

Genetic analysis in cotton (*Gossypium hirsutum* L.) for seed cotton yield and its component characters

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Abstract

The choice of plant breeding methodology for upgrading the yield potential largely depends on the availability of reliable information on the nature and magnitude of gene effects present in the population. The present study was undertaken during 2021-2022 with the objective to study the gene action of seed cotton yield and other important traits in cotton using the full diallel technique involving seven parents namely MCU 5, MCU 7, SVPR 2, SVPR 4, Swaraj, Surabhi and Kumbakonam local. Data from the F1 generation and parents were analyzed using Hayman⁴ method of diallel analysis. Additional statistics needed for the genetic interpretation indicated that all the traits were controlled by the both additive and non-additive genetic variance. Estimates of genetic component variance due to additive (D) were significant for traits days to 50% flowering, fiber length, seed index, ginning outturn and seed cotton yield per plant. Dominant components (H₁ and H₂) were also significant for all the traits studied. The positive F value and KD/KR (>1) indicated the distribution of more dominant alleles for most of the traits. The negative value of F and KD/KR (<1) indicated the distribution of more recessive alleles for the traits number of sympodial branches, boll weight and lint index. The potence ratio indicated the presence of over dominance in the inheritance of most of the traits. Narrow sense heritability indicated the importance of non-additive genetic variance in the inheritance of most of the traits.

Key words : Full diallel, genetic parameters, narrow sense heritability, cotton.

The choice of plant breeding methodology for upgrading the yield potential largely depends on the availability of reliable information on the nature and magnitude of gene effects

present in the population. Hayman's method of diallel analysis, which provides the estimates of the six components such as D-additive genetic variance, H1- dominance variance,

H²-positive and negative gene effect, E-environmental component of variance, F-covariance of additive and dominant effect and h²-dominant effect help in understanding the performance of parents used in the cross and indetermining the characters. Therefore, the present study was undertaken with the objective to study the gene action of seed cotton yield and other important traits in cotton using the full diallel technique involving seven parents.

Seven genotypes of cotton namely, MCU 5, MCU 7, SVPR 2, SVPR 4, Swaraj, Surabhi and Kumbakonam local were mated in a full diallel fashion. The resulting forty two hybrids were evaluated along with their parents for seed cotton yield and its component characters namely, days to first flowering, days to 50% flowering, plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, fiber length, lint index, seed index, ginning outturn and seed cotton yield per plant were laid out in Randomized Block Design with three replications during Jan-June, 2022. Each entry was grown in a 10 m long single row plot with a spacing of 75 × 30 cm. Observations were recorded on five randomly selected plants in each plot on ten bolls in seed cotton yield traits. The genetic parameters were estimated as per Hayman's analysis of diallel crosses⁴.

The mean sum of square for combining ability revealed that the GCA variance was significant for most of the characters except days to 50% flowering and lint index studied (table-1). This indicated the presence of additive genetic variance for all the eleven

characters studied. The SCA variances were also significant for all the eleven traits studied. The Reciprocal variances were also significant for all the eleven traits studied. This implied the presence of dominance and non-additive genetic variance in the inheritance of these traits. The results amply revealed the importance of both the additive and non-additive genetic variance for all the eleven traits.

However, the ratio of GCA/SCA was less than unity for most of the traits except days to first flowering, plant height and number of sympodial branches per plant. The SCA variance was greater in magnitude than GCA variance for all the characters studied, indicating the predominance of non-additive gene action for all the characters (Table-1). This showed the possibilities of improvement of these traits through heterosis breeding. Shanti and Selvaraj⁸, Mandloi *et al.*,⁶ reported similar results. Estimates of genetic component variance due to additive (D) component were significant for traits days to 50% flowering, fiber length, seed index, ginning outturn and seed cotton yield per plant.

The dominant components (H₁ and H₂) were significant for all the eleven traits studied (table-2). Hence, the genetic components of the variance viz., H₁ and H₂ suggested the importance of both additive and dominant genes for all the traits of interest. This was also supported by the significance of both GCA and SCA variances for all the traits studied. The additive and non-additive gene effect may be exploited following inter mating among the progenies within and between

Table-1. Analysis of variance for combining ability for Eleven different characters

Sources	DF	Mean Sum of Squares										
		Days to first flowering	Days to 50% flowering	Plant height	No. of sympodial branches per plant	Number of bolls per plant	Boll weight	Fiber length	Lint Index	Seed Index	Ginning Outturn	Seed cotton yield per plant
GCA	6	2.35**	1.01	33.32**	4.47**	4.82**	0.07**	0.07**	0.13	0.17**	1.91**	308.20**
SCA	21	0.79*	1.72**	24.66**	3.35**	31.74**	0.10**	0.24**	0.28**	0.29**	7.64**	497.64**
Reciprocal	21	1.90**	2.73**	14.14**	2.90**	3.60**	0.10**	0.12**	0.18*	0.18**	2.43**	408.41**
GCA/SCA	-	2.97	0.59	1.35	1.33	0.15	0.70	0.29	0.46	0.59	0.25	0.62
Error	96	0.40	0.58	1.33	0.43	0.60	0.01	0.01	0.09	0.01	0.41	0.62

** - Significant at 1 per cent level * - Significant at 5 per cent level

Table-2. Estimates of genetic components and their ratio for eleven characters studied

Traits	Days to first flowering	Days to 50% flowering	Plant height	No. of sympodial branches per plant	No. of bolls per plant	Boll weight	Fiber length	Lint Index	Seed Index	Ginning Outturn	Seed cotton yield per plant
D	0.45	0.91*	3.15	0.78	4.99	0.00	0.18**	0.02	0.21*	3.24*	228.73*
F	0.92	2.06*	5.31	0.27	7.24	0.00	0.35**	0.01	0.40	6.66*	534.30*
H ₁	1.69*	3.32**	57.97**	5.92**	65.70**	0.20**	0.65**	0.39**	0.79**	18.31**	1376.21**
H ₂	0.67	2.09*	46.67**	5.82**	62.25**	0.19**	0.46**	0.37**	0.55*	14.46**	984.19**
h ²	0.02	0.26	98.29**	19.22**	270.27**	0.49**	0.01	0.38**	0.01	37.93**	137.42
E	0.45**	0.67**	1.32	0.44*	0.61	0.01	0.01	0.09**	1.01	0.41	5.56
(H ₁ /D) ^{1/2}	1.93	1.91	4.29	2.75	3.63	7.02	1.93	4.80	1.91	2.38	2.45
H ₂ /4H ₁	0.01	0.16	0.20	0.25	0.24	0.24	0.18	0.24	0.81	0.20	0.18
K _D /K _R	3.24	3.88	1.49	0.88	1.50	0.85	3.17	0.90	2.92	2.52	2.82
h ² /H ₂	0.03	0.19	2.11	3.30	4.34	2.63	0.02	1.02	0.02	2.62	0.29
h(ns)%	20.03	1.73	21.22	32.64	2.56	18.69	1.80	5.86	4.01	2.03	5.25

** - Significant at 1 per cent level * - Significant at 5 per cent level

promising crosses in early segregating generations.

The positive F value and the ratio of KD/KR (more than unity) suggested the distribution of more dominant alleles for almost all the traits except number of sympodial branches, boll weight and lint index. The negative value of F component and the ratio of KD/KR (less than unity) indicated the distribution of more recessive alleles for the traits number of sympodial branches, boll weight and lint index. The environment effect (E) was non-significant for almost all the traits except days to first flowering, days to 50% flowering, number of sympodial branches and lint index studied. The potence ratio $(H_1/D)^{1/2}$ was more than unity, indicating the presence of over dominance in the inheritance of all the traits including seed cotton yield per plant.

The ratio of $H_2/4H_1$ was less than 0.25 for all the eleven traits studied. This indicated the unequal allelic frequency or asymmetrical distribution of positive and negative genes in the parents at the loci exhibiting dominance. The ratio of h^2/H_2 was less than one for almost all the traits studied except plant height, number of sympodial branches, number of bolls, boll weight, lint index and ginning out turn. This revealed that five traits were found to be under the control of at least single group of genes.

Plant height, number of sympodial branches, number of bolls, boll weight, lint index and ginning out turn were found to be under the control more than one group of genes. The narrow sense heritability was low for almost

all the traits except number of sympodial branches. This indicated the importance of non-additive genetic variance or the number of genes controlling these characters may be more or these traits may largely be influenced by environment. Simple selection would be more effective in the sets of materials exhibiting greater additive genetic variability and desirable mean performance. Present study revealed the importance of both additive and non-additive gene action in the improvement of seed cotton yield traits. In such case, simple pure line selection or modified pedigree selection may not be possible.

Hence, improvement can be expected by delaying the selection to later segregating generations, when the dominance and epistatic interactions disappear and resorting to intermating of superior segregants followed by recurrent selection¹⁻³. Diallel selective mating system can also be adopted,⁵. In the presence of over dominance, the best scheme to develop hybrids would be reciprocal recurrent selection.

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