RESEARCH ARTICLE

COMBINING ABILITY ANALYSIS IN F_1 AND F_2 POPULATION FOR COTTON LEAF CURL VIRUS DISEASE AT MULTIPLE LOCATIONS

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ARTICLE DETAILS

ABSTRACT

Genetic studies were conducted to examine the heritage of resistant to cotton leaf curl virus. Genetic components of variance revealed higher $\sigma^2 GCA$ and Additive ($\sigma^2 A$) than $\sigma^2 SCA$ and Dominance ($\sigma^2 D$), which indicated additive genes were more reliable for inheritance of resistance to CLCV. The ratio of variances $\sigma^2 gca/\sigma^2 sca$ was higher than unity (one) and further proved from degree of dominance $[\sigma^2 A/\sigma^2 D]^{0.5}$ which was greater than one and confirmed supremacy of additive genes at both locations and generations. The heritability narrow sense (h^2) and broad sense (H^2) was found higher which suggested role of additive genes, which are fixable. Therefore selection would be effective in early segregating generation according to the symptoms of cotton leaf curl virus. The GCA effects for CLCV showed that among the parents, Mac-7 found as good general combiner with highest significant negative GCA effects at both locations in F_1 and F_2 which considered as CLCV resistant parent. The SCA effects exhibited that hybrid, Mac-7 x USD16-3058, CIM-602 x Mac-7 and NIA-Noori x Mac-7 showed significant negative SCA effect in both generations and locations. It was noted that cross combinations involved good x poor and poor x good general combiner with significant SCA effect was due to complementary gene action which produce desirable transgressive segregants, these can be further studies through bi-parental mating of diallel selective mating or any other form of recurrent selection in early generation with single plant selection to exploited both additive an non-additive gene action.

KEYWORDS

Cotton Leaf Curl Virus, Diallel analysis, combining ability, gene action, Locations

1. INTRODUCTION

Cotton is a main fiber crop; it has a significant importance at globally with high commercial value. It is being grown in temperate and tropical regions of more than 70 countries. The specific areas of production include countries such as China, USA, India, Pakistan, Uzbekistan, Turkey, Australia, Greece, Brazil, Egypt etc., where climatic conditions suit the natural growth requirements of cotton. This includes periods of hot and dry weather and adequate moisture obtained through irrigation. Pakistan is 4th largest cotton producing country in the world, whereas 3rd in consumption globally during last five years from 2014-15 to 2018-19. County economic development depends upon the production of cotton, because the nation mainly dependent on industry of cotton and related to its textile sector.

That's why the principal status has been given to the cotton crop. Cotton crop for year 2018-19 season has been cultivate over 2.7 million hectares showing an increase of about 2% as compared to cultivation of 2.6 million hectares recorded during last year season 2017-18. The area under cotton crop in Pakistan during 2017-18 was 2808.66 million hectares with the production of 11.98 million bales. In Sindh Province cotton crop was sown under 612.0 million hectares and the production was 3.77 million bales recorded during the year 2017-18. The crop cultivation in Sindh during current season witnessed decreased of 31.0% as compared to corresponding period of last season. Due to severe shortage of water only 68% sowing had been recorded against the target. In the standing crop

severe attack of whitefly was observed and cotton leaf curl virus was also spreading rapidly due to its vector whitefly (Cotton Review, 2018).

Cotton leaf curl virus (CLCV) found to be most important disease, considered as most severe and destructive for cotton crop. CLCV belongs to the family gemini virus and genus begomo virus. CLCV is a *Bemisia tabaci* (whitefly) transmitted virus and is associated to the viral family Geminiviridae. Cotton leaf curl virus (CLCV) first time appeared in Pakistan during 1967 at Tiba Sultan Pur near Multan District. During the earlier time disease was un-noticed but in 1993-1995 drastic losses was observed and appeared epidemic form in Pakistan. In 1997 CLCV was reported from Province of Sindh which was free from CLCV (Mansoor et al., 1998). A researcher reported that segregating generation for CLCV resistant controlled through single dominant gene (Mahmood, 2004). A group researchers observed CLCV resistant plants in F_1 generation due to absence of extra-chromosomal inheritance and further reported that in F_2 generation 3 plants showed symptoms of CLCV due to segregation (Rehman et al., 2005).

Some researcher noted that additive gene effect specified more to CLCV resistant than susceptible in divergence with dominance gene effect (Khan et al., 2007). A study reported 100% CLCV resistant plants in F_1 generation when resistant parent were used in cross combinations (Khan et al., 2007). However, in F_2 generation from 83-91% resistant plants were observed due to segregation. According with the finding of the un-tired and massive efforts of cotton breeder, four cotton varieties were developed which were resistant against cotton leaf curl virus (Ihsan et al., 2011). However, the

CLCV resurfaced during 2001 and all the varieties proved susceptible. At that present all the breeding material and released varieties are susceptible to CLCV strain and scientists are in search of resistant sources to develop the resistant or highly tolerant germplasm (Haider et al., 2012). The prime objective of cotton breeder to evolve variety which possess resistant/tolerant for cotton leaf curl virus (CLCV) along with potential of seed cotton yield and earliness (Farooq et al., 2014). Diallel analysis is one of the methods among them which is widely used for the evaluating type of gene action (additive and non-additive). Thus, it facilitates for selecting appropriate parent for the exploitation in hybridization and selection program to produce genotypes resistant with cotton leaf curl virus.

2. MATERIAL AND METHOD

The breeding material 10 parents, 45 F_1 hybrids and 45 F_2 population were grown during the Kharif season 2017 and 2018 in randomized complete block design with three replications at two locations Sakrand and Mirpurkhas. Breeding material was developed by crossing 10 cotton cultivars viz. CRIS-129, MNH-886, FH-142, NIA-Noori, Baghdadi, CIM-602, NIAB-824, CEMB-33, Mac-7 and USD16-3058. The 200 square feet plot size was arranged for each treatment. The inputs and plant protection measures were applied as per need whenever required. The cotton leaf curl virus (CLCV) disease percentage, severity and index was analyzed by using disease rating scale suggested (Akhtar et al., 2010; Farooq et al., 2011). The data of both locations were individually employed for analysis of variance (ANOVA). The LSD (least significance difference) was examined for mean separation. The general combining ability and specific combining ability were estimated according to Diallel Method-II Model-1 described by Griffings by using the statistical software Plant Breeding Tool 1.4 and Statistix 8.1 (Griffings, 1956).

3. RESULTS AND DISCUSSION

The present research exposed significant mean square values of parents, hybrids and genotypes for cotton leaf curl virus (CLCV) at both the locations (Sakrand and Mirpurkhas) in F_1 generation and F_2 segregating population which suggested genetically diverse material were studied. Similar results reported (Randhawa et al., 1998; Ilhai et al., 2013; Shakeel et al., 2015). Significant mean squares of CLCV in F_1 and F_2 generation also documented (Khan, 2013). The mean squares due to general combining ability (GCA) and specific combining ability (SCA) was also significant at both the environments (Sakrand and Mirpurkhas) in F_1 and F_2 generation designated additive and non-additive gene action was involved for inheritance of CLCV. A group researchers observed significant GCA and SCA means squares for CLCV and specified role of additive and non-additive gene action (Shakeel et al., 2015; Khan et al., 2017).

The genetic components of variance for CLCV revealed higher variance of GCA (σ^2GCA) and Additive (σ^2A) than SCA (σ^2SCA) and Dominance (σ^2D) that additive genes were more reliable for inheritance of resistant to CLCV. It was further confirmed with ratio of variances σ^2gca/σ^2sca was higher than unity (one) and further proved from degree of dominance $[\sigma^2A/\sigma^2D]^{0.5}$ which was greater than one and confirmed that supremacy of additive genes of CLCV at both the environments in F_1 generation and F_2

population. A study reported higher portion of additive variance than dominance (Randhawa et al., 1998). A group researcher described that additive gene effect contributed more to resistance than susceptible (Khan et al., 2007). The heritability narrow sense (h^2) and broad sense (H^2) was found higher as well at both individual environments in both the generations (F_1 and F_2), suggested role of additive genes, which are fixable. Therefore, selection would be effective in early segregating generation according to the symptoms of cotton leaf curl virus (CLCV). A group researchers found high narrow sense heritability for CLCV and suggested that resistant could be improved through single plant selection (Hussain et al., 2012; Khan, 2013).

General combining ability (GCA) effect are corresponding to additive effect, which is an important for genetic information by finding desirable good general combiner to improve characters with interest (Wu et al., 2010). The GCA effects for CLCV showed that among the parents Mac-7 found as good general combiner with highest significant negative GCA effects at individual locations and generations F_1 and F_2 which considered as CLCV resistant parent. However, highest significant positive GCA effect showed by USD16-3058 which measured as CLCV susceptible and poor parent at both the locations (E-1 and E-2) and generations (F_1 and F_2). The parent FH-142 and Baghdadi also showed negative GCA effect for CLCV and excelled as average parent with tolerant for CLCV. While, remaining poor parents which exhibited positive GCA effect and noted as susceptible. The similarity in estimation of GCA effects in F_1 and F_2 generation specified that the best combiners are stable in their performance over generation to generation.

The specific combining ability (SCA) effects proposed that, in hybrids combinations Mac-7 x USD16-3058, CIM-602 x Mac-7 and NIA-Noori x Mac-7 proved as good specific combiner which contributed significant negative SCA effect for CLCV at both environments and generations F_1 and F_2. It was noted that cross combinations involved good x poor and poor x good general combiner with significant SCA effect was due to complementary gene action which produce desirable transgressive segregants, these can be further studies through bi-parental mating of diallel selective mating or any other form of recurrent selection in early generation with single plant selection to exploited both additive an non-additive gene action. However, some hybrids also showed negative SCA effect but non-significant and combined with the Mac-7.

The remaining cross combinations were noted with negative to positive SCA effect which was likely combinations of average x poor and poor x poor general combiner may be due to nicking ability/genetic diversity of their parents in form of dispersed genes for cotton leaf curl virus (CLCV). It is further suggested that GCA and SCA effects are not alone feasible to pic good combiner for exploitation in breeding program. Therefore, per se performance of parents and hybrids particular cotton leaf curl virus disease data in F_1 and F_2 generation will support to choose appropriate cross combinations for further exploitation in cotton improvement program. Similar results of negative and positive GCA and SCA effect for CLCV was obtained (Randhawa et al., 1998; Shakeel et al., 2016; Khan et al., 2017).

Table 1: Analysis of Variance (ANOVA) For Cotton Leaf Curl Virus Disease Incidence %.

Source of Variation	D.F	F_1 Generation 2017		F_2 Population 2018	
		Sakrand	Mirpurkhas	Sakrand	Mirpurkhas
Replications	2	21.07	166.819	21.07	61.357
Parents	9	1360.76**	398.029**	1515.32**	318.247**
Crosses	44	1009.13**	253.331**	1009.13**	251.338**
Genotypes	54	1050.5**	273.07**	1544.47**	259.55**
General Combining Ability (GCA)	9	1732.4**	444.01**	2770.26**	427.283**
Specific Combining Ability (SCA)	44	73.707**	20.425**	63.7361**	18.3634**
Error	216	27.921	12.245	12.588	7.415

Table 2: Genetic Components of Variance For Cotton Leaf Curl Virus Disease Incidence %.

Genetic Components	F_1 Generation 2017		F_2 Population 2018	
	Sakrand	Mirpurkhas	Sakrand	Mirpurkhas
σ^2 GCA	138.22	35.29	225.54	34.07
σ^2 SCA	45.78	8.17	51.14	10.94
σ^2 A	552.91	141.19	902.17	136.31
σ^2 D	183.14	32.71	204.58	43.79
h^{ns}	0.72	0.75	0.80	0.72
H^{bs}	0.96	0.93	0.98	0.96
σ^2gca/σ^2sca	3.02	4.32	4.41	3.11
$[\sigma^2A/\sigma^2D]^{0.5}$	1.73	2.07	2.10	1.76

Table 3: General Combining Ability (GCA) Effects For Cotton Leaf Curl Virus Disease Incidence %.				
Parents	**F_1 Generation 2017**		**F_2 Population 2018**	
	Sakrand	**Mirpurkhas**	**Sakrand**	**Mirpurkhas**
CRIS-129	4.35**	1.74	0.72	2.77**
MNH-886	-1.39	1.34	1.17	0.27
FH-142	-3.00*	-0.53	-2.27*	-0.95
NIA-Noori	2.95*	1.61	7.80**	1.36
Baghdadi	-4.34**	-2.70**	-0.93	-1.84*
CIM-602	10.67**	4.12**	8.82**	5.25**
NIAB-824	0.11	-1.90*	2.04*	-0.79
CEMB-33	-1.60	-1.00	3.78**	-0.71
Mac-7	-27.28**	-13.44**	-39.63**	-14.16**
USD16-3058	19.53**	10.76**	18.50**	8.79**
S.E (gi)	1.44	0.95	0.97	0.75
S.E (gi-gj)	2.15	1.42	1.44	1.11
C.D @5%	2.27	2.83	2.87	2.20

Table 4: Specific Combining Ability (SCA) Effects For Cotton Leaf Curl Virus Disease Incidence %.				
Crosses	**F_1 Generation 2017**		**F_2 Population 2018**	
	Sakrand	**Mirpurkhas**	**Sakrand**	**Mirpurkhas**
CRIS-129 x MNH-886	7.79	1.94	-0.80	4.06
CRIS-129 x FH-142	0.43	-1.32	-1.43	-0.36
CRIS-129 x NIA-Noori	0.42	-1.90	3.37	-1.16
CRIS-129 x Baghdadi	-6.03	1.31	-5.10	-5.16*
CRIS-129 x CIM-602	16.86**	4.39	-1.65	11.11**
CRIS-129 x NIAB-824	4.32	-0.82	2.90	-2.25
CRIS-129 x CEMB-33	-4.24	4.78	1.43	2.31
CRIS-129 x Mac-7	-7.03	-3.28	-3.76	-4.47
CRIS-129 x USD16-3058	-4.20	2.62	9.41**	-1.53
MNH-886 x FH-142	12.64**	1.72	-7.97*	3.27
MNH-886 x NIA- Noori	-6.54	-1.89	-5.61	-3.90
MNH-886 x Baghdadi	-3.92	-1.51	-1.01	-3.14
MNH-886 x CIM-602	-5.09	2.20	7.04*	-0.96
MNH-886 x NIAB-824	2.84	-2.38	15.72**	3.28
MNH-886 x CEMB-33	-3.83	0.82	-0.82	5.60*
MNH-886 x Mac-7	-1.28	-2.87	-4.45	-2.24
MNH-886 x USD16-3058	-4.42	7.13*	-0.07	-2.33
FH-142 x NIA- Noori	1.24	6.07	12.30**	-2.52
FH-142 x Baghdadi	1.69	-0.45	0.53	1.82
FH-142 x CIM-602	11.75*	1.13	-1.52	8.89**
FH-142 x NIAB-824	-3.69	-2.45	1.32	0.46
FH-142 x CEMB-33	-8.49	-0.18	-4.75	-5.95*
FH-142 x Mac-7	0.33	-1.01	-2.41	-0.72
FH-142 x USD16-3058	-5.92	0.86	3.53	-3.01
NIA- Noori x Baghdadi	5.34	1.01	-5.44	-1.86
NIA- Noori x CIM-602	6.71	10.02**	0.17	-1.14
NIA- Noori x NIAB-824	0.20	4.11	-8.45**	4.63
NIA- Noori x CEMB-33	5.14	-2.59	6.15	4.31
NIA- Noori x Mac-7	-5.62	-3.15	-11.01**	-1.43
NIA- Noori x USD16-3058	9.14	-2.62	-3.74	5.98*
Baghdadi x CIM-602	-6.64	-5.66	4.44	-1.04
Baghdadi x NIAB-824	-6.05	2.83	-6.71*	-1.27
Baghdadi x CEMB-33	-3.65	-0.51	-1.25	-3.72
Baghdadi x Mac-7	1.67	1.16	-3.24	0.50
Baghdadi x USD16-3058	1.82	-3.37	-1.87	2.18
CIM-602 x NIAB-824	-0.39	4.84	-2.53	-4.16
CIM-602 x CEMB-33	5.72	-3.13	4.03	-0.44
CIM-602 x Mac-7	-13.34**	-5.66	-10.50**	-4.85
CIM-602 x USD16-3058	-4.01	-3.62	-0.32	-1.87
NIAB-824 x CEMB-33	16.54**	-0.94	-3.89	0.06
NIAB-824 x Mac-7	-2.78	0.36	-5.85	-0.92
NIAB-824 x USD16-3058	3.08	-3.87	-1.25	-0.84
CEBM-33 x Mac-7	-1.07	2.93	-7.65*	-0.43
CEBM-33 x USD16-3058	-1.95	-1.57	3.75	-4.72
Mac-7 x USD16-3058	-20.10**	-12.30**	-16.17**	-5.96*
S.E (si)	4.87	3.22	3.27	2.51
S.E (si-sj)	6.10	4.04	4.09	3.14
C.D @5%	12.09	8.01	8.12	6.23

4. CONCLUSION

It is concluded from present research that the additive genes are reliable for inheritance of resistant to cotton leaf curl virus, because of the higher variance of additive and GCA were obtained. It was further proved degree of dominance and heritable which suggested role of additive genes that are fixable. Therefore, Mac-7 considered as CLCV resistant parent for CLCV, it shown negative GCA effect and hybrid that were combined with Mac-7 showed significant negative SCA effect in both generations and locations. Therefore, single plant selection would be effective in early segregating generation with the symptoms of cotton leaf curl virus disease.

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