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Genetic Analysis and Inheritance Studies in F_2 Population of Upland Cotton (*G. hirsutum* L.)

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ABSTRACT

Cotton is vital in economic, political and social affairs of most countries of the world including India. There is increasing demand of cotton in local and international market, hence urgent need to exploit potential of available germplasm through hybridization and selection programme. Thorough study of F_2 populations may highlight proper knowledge for the design of different breeding programmes. This study was on F_2 generation of the cross ARBC1301 x Surabhi along with their parents. Observation was made on 230 F_2 progenies and 15 randomly selected plants for parents. Sixteen biometric observations; days to flowering (DF), plant height (PH), number of monopodia per plant (NMPP), number of sympodia per plant (NSPP), number of nodes per plant (NNPP), first internode length (FIL), number of fruiting points per plant (NFPP), number of bolls per plant (NBPP), boll weight (BW), ginning outturn (GO), single plant yield (SPY), 2.5% span length (SL), bundle strength (BS), uniformity ratio (UR), fibre fineness (FF) and elongation percentage (EP) were recorded. Single plant yield ranged from 6.17g to 97.04g for the F_2 with a mean of 33.64. F_2 hybrids were earliest to flower, they also recorded the least in plant height, first internode length, boll weight, 2.5% span length, uniformity ratio, elongation percent, fibre fineness and single plant yield. However, in number of nodes per plant, number of fruiting points per plant, number of sypodial branches per plant and number of bolls per plant, F_2 hybrids performed better than either of the parents. The parents ARBC1301 and Surabhi recorded 33.97 and 36.13 for mean of single plant yield respectively. Principal component analysis revealed that number of bolls per plant, number of fruiting point per plant, number of sympodia per plant contributed more variation and can be considered as major traits for selection while handling a large population. Step wise regression showed that number of sympodia per plant, number of bolls per plant and boll weight were major predictor for single plant yield. Leaf anatomical parameters study indicated that the progeny #197 has highest thickness of spongy parenchyma (25.14µ) and highest palisade cell height (16.02µ) which indicated its tolerance to the sucking pest Leaf hopper.

Key words: *Cotton, Variability, Correlation, Regression, Selection*

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INTRODUCTION

Proper knowledge and study of genetic variability is paramount milestone in understanding of interspecies as well as intra-species crop performance resulting in crop yield improvement[23]. Broad sense heritability (h^2) values enable plant breeders to assess magnitude of heritable attributes and prognosticate the chances of transmitted attributes from parents to next generation[1]. Broad sense heritability with more than 80% value is high, while values between 60-79% are partially high and values less than 59% are regarded as low which are not desirable[25]. In order to meet the increasing demand of cotton in local and international market, there is need to exploit potential of available germplasm through hybridization and selection programmes. So it is important to investigate the associations between yield, its components and fibre quality traits because selection for one character may improve or deteriorate associated characters, depending on the nature and magnitude. Correlations between traits allow the measurement of the magnitude of the relationship between several traits and help to set selection criteria to improve yield, earliness, and fibre quality in cotton [12]. Multivariate biometrical techniques like principle component analysis (PCA), correlation analysis and multidimensional scaling method have been frequently utilized by plant breeders to explore genetic diversity among genotypes and direct and indirect effects of attributes [6]. Mechanical resistance of host plant leads obstruction to feeding and oviposition. These obstructions are toughness and thickness in epiderminal tissues, which are important factors in reducing insect infestation. Toughness of leaf veins, thickness of lamina and palisade cell play a major role in jassid resistance [20]. Based on above concern the objective of this study is to estimate variability, correlation, regression, principal component analysis to exploit potential for selection in F_2 population.

MATERIAL AND METHODS

This study was carried out on F_2 generation of the cross ARBC1301 x Surabhi along with their parents at Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore. Observations were recorded in 230 single plants of the F_2 population, in parents observations were on 15 randomly selected plants. Sixteen biometric observations *viz.*, days to first flowering (DFF), plant height (PH), number of monopodia per plant (NMPP), number of sympodia per plant (NSPP), number of nodes per plant (NNPP), first internode length (FIL), number of fruiting point per plant (NFPP), number of bolls per plant (NBPP), boll weight (BW), ginning outturn (GOT), single plant yield (SPY), 2.5% span length (SL), bundle strength (BS), uniformity ratio (UR), fibre fineness (FF) and elongation percentage (EP) were recorded

Statistical analysis

Phenotypic variance (PV), genotypic variance (GV), phenotypic coefficient of variability (PCV) and genotypic coefficient of variability (GCV) were obtained for various characters. Broad sense heritability (H^2) and Genetic advance over mean (GAM) were worked out using the methods of Lush[18] and Singh and Choudary [25] respectively.

The simple correlation coefficients were worked by using the formula given by Falconer[9]. Skewness and Kurtosis were calculated using the frequency distribution as per the method suggested by Kapur[16]. PCA was performed as per Jackson[13]. The goodness of fit to Mendelian segregation ratio of different classes in segregating crosses of F_2 population was tested by chi square test [17]. To study the anatomical parameters associated with jassid resistance, histological studies of leaves were carried out following the method described by Johansen[14].

EXPERIMENTAL RESULTS

Mean performance and variance components

The mean performances and variance components of the 2 parents and the 230 F_2 progenies are presented in Table 1. Days to first flowering for parents were about 51 days and the overall mean for F_2 population was 46 days. The F_2 population flowered earlier than either of the parents with a range of 47 to 61 days. Also, F_2 population recorded the lowest value for plant height, inter node length, boll weight, span length, uniformity ratio, elongation percent and single plant yield than either of the parents. However, in number of nodes per plant, number of fruiting points per plant, number of sympodial branches per plant and number of bolls per plant F_2 hybrids performed superiorly over either of the parents. For number of monopodial branches per plant, ginning outturn and bundle strength, mid parent heterosis is experienced in F_2 segregants as the expressed values are in between the better parents and the lower parents.

Phenotypic and Genotypic coefficients of variability

F_2 segregants recorded high PCV, high GCV, high heritability and high genetic advance over mean for three characters viz; number of bolls per plant, ginning outturn and 2.5% span length. However, for inter node length, number of sympodia and boll weight the PCV, GCV and GAM were high but with moderate heritability. Number of nodes per plant recorded high PCV, high heritability, high GAM but moderate GCV. Fibre fineness and single plant yield recorded high heritability and high genetic advance but with moderate PCV and GCV. Similar results were reported by Preetha and Raveendran[22], Dinakaran *et al.*[7] and Abbas *et al.*[1]. High PCV and GCV with high heritability and GAM recorded for ginning outturn, number of bolls per plant, nodes per plant, internode per plant indicates that these traits have more variability in this population and are highly amenable for selection

Population Structure

For days to first flowering, the population performance was positively skewed and platykurtic. Plant height, inter node length, number of nodes per plants, number of fruiting points per plant, number of monopodia, number of sympodia per plant, number of bolls per plant, boll weight and ginning outturn were all leptokurtic and positively skewed. 2.5% span length and uniformity ratio exhibited negative skewness with platykurtic curve, while bundle strength was positively skewed and leptokurtic. Single plant yield demonstrated positively skewed and leptokurtic population structure.

The mean performance of the entire transgressive segregants had recorded higher value than the parents. Also, effective population structure was observed for the traits; days to first flowering, 2.5% span length, uniformity ratio and elongation percentage.

Correlation and Regression

Single plant yield was positive and significantly correlated with fibre fineness (0.281), boll weight (0.667), number of bolls per plant (0.327), number of fruiting points per plant (0.268), number of nodes per plant (0.17) and inter node length (0.15). Ginning outturn was negative and significantly correlated with single plant yield (0.15). However, Fibre fineness was significant and positively correlated with uniformity ratio (0.237), 2.5% span length (0.134) and boll weight (0.294), while it was also negatively correlated with elongation percent. Elongation percent was significant and positively correlated with uniformity ratio (0.27) but significant and negatively correlated with 2.5% span length (0.406), ginning outturn (0.173) and boll weight (0.143). According to Table 2 other characters also recorded positive and significant correlations amongst themselves. Fibre fineness, boll weight, bolls per plant, fruiting point per plant, nodes per plant, internode per plant has positive significant correlation with single plant yield. Hence, selection for these traits will help in selecting segregants with high seed cotton yield. Similar results of positive correlation between yield and other component was reported by Percy *et al.*[21], Baloch *et al.*[5], Hussain *et al.* [11], Altaher and singh [2].

In F_2 population, 85 percent of variability for single plant yield was relatively contributed by other independent traits. Number of bolls per plant (2.42) and boll weight (12.94) exhibited positive and significant regression value for single plant yield, which indicates that unit increase in boll number and boll weight increases single plant yield up to 2.42g and 12.94g. Number of sympodia per plant (0.45) exhibited negative and significant regression value for yield. Unit increase in number of sympodia decreases yield up to 0.45g similar to the report by Kamrul *et al.*[15] and Baloch *et al.*[4]. Step wise regression revealed that number of sympodia per plant, number of bolls per plant [8] and boll weight contributed as major predictor for single plant yield in ARBC1301 x Surabhi.

Principal component analysis (PCA) in F_2 segregating population

PCA analysis revealed that first six components contributed 69.3% of variability among 230 F_2 segregants. These six principal components were retained based on the scree plot and threshold eigen value greater than 1. The eigen value for PC1, PC2, PC3, PC4, PC5, PC6 were 3.4, 2.1, 1.8, 1.5, 1.2 and 1.1 respectively (Table 4). Principal component analysis facilitates in depth analysis of genetic divergence between genotypes in terms of spatial distance (Haritha and Ahmad 2013).

The first principal component accounted for 21.2% of total variability. Higher variation to the PC1 was contributed by number of bolls per plant (0.85), number of fruiting point per plant (0.85), number of sympodia per plant (0.76), number of nodes per plant (0.67), plant height (0.61), 2.5% span length (0.45) and single plant yield (0.24). The second (13.4%), third (11.1%), fourth (9.5%), fifth (7.5%) and sixth (6.7%) principal components also contributed to the total variability. Principal component analysis also revealed that number of bolls per plant, number of fruiting point per plant, number of sympodia per plant contributed more variation, wherefore these traits can be considered as major for selection while handling a large population.

Inheritance studies for hairiness in F_2 population

Inheritance pattern for hairiness trait was studied in the F_2 population. The 251 plants were scored for hairiness as pilose (presence of hair) and glaborous (absence of hair). Among them 77 were found to have hairs and 177 without hairs. The segregation ratio for glaborous to pilose was 3:1. The calculated value of chi square was non-significant for this monohybrid ratio and expressed the goodness of fit (Table 5). Inheritance studies could be used for studying gene action involved in controlling the traits which will be useful for future breeding programmes. However Nawab *et al.*[19] and Simpson[24] revealed 1:2:1 segregation pattern for hairiness trait indicating incomplete dominance.

Leaf anatomical parameters

Anatomical features like thickness of phloem, distance of phloem from lower epidermis, palisade height, spongy parenchyma height and arrangement of palisade cells were recorded for parents (ARBC1301 and Surabhi) and two F_2 progenies of the cross. Significant differences were noticed for all the parameters. Mean performance for anatomical parameters are furnished in Table 6. Thickness of phloem was more in Surabhi (27.24µ) followed by ARBC-1301 (26.41µ). The progeny #217 recorded high mean performance with 25.83µ. Distance of phloem from epidermis ranged from 77.73µ to 119.14µ. ARBC-1301 exhibited significantly higher distance of phloem from lower epidermis (119.14µ). Spongy parenchyma ranged from 15.21µ to 25.14µ. Thickness of spongy parenchyma was significantly higher in progeny #197. Palisade cell height ranged from 11.45µ to 16.02µ. Highest palisade cell height was recorded by progeny #197 (16.02µ). Anatomical study revealed that parents were more superior to the two F_2 progeny plants. Anotomical features were not inherited effectively under the study. This revealed that some other factors like hairiness would cause resistance to sucking pest for the selected progeny. Palisade mesophyll height is major criteria in water use efficiency. From the study it revealed all genotypes are susceptible to water stress but resistance to sucking pest. According to Ansingkar[3], various leaf anatomical parameters like distance to phloem elements from lower abaxial surface and structure of parenchyma tissues were reported to be associated with resistance to sucking pest.

Table 1: Mean performance and components of variance in ARBC1301 x Surabhi F_2 cross

	DFF	**PH**	**FIL**	**NNPP**	**NFPP**	**NMPP**	**NSPP**	**NBPP**	**BW**	**GOT**	**SL**	**UR**	**BS**	**EP**	**FF**	**SPY**
ARBC-1301	51.33	70.73	3.93	10.86	13.93	0.73	8.00	11.60	3.08	33.45	28.24	49.98	17.80	6.32	3.84	33.97
Surabhi	51.44	97.00	4.33	10.86	17.00	1.20	7.73	13.00	3.24	24.26	32.08	47.20	21.66	6.16	3.26	36.13
F_2 hybrid	46.88	63.94	3.34	13.55	20.17	0.89	9.49	15.45	2.02	24.31	25.51	41.80	19.18	5.41	3.24	33.64
Maximum	61	124	10	35	49	7	29	40	5.65	42.5	34.1	56	28.8	8.4	6.5	97.04
Minimum	47	40	0.7	9	7	0	2	5	0.54	7.45	21.3	40	17.5	3.9	2.1	6.17
Mean-2SE	53.46	71.67	3.59	15.09	22.34	0.89	10.28	17.00	2.17	26.99	29.00	47.69	21.79	6.11	3.65	36.48
Mean+2SE	54.37	75.39	4.09	16.07	24.05	1.16	11.55	18.54	2.47	28.93	29.68	48.46	22.34	6.33	3.82	40.91
Skewness	0.25	0.34	1.03	0.91	0.55	1.22	1.20	0.55	1.62	2.17	-0.49	-0.08	0.49	-0.10	0.38	0.60
Kurtosis	-1.05	0.41	0.56	4.00	0.54	4.41	1.26	0.36	4.88	13.93	-0.33	-0.21	0.32	-0.04	1.10	0.38
PCV	6.51	23.51	35.66	20.95	28.13	106.87	33.23	41.23	52.43	26.45	44.74	6.76	5.51	10.79	15.86	19.52
GCV	5.81	15.72	24.6	17.07	19.81	51.41	21.83	33.51	29.55	23.78	43.81	3.76	5.27	9.08	14.42	16.24
Heritability	79.66	44.67	47.56	66.41	49.6	23.14	43.14	66.07	31.78	80.83	95.9	31.03	91.81	70.86	82.63	69.22
GAM	10.68	21.64	34.94	28.66	28.74	50.94	29.53	56.11	34.32	44.05	88.39	4.32	10.41	15.75	27	27.83

Table 2: Simple correlation coefficients between single plant yield with yield components and fibre quality traits in ARBC1301 x Surabhi

	DFF	**PH**	**FIL**	**NNPP**	**NFPP**	**NMPP**	**NSPP**	**NBPP**	**BW**	**GOT**	**SL**	**UR**	**BS**	**EP**	**FF**	**SPY**
DFF	**1.000**	0.099	-0.043	0.086	-0.030	0.176**	-0.049	0.002	-0.075	-0.044	0.023	0.086	0.147*	0.110	-0.044	-0.124
PH		**1.000**	0.001	0.509**	0.383**	0.146*	0.523**	0.357**	-0.140*	0.011	0.096	0.027	0.142*	0.070	0.042	0.073
IL			**1.000**	0.092	0.034	-0.117	0.087	0.031	0.134*	-0.065	0.011	-0.036	-0.052	-0.050	-0.014	0.153*
NN				**1.000**	0.372**	0.032	0.600**	0.364**	-0.050	-0.014	0.232**	-0.082	-0.066	0.021	0.063	0.170**
NFP					**1.000**	0.076	0.484**	0.924**	-0.364**	-0.155*	0.271**	-0.203**	-0.013	0.108	-0.038	0.268**
NM						**1.000**	-0.169*	0.083	-0.088	0.030	-0.037	0.107	0.092	0.007	0.029	-0.037
NS							**1.000**	.500**	-0.204**	-0.059	0.243**	-0.149*	-0.085	-0.016	-0.009	0.080
NB								**1.000**	-0.377**	-0.162*	0.257**	-0.163*	-0.043	0.078	-0.013	0.327**
BW									**1.000**	-0.042	-0.064	0.087	-0.099	-0.143*	0.294**	0.667**
GOT										**1.000**	0.122	0.008	0.145*	-0.173**	0.101	-0.157*
SL											**1.000**	-0.589**	0.067	-0.406**	0.134*	0.102
UR												**1.000**	0.048	0.275**	0.237**	-0.018
BS													**1.000**	-0.074	-0.008	-0.117
EP														**1.000**	-0.376**	-0.115
FF															**1.000**	0.281**
SPY																**1.000**

Table 3: Regression coefficient between single plant yield with yield and fibre components in F_2

Character combination	**Regression value**
Constant	-4.468
DFF and SPY	-0.318
PH and SPY	0.010
FIL and SPY	0.040
NNPP and SPY	0.186
NFPP and SPY	-0.332
NMPP and SPY	-0.528
NSPP and SPY	-0.455*
NBPP and SPY	2.423*
BW and SPY	12.941*
GOT and SPY	-0.048
SL and SPY	-0.041
UR and SPY	0.091
BS and SPY	0.011
EP and SPY	-0.875
FF and SPY	-0.006

Table 4: Principal component matrix in ARBC1301 x Surabhi

ARBC1301 x Surabhi	Component					
	1	2	3	4	5	6
NBPP	0.855	-0.076	0.127	-0.086	-0.327	-0.183
PH	0.618	-0.123	0.164	0.418	0.274	0.079
FIL	0.084	0.249	0.156	-0.228	0.265	0.431
NNPP	0.673	0.078	0.145	0.211	0.367	0.168
NFPP	0.857	-0.098	0.098	-0.099	-0.306	-0.171
NMPP	0.030	-0.206	0.044	0.495	-0.518	0.042
NSPP	0.765	0.007	0.051	-0.019	0.435	-0.034
SPY	0.247	0.708	0.459	-0.022	-0.285	0.061
GO	-0.126	0.044	-0.419	0.387	0.318	-0.261
SL	0.450	0.367	-0.636	0.000	-0.123	0.153
UR	-0.323	-0.203	0.632	0.417	0.144	-0.255
BS	-0.028	-0.164	-0.258	0.477	-0.074	0.217
EP	-0.009	-0.587	0.527	-0.202	0.024	0.081
FF	-0.015	0.570	0.092	0.493	-0.016	-0.331
DF	0.016	-0.278	0.018	0.388	-0.172	0.632
BW	-0.331	0.740	0.369	0.063	0.000	0.237

Table 5: Chi square test for inheritance studies for hairiness trait

Pilose	3	177	188.25	126.56	0.67	7.81
Glaborous	1	74	62.25	126.56	2.01	
Total	2	251	251		2.68^{ns}	7.81

Table 6: Leaf Anatomical parameters in parents and F_2 progenies

Acession name	Thickness of phloem	Distance of phloem from lower epidermis	Spongy parenchyma thickness	Palisade cell height
ARBC-1301	26.41	119.14*	15.21	11.45
Surabhi	27.24	92.33	18.35	14.02
#197	25.83	99.59	18.81	16.02
#217	18.48	77.73	25.14*	14.23
Mean	24.49	89.88	17.46	13.93
CD (5%)	5.31	3.01	3.21	2.98

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