodial branches (Farooq *et al.*, 2011). Disease symptoms appear at seedling stage hinders boll formation, flowering, maturation, yield of seed cotton and reduced fiber quality (Monga *et al.*, 2011). Genetic diversity plays an important role to reduce damage by insects and pests, facilitating the development of segregating population. Parental selection for future breeding program is important to reduce the damage caused by CLCuV (Esbroeck and Bowman, 1998).

COTTON PLANT TRAITS UNDER CLCuV EPIDEMIC CONDITION

Combining ability analysis is an important tool to select desirable parents and collect information from genes and their effects in quantitative traits, thus define the pattern of genetic effects on the expression of quantitative characters by identifying superior parents and hybrids. Good general combining ability is mandatory for parent's selection while hybrids are selected based on specific combining abilities (Ahuja and Dhayal, 2007). Information about the genetic mechanisms of parents governing different plant traits like the number of bolls per plant, number of monopodial and sympodial branches, boll weight and seed cotton yield may help to improve the genetic makeup of plant in direction to maintaining and improving proper crop production. In early plant breeding era, large number of crosses were attempted by plant breeders and parents were recognized on the basis of progeny performance. Various matting designs in this regard have been valuable. Diallel analysis has been used more than any other design to estimate GCA of parents and SCA of hybrids along with information related to gene action controlling different traits. In diallel matting design, less number of parents are used with more resources. On the other hand, North Carolina Design II (NCMII) involves a higher number of parents with the same resources and provides information for parents with reliable genetic parameters. Our aim was to estimate the genetic effects controlling different plant traits with general and specific combining ability of cotton inbred under CLCuV

epidemic conditions by North Carolina Design II genetic analysis.

MATERIAL AND METHODS

The field work was performed in the experimental area at the Department of Plant Breeding and Genetics, University of Agriculture Faisalabad, during 2013-14. The plant material was developed by crossing nine genotypes of *Gossypium hirsutum*, including four Non-Bt males (CIM-1100, CIM-506, FH-942 and FH-900) and five Bt females (FH-113, FH-114, MNH-886, IR-3701 and AA-703) in NCMII design in the greenhouse. Seeds of 20 hybrid genotypes along with nine parents were sown in the field during June 2013 in randomized complete block design (RCBD) using two replications. At maturity stage, five plants in each row were tagged to data collection on the CLCuV percentage, plant height, sympodial branches/plant, bolls/plant, locules/boll, boll weight, seed index, GOT, seed cotton yield, fiber length, fiber strength and fiber fineness. Genetic effects were calculated as described by Comstock *et al.* (1949). Combining ability analysis was also carried out by the method given by Kearsy and Pooni (1996).

RESULTS

The responses of cotton varieties and their hybrids showed significant mean square differences (*Table 1*), which indicated the presence of genetic variations among cotton genotypes. The significant mean squares due to males and females shows that both, additive and non-additive (Dominant or Epistasis) genetic effects were important in the expression of the studied traits.

Table 1 - Mean square from variance analysis of NCM-II for various characters in *Gossypium hirsutum*

Source of variations	d.f.	CLCuV (%)	Plant height (cm)	Sympodial branches/plant	Bolls/plant	Locules/boll	Boll weight (g)	Seed index (g)	GOT	Seed cotton yield (g)	Fiber length (mm)	Fiber strength (g/tax)	Fiber fineness (micronaire)
Replications	1	1.29	0.04	3.05	0.436	0.01	0.02	1.27	9.20	0.23	2.74	1.04	0.04
Male (GCA)	3	7.15	248.05	14.52	122.96	0.14	0.44	4.27	35.89	1238.2	7.96	7.42	0.53
Female (GCA)	4	1.06	47.32	5.95	79.90	0.05	0.27	5.08	58.97	127.12	3.24	5.41	0.49
Male × female (SCA)	12	1.57	68.54	8.34	75.82	0.08	0.41	2.53	33.59	617.92	2.72	3.94	0.32
Error	20	0.31	16.34	0.75	1.74	0.02	0.05	1.10	5.06	12.83	0.72	1.14	0.14

CLCuV= Cotton leaf curl virus; d.f.=degree of freedom; GOT= Ginning out turn

Table 2 - General combining ability effects of male and female parents for various characters in *Gossypium hirsutum* L.

Inbred parents	CLCuV (%)	Plant height (cm)	Sympodia branches/plant	Bolls/plant	Locules/boll	Boll weight (g)	Seed index (g)	GOT	Seed cotton yield (g)	Fiber length (mm)	Fiber strength (g/tax)	Fiber fineness (micronaire)
Male inbreds												
CIM-1100	2.38	4.83	-0.99	-2.40	0.02	0.189	-0.03	1.48	-8.27	-1.16	0.68	-0.15
CIM-506	3.84	-4.95	0.72	1.07	-0.03	0.111	-0.02	1.72	-4.13	0.27	0.41	0.11
FH-900	-5.02	3.71	0.23	-0.13	0.07	-0.113	-0.24	0.07	9.55	0.29	-1.03	0.01
FH-942	-1.20	-3.59	0.05	1.47	-0.06	-0.187	0.27	-3.27	2.86	0.60	-0.07	0.03
S.E. (s.i.)	0.196	1.43	0.31	0.47	0.05	0.080	0.37	0.79	1.27	0.30	0.38	0.13
Female inbreds												
FH-113	3.15	3.13	-0.41	3.98	0.21	0.337	0.90	-1.53	12.04	1.74	1.18	0.22
FH-114	0.70	0.07	-1.41	-3.01	0.05	0.082	-0.02	2.19	-9.33	0.19	-0.15	0.26
MNH-886	-19.22	-3.65	1.11	-3.19	-0.12	-0.32	-1.84	-0.33	7.28	-1.10	0.84	-0.13
IR-3701	-3.18	-0.25	-0.08	2.83	0.01	0.072	0.54	0.78	-0.79	-0.65	-1.09	-0.39
AA-703	18.55	0.69	0.79	-0.61	-0.15	-0.172	0.42	-1.12	-9.19	-0.18	-0.78	0.04
S.E. (s.i.)	0.175	1.28	0.27	0.42	0.04	0.07	0.33	0.71	1.13	0.27	0.34	0.12

CLCuV= Cotton leaf curl virus; d.f.=degree of freedom; GOT= Ginning out turn

COTTON PLANT TRAITS UNDER CLCuV EPIDEMIC CONDITION

The general combining ability analysis gives information about the superior parents based on their hybrid performance to exploit heterosis breeding. The genotype FH-900 showed a maximum negative GCA effect (5.02) for CLCuV and maximum positive GCA effects (0.069, 9.547) for locules/boll and seed cotton yield. CIM-1100 performed well against boll weight (0.189), fiber strength (0.683) and fiber fineness (0.145). CIM-506 was found to be a good general combiner for plant height (4.945), number of sympodial branches (0.718) and GOT (1.716). Maximum boll number, seed index and fiber length were shown in FH-942 with GCA effects 1.466, 0.269 and 0.604. Among five female parents, MNH-886 showed good performance against CLCuV (19.22), plant height (3.654) and number of sympodial branches (1.113), FH-113 against boll number (3.976), number of locules per boll (0.213), boll weight (0.337), seed index (0.903), seed cotton yield (12.038), fiber length (1.738) and fiber strength (1.181). High GOT was obtained from FH-114 (2.192) and fiber fineness (0.388) from IR-3701. Parents showing maximum GCA effects were considered as the best general combiners as they contained valuable genes for the improvement of characters and may be preferred for selection and hybridization program (Table 2).

Among twenty hybrids, FH-113×FH-942 was found to be the best specific combiner for fiber fineness as it showed maximum negative SCA effect (0.565). MNH-886×CIM-1100

performed well for seed index (1.401). Maximum GOT and sympodial branches were exhibited by MNH-886×FH-942 having SCA effects 5.982 and 3.992, respectively. IR-3701×CIM506 showed in the number of bolls (10.809) and seed cotton yield (20.290), MNH-886×FH-900 for plant height (12.84), FH-114×FH-942 showed the maximum locules number per boll (0.256) and high fiber length (2.296) was exhibited by FH-114×CIM-1100. The hybrid AA-703×CIM-1100 performed well under a CLCuV epidemic condition with good fiber strength (Table 3). The selection of such crosses would be beneficial to the development of superior hybrid through heterosis breeding. Khan *et al.* (1991) and Haq and Azhar (2005) reported that parental exhibiting best general combining ability for a specific trait may yield good hybrids and it was partially substantiated by the results of the present study that crosses of parent MNH-886, e.g. MNH-886×FH-900 and MNH886×FH-942 showed a high specific combining ability for plant height and number of sympodial branches per plant, respectively. It is not a rule that parents should be the best by general combiners for hybrid production, sometimes hybrid with high SCA may be produced by the combination of either parent with poor GCA (Patel *et al.*, 1997), e.g. FH-114×CIM-1100 for fiber length, MNH886×CIM-1100 for seed index and MNH-886×FH-900 for plant height, respectively, in this study.

Table 3 - Specific combining ability effects of 20 crosses for various characters in *Gossypium hirsutum* L.

Hybrids	CLCuV (%)	Plant height (cm)	Symptodial branches/plant	Bolls/plant	Locules / boll	Boll weight (g)	Seed index (g)	GOT	Seed cotton yield (g)	Fiber length (mm)	Fiber strength (g/tax)	Fiber fineness (micronaire)
FH-113× CIM-1100	1.47	-2.30	1.26	-3.42	0.08	-0.03	-0.51	-3.08	7.85	0.48	-1.86	0.16
FH-113× CIM-506	14.80	-3.76	-2.21	-5.04	0.05	-0.05	-1.22	2.21	-32.28	-0.63	0.11	-0.53
FH-113× FH-900	-15.29	5.97	-0.57	6.39	-0.08	-0.05	0.83	5.46	8.79	-0.67	1.02	0.93
FH-113× FH-942	-0.99	0.10	1.52	2.06	-0.05	0.13	0.89	-4.59	15.65	0.82	0.74	-0.57
FH-114× CIM-1100	3.09	2.57	-0.30	1.62	-0.36	-0.19	-0.70	-2.67	9.60	2.29	-0.06	-0.39
FH-114× CIM-506	2.67	-0.74	1.02	-1.20	0.06	-0.38	0.52	-1.78	7.534	-1.167	-0.99	0.43
FH-114× FH-900	1.11	4.74	-0.12	-0.66	0.05	0.32	-0.612	-0.10	-1.48	-0.79	0.10	-0.02
FH-114× FH-942	-6.87	-6.56	-0.60	0.25	0.26	0.25	0.80	4.55	-15.65	-0.34	0.95	-0.02
MNH-886× CIM-1100	17.81	2.57	-0.74	-3.19	0.09	-0.41	1.40	4.90	-18.22	-0.51	0.80	0.00
MNH-886× CIM-506	-17.40	8.07	-2.44	-1.17	0.03	0.62	0.56	-2.76	-1.22	1.28	-0.73	0.03
MNH-886× FH-900	3.20	-12.84	-0.82	-5.97	-0.17	0.42	-1.07	-8.12	10.45	0.41	-0.79	-0.09
MNH-886× FH-942	-3.61	2.21	3.99	10.33	0.05	-0.64	-0.88	5.98	8.99	-1.18	0.73	0.06
IR-3701× CIM-1100	1.77	-2.39	-1.20	-3.22	-0.01	0.29	0.18	0.78	-5.82	-0.78	-0.65	0.14
IR-3701× CIM-506	-10.11	-2.71	2.65	10.81	-0.00	-0.21	-0.89	0.06	20.29	-0.32	0.22	0.02
IR-3701× FH-900	-11.17	3.82	1.67	3.00	0.15	-0.10	0.84	1.43	-0.02	0.67	0.41	-0.29
IR-3701× FH-942	19.52	1.27	-3.13	-10.59	-0.14	0.02	-0.13	-2.27	-14.45	0.43	0.01	0.14
AA-703× CIM-1100	-24.14	-0.45	0.98	8.22	0.20	0.34	-0.37	0.08	6.59	-1.48	1.77	0.09
AA-703× CIM-506	10.04	-0.86	0.97	-3.40	-0.14	0.02	1.03	2.26	5.68	0.83	1.39	0.06
AA-703× FH-900	22.15	-1.69	-0.17	-2.76	0.05	-0.59	0.02	1.32	-17.73	0.37	-0.74	-0.52
AA-703× FH-942	-8.05	2.99	-1.79	-2.05	-0.12	0.23	-0.68	-3.66	5.46	0.28	-2.42	0.38
S.E. (s.e.)	0.393	2.86	0.61	0.93	0.09	0.16	0.74	1.59	2.53	0.59	0.75	0.26

COTTON PLANT TRAITS UNDER CLCuV EPIDEMIC CONDITION

Table 4 - Components of variation and heritabilities for various characters in *Gossypium hirsutum* L.

Genetic Components	CLCuV %	Plant height (cm)	Symptodial branches/plant	Bolls/plant	Locules/boll	Boll weight (g)	Seed index (g)	GOT	Seed cotton yield (g)	Fiber length (mm)	Fiber strength (g/tax)	Fiber fineness (micronaire)
σ^2m	0.56	17.95	0.62	4.71	0.01	0.002	0.17	0.23	62.03	0.52	0.35	0.02
σ^2f	-0.06	-2.65	-0.30	0.51	-0.003	-0.02	0.32	3.17	-61.35	0.06	0.18	0.02
$\sigma^2m \times f$	0.63	26.10	3.80	37.04	0.03	0.18	0.72	14.27	302.55	1.00	1.40	0.09
σ^2A	2.23	71.80	2.47	18.86	0.03	0.01	0.69	0.92	248.11	2.10	1.39	0.08
σ^2D	2.52	104.41	15.18	148.15	0.12	0.72	2.86	57.07	1210.19	4.00	5.61	0.36
σ^2E	0.31	16.34	0.75	1.74	0.02	0.05	1.10	5.06	12.83	0.72	1.14	0.14
σ^2P	5.06	192.55	18.40	168.75	0.16	0.79	4.66	63.05	1471.13	6.82	8.14	0.58
σ^2G	4.75	176.22	17.65	167.01	0.14	0.73	3.55	57.99	1458.30	6.10	6.99	0.44
h^2ns	0.44	0.37	0.13	0.11	0.15	0.013	0.14	0.01	0.16	0.30	0.17	0.14
h^2bs	0.93	0.91	0.95	0.98	0.89	0.93	0.76	0.91	0.99	0.89	0.85	0.76

CLCuV= Cotton leaf curl virus; d.f.=degree of freedom; GOT= Ginning out turn; σ^2m = variance of male; σ^2f = variance of female; $\sigma^2m \times f$ = variance of male and female; σ^2A = additive variance; σ^2D = dominance variance; σ^2E = environmental variance; σ^2P = phenotypic variance; σ^2G = genotypic variance; h^2ns = narrow sense heritability; h^2bs = broad sense heritability

DISCUSSION

The presence of genetically controlled variation may be advantageous and helpful to breeders. The estimation of genetic effects of seed cotton yield (Ahmad *et al.*, 2002; Tarr, 1957), number of bolls per plant (Moskovet, 1940) and fiber quality traits (Moskovet, 1940) were used under cotton leaf curl virus. Estimation of additive and non-additive genetic effects for the studied characters are presented in (*Table 4*). Estimates of dominance variance were higher than estimates of additive variance for the studied characters. Genes responsible for resistance against CLCuV were dominant to their alleles (Hussain *et al.* (2012). Previous study also indicated the same results that a single dominant gene was responsible for CLCuV resistance (Aslam *et al.*, 2000 and Mahmood, 2004). Predominance of non-additive gene action for plant height was observed by Deva *et al.* (2002), number of sympodia per plant was reported by Valarmathi and Jehangir (1998), GOT under non-additive gene action was observed by Sandhu *et al.* (1993). Studies of Ahuja and Dhayal (2007) revealed that the number of bolls, boll weight and seed cotton yield were influenced by genes acting non-additively.

High dominance variance was observed for a number of locules per boll, which indicated that particular character was under dominant genes control. In contrast to our results, Patil *et al.*, (1997) reported additive type of

gene actions for a particular trait. Seed index was controlled by non-additive genetic effects as reported by Deva *et al.* (2002) and Subhan *et al.* (2002). Amudha *et al.* (1997), Mandloi *et al.* (1998), Modi *et al.* (1999) and Krishna (1998) concluded non-additive genetic effects for the inheritance of ginning out turn. Fiber quality characters, i.e. fiber length, fiber strength and fiber fineness, were controlled by dominant genes, as it was also reported by the previous studies of Baloch *et al.* (1997), Hassan *et al.* (1999 and 2000), Ahuja and Dhayal (2007), Preetha and Ravendran (2008). Estimates of additive variance were found higher than dominance variance for seed cotton yield meaning that selection based on additive genes in early segregation population would be effective to produce superior inbreds. However, the dominance variances were higher than additive variances for CLCuV %, plant height, number of sympodial branches per plant, bolls/plant, locules/boll, boll weight, seed index, GOT and fiber quality traits. Falconer and Mackay (1996) also reported that segregating populations were not liable for selection in early generations, i.e. F₂ and thus selection must be delayed until the genes are established in the breeding population.

CONCLUSION

Our results indicated the importance of dominant genes in the inheritance of these characters. Heritability is an effective tool for

COTTON PLANT TRAITS UNDER CLCuV EPIDEMIC CONDITION

plant breeders to separate heritable variations from phenotypic variations. The selection's efficiency of both yield and yield components depend on the genetic variation and heritability percentage. High heritability estimates suggest the possibility of genetic improvement in our study material. In the present study, the estimate of narrow sense heritability ranged from 0.01 to 0.44. Broad sense heritability was found greater than narrow sense heritability ranging from 0.76 to 0.98, respectively. Low broad sense heritability was found in fiber fineness, which indicates that such character was highly depended on environmental factors. Low narrow sense heritability in various traits was found due to less additive variance with dominance genetic variance. So, it is concluded that the selection of desirable traits based on narrow sense heritability would be effective in late generations.

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