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Estimation of Genetic Effects Controlling Different Plant Traits in *Gossypium hirsutum* under CLCuV epidemic Condition

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ABSTRACT: A study was conducted in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad during year 2013 to estimate the genetic effects controlling different plant traits in Gossypium hirsutum under epidemic CLCuV condition following North Carolina Design II. The genotypes comprised of four non- Bt males (CIM-1100, CIM-506, FH-942 and FH-900) and five Bt females (FH-113, FH-114, MNH-886, AA-703 and IR-3701). Twenty crosses along with parents were sown in two replications under RCBD. The mean squares were significant for all traits which is the indication of both additive and non-additive genes controlling the characters but non-additive genes were more important because, variance due to dominant genes were higher than additive genes. Among testers FH-900 showed best performance against CLCuV, number of locules per boll and seed cotton yield. CIM-1100 performed well against boll weight, fiber strength and fiber fineness. CIM-506 was good general combiner for plant height, number of sympodial branches and GOT. Maximum boll number, seed index and fiber length was shown by FH-942. Among lines, MNH886, FH-113, IR-3701 and FH-114 exhibited best general combiners against many traits. Hence these parents may be preferred for hybridization program to improve 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 were best specific combiners for different traits. These results indicated that in order to improve various traits, different hybrids may be exploited for hybrid crop development.

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Key Words: *Gossypium hirsutum*, Cotton leaf curl virus (CLCuV), Genetic effects, General and Specific Combing ability, North Carolina Design II.

INTRODUCTION:

Agriculture is the back bone 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; Fryxell, 1992). Pakistan ranks 4th in world cotton production after China, USA and India (Akhtar, 2005). Cotton is an essential source of foreign exchange earnings and brings about 60% through export products (Igbal et al., 2005). The contribution of cotton in total agriculture is about 8.6% and 1.8% contribution in 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 are dependent upon cotton farming, ginning and textile.

Cotton crop not only produce fiber, it also provide edible oil and seed cake for animals.

Cotton is a summer crop and is sown in the month of May-June. Late sown crop is affected by many biotic and abiotic factors like high temperature in the month of August, attack of sucking insects and wide spread of cotton leaf curl virus. Many important plant diseases are caused by biotic stresses like viruses and are also responsible for production and quality losses. Cotton leaf curl virus is an epidemic disease transmitted by white fly. Cotton producers in Pakistan are facing production problems and heavy loss due to cotton pests (Haidar et al., 2007). CLCuV is considered as a major threat to the production of cotton in Pakistan (Ahmad et al., 2010). A loss of about 2.3 million bales had been reported in Pakistan due to CLCuV in the last year (Pakistan Economic Survey, 2012-13). It not only affects the seed cotton vield but also results in stunted growth of plant; deteriorate fiber quality, decrease boll weight, seed weight, number of monopodia land sympodial branches (Farooq et al., 2011). Appearance of disease

at seedling stage hinders boll formation, flowering, maturation, yield of seed cotton and destroys fiber quality (Monga *et al.*, 2011).

Genetic variability plays an important role in protection of losses due to insects and pests and facilitates development of segregating populations (Esbroeck et al., 1999). The selection of parents is very important in future breeding programs (Esbroeck & Bowman, 1998) which may be helpful for the development of allelic variation and in the creation of favorable gene combinations. Combing ability analysis is an important tool for the selection of desirable parents together with the information regarding gene effects controlling quantitative traits. Combining ability define the pattern of genetic effects in the expression of quantitative characters by identifying superior parents and hybrids (Ahuja and Dhayal, 2007). Good general combing ability is mandatory for parents selection while hybrids are selected on the basis of specific combing ability.

Information about genetic mechanisms of parents governing different plant traits like 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 particular direction for maintaining and improving proper crop production. In early plant breeding era, large number of crosses was 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 parent is used with more resources. On the other hand North Carolina Design-II involves more number of parents with same resources and provides information for parents with reliable genetic parameters.

The objective of present study was to estimate genetic effects controlling different plant traits and general and specific combing ability of cotton inbreds under CLCuV using North Carolina Design-II genetic analysis.

MATERIAL AND METHODS:

The present study regarding the estimation of genetic effect was carried out in the experimental area of Department of Plant Breeding and Genetics, University of Agriculture Faisalabad during year 2013. The experimental 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 fashion in glass house. Seeds of twenty hybrids along

with nine parents were sown in the field during June 2013 in two replications in randomized complete block design. At maturity, five plants in each row were tagged to obtain data 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. The genetic effects were calculated according to the procedure as described by Comstock *et al.*, (1949). Combing ability analysis was also carried out by the method given by Kearsey and Pooni (1996).

RESULTS:

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

The general combing ability analysis (Table 3) gives information about the selection of superior parents on the basis of their hybrids performance to exploit heterosis breeding. Among testers FH-900 showed maximum negative GCA effect (5.02) for CLCuV and maximum positive GCA effects (0.069, 9.547) for locules/boll and seed cotton vield. CIM-1100 performed well against boll weight (0.189), fiber strength (0.683) and fiber fineness (0.145). CIM-506 was found to be 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 was 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.

Among twenty hybrids, FH-113× FH-942 was found to be 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 effects5.982 and3.992 respectively.IR-3701× CIM506against 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 maximum locules number per boll (0.256) and high fiber length (2.296) was exhibited by FH-114× CIM-1100. Hybrid AA-703× CIM-1100 performed well under CLCuV epidemic condition with good fiber strength (Table 4). Selection of such crosses would be beneficial for the development of superior hybrid through heterosis breeding.

Khan *et al.*, (1991), Haq and Azhar (2005) reported that parents exhibiting best general combining ability for a specific trait may yield good

hybrids and it was partially substantiated by the results of present study that crosses of parent MNH-886 e.g. MNH-886× FH-900 and MNH886× FH-942 showed high specific combing ability for plant height and number of sympodial branches per plant respectively. It is not necessary that parents should be best 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.

1 able 1. Mean Squares non analysis of variance of NCN-11 for various characters in Oossyptum nu sutum 1	Table 1: Mean So	quares from anal	vsis of variance of	f NCM-II for various	characters in Goss	vpium hirsutum L
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Source of variations	d.f	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 (micronarine)
Replications	1	1.288	0.037	3.044	0.436	.0058	0.023	1.273	9.204	0.233	2.743	1.043	0.034
Male (GCA)	3	7.147	248.053	14.517	122.962	0.139	0.439	4.270	35.889	1238.2	7.958	7.421	0.527
Female (GCA)	4	1.062	47.320	5.944	79.904	0.050	0.266	5.077	58.966	127.127	3.237	5.405	0.489
Male × female (SCA)	12	1.570	68.543	8.343	75.814	0.075	0.413	2.534	33.591	617.923	2.718	3.942	0.320
Error	20	0.309	16.337	0.752	1.738	0.017	0.052	1.104	5.055	12.828	0.718	1.139	0.139

Table 2: Components of variation and heritabilities for various characters in Gossypium hirsutum L.

Genetic Componnets	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 (micronarine)
σ²m	0.557	17.950	0.617	4.714	0.006	0.002	0.173	0.229	62.027	0.524	0.347	0.020
σ²f	-0.063	-2.652	-0.299	0.511	-0.003	-0.018	0.317	3.171	-61.349	0.064	0.182	0.021
σ²m×f	0.630	26.103	3.795	37.037	0.029	0.180	0.715	14.267	302.547	1.00	1.401	0.090
σ²A	2.230	71.803	2.469	18.859	0.025	0.010	0.694	0.919	248.110	2.096	1.391	0.082
σ²D	2.523	104.412	15.182	148.151	0.117	0.722	2.860	57.070	1210.19	4.00	5.606	0.362
σ²E	0.309	16.337	0.752	1.738	0.017	0.052	1.104	5.055	12.828	0.718	1.139	0.139
σ²P	5.063	192.553	18.404	168.749	0.159	0.785	4.659	63.045	1471.129	6.815	8.137	0.583
σ²G	4.753	176.216	17.652	167.011	0.142	0.732	3.554	57.989	1458.301	6.096	6.998	0.44
h²ns	0.44	0.37	0.13	0.11	0.15	0.013	0.14	0.01	0.16	0.30	0.17	0.14
h²bs	0.93	0.91	0.95	0.98	0.89	0.93	0.76	0.91	0.99	0.89	0.85	0.76

Table 3: General combining ability effects of male and female parents for various characters in *Gossypium* hirsutumL.

Inbred parents	CLCuV %	Plant height (cm)	Sympodia branches/ plant	Bolls/ plant	Locule s/ boll	Boll weight (g)	Seed index (g)	GOT	Seed cotton yield (g)	Fiber length (mm)	Fiber strength (g/tax)	Fiber fineness (micronarine)
Male inbreds												
CIM- 1100	2.38	4.825	-0.996	-2.404	0.021	0.189	-0.026	1.484	-8.269	-1.156	0.683	-0.145
CIM-506	3.84	-4.945	0.718	1.066	-0.032	0.111	-0.002	1.716	-4.133	0.266	0.413	0.106
FH-900	-5.02	3.713	0.228	-0.128	0.069	-0.113	-0.240	0.066	9.547	0.286	-1.026	0.006
FH-942	-1.20	-3.593	0.05	1.466	-0.058	-0.187	0.269	-3.267	2.855	0.604	-0.070	0.032
S.E. (si.)	0.196	1.429	0.306	0.466	0.046	0.080	0.371	0.794	1.266	0.299	0.377	0.131
Female inbreds												
FH-113	3.15	3.134	-0.414	3.976	0.213	0.337	0.903	-1.525	12.038	1.738	1.181	0.217
FH-114	0.70	0.074	-1.409	-3.006	0.048	0.082	-0.024	2.192	-9.331	0.188	-0.153	0.259
MNH-886	-19.22	-3.654	1.113	-3.194	-0.124	-0.32	-1.839	-0.332	7.276	-1.097	0.841	-0.130
IR-3701	-3.18	-0.250	-0.076	2.831	0.010	0.072	0.538	0.782	-0.786	-0.652	-1.086	-0.388
AA-703	18.55	0.687	0.786	-0.606	-0.147	-0.172	0.423	-1.117	-9.196	-0.177	-0.783	0.042
S.E. (si.)	0.175	1.278	0.274	0.416	0.041	0.072	0.332	0.711	1.132	0.268	0.337	0.117

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Hybrids	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 (micronarine)
FH-113× CIM-1100	1.47	-2.302	1.256	-3.416	0.081	-0.031	-0.511	-3.077	7.851	0.476	-1.863	0.163
FH-113× CIM-506	14.80	-3.762	-2.208	-5.036	0.045	-0.053	-1.215	2.211	-32.284	-0.626	0.106	-0.529
FH-113× FH-900	-15.29	5.969	-0.568	6.388	-0.077	-0.049	0.833	5.461	8.785	-0.666	1.016	0.931
FH-113× FH-942	-0.99	0.095	1.52	2.064	-0.049	0.134	0.893	-4.595	15.647	0.816	0.740	-0.565
FH-114× CIM-1100	3.09	2.567	-0.299	1.616	-0.364	-0.186	-0.703	-2.674	9.601	2.296	-0.058	-0.389
FH-114× CIM-506	2.67	-0.742	1.017	-1.203	0.06	-0.378	0.522	-1.776	7.535	-1.166	-0.988	0.428
FH-114× FH-900	1.11	4.739	-0.123	-0.659	0.048	0.315	-0.619	-0.096	-1.484	-0.786	0.101	-0.021
FH-114× FH-942	-6.87	-6.564	-0.595	0.246	0.256	0.249	0.800	4.547	-15.652	-0.344	0.945	-0.017
MNH-886× CIM-1100	17.81	2.567	-0.741	-3.196	0.088	-0.414	1.401	4.900	-18.216	-0.509	0.796	0.000
MNH-886× CIM-506	-17.40	8.067	-2.435	-1.166	0.032	0.624	0.557	-2.761	-1.222	1.279	-0.733	0.028
MNH-886× FH-900	3.20	-12.84	-0.815	-5.972	-0.169	0.428	-1.074	-8.121	10.448	0.409	-0.793	-0.091
MNH-886× FH-942	-3.61	2.205	3.992	10.334	0.048	-0.638	-0.884	5.982	8.99	-1.179	0.730	0.062
IR-3701× CIM-1100	1.77	-2.387	-1.201	-3.221	-0.006	0.293	0.184	0.775	-5.823	-0.784	-0.646	0.138
IR-3701× CIM-506	-10.11	-2.707	2.654	10.809	-0.002	-0.208	-0.89	0.063	20.290	-0.316	0.224	0.016
IR-3701× FH-900	-11.17	3.824	1.674	3.003	0.145	-0.104	0.838	1.433	-0.019	0.674	0.414	-0.294
IR-3701× FH-942	19.52	1.270	-3.127	-10.59	-0.136	0.019	-0.132	-2.272	-14.447	0.426	0.008	0.14
AA-703× CIM-1100	-24.14	-0.445	0.986	8.216	0.201	0.338	-0.371	0.075	6.586	-1.479	1.771	0.088
AA-703× CIM-506	10.04	-0.855	0.972	-3.403	-0.135	0.016	1.025	2.263	5.680	0.829	1.391	0.056
AA-703× FH-900	22.15	-1.693	-0.168	-2.759	0.053	-0.589	0.023	1.323	-17.729	0.369	-0.738	-0.524
AA-703× FH-942	-8.05	2.993	-1.79	-2.053	-0.119	0.234	-0.677	-3.662	5.462	0.281	-2.424	0.38
S.E. (si.)	0.393	2.858	0.613	0.932	0.092	0.161	0.743	1.589	2.532	0.599	0.754	0.263

Table 4: Specific combing ability effects of 20 crosses for various characters in Gossypium hirsutum L.

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 (Andrew, 1936; 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 2. Estimates of additive 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 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 number of

bolls, boll weight and seed cotton yield were influenced by genes acting nonadditively.

High dominance variance was observed for number of locules per boll which indicated that particular character was under the control of dominant genes. In contrast to the results of present study, Patil *et al.*, (1997) reported additive type of gene actions for particular trait. Seed index was controlled by nonadditive 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 outturn.

Fiber quality characters i.e. fiber length, fiber strength and fiber fineness was 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), Pareetha and Ravendran (2008).

Estimates of additive variance was found higher than dominance variance for seed cotton yield so it could be concluded that selection based on additive genes in early segregation population would be effective to produce superior inbreeds. However, the dominance variances were higher than additive variances for CLCuV %, plant height, no of sympodial branches per plant, bolls/plant, locules/boll, boll weight, seed index, GOT and fiber quality traits. Results indicated the importance of dominant genes in the inheritance of these characters.

Heritability is an effective tool for plant breeders to separate heritable variations from phenotypic variations. The efficiency of selections of both yield and yield components depend on the genetic variation and heritability percentage. High heritability estimate suggested the possibility of genetic improvement in the under study material. In 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 indicated 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 selection of desirable traits on the basis of narrow sense heritability would be effective in late generations. Falconer and Mackav (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 population of breeding.

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