ESTIMATE OF GENE EFFECTS FOR SEED AND FIBRE CHARACTERS IN DESI COTTON (*G. arboreum L.*)

S. S. BHATADE[1] and N. L. BHALE[x]

A (7 x 7) parent diallel cross in *G. arboreum L.* was studied over four locations to estimate gene effects for seed and fibre characters. Ginning out-turn, seed index and lint index were observed to be controlled by both additive and non additve types of gene action whereas halo-length was predominantly controlled by additive gene action. Moderate to high heritability estimates in the range of 57-90% for ginning out-turn and 46-99% for halo-length were observed in different experiments. Seed index and lint index showed relatively low heritability estimates and the gene effects controlling these traits were not consistent in different experiments. One to two gene groups exhibiting dominance controlled ginning out-turn and lint index. In general, the gene effects were influenced to a considerable extent by environmental variation for all the traits except halo length for which gene effects were relatively stable. Implications of the study for designing appropriate breeding procedures with a view to improve ginning out turn and halo length is discussed.

Information regarding the type of gene effects involved in the inheritance of economic traits is a prerequisite for adopting an efficient breeding methodology aimed at harnessing fixable I. e. additive and additive x additive interaction part of total genetic variation present in the breeding material. In a successful breeding programme, it is envisaged to bring about maximum assembly of favourable genes. In view of this, it is necessary that genetic architecture of important characters should be studied precisely before initiating crop improvement programme. Previous studies were based on single environment. For obtaining reliable estimates of gene effects, it is suggested to study the material over as many environments as possible since the genotype x environment interaction cause bias in estimates of gene effects (Mather and Jinks, 1971) In the present investigation, a diallel cross involving seven elite and diverse cultivers of *G. arboreum* was studied over four locations to obtain information on genetic components of variation for some seed and fibre characters in desi cotton (*G. arboreum L.*).

MATERIALS AND METHODS

A set of diallel crosses (excluding reciprocals) among seven elite and diverse cultivars of *G. arboreum* was attempted during 1978-1979. The material comprising of seven parents and their 21 F_1's were sown at four locations viz. Parbhani (L_1), Badnapur

(L₃), Nanded (L₃), and Somnathpur(L₄) during kharif season of 1979-80 in a randomized block design with four replications. Two to three seeds were dibbled 22.5 cm, apart in a row spaced at 45 cm., each row consisting of 20 hills. At every hill, one plant was maintained after thinning. Border rows were grown around the plots to avoid border effect. Recommended doses of fertilizer and plant protection schedule was followed at all the four locations for raising a healthy crop. The observations on ginning out-turn, lint index and halo-length were recorded as per procedure suggested by *Santhanam* (1967). Diallel analysis was carried out according to *Hayman* (1954) for all the traits under study.

RESULTS AND DISCUSSION

The genetic components of variation and their ratios obtained from analysis of (7X7) diallel experiment conducted over four locations is presented in Table 1. The values for genetic components of variation obtained from diallel analysis based on data pooled over four locations (L) is also presented in the same table. The characterwise results obtained are discussed below.

Ginning out-turn

Both "D" and H₁ components, were significant in all the experiments for ginning out-turn. Component$_s$ 'D' was greater than H₁ under L₁. L₂, L₃, and in diallel analysis based on mean values (L) whereas under (L₄), H₁ exceeded D which suggested that, in general, additive genetic variance played an important role in control of ginning percentage although presence of considerable non additive genetic variance was also noticed. However, the proportion of the two types of gene effects varied under different environments due to G x E interaction. Bhatate, (1981), in another study with the same material reported significant interaction of additive (δ² g. c. a.) and non additive gene effects (δ² s. c. a.) with locations for ginning out-turn. This was also reflected in degree of dominance which indicated partial dominance under L₁, L₂, and L₄ and complete dominance under L₃.

Moderately high heritability estimates ranging from 57.7 - 78.1 were observed under four locations whereas in pooled analysis, heritability was high (90.0%) which suggested the preponderance of additive genetic variance for this trait. White and Kohel (1964), Chahal and Singh(1976) in *G. arboreum* also reported predominance of additive type of gene action for ginning out-turn. On the other hand, Gupta and Singh (1970), Deshmukh *et. al* (1980) and Singh and Singh observed importance of both additive and non additive components of genetic variance in the inheritace of ginning out-turn. The ratios of genetic components of variations were not consistent over different locations and did not indicate specific trend. However, the analysis based on pooled data revealed that one or two gene groups exhibiting dominance controlled the character. On the contrary, Chandramati and Menon (1973) reported that large number of groups of genes governed

the ginning out-turn in *G. hirsutum*. Positive and significant value of 'F' and KD/KR which exceeded unity in most of the experiments suggested prevalence of dominant alleles in the parents. However, distribution of allels at loci exhibiting dominance was not symmetrical as brought out from ratio $(H_2/4H_1)$ which was less than 0.25 in all the experiments.

Seed Index

The genetic effects were not consistent under different locations. Both 'D' and 'H$_t$' were significant under L$_2$, L$_1$, whereas, only 'D' or 'H$_1$' were significant under L$_4$, and L$_1$. However, 'H$_1$' was greater than 'D' under all the environments and diallel analysis based on mean values (L) which indicated greater role of non additive genetic variance in control of seed index. Mean degree of dominance indicated over dominance under L$_1$, L$_1$, L$_3$, and L whereas, partial dominance was noticed under L$_4$ only. This indicated that seed index was mainly controlled by dominant gene action, even though both additive and non additive gene effects were involved in the inheritance of this trait. Low to medium heritability estimates in the range of 5.44-40.23 obsereved for this trait confirmed the importance of additive as well as non additive genetic variance in the genetic control of this trait. These findings are in agreement with several workers such as *Gupta and Singh*(1970), Singh *et al* (1972) and Singh and Sandhu (1979). Chahal and Singh (1976) in a 10X10 diallel of *G. arboreum* observed that the non additive compo-

nent of genetic variation was predominant as it was higer than 'D' component. The genetic parameters viz, h^2/H, H$_2$/4H$_1$ and KD/KR were not consistent over environment since GxE interaction considerably influenced gene effects governing this trait as observed by Bhatade (1982). This indicated necessity to repeat experiment over till wider range of environments for obtaining reliable estimates of gene effects governing quantitative characters.

Lint Index

Both "D" and H$_1$ components were significant in all the experiments except L$_1$. The component H$_1$ was greater than "D" in case of all the experiments which suggested that non additive gene action was important in controlling this trait although additive gene action also played considerable role. Mean degree of dominance suggested involvement of over dominance in all the experiments. The over dominance might have resulted due to the effect of non-allelic interactions which inflated the dominance component in the genetic components of variation analysis, *Chahal and Singh* (1976) and Mittal (1981) reported importance on non-allelic interactions in the inheritance of this trait. Low to moderate estimates in the range of 14.32 - 57.0% were obtained under differerent locations. Importance of non additive gene action in genetic control of this trait was reported by Chahal and Singh (1976) Bhardwaj and Chaturvedi (1970); Gupta and Singh (1970) in cotton crop. Positive 'F' value and KD/KR which exceeded

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unity in most of the experiments suggested prevalence of dominant alleles in the parents. However, distribution of alleles at loci exhibiting dominance was not symmetrical as brought out from $H_2/4H_1$ ratios. The value of H^2/H_1 suggested one or two gene groups exhibiting dominance controlled this trait.

Halo length

Both "D" and H_1 components were significant under all the environments for halo length. However, "D" was grater than "H_1" which suggested that additive genetic variance played an important role in control of this trait. However, non additive genetic effects also played significant role in the control of halo length since "H_1", "H_2", were significant in most of the experiments. The genetic effects were relatively constant over different locations for this trait which revealed that small number of genes showing less interaction with environment were involved in the inheritance of halo length (Gamble, 1962). Relative stability of additive effects over different locations also indicated possibility of selecting for high staple length with wider adaptability. Degree of dominance indicated partial dominance in all the experiments. Moderate to high heritability estimates in the range of 46.1 - 99.7% was observed for this trait which implied that additive genetic variance played major role. Verhalen and Murray (1969) and Inns (1974) observed importance of additive gene action for halo length with low degree of

dominance. Significantly positive F value and KD/KR exceeding unity in the case of all the experiments suggested excess of dominant alleles with assymetrical distribution in the parents.

The present investigation clearly revealed that ginning out-turn, lint index and seed index are controlled by both additive and non additive types of gene action. Under such a situation, a breeding methodology which may mop up both additive and non additive genetic variance would be more useful for improvement of ginning out-turn. The available additive genetic variance should be exploited by adopting mass pedegree selection in early generation and some form of inter se mating may be followed among elite selections in later generations which may help in fixing a part of non additive effects. On the other hand, halo length can be improved by following mass selection as additive gene action is predominantly involved in its inheritance and also the character has revealled high heritability estimates under different locations. Diallel selective mating system as propossed by Jension (1970) appears on appropriate breeding procedure for improving ginning out turn and halo length simultenously. Also, the study emphasized the need to test the material over as many environments as possible to obtain reliable estimates of gene effects governing quantitative traits.

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Table 1. Genetic component of variation and their ratios for four characters.

Component.	Location.	Ginning out turn	Seed Index	Lint Index	Halo-length
1	2	3	4	5	6
D	L_1	3.701**±0.1878	0.009±0 0401	0.025 ±0.0299	3.878**±0.2368
	L_3	3.777**±0.3415	0 155*±0.0413	0.128**±0 0176	8.027**±0.4220
	L_6	5.321**±0.2507	0.123 ±0.0504	0.092**±0.0142	8.091**±0.1871
	L_4	3.834**±0.2845	0.095*±0.0088	0.022* ±0.0066	2.013**±0.163
	L	4.202**±0.1023	0.061**±0.0087	0.054**±0.0077	4 837**±0.0848
F	L_1	1.744* ±0.4504	−0.012 ±0.0963	0.001 ±0.0718	2.466**±0.0568
	L_3	1.216 ±0.8192	0.075 ±0.0991	0 095 ±0.4422	5.333**±1.0124
	L_5	6.412**±1.2031	−0.253 ±0 2420	0 115 ±0.0683	6.186**±0.5979
	L_4	−0.225 ±0.6826	−0.019 ±0.2110	0.004 ±0.0157	1.395**±0 3930
	L	1.492**±0.2455	−0.058 ±0.0210	0.039 ±0.0185	2.653**±0.2034
H^D	L_1	2.107* ±0.4520	0.193*±0.0966	0.145 ±0.0721	1.730* ±0 5701
	L_3	2.888* ±0.8221	0.381 ±0 0994	0.139* ±0.0423	3.608* ±1 0159
	L_5	8.057* ±2.4247	1.726 ±0.4257	0.631**±0.1371	6.121* ±1.8021
	L_4	1.734* ±0.6831	0.032 ±0.0211	0.418* ±0.0158	1.482* ±0.3940
	L	1.032* ±0.2464	0 030*±0.0210	0.074* ±0.0186	1.003**±0 2041
H_2	L_1	1.715**±0.3983	0.147 ±0.0851	0 112 ±0.0635	1.160 ±0 5020
	L_2	2.237* ±0.7244	0.24.*±0.0876	0.1073 ±0.0373	2.594* ±0 8952
	L_5	5.110 ±2.1277	1.601*±0.4279	0.441* ±0.1205	5.081* ±1.5800
	L_4	1.524* ±0.6036	0.027 ±0 0186	0.036* ±0.0139	1.034* ±0.3470
	L	1.718* ±0.0271	0.049*±0 0185	0.043* ±0.0164	0 575* ±0.1799
h^2	L_1	5 259**±0 2675	0.356**±0 0572	0.054 ±0.0427	−0.002 ±0 3125
	L_2	1.103 ±0.4865	−0 012 ±0.0580	−0.004±0.0250	1.064±0.6012
	L_5	0.077 ±0.3573	0.011 ±0.0719	0.088**±0 0203	0.077±0.2660
	L_4	0.793 ±0.4050	0.053 ±0.0120	0.074**±0 0093	1 129**±0 2334
	L	1.390**±0 1458	0.037 ±0.0125	0.036* ±0.0100	0.455* ±0.1200
$(H_1/D)\frac{1}{2}$ Degree of dominance	L_1	0.7545	4.6545	2.4020	0.6679
	L_2	0.8743	1 5696	1.0462	0 6744
	L_3	1.0306	3.7480	2.6166	0.8598
	L_4	0.6724	0.5846	1 4650	0.8581
	L	0.4957	1.1481	1.1754	0.4550

1	2	3	4	5	6
h'/H_2	L_1	3.0667	2.4990	0.4846	−0.0014
No. of.	L_2	0.4931	0.0506	−0.0489	0.4102
allels	L_3	0.0151	−0.0068	0.2002	0.0152
allele groups	L_4	0.5203	1.8428	2.0600	1.0911
or showing dominance	L	1.9349	0.7377	0.8280	0.7900
$H_2/4H_1$	L_1	0.2035	0.1903	0.1931	0.1675
(Proporation	L_2	0.1937	0.1582	0.1302	0.1793
of Possitive	L	0.2014	0.2319	0.1742	0.2075
and Nega-	L_4	0.2198	0.2204	0.1896	0.1744
tive allels among the parents)	L	0.1748	0.2346	0.1513	0.1789
KD/KR	L_1	1.9082	0.3636	1.0234	2.8166
(Pro-	L_2	1.4506	1.3646	2.1057	2.9646
porti-	L_3	2.9186	0.5693	1.6231	2.1677
ion of	L_4	0.9163	0.7055	1.1646	2.3536
domin-ant and recessivegencs in the parents)	L	2.1640	0.4170	1.9025	4.0269
h^2	L_1	78.13	18.13	19.52	46.05
Heri-	L_2	61.36	27.52	56.98	99.65
tabil-	L_3	69.51	5.44	14.32	86.20
lity%	L_4	57.71	40.23	19.72	86.39
	L	90.09	25.74	52.57	90.89
E	L_1	0.168 ±0.0664	0.073 ±0.142	0.023 ±0.106	0.087 ±0.0837
(Envir-	L_2	0.176 ±0.2207	0.026 ±0.0146	0.013 ±0.0662	0.438 ±0.1492
onmen-	L_3	0.171 ±0.0887	0.038 ±0.0178	0.009 ±0.0050	0.091 ±0.0062
tal effect	L_4	0.212 ±0.1006	0.022 ±0.0032	0.010**±0.0023	0.057 ±0.0579
	L	0.042 ±0.0362	0.008 ±0.0031	0.0003 ±0.0027	0.042 ±0.0300

* P = 0.05

** P = 0.01

D, Additive genetic variance, H_1, H_2 h', dominance components of genetic variance, F. measure of covariance between additive and dominance effects.