

PREDICTION OF F₁ YIELD FROM PARENTAL PERFORMANCE IN UPLAND COTTON

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ABSTRACT

The investigations were carried out to develop a numerical relationship of yield of F₁ hybrids with the characters of the parents in upland cotton. Eight parental diallel cross and line x tester of 15 male with four female parents were analysed. The prediction of yield level of F₁ hybrids was worked out through the application of linear multiple regression model using mean of parents or differences of parents for various morphological and biochemical characters of parents as independent variables. The regression equations in both the sets showed that mid parental values were more appropriate, to predict the yield performance of F₁ hybrids. When regression equations from diallel crosses were used to predict the performance of crosses included in line x tester and vice versa, no general relationship was established that could be used to precisely predict the performance of F₁ hybrids entirely on the basis of characters of their parental lines.

INDEX WORDS: Cotton, prediction, regression analysis, heterosis

The manifestation of heterosis has been reported and commercially exploited in a number of crops but no sound genetic theory is yet available to help in precisely identifying the specific parents that would result in the most productive hybrids. The combining ability of parental lines is the predominant criterion that is being used to shortlist the most probable parents in heterosis breeding programmes. Davis (1978) suggested some guidelines by which the parents having greater probability of producing early maturing and high yielding hybrids of cotton can be selected. It, however, is worth mentioning that even these guidelines do not provide a precise estimate of the actual yield performance of

F₁ crosses.

There is need to identify some morphological and agronomic characters which can help to select the parents for getting maximum level of heterosis and highly productive hybrids. Such an association of easily observable characters of parents with heterosis, which combined with combining ability analysis can be helpful to identify high yielding hybrids with less resources and efforts.

MATERIAL AND METHODS

The experimental material consisted of two sets of crosses of upland cotton (*G. hirsutum* L.). Set I included eight parental

diallel crosses, excluding reciprocals, whereas crosses of 15 male with four female parents represented the second set i.e. set II. These two sets included eight exotic genotypes in set I (diallel) and crosses of four locally bred female parents and 15 diverse male parents from different sources in set II (line x tester). The hybrids were sown at the spacing of 67.5 x 60 cm (wide) and the others at 67.5 x 30 cm (normal) which is recommended for cultivation of cotton varieties in the state. Both the sets were evaluated for eighteen morphological characters viz. plant height, number of days to flowering, number of node at which first sympod appears, number of monopods, number of sympods, number of fruiting points, number of bolls, boll setting, boll size, number of locks per boll, number of seeds per lock, number of days to final maturity, yield of seed cotton per pant, ginning outturn, seed index, lint index, 2.5 percent span length and harvest index. In addition the parents were also evaluated for four biochemical characters namely peroxidase activity, total soluble proteins, total sugars and chlorophyll content. A relationship between the yield of F_1 hybrids and the performance of parental lines of such hybrids was calculated through the application of linear multiple regression analysis. The yield of F_1 crosses was taken as dependent variable which was regressed upon two groups of independent variables obtained from data of parental lines. The mid parental values for different characters of corresponding parents of each cross, constituted the first group of independent variables whereas the

absolute differences between the scores of such characters from parental lines were taken as the second group of independent variables. Since the parental lines were evaluated at two spacings so the parents at each spacing provided two groups of independent variables. In this way, four multiple regression equations were derived for each of the two sets of the experimental material resulting in the eight multiple regression equations. In the beginning the data on all the morphological characters, quality characters and biochemical characters of parents were included as independent variables. The best regression was, however, determined by deleting some of these characters on the basis of correlation among independent characters as well as with yield of hybrids, partial regression coefficients and the R^2 values of different regressions following Draper and Smith (1981).

RESULTS AND DISCUSSION

The analysis of variance for regression including all the characters for both the sets (Table 1 and 2) showed that the use of mid parental values as independent variables gave a significant regression function only for set II of crosses. Furthermore mid parental values, observed both under normal as well as wider spacing of parental lines, produced significant regression function for this set. On the other hand the use of differences between parental values produced a significant regression for both the sets but only when the parental values were obtained under wider spacing. The R^2

Table 1 Analysis of variance (mean squares) for complete regression

Source	d.f.	Normal spacing of parents		Wider spacing of parents	
		Mid parents	Differences	Mid parents	Differences
Set I					
Regression	22	263.734	224.532	214.457	269.051*
Error	5	66.679	239.215	283.542	43.329
R ²		0.9457	0.8051	0.7774	0.9647
Set II					
Regression	22	891.539*	744.045	968.042**	786.852*
Error	37	372.123	459.8219	326.634	434.369
R ²		0.5876	0.4308	0.6381	0.5186

* P ≤ 0.05; **P ≤ 0.01

Table 2 Analysis of variance for restricted regression

Source	Normal spacing of parents				Wider spacing of parents			
	Mid parents		Differences		Mid parents		Differences	
	d.f.	m.s.	d.f.	m.s.	d.f.	m.s.	d.f.	m.s.
Set I								
Regression	14	233.695	8	409.423	12	255.444	9	371.862
Error	14	221.25	19	150.546	15	204.699	18	154.945
R ²		0.4952		0.5338		0.5064		0.5455
Set II								
Regression	9	1829.484**	10	1149.155*	12	1487.62**	12	1129.089**
Error	50	338.341	49	446.752	47	330.446	47	421.986
R ²		0.4932		0.3442		0.5348		0.4059

* P ≤ 0.05; **P ≤ 0.01

values in general, were quite high for regression function involving set I as compared to those of set II of crosses. It thus appears that rather than mid parents, it is the difference of the scores of parental characters evaluated under wider spacing that may be helpful to predict the yield performance of F₁ crosses. But the inclusion of such a large number of characters in the prediction process may not be practicable. So an

attempt was made to derive restricted regression functions by excluding some characters which have strong correlation with other characters included in the function. The analysis of variance for regression of such sub-sets (Table 2) for set I of crosses did not show any consistency with respect to the type of independent variable (i.e. mid parent or differences) or the spacing among plants of parental lines i.e. normal or wide. But

for set II (Table 2) of crosses both mid parents as well as differences of parental scores resulted in significant regression functions at both the spacings. The R^2 values of all these functions, however, were quite low as compared to the full regression function. Though there is no unambiguous functional relationship but it appears that differences between scores of parental characteristics observed under wider spacing may have some utility in the prediction of F_1 performance.

On the other hand, a statistical peculiarity of regression function is that significance of regression function and R^2 values can usually be increased by inclusion of more number of variables

(Draper and Smith, 1981). In such a situation the actual utility of regression function can be judged from the comparison of expected values with the observed ones based on given regression equation. In the present study two sets i.e. diallel and line x tester were included yielding two sets of regression functions that can be used to predict the yield of crosses not included in the construction of regression function. The values of top ten crosses of set I (diallel) expected from regression function derived from set II have been given in Table 3. Similarly, regression function derived from diallel (set I) was used to predict the values of top ten crosses of line x tester (Set II) by using only the

Table 3 The expected yield of top ten crosses of diallel (set I) based on regression equations derived from line x tester (set II)

Crosses	Observed yield (gm per plant)	Expected yield (gm/yield)			
		Mid parents		Differences	
		NS	WS	NS	WS
KW61 - 276 X MATGRS 75-75	94.56	61.70	38.65	87.56	71.62
AKH8646 X AKH8652-90	87.18	43.91	25.77	98.70	61.62
TH46 X AKH 8646	85.37	83.21	31.04	110.00	45.09
TH46 X KW61 - 276	81.61	66.67	70.05	111.79	76.16
MATGRS 75-75 X 701H-452	80.88	78.70	106.36	94.41	65.50
AKH8646 X MATGRS 75-75	78.42	73.67	1.73	83.40	47.38
KW61 - 276 X 701H-452	78.22	85.82	101.44	110.85	91.62
701H-452 X H655-C	77.78	96.38	159.81	81.63	58.29
Macha X MATGRS 75-75	76.67	57.91	-31.07	54.24	51.34
TH6 X 701H-452	74.50	96.54	138.03	89.13	66.50
Correlation (r) between observed and expected		-0.54	-0.31	0.27	0.05
NS = Normal spacing		WS = Wider spacing			

differences of parents (Table 4). The mid parental values were also used but gave negligible correlation between observed and expected values and therefore, have not been included in the table. The highest value of correlation was between observed and expected values was 0.27 and -0.54. Even the remaining four correlations were negative in sign. It, thus does not support the idea of using the parental data, in this form, to estimate the potential F_1 crosses. Singh, Chahal and Singh (1986) also used the transformed data of sequential characters for predicting the yield of F_1 crosses and reported that prediction was not reliable especially for highly heterotic hybrids. Furthermore a perusal of individual regression functions in the

present study also did not reveal the importance of a particular character (s), like components of yield or biochemical characters which might have been included in all the regression functions. It thus appears that final yield of seed cotton displays complex interaction of various characters which are largely dependent on the genetic constitution of specific pairs of parents of F_1 crosses. No general relationship of such easily observable characters seems to be helpful to get an idea of the magnitude of their interactions. It thus indicates the need to explore the possibility of using more specific molecular markers to determine the genetic diversity and hence heterotic potential of parental materials.

Table 4 The expected yield of top ten crosses of line x tester (set II) based on regression equations of diallel crosses (set I)

Crosses	Observed yield (gm/plant)	Expected yield (gm/yield) Differences	
		NS	WS
LH1134 X ELS 358	132.78	70.11	55.85
LH1134 X IC822	127.73	72.59	66.60
LH1134 X IC822	125.75	79.64	79.78
F1054 X	121.59	75.79	73.33
F1054 X MATGRS 75-75	120.09	81.69	91.96
LH1134 X MATGRS 75-75	116.08	66.80	61.61
LH1134 X ELS 358	101.08	77.18	68.78
LH1134 X Macha	99.45	108.08	81.26
F1054 X Macha	93.99	66.20	67.78
LH1134 X Macha	93.40	90.35	88.31
Correlation (r) between observed and expected		-0.39	-0.32
NS = Normal spacing		WS = Wider spacing	

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