Rs-P and other P fractions

Rs-P fraction was found to be not related to any of the P fractions with the first crop. However in the maize crop, the first residual effect showed a positive relationship between Rs-P and available P and the cumulative effect recorded significant correlation values between Rs-P and A1-P and also Ca-P fractions. This was found to hold good with the second reidual effect of blackgram as well. These results suggested that the Rs-P is not dependant on available P as a general rule and showed the other fractions like A1-P and Ca-P and even Saloid-P in certain cases increased. There occured a concomitant increase in the Rs-P as well. It may be mentioned that the A1-P and Ca-P are the other fractions that resulted from the liquidation of Rs-P and obviously such relationship between Rs-P and A1-P and Ca-P fractions could be expected.

Ca-P and other P fractions

With fingermillet crop, a positive correlation between Ca-P and Fe- P was observed. Any increase in soluable phosphate ion which tend to form $CaPO_4$ also bring about enhanced Fe-P fraction. However the long period of incubation transformed the above picture and positive relationship between Ca-P and available P and A1-P could be recognised. This indicates that over a period of time, the Ca-P also contribute to the available P pool of the soil. The fact that Ca-P. available P relationship existed even under the third crop of blackgram provide evidence for the continued beneficial effect of Ca-p fraction in favourably influencing the available P status of the soil.

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Madras Agric. J., 81(6): 308-311 June, 1994

https://doi.org/10.29321/MAJ.10.A01521

ASSOCIATION OF CHARACTERS AND PATH COEFFICIENT ANALYSIS IN UPLAND COTTON (*G. hirsutum*, L).

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ABSTRACT

The present study consisted of 13 genotypes of *G. hirsutum* cottons. Wide range of variability for no.of bolls/plant, seed cotton yield/plant, mean fibre length, seed index, bundle strength, micronaire value and ginning out-turn was observed, offering ample scope for improvement in those characters. High heritability coupled with high genetic advance was manifested by seed index, indicating additive gene action. High heritability and moderate genetic advance estimates for mean fibre length, bundle strength and lint index suggests that variability is partly under non-additive gene control.

Any improvement brought forth in field crops can be quantified in terms of increase in yield. Yield is a complex character, mainly dependent on many genetically controlled quantitative characters as well as environment. The nature and association of such characters with yield and among themselves plays vital role in choosing superior genotypes. It also depends upon the magnitude of genetic variability present in the genetic stock for the maximum improvement of yield. Heritability and genetic advance serves as a tool to the breeder in determining the direction and magnitude of selection.

MATERIALS AND METHODS

The experimental material consisted of thirteen genotypes of *G. hirsutum* cotton that are being

Table 1. Estimates of range, mean, GCV, PCV, heritability and G.A. as % of mean for different characters of up land cotton.

Character	Mean	Range Minimum	Range Maximum	Phenotypic variance	Genotypic variance	G.C.V.	P.C.V	Heritability %	G.A. as % of mean at K=2.06
1.	2.	3.	4.	5.	6.	7.	8.	9.	10.
No. of bolls / plant	22.10	18.00	31.87	32.494	8.220	12.3748	25.7988	25.30	13.40
Boll weight (g)	3.55	3.03	4.03	0.188	0.058	6.6324	12.2211	28.45	7.00
No. of locs / boll	4.08	3.83	4.23	0.027	0.009	2.3846	4.0636	34.44	2.69
No. of seeds/boll	28.88	25.60	31.20	5.985	1.524	4.2740	8.4709	25.46	4.43
Lint index (g)	4.81	4.24	5.69	0.244	0.163	8.5483	10.2717	69.27	14.55
Seed index (g)	8.10	7.14	10.62	1.070	1.008	12.3970	12.7719	94.22	24.69
G.O.T. (%)	35.78	33.70	38.40	3.326	1.865	3.8161	5.0961	56.07	5.87
Mature fibre %	53.97	49.67	57.00	9.263	2.267	2.7897	5.6407	24.46	2.83
Bundle strength (g/tex) at 'O' gauge	38.48	34.43	42.20	6.488	4.359	5.7863	6.6185	76.43	10.42
Fibre fineness (µg/inch)	3.55	2.85	4.07	0.187	0.107	9.1910	12.1674	57.06	14.08
Mean fibre length (mm)	24.11	20.67	27.10	4.030	3.557	7.8223	8.3264	88.26	15.14
Seed cotton yield/plant (g)	57.47	38.17	83.83	254.161	57.7771	13.2245	27.7383	22.73	12.98

cultivated in different agro climatic regions of Andhra Pradesh. The material was sown in RBD with three replications at Regional Agricultural Research Station, Lam,Guntur. The plants were spaced at 105 x 60 cm apart, and the plot size was 37.8 m^2. Agronomic and plant protection practices recommended were adopted. Data were collected on quantitative characters like seed cotton yield/plant(g), no.of locules/boll, no.of seeds/boll, lint index(g), seed index(g), ginning out turn (%) from five randomly chosen plants in each replication. Fibre quality aspects like fibre maturity per cent, bundle strength (g/tex), fibre fineness (micronaire value/inch), and mean fibre length (mm) were also estimated from pooled lint samples. The plot means in each replication was used for statistical analysis. Analysis of variance for individual character was carried out by following the standard procedure.Phenotypic Coefficient of Variance (GCV), heritablity (Broad sense), phenotypic and genotypic correlation coefficients were computed as per Singh and Chaudhary (1977). Genetic advances as per cent of mean was calculated. The correlation coefficients were further partitioned into direct and indirect effects by path coefficient analysis.

RESULTS AND DISCUSSION

Among twelve characters including yield, studied, wide range of variability (Table-1) was observed for no.of bolls/plant (18.00 to 31.87), seed cotton yield/plant (38.17 g to 83.83 g), mean fibre length (20.67 mm to27.10 mm), boll weight (3.03 g to 4.03 g), seed index (7.14 g to 10.62 g), bundle strength (34.43 g/tex to 42.20 µg/tex), fibre fineness (2.85µg/inch to 4.07 µg/inch), and ginning out turn (33.70% to 38.40%) offering great scope for the improvement of these characters. Phenotypic coefficient of variability for all the characters studied. Wide differences between phenotypic and genotypic coefficient of variation was observed for all the characters studied, except seed index, indicating that environment plays an important role in governing these attributes. High heritability estimates, coupled with high genetic advance may be useful in identifying the characters possessing additive and non-additive gene effects (Allard, 1960). Heritability estimates in broad sense ranged from 22.73% to 94.22%. High heritability values were recorded for seed index (94.22%), mean fibre length (88.26%), bundle strength (76.43%), and lint index (69.27%). As the high heritability values indicate the presence of additive gene action, further improvement in the population can be achieved through mass selection and pedigree selection. Moderate heritability was found for ginning out turn (56.07%), while other characters exhibited low heritability estimates. Seed index had high genetic advance (24.69) coupled with high heritability estimates. Additive gene action seems to be important for this character. Similar results were reported by Shinde and Deshmukh (1985).High heritability and

Table 2. Path analysis of phenotypic correlation coefficient for 12 characters in upland cotton

Character	Direct effect on yield	Indirect effects (via)									
		Boll weight	No. of locs/boll.	No. of seeds/ boll.	Link index	Seed index	G.O.T.%	Mature fibre %	Bundle strength	Micronaire value	Mean fibre length
1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.
No. of bolls / plant	0.7870	0.0403	0.0523	0.0008	0.0051	0.0191	0.0024	0.0021	-0.0049	-0.0051	0.0011
Boll weight (g)	0.1300	0.2438	0.0251	0.0029	0.0076	-0.0195	0.0029	0.0203	0.0031	0.0014	0.0062
No. of locs / boll	0.2445	0.0363	0.1682	0.0041	-0.0070	0.0522	0.0016	-0.0071	0.0004	0.0005	-0.0290
No. of seeds/boll	0.0878	0.0947	0.0913	0.0075	-0.0051	0.0394	0.0028	0.0231	0.0006	0.0106	-0.0314
Lint index (g)	0.1501	0.0693	-0.04444	-0.0016	0.0287	-0.0480	0.0040	-0.0082	0.0040	0.0161	0.0085
Seed index (g)	-0.1501	0.0482	-0.0893	-0.0030	0.0125	-0.0983	-0.0033	0.0189	0.0008	0.0111	0.0259
G.O.T. (%)	0.1705	0.0642	0.0250	0.0019	0.0097	0.0299	0.0110	-0.0275	0.0062	0.0081	-0.0126
Mature fibre %	0.0197	0.0580	-0.0140	0.0020	-0.0026	-0.0217	-0.0035	0.0854	-0.0032	-0.0041	0.0071
Bundle strength	0.1900	-0.0375	-0.0035	-0.0002	-0.0053	0.0037	-0.0034	0.0136	-0.0202	-0.0099	-0.0018
Micronaire value	-0.0603	0.0051	0.0017	0.0017	0.0084	-0.0164	0.0018	-0.0052	0.0030	0.0660	-0.0283
Mean fibre length	0.0131	0.0224	-0.0721	-0.0035	0.0035	-0.0377	-0.0021	0.0090	0.0005	-0.0278	0.0676

moderate genetic advance was observed for mean fibre length, bundle strength and lint index indicating that the variability was partly due to non-additive gene effects. This provides scope for further genetic improvement through selection. Moderate heritability and low genetic advance was mainfested for the character ginning out turn, suggesting the involvement of non-additive gene action in their inheritance. Futher improvement in this trait can be brought forth through heterosis breeding.

In general, genotypic correlation coefficient was higher than phenotypic correlation coeficient, which indicates that strong inherent association between characters governed largely by genetic causes, are largely subjected to environmental forces.

Seed cotton yield/plant exhibited highly significant positive association with no.of bolls/plant both at genotypic level (0.9541) and phenotypic level (0.9002) and with ginning out turn (0.8598) at genotypic level only. The results are inaccordance with those reported by Shinde and Deshmukh (1985). The association between seed cotton yield/plant was significantly and positively associated with boll weight (0.4238) and no. of locs/boll (0.4647).

For other characters studied, the pairs no.of locs/boll and no.of seeds/boll (0.8338, 0.5427), lint index and seed index (0.5430, 0.4661) manifested significantly positive association at genotypic and phenotypic levels respectively. At the same time negatively significant correlation was observed between the pairs no.of locs/boll and seed index (-0.9497, -0.5308) no. of locs/boll and mean fibre length (-0.9912, -0.4284), no.of seeds/boll and seed index (-0.6638, -0.4004), fibre fineness and mean fibre length (- 0.6759.-0.4183) at genotypic levels respectively. Negative and significant association was observed between no. of seeds/boll and mean fibre length (-0.4646) at phenotypic level.

Positive and significant association of the character ginning out turn, at genotype level, with no. of bolls/plant, boll weight, no. of locs/boll, no. of seeds/boll and lint index was observed whereas the character mature fibre per cent showed significantly negative association at genotype level, with no. of locs/bool, no. of seeds/boll, lint index. seed index and ginning out turn.

Partitioning of phenotypic correlation coefficient (Table 2) into direct and indirect effects revelaed that only no. of bolls/plant had high positive direct influence (0.7870) on seed cotton yield followed by no. of locs/boll (0.2445), whereas seed index had moderate direct negative effect (-0. 1529) on seed cotton yield/plant. The other characters, though did not have any direct effect on yield, they showed indirect influence via other characters.

Thus, it can be concluded that in the improvement of seed cotton yield, emphasis should be given to selection of plants with high boll number, coupled with boll weight, high ginning out turn and more no. of locks/boll.

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Madras Agric. J., 81(6): 311-312 June, 1994

GENETICS OF YIELD AND ITS COMPONENTS IN TOMATO UNDER MOISTURE STRESS

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ABSTRACT

The nature of gene action for yield and its component characters in tomato under moisture stress was studied in a six parent full diallel cross. Presence of additive gene action for days to flowering and number of fruits set per cluster and additive and non-additive genetic systems for number of fruits per plant, mean fruit weight and yield per plant was indicated. High heritability estimates were observed for days to flowering, mean fruit showed partial dominance. All the traits except number of fruits per plant showed partial dominance. Asymmetrical distribution of genes with positive and negative effects was noticed. The number of genes controlling inheritance of the traits was established.

Tomato (*Lycopersicon esulentum Mill.*) production is affected by various environmental stresses, the major limiting factor being the moisture stress. Yield is a complex trait and depen dent on many attributes. A knowledge of nature of gene action is a pre-requisite in breeding programmes. Though gene action has been reported in tomato under irrigation, genetic information under moisture stress is scanty. Hnece, studies were under taken to elicit information on the genetics of yield and its attributes in tomato under moisture stress.

MATERIALS AND METHODS

The investigations were carried out at the Agricultural College and Research Institute, Madurai during 1986. Six homozygous lines of tomato exhibiting different magnitudes of resistance and varied *per se* performance under moisture stress viz., resistant with high yield (LE 3, LE 75 and LE 76), moderately resistant with moderate yield (LE 74), moderately resistant with low yield (LE 22) and susceptible with low yeild (LE 11) were selected from the germplasm of diverse origins. The lines wec inovlved in full diallel mating and hybrids of direct and reciprocal crosses along with the parents were evaluated in pot-culture under simulated soil moisture stress condition. The seeds were sown in seed pans and 25- day old seedlings were planted in full size earthern pots filled with pot mixture consisting of 1:1:1 red earth, sand and powdered farmyard manure. The pots were arranged in randomised block design with two replications and twenty plants were maintianed for each parent and hybrid in each replication.

Moisture stress was included uniformly by watering to field capacity and withholding water till soil moisture depleted to the level of 25 per cent of available moisture (Dastane, 1972). The soil moisture content was estimated periodically by thermogravimetric method. Observations on days taken for first flowering, number of fruits set per cluster, number of fruits per plant, mean fruit weight and yield per plant were made on ten randomly selected plants in each replication. The data were subjected to analysis of variance (Panse and Sukhatme, 1967) and the genetic components of variation were worked out following the methods of Hayman (1954 a,b).

RESULTS AND DISCUSSION

The estimates of genetic parameters and their ratios for yield and its components are presented in Table. The data showed that days to flowering and number of fruits set per cluster were governed by additive factors as evident from the significant D and the results are in conformity with the findings of Anand (1977) and Singh and Singh (1980). The significant D, H_1 and h^2 components for number of fruits per plant, mean fruit weight and yield per