DESIGN-11 ANALYSIS FOR ESTIMATIMG GENERAL AND SPECIFIC COMBINING ABILITY EFFECTS OF COTTON LEAF CURL VIRUS RESISTANT INBRED PARENTS

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ABSTRACT Combining ability estimates are very important attributes to cotton breeders in predicting genetic improvement that could be made through hybridization and selection. Cross Classification Design-11 analysis that involved 5 cotton leaf curl virus (clcv) susceptible male and 5 clcv resistant female inbred parents were crossed in cotton research institute, Sindh, Pakistan, during summer Season 2000 and 2001, thus forming 25 intrahirsutum F1 hybrids were studied. The mean squares due to male and female parents both determined general combining ability (GCA) variances and males x females which pertained to specific combining ability (SCA) variances were significant for all the six characters. The significance of GCA and SCA variances suggested that both additive and dominant genes were controlling the traits, thus selection in segregating populations could be very effective or choice parents could be used for hybrid crop development. The significance of GCA and SCA variances as such, however, do not provide the information on the nature of genes of individual inbred parents, hence GCA and SCA effects of males and females were also detemined. Among the males, parents CRIS-121 for seedcotton yield and number of bolls; CRIS-226 for boll weight and lint %; CRIS-134 for fibre length and CRIS-154 for earliness, exhibited maximum GCA estimates. Whereas among the female parents, the higher GCA estimates were displayed by VH-137 for seedcotton yield, boll weight and fibre length; FH-901 for bolls per plant and LRA-5166 for lint % and earliness %. The parents gave variable GCA estimates for different characters implied

that parental choice could be made according to the characters to be improved. It is, generally, predicted that hybrid's performance per se is also reflected in SCA of the parents. However this assumption did not always hold true. In the present studies, the *per se* hybrid performance and their SCA, though not exactly attended the similiar positions, yet top three scoring hybrids have only changed their rank orders. These results thus indicated that per se hybrid performance could be persuaded to select the parents for SCA, consequently for hybrid cotton development.

Kay words: General and specific combining ability, cotton leaf curl virus, upland cotton.

Running Title: Estimating general and specific combining ability effects in intrahirsutm F1 hybrids.

INTRODUCTION

Early evidences indicated that certain inbred parents perform better than the others in transmitting favorable genes to their off-springs. Richey and Mayer (1925) thus emphasized that due to lack of any definite correlation in the performance between the parents and their off-springs, selection for combining ability therefore must be based on the performance of the inbreds in cross combinations rather than the inbreds per se. Cotton breeders hence are very ardent in determining the genetic potential of their inbred parents in hybrid combinations for two reasons. First is that, inbred parents be identified which form good individuals in specific combination what is commonly referred as specific combining ability (SCA) of the inbred parents. Second purpose is to locate those inbred lines which form good combinations with series of other inbred parents is referred as general combining ability (GCA) of the parents (Sprague and Tatum, 1942). Thus, former types of inbreds are useful for hybrid cotton development whereas later types are desirable for hybridization and selection from segregation populations.

In quantitative genectics, genotypic value of an individual is determined by various types of

gene actions such as additive, dominantce, and their interactions (Falconer, 1989). Theoretically, inbreds which show good SCA are those predominantly with dominant genes and these are not transferable to their off-springs. Whereas inbreds which perform well in general terms referred as general combining ability are those preponderant with additive genes. Among number of cotton breeders, Baloch *et al.* (1993, 1995, 1997, 1999, 2000 and 2002 and Bhutto *et al.* (2001) reported that inbred parents were very inconsistent for their GCA and SCA estimates. Generally, parents that formed best GCA effects were not always best for SCA effects. It was therefore, believed that combining ability is the property of an individual parent in hybrid combination rather than inbred parents *per se* performance. Therefore it is utmost important to cotton breeders that every inbred parents be specified for their potentiality in terms of GCA or SCA.

Ever since cotton leaf curl virus (clcv) disease erupted in Pakistan during 1991, cotton breeders had no choice but to use at least one of the (clcv) parents in their hybridization programme. Breeders are also well known of the fact that making huge number of crosses between (clcv) resistant and other high yielding strains thereby isolate potential inbreds based on progeny performance seems a chance game. This approach of isolating desirable inbreds naturally is very tedious and expenive in terms of inbreds also require vigorous selection in segregating populations. Thus, it becomes imperative for Pakistani cotton breeders to determine the GCA and SCA of (clcv) parents with our high yielding parents before their usefulness for extracting potential progenies is established. In this way an effective and more reliable hybridization programme could be launched.

Additive and domionance genetic variances are important to breeders in that, they arbitrate as how far a particular trait is amenable to selection in segregating generation or useful for hybrid cotton development. For these purposes, diallel analysis has been extensively used but Cross Classification Design-11 analysis is still superior mating design against diallel in that, it uses more number of parents with relatively small number of crosses, thus it provides more reliable estimates of genetic components of variances as

compared to diallel analysis. Hence the knowledge of relative contribution of desirable genes of (clcv) resistant inbreds and also the nature of genes whether those are additive or dominance are very useful to cotton breeders for conducting effective breeding programmes.

Thus, the objectives of the present study were to determine the GCA and SCA effects of (clcv) resistant inbreds and also genetic variations due to GCA and SCA thereby knowing the importance of additive and dominance genes attributable to various quantitative traits in intrahirsutum F1 hybrids.

MATERIALS AND METHODS

The Cross Classification Mating Design-11 analysis that involved 5 Cotton leaf curl virus (clcv) susceptible male parents (DNH-49, CRIS-226, CRIS-121, CRIS-134 and CRIS-154) and 5 (clcv) resistant parents (Cyto 9/91, FH-901, VH-137, LRA-5166 and CIM-443) were crossed in cotton research institute in Sindh, Pakistan in all possible combinations, thus forming 25 F_1 hybrids. Enough numbers of flowers were pollinated during 2000 crop year so as to obtain sufficient quantity of seed for replicated trial. The seeds of 25 F_1 hybrids were raised in a randomized complete block design with four replications during summer season of 2001 in plot size of 30 x 7.5 feet length where row to row and plant to plant distances were kept at 2.5 feet and 9.0 inches, respectively. After 30 days from sowing, primary thinning was carried out in order to minimize un-necessary plant competition for healthy growth and also maintain optimum plant stand. All the inputs like fertilizer, irrigations and insecticides were applied on the basis of as and when required. For recording the observations, 10 plants per hybrid per repeat thus a total of 40 plants per entry were rendomly tagged. The data on six quantitative traits were recorded as seedcotton yield in gm, number of bolls per plant, boll weight in gm, lint % as the ratio of lint from seedcotton sample, fibre length at 5% span length, and earliness as the percentage of open bolls at 125 days after planting.

The Cross Classification Design-11 analysis was carried-out for determining the genetic variability due general combining ability (GCA) and specific combining ability (SCA) as described by Comstock and

Robinson (1948) abopted by Hallauer and Miranda (1986). The GCA and SCA effects of inbred parents were also calculated by adopting Griffing's (1956) statistical procedures described by Singh and Choudhry (1979).

RESULTS AND DISCUSSION

Predicting relative contribution of desirable genes of inbred parents to their off springs is imperative in designing effective plant breeding programmes. Various mating designs in this regard have been very useful. The diallel analysis has been used more than any mating design to designate general combining ability (GCA) and specific combing ability (SCA) of the parents, thereby, obtaining the information on the types of gene actions controlling different quantitative traits in cotton. Yet, dialled mating design has its limitations in using less number of parents but requires more resources. Cross classification Design-11 as compared to diallel, involves more parents with same resources. Thus Design-11 analysis provides information for large number of parents with more reliable estimates of genetic parameters.

The mean squares (Table-1) of the crosses (F_1 hybrids) for the characters; seed seedcatton yield, number of open bolls per plant, boll weight (g.), lin %, fibre length (mm) and earliness were all significant which allowed arbitrating the proportions of genetic variability due to general combining ability (GCA) and specific combining ability (SCA).

The *per se* performance of all 25 (clcv) resistant F1 hybrids is presented in (Table-1). For seedcotton, hybrid VH-137 x CRIS-226 produced maximum yield (112.4gm), next in the rank was VH-137 x DNH-49 (94.5gm) and third in the order was Cyto. 9.91 x CRIS-226 (89.3gm) and CIM 443 x CRIS-154. These top four high yielding hybrids also secured similar rankings for number of bolls per plant which were 39.0, 33.0, 30.8 and 30 bolls, respectively. These results thus suggested that yield and bolls are highly associated traits. However, the hybrids producing higher yields and setting more number of bolls did not perform similar for boll weight, except VH-137 x DNH-49 which was first rank for yield and bolls, ranked only third in producing bigger bolls (2.9gm). Such results thus implied that

Table 1. Mean squares from Cross Classification Design-11 analysis for six quantitative traits in intrahirsutum cotton leaf curl virus resistant F_1 hybrids.

Source of variation	Degres of freedom	Mean Squares					
		Seedcotton yield (g)	Open bolls per plant	Boll weight (g)	Lint percent	Fibre length (mm)	Earliness % at 125 dap+
Crosses	24	695.178**	71.778**	0.191**	5.540**	2.288**	329.660**
Males (GCA)	4	941.835**	130.084**	0.162**	3.011**	3.684**	603.195**
Females (GCA)	4	190.475**	34.721**	0.283**	9.694**	2.409**	280.790**
Males x Females (SCA)	16	759.689**	66.465**	0.168**	5.134**	1.910**	273.495**
Error	72	1.161	0.171	0.003	0.037	0.038	2.910

** Highly significant at 1% probability level.

dep + = days after planting.

bigger bolls do not necessarily mean to increase the seedcotton yield. However, bigger bolls were set by the hybrids FH-901 x DNH-49 and CIM-443 x CRIS-121 which weighted 3.1gm. The hybrids FH-901 x CRIS-134 and CIM-443 x CRIS-226 ginned higher lint % of 37.8 and 36.5, respectively. In respect of fibre length, none of the high yielding hybrids gave longer fibre, yet two hybrids VH-137 x CRIS-121 and LRA-5166 x CRIS-121 produced equally longer fibre measuring 27.6mm. The top three early maturing hybrids were also not among the high yielders, except VH-137 x DNH-49 which ranked second in yield and number of bolls, ranked only third in earliness. These results generally demonstrated that earliness is not correlated with higher yield but compromise could be made while selecting for both the traits simulaneously. Nevertheless hybrids CIM-443 x CRIS-134 (92.2%) ranked first, and Cyto. 9/91 x CRIS-134, CIM-443 and CRIS-226 for lint %; VH-137, CRIS-121, LRA-5166, FH-901 and CRIS-226 for fibre length and CIM-443, CRIS-134, Cyto. 9/91, CRIS-154, VH-137 and DNH-49 for earliness, are choice parents.

The crosses (F1 hybrids) mean squares (Table-2) for all the six characters being significant permitted to further partition this factor into the components of males and females both pertain to GCA and also into males x females which designate to SCA source of variations. All these source of variations were also significant implied that both the types of gene actions, additive and dominance genes were important for all the studied characters. However, mean squares due to GCA (males or females) were higher than SCA (males x females) suggested that though both types of genetic variances were substantial, yet additive variances were greater than the dominance variances for all the characters, Ubaidullah and Hussain (1997), Baloch *et al.* (2000 and 2002) and Bhutto *et al.* (2001) also reported significant GCA and SCA variances for seedcotton yield, bolls per plant, boll weight, lint % and fibre length. The proportion of GCA being higher than SCA was also noted by these researchers. There also existed significant differences between males and females (both pertain to GCA variance) for various characters. With respect to seedcotton yield, bolls per plant,

Table 2. Per se hybrid performance of cotton leaf curl virus resistant intrahirsutum F1 hybrids for six quantitative traits.

F1 Hybrids	Seedcotton yield per plant (gm)	Open bolls per Plant	Boll weight (gm)	Lint percent %	Fibre length (mm)	Earliness % at 125 dap*
1. Cyto. 9/91 x DNH-49	69.3	26.0	2.7	35.0	26.2	74.6
2. Cyto. 9/91 x CRIS-226	89.3	30.8	2.9	33.2	25.7	76.5
3. Cyto. 9.91 x CRIS-121	80.4	27.7	2.9	33.5	26.5	81.2
4. Cyto. 9/91 x CRIS-134	60.0	22.2	2.7	36.1	25.7	86.2
5. Cyto. 9/91 x CRIS-154	76.6	27.3	2.8	33.4	25.1	71.5
6. FH-901 x CRIS-226	71.3	22.8	3.1	34.0	26.4	76.7
7. FH-901 x CRIS-226	55.5	20.6	2.7	34.4	27.2	65.7
8. FH-901 x CRIS-121	89.2	29.7	3.0	34.5	26.1	72.2
9. FH-901 x CRIS-134	74.8	25.8	2.9	37.8	26.7	84.0
10. FH-901 x CRIS-154	62.0	25.5	2.7	34.5	26.2	64.5
11. VH-137 x DNH-49	94.5	33.0	2.8	33.2	26.3	84.7
12. VH-137 x CRIS 226	112.4	39.0	2.9	34.2	26.3	73.5
13. VH-137 x CRIS-121	70.4	24.3	2.8	34.0	27.6	64.5
14. VH-137 x CRIS-134	78.6	28.0	2.8	34.6	24.5	67.2
15. VH-137 x CRIS-154	73.1	27.0	2.7	35.2	26.1	61.2
16. LRA-5166 x DNH-49	80.5	29.8	2.7	35.5	27.5	58.7
17. LRA-5166 x CRIS-226	60.5	30.5	1.9	32.2	26.1	56.5
18. LRA-5166 x CRIS-121	74.6	25.7	2.9	34.8	37.6	71.7
19. LRA-5166 x CRIS-134	70.9	25.0	2.8	35.6	27.3	63.7
20. LRA-5166 x CRIS-154	78.0	28.9	2.7	35.6	26.4	80.2
21. CIM-443 x DNH-49	65.3	23.1	2.8	34.0	25.3	82.2
22. CIM-443 x CRIS 226	62.4	24.0	2.6	36.5	26.8	76.5
23. CIM-443 x CRIS-121	68.1	22.0	3.1	34.5	26.6	73.0
24. CIM-443 x CRIS-134	88.2	30.0	2.9	35.0	26.5	92.2
25. CIM-443 x CRIS-154	56.0	21.5	2.6	35.0	26.1	73.5
Grand Mean	74.5	26.7	2.8	34.7	26.4	73.3
LSD (5%)	1.51	0.58	0.08	0.27	0.27	2.39

Dap * = days after planting

fibre length and earliness, the GCA of males were higher than females, except for boll weight and lint %, it was *vice versa*. These results thus connoted that comparatively, male parents retain more additive genes for the improvement of yield, boll, fibre lengh and earliness and clcv resistant female parents for boll weight and lint %. Nevertheless, male and female parents were equally important if non-additive genetic variance is to be exploited for the improvement of all the six characters.

The significance of GCA and SCA variances as such does not provide the information on the nature of genes present in individual inbred parents. Therefore, general combining ability and specific combining ability effects of both (clcv) susceptible male and (clcv) resistant female inbred parents were also detemined (Table-3). For seed cotton yield, parents CRIS-121 (11.327) and CRIS, 134 (1.568) among the males and V.H-137 (2.067) and Cyto. 9/91 (1.172) respectively ranked first and next good general combiners. In respect to bolls per plant, parents CRIS-121 (3.571) and CRIS-134 (1.296) among the males, FH-901 (2.136) and Cyto. 9/91 (0.251) among the

(clcv) resistant female parents secured first two positions, respectively. In *per se* hybrid performance, it was generally observed that hybrids which were good for seedcotton yield were also good for number of bolls, but for GCA effects, this exact trend of the parents for both traits did not exist. Regarding boll weight and lint %, parents CRIS-226 and CRIS-154 among the males and VH-137 and LRA-5166 among the females ranked top for both the traits, respectively. For fibre length, parents CRIS-134 (0.624) and CRIS 266 (0.189) among the males and VH-137 (0.544) among the females exhibited maximum GCA effects. Whereas for earliness parents CRIS 134 (-7.136) and CRIS-121 (-3.036) among the males, FH-901 (-3.586) parents CIM-443 (-3.086) among the (clcv) resistant female parents ranked as first and next good general combiners, respectively. The results in Table-3 thus generally suggested that among the male parents CRIS-121, for yield and number of bolls; CRIS-226 for boll weight and lint %; CRIS-134 for fibre length and CRIS 134 for earliness exhibited maximum GCA estimates conferring saturation of additive genes in these parents.

Table 3. General combining estimates of (clcv) susceptible male and (clcv) resistant female parents for six quantitative characters in intrahirsutum F_1 hybrids.

Inbred parents	Seedcotton yield (gm)	Open bolls per plant	Boll weight (gm)	Lint %	Fibre length (mm)	Earliness % at 125 dap
CLCV susceptible male inbreds :						
1. DNH-49	0.631**	-0.052	0.022	-0.400**	-0.511**	4.694**
2. CRIS-226	-3.918**	-2.405**	0.102**	0.390**	0.189**	-0.686**
3. CRIS-121	11.327**	3.571**	0.027*	-0.410**	-0.021	-3.036**
4. CRIS-134	1.568**	1.296**	-0.163**	0.080	0.624**	-7.136**
5. CRIS-154	-6.473**	-2.401**	0.012	0.340**	-0.101*	6.164**
S.E. (gi.)	**0.241**	**0.092**	**0.012**	**0.043**	**0.044**	**0.381**
CLCV resistant female inbreds :						
1. Cyto. 9/91	1.712**	0.251**	0.032**	-0.310**	-0.021	2.064**
2. FH-901	1.542**	2.136**	-0.158**	-0.560**	0.064*	-3.586**
3. VH-137	2.067**	-0.807**	0.157**	-0.390**	0.544**	-0.786**
4. LRA-5166	0.022	-0.331**	0.037**	1.170**	-0.226**	5.364**
5. CIM-443	-5.338**	-1.250**	-0.068**	0.090**	-0.361**	-3.086**
S.E. (gi.)	**0.241**	**0.092**	**0.012**	**0.043**	**0.044**	**0.381**

* and ** refer to 5% and 1% level of significancy, respectively.

Whereas, among the (clcv) resistant female parents, the maximum GCA displaying parents were; VH-137 for yield, boll weight and fibre length; FH-901 for bolls per plant and LRA-5166 for lint % and FH-901 for earliness suggested that these parents retain more additive genes. Thus, parents could be employed for hybridization and extraction of desirable progenies from segregating populations.

It is generally predicted that the parents that perform well as *per se* hybrids also perform similar for general combinations and for sure in specific combinations. This type of assumption did not always hold true (Srinivasan and Gururajan, 1973; Baloch *et al.*, 1993, 1995, 1997 and 2000 and Bhutto *et al.* 2001). In hybrids *per se* (Table-1), VH-137 x CRIS-226, VH-137 x DNH-49 and Cyto. 9/91 x CRIS-226 which ranked first, second and third for seedcotton yield and number of bolls did not perform similar for specific combining ability, except only hybrid VH-137 x CRIS-226 which was still top scoring in both hybrids *per se and* in SCA for yield and next in both hybrids *per se* and in SCA for yield and next in number of bolls. In respect of boll weight, the rank

order of the hybrid VH-137 x CRIS-226 as *per se* and for SCA though changed, but it still stood among the top three scoring hybrids (Table, 4). Regarding lint %, hybrids FH-901 x CRIS-134 and CIM-443 x CRIS-226 though changed the rank orders as *per se* hybrid performance and for SCA, yet both the hybrids secured top two positions. In respect to fibre length, hybrids FH-901 x CRIS-226, VH-137 x CRIS-121 and LRA-5166 x CRIS-134 which also changed the rank orders but still remained at first three positions for SCA also. The hybrids VH-137 x DNH-49 and CIM-443 X CRIS-134 except changing their rank positions for earliness as *per se* and for SCA performance, were still among the top three good performing hybrids for SCA. Present results are in accordance with those of Baloch *et al.* (1993, 1995, 1997 and 2000) and Bhutto *et al.* (2001) who also noted that not all but some of the parents perform equally better as hybrids *per se* and for SCA. The close association between the performances of hybrids *per se* and for SCA in present studies suggested that F_1 hybrids between (clcv) susceptible and (clcv) resistant parents could be reliably persuaded for hybrid cotton development.

Table 4. Specific combining ability estimates of intrahirsutum F₁ hybrids obtained from the crosses between (clcv) susceptible and (clcv) resistant inbreds for six quantitative traits.

F1 Hybrids	Seedcotton yield per plant (gm)	Open bolls per Plant	Boll weight (gm)	Lint percent %	Fibre length (mm)	Earliness % at 125 dap*
1. Cyto. 9/91 x DNH-49	-7.532	-0.888	-0.162	1.05	0.366	-5.474
2. Cyto. 9/91 x CRIS-226	12.641	1.227	0.328	-0.50	-0.194	2.056
3. Cyto. 9.91 x CRIS-121	3.213	1.857	-0.087	-0.30	0.101	4.006
4. Cyto. 9/91 x CRIS-134	-15.142	-4.108	-0.142	0.72	0.071	2.856
5. Cyto. 9/91 x CRIS-154	6.821	1.912	0.063	-0.95	-0.344	-3.444
6. FH-901 x DNH-49	-0.977	-1.736	0.183	-0.74	-1.109	2.006
7. FH-901 x CRIS-226	-16.605	-5.821	-0.002	-0.24	0.606	-3.314
8. FH-901 x CRIS-121	16.593	6.247	-0.067	-0.16	-0.949	0.386
9. FH-901 x CRIS-134	4.213	1.845	-0.047	1.58	0.396	5.986
10. FH-901 x CRIS-154	-3.225	-0.536	-0.067	-0.59	0.056	-5.064
11. VH-137 x DNH-49	7.006	2.490	-0.017	-0.69	0.181	12.356
12. VH-137 x CRIS 226	25.053	6.605	0.223	0.51	0.071	6.786
13. VH-137 x CRIS-121	-17.475	-5.153	-0.117	0.14	0.891	-5.014
14. VH-137 x CRIS-134	-7.229	-1.931	-0.047	-0.82	-1.464	-8.414
15. VH-137 x CRIS-154	-7.355	-2.011	-0.042	0.86	0.321	-5.714
16. LRA-5166 x DNH-49	5.901	1.589	0.048	1.07	0.506	-9.544
17. LRA-5166 x CRIS-226	-13.939	0.405	-0.512	-1.98	-0.929	-6.114
18. LRA-5166 x CRIS-121	-0.380	-1.478	0.098	0.45	0.116	6.336
19. LRA-5166 x CRIS-134	-2.009	-2.656	0.193	-0.31	0.511	-7.814
20. LRA-5166 x CRIS-154	10.428	2.165	0.173	0.77	-0.204	17.136
21. CIM-443 x DNH-49	-4.397	-1.431	-0.052	-0.69	-0.944	0.656
22. CIM-443 x CRIS 226	-7.149	-2.416	0.037	2.06	0.466	0.586
23. CIM-443 x CRIS-121	-1.953	-1.473	0.173	-0.11	-0.159	-5.714
24. CIM-443 x CRIS-134	20.168	6.849	0.043	-1.17	0.486	7.386
25. CIM-443 x CRIS-154	-6.669	-1.531	-0.127	-0.09	0.171	-2.914
S.E. (Si.)	0.539	0.207	0.027	0.10	0.097	0.853

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تحليل التصميم الثاني لتقدير القدرة العامة والخاصة للائتلاف لمقاومة السلالات الأبوية لفيرس تجعد الورقة في القطن

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تعتبر تقديرات القدرة للائتلاف مؤشرات مهمة جدا بالنسبة لمربي القطن للتبؤ بالتحسين الوراثي والتي يمكن تقديرها من خلال التهجين والانتخاب. استخدم تحليل التصميم الثاني من خلال التهجين ٥ سلالات أبوية قابلة للأصابة بفيرس تجعد الورقة في القطن (clcv) (ذكور) مع ٥ سلالات مقاومة لفيرس تجعد الورقة في القطن (إناث) (في معهد بحوث القطن سندو – باكستان خلال الموسمين الصيفين ٢٠٠٠ ، ٢٠٠١). وتم الحصول على ٢٥ هجين فيما بين القطن الأمريكي، كان متوسط مربع الانحرافات (التباين) الراجع للذكور والإناث (قدرة عامة) والذكور والإناث (قدرة خاصة للائتلاف) معنوياً للصفات الستة التي تم دراستها. ولقد أوضحت النتائج معنوية تباين القدرة العامة والخاصة للائتلاف وأن كل من الفعل الجيني المضيف والسيادي تحكم وراثة هذه الصفات لذلك فأن الانتخاب في الأجيال الانعزالية سيكون فعالا. أتضح أن اختيار الآباء يمكن استخدامه لتحسين الهجين ولم تعطي معنوية تباينات القدرة العامة والخاصة للائتلاف للذكور والإناث. وأظهرت النتائج أعلى تقديرات للقدرة العامة للائتلاف بين الذكور: الأب CRIS 121 (القطن الزهر وعدد اللور)، الأب CRIS 226 (وزن اللـــوزة ونسبة التيلة) الأب CRIS 134 (طول التيلة) والأب CRIS-154 بالنسبة لصفات التبكير .

وبينما نجد أنه بين الآباء المستخدمة كأناث فأنه كانت التقديرات عالية بالنسبة للقدرة العامة للائتلاف أمكن الحصول عليها في الأب VH-137 بالنسبة لمحصول القطن الزهر ووزن اللوزة وطول التيلة والأب FH-501 لعدد اللـوز/نـبات والأب LRA-5166 بالنسبة لنسبة التيلة والتبكير . ولقد أعطت الآباء تقديرات مختلفة بالنسبة للقدرة العامة للائتلاف (GCA) للصفات المختلفة وهذه النتائج تشير أن اختيار الآباء تم على أساس تحسين هذه الصفات.

وعلى وجه العموم فقد تنبأ أن متوسط سلوك الهجين ينعكس أيضاً على قيمة SCA لكل هجين وبالرغم من ذلك فأن هذه الاقتراضات ليست دائما حقيقية وفي الدارسة الحالية فأن متوسط سلوك الهجن وكذلك قيمة القدرة الخاصة للائتلاف SCA لم يتلازم مع النتائج المتشابهة وبالرغم من ذلك فأن الثلاث هجن التي أعطت متوسط سلوك عالي غيرت ترتيبها فقط.

وهذه النتائج تشير إلى أن متوسط سلوك الهجن يمكن التبؤ به لا نتخاب أو أختيار الآباء الداخلة في الهجن وبالتالي فأن هذه النتيجة مهمة لتطوير الهجن في القطن.