



IDENTIFICATION OF FAVOURABLE ALLELES IN THE DONOR PARENTS FOR IMPROVING AMERICAN COTTON HYBRID (NDLH 1938 × MCU 5)

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Abstract

Egyptian cotton genotypes are the only source for developing extra long staple cotton with high bundle strength. There is a need to identify genotypes containing favourable alleles not present in the American cotton hybrid to be improved. The objective of the present investigation was to evaluate six Egyptian cotton genotypes and to determine, which ones have the greatest relative values of favourable alleles for the improvement of 2.5% span length and bundle strength in the elite single cross cotton hybrid (NDLH 1938 × MCU 5). The estimates of $\mu G'$ values revealed the genotype SUVIN may be used as source of favourable alleles for improving elite hybrid with respect to 2.5% span length. This improvement may be possible by transferring favourable alleles from SUVIN to NDLH 1938 through back crossing as it has high genetic affinity with NDLH 1938. The bundle strength can be improved through transferring favourable alleles from GSB 40 to NDLH 1938 as it exhibited high $\mu G'$ estimates. The parent, NDLH 1938 has great genetic affinity with both the donors hence; this parent can be improved for both the traits through backcrossing.

Key words : American cotton, donors, quality traits, favourable alleles.

Introduction

The widespread use of high speed spinning technology in the textile mills has increased the demand for raw cotton fibre with higher strength and length. Hence, cotton fibre quality must be improved to remain competitive with synthetic fibres and to meet the needs of new spinning and weaving methods (Kohel, 1999). In this day by day, quality and quantity requirement changing scenario, the cotton hybrids usage in the present day agricultural production is limited. Therefore, they have to be replaced by new hybrids that will exceed the existing ones in their performance. Egyptian cotton genotypes may serve for the improvement of existing cotton hybrids in terms of important fibre quality traits *viz.*, 2.5% span length and bundle strength as the donors of favourable alleles.

Dudley (1984) proposed a methodology for identification of unique favourable alleles in donor inbred lines of maize for improving the parental constituents in a desirable single cross. This method was followed by several modifications by him as well as by other workers (Dudley, 1987b; Zanoni and Dubley, 1989b and Bernardo,

1990) devising new parameters for evaluating the donor inbred lines from all aspects like frequency of favourable alleles present, frequency of alleles lacking in the parental parents, estimating the relative relationships of the donor inbred and also estimating the loss of alleles not only in the donor parents, but also in the single cross hybrids of maize. In the present experiment, a target cross (NDLH 1938 × MCU 5), which has been a *priori* projected to be improved was considered based on its proven performance in the previous yield trials.

Materials and Methods

The experimental material for identification of favourable alleles consisted of two lines, NDLH 1938 and MCU 5 parents of target cross (NDLH 1938 × MCU 5) and six testers *viz.*, GSB 40, DB 16, DB 11, GSB 41, TCB 37 and SUVIN. These eight parents mated in line × tester fashion to get 12 F_1 s during off season (2014-15). The parents and crosses were evaluated at three locations *i.e.*, RARS, Lam Farm; ARS, J.M. Puram and Agricultural College Farm, Bapatla during *khariif*, 2014-15. Data was collected on 2.5% span length (mm) and bundle strength (g/tex). Statistical analysis carried out as per methodology

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suggested by Dudley (1987b).

A positive value $\mu G'$ shows that line (P_w) has favorable alleles on loci where parental lines (P₁ and P₂) have unfavorable alleles. Value $\mu B'$ gives relative number of loci where P₁ and P₂ have favorable alleles, $\mu C'$ gives relative number of loci where P₁ and P_w have favorable alleles and P₂ does not, and $\mu E'$ gives to the relative number of loci where P₂ and P_w have favorable alleles and P₁ does not. Values $\mu D'$ and $\mu F'$ show that P₁ or P₂ have favorable alleles at the loci where other two lines do not have favorable alleles. The sum of $\mu C'$ and $\mu F'$ gives relative number of loci, where P₁ and P_w have the same (+ or -) alleles, while $\mu D' + \mu E'$ give relative number of loci where P₂ and P_w have the same (+ or -) alleles. If: 1. $\mu C' + \mu F' > \mu D' + \mu E'$ – line P_w is more closely related to P₁ and is used for the improvement of parent P₁. 2. $\mu C' + \mu F' < \mu D' + \mu E'$ – donor line P_w is more closely related to P₂ and is used for the improvement of parent P₂. Evaluation of parentage of donor (P_w) with elite hybrid parents (P₁ and P₂) can be performed by using the following formulas $[(P_2 \times P_w) - (P_1 \times P_w) + (P_1 - P_2)/2]$. Positive value points to the parentage between P₁ and P_w, while negative value points to the parentage between P₂ and P_w. Depending on which parent is being improved, P₁ or P₂, the founding initial population for selection is determined by comparing values $\mu D'$ or $\mu F'$ with value $\mu G'$. If parent P₁ is improved, there are three possibilities:

1. $\mu D' = \mu G'$; the probability that the new line will have more loci with favorable alleles in class D and G than either P₁ or P_w is maximum. Then the approach will be hybrid self-fertilization (P₁ × P_w).
2. $\mu D' > \mu G'$; points to the back crossing of hybrids (P₁ × P_w) with parent P₁.
3. $\mu D' < \mu G'$; back crossing of hybrids (P₁ × P_w) with donor P_w is recommended.

The standard error (SE) of the estimators for $\mu B'$ to $\mu G'$ were calculated as the square root of the variance of the linear function associated with each estimator ignoring covariance. All estimates were considered different from zero, if they exceeded twice their standard error.

Results and Discussion

The estimates of $\mu G'$ for the cross NDH 1938 × MCU 5 for 2.5% span length and bundle strength were presented in table 1. For 2.5% span length, in combined analysis and at Lam farm all the six donors recorded significant positive $\mu G'$ estimates. Only one donor *i.e.*, SUVIN exhibited significant $\mu G'$ estimates at J. M. Puram. All the donors registered significant $\mu G'$ values

at Bapatla except DB 11 and SUVIN. The donor, SUVIN showed highest $\mu G'$ estimate at Lam Farm and J.M. Puram. Whereas, GSB 40 recorded the highest $\mu G'$ value at Bapatla. In combined analysis, SUVIN had shown the highest $\mu G'$ estimate followed by GSB 40 and TCB 37. However, DB 11 showed the lowest $\mu G'$ estimate among all donors.

For bundle strength, all the donors showed significant positive $\mu G'$ estimates in combined analysis, of which GSB 40 gave the highest $\mu G'$ estimate followed by SUVIN and DB 16. The donor, DB 11 recorded the lowest $\mu G'$ estimate in combined analysis. Considering the individual environments, all the six donors except DB 11 at Lam farm; GSB 40 and DB 16 at Bapatla recorded significant positive $\mu G'$ estimates. It is interesting to note that at J M Puram, $\mu G'$ estimates could not be obtained for all the donors. The reasons may be due to the failure of the assumptions of complete dominance or epistasis (Dudley, 1988).

Considering the overall data, it may be inferred that estimates of $\mu G'$ in various donors greatly differed in different environments for the same trait. This may be attributed to the differential environmental effects on the same set of genes governing the expression of the same trait. It is also observed that almost all the donors showed significant positive $\mu G'$ estimates for the two characters studied in combined analysis indicating existence of favourable alleles for further improvement of the target hybrid.

However, further characterization of various donors and their genetic similarity estimates (tables 2 and 3) have to be analyzed critically along with the other estimates ($\mu B'$ to $\mu G'$) to initiate the improvement programme for this cross. For this cross, the genetic enhancement for 2.5% span length and bundle strength was considered.

A perusal of the results obtained with respect to the donors (table 1) is quite encouraging. The donors *viz.*, SUVIN, GSB 40 and TCB 37 gave the highest significant positive $\mu G'$ estimates indicating their worth in transferring favourable alleles in the target cross for 2.5% span length. In order to obtain further details about the nature and frequency of alleles in the donor parents *vis-a-vis* concerned target cross, the various parameters to represent the different classes and the relationship of the donors with the parents of the cross concerned are presented in table 2. Critical study of mean *per se* value of the crosses and different parameters of the model taken into consideration together indicates that the findings are not beyond expectations. For example, the donor, SUVIN showed the highest significant $\mu G'$ estimate

Table 1 : Estimates of $\mu G'$ in the donor parents for 2.5% span length and bundle strength combined over environments, when the hybrid NDLH 1938 \times MCU 5 was designated as the hybrid to be improved.

Parent	$\mu G'$							
	RARS, Lam Farm		ARS, J. M. Puram		Agricultural College Farm, Bapatla		Pooled	
	2.5% span length (mm)	Bundle strength (g/tex)	2.5% span length (mm)	Bundle strength (g/tex)	2.5% span length (mm)	Bundle strength (g/tex)	2.5% span length (mm)	Bundle strength (g/tex)
GSB 40	2.342 ^{aa} *	1.940 ^{a*}	N	N	3.530 ^{c*}	5.305 ^{c*}	3.097 ^{c*}	3.552 ^{c*}
DB 16	2.365 ^{aa} *	1.015 ^{b*}	N	N	2.470 ^{c*}	2.045 ^{c*}	2.757 ^{c*}	2.000 ^{b*}
DB 11	1.550 ^{c*}	0.355 ^b	N	N	N	N	1.748 ^{c*}	1.545 ^{b*}
GSB 41	2.557 ^{aa} *	1.370 ^{b*}	N	N	2.240 ^{c*}	N	2.267 ^{c*}	1.767 ^{b*}
TCB 37	2.622 ^{aa} *	1.315 ^{a*}	N	N	3.075 ^{c*}	N	2.852 ^{c*}	1.887 ^{b*}
SUVIN	3.437 ^{aa} *	2.022 ^{aa} *	4.072 ^{c*}	N	N	N	3.467 ^{c*}	2.587 ^{c*}
SE a	0.247	0.224	-	-	-	-	-	-
SE b	-	0.224	-	-	-	-	-	0.238
SE c	0.294	-	0.266	-	0.339	0.316	0.301	0.297
SE d	-	-	-	-	-	-	-	-

* Larger than 2 \times SE; N = $\mu G'$ values could not obtained

a = q_{j_0}, q_{k_1}

b = q_{j_1}, q_{k_0}

c = q_{j_0}, q_{j_1}

d = q_{k_0}, q_{k_1}

Table 2 : Estimates of $\mu B' \dots \mu G'$ for 2.5% span length in six donor parents when NDLH 1938 \times MCU 5 is the hybrid to be improved.

Parents	Class of loci										
	$\mu B'$	$\mu C'$	$\mu D'$	$\mu E'$	$\mu F'$	$\mu G'$	$\mu C+F'$	$\mu D+E'$	Genetic affinity with	Mean <i>per se</i> of NDLH 1938 \times donor	Mean <i>per se</i> of MCU 5 \times donor
GSB 40	0.477	-0.062	-0.062	-0.097	1.417*	3.097*	1.355*	-0.160	NDLH 1938	32.98	37.79
DB 16	0.252	-0.062	-0.062	-0.152	1.472*	2.757*	1.410*	-0.215	NDLH 1938	33.69	35.67
DB 11	0.132	-0.062	-0.062	0.682	0.638	1.748*	0.575	0.620	MCU 5	32.82	33.69
GSB 41	-0.782	-0.062	-0.062	0.408	0.912*	2.267*	0.850	0.345	NDLH 1938	32.76	34.91
TCB 37	-0.608	-0.062	-0.062	0.387	0.933*	2.852*	0.870*	0.325	NDLH 1938	34.93	37.02
SUVIN	0.112	-0.062	-0.062	0.023	1.298*	3.467*	1.235*	-0.040	NDLH 1938	35.92	38.10

® Mean *per se* of the cross NDLH 1938 \times MCU 5 is: 28.63

* Larger than 2 \times S.E.

Table 3 : Estimates of $\mu B' \dots \mu G'$ for bundle strength in six donor parents when NDLH 1938 \times MCU 5 is the hybrid to be improved.

Parents	Class of loci										
	$\mu B'$	$\mu C'$	$\mu D'$	$\mu E'$	$\mu F'$	$\mu G'$	$\mu C+F'$	$\mu D+E'$	Genetic affinity with	Mean <i>per se</i> of NDLH 1938 \times donor	Mean <i>per se</i> of MCU 5 \times donor
GSB 40	0.108	0.283	0.283	-1.108	1.807*	3.552*	2.090*	-0.825	NDLH 1938	26.75	30.67
DB 16	-0.535	0.090	0.475	0.610	0.090	2.000*	0.180	1.085*	MCU 5	27.90	27.20
DB 11	-0.415	0.210	0.355	0.490	0.210	1.545*	0.420	0.845*	MCU 5	25.76	25.88
GSB 41	-1.223	0.043	0.523*	0.657*	0.043	1.767*	0.085	1.180*	MCU 5	26.84	26.12
TCB 37	-1.628	0.198	0.368	0.502	0.198	1.887*	0.395	0.870*	MCU 5	27.79	27.12
SUVIN	-0.653	0.283	0.283	0.318	0.382	2.587*	0.665	0.600	NDLH 1938	28.61	28.85

® Mean *per se* of the cross NDLH 1938 \times MCU 5 is: 22.89

* Larger than 2 \times S.E.

(3.467*) among the donors and expectedly should have given higher mean value in its cross combinations with the constituents (NDLH 1938 and MCU 5) of the target cross.

The cross, MCU 5 (P_2) \times P_w recorded high *per se* performance and higher $\mu F'$ values (class where P_1 and P_w have unfavourable alleles and P_2 has favourable alleles) indicating for further improvement of the target cross for 2.5% span length can be possible through replacement of P_1 with the donor line, if other yield contributing traits are unaltered. On the other hand, if the improvement of this cross is sought *via* parental improvement the genotype SUVIN can be used as donor for recycling as it showed high $\mu G'$ values compared with other donors. Considering the parameters ($\mu C' + \mu F'$) and ($\mu D' + \mu E'$), the donor has genetic affinity with NDLH 1938 and it may be summarized that enhancement of NDLH 1938 by this will not cause any canceling effect which usually emanate from wide diversity of alleles coming together causing disequilibrium in the degree of association of dominant genes acting in opposite directions.

For enhancing bundle strength in the target cross, NDLH 1938 \times MCU 5 through parental improvement, GSB 40 (3.552*) could be suggested, as this donor recorded highest positive and significant $\mu G'$ value. This revealed its worth in transferring favourable alleles. The cross MCU 5 (P_2) \times P_w had recorded high *per se* performance and at the same time, it had also recorded high $\mu F'$ value (class where P_1 and P_w have unfavourable alleles and P_2 has favourable alleles) (table 3). For increased bundle strength in elite hybrid, P_1 may be replaced by the donor line GSB 40 or otherwise improvement of elite hybrid may be possible through improving the parental line NDLH 1938 (P_1) through back crossing with GSB 40 as the donor has high genetic affinity with NDLH 1938. Similarly, several workers (Bernardo, 1990; Dudley *et al.*, 1996; Malvar *et al.*, 1997 and Ayrault *et al.*, 1999) used this model for population improvement and several workers (Dudley, 1984; 1987a, Malvar *et al.*, 2004; Reddy *et al.*, 2005 and Rodriguez *et al.*, 2007) used this model for inbreds improvement and supported the contention that the single cross hybrid improvement could be possible by selecting donors with significant favourable alleles.

The perusal of results revealed the donor parent, SUVIN for 2.5% span length and for bundle strength, GSB 40 recorded significant positive $\mu G'$ estimates and exhibited presence of favourable alleles in combined analysis. The ($\mu C' + \mu F'$), ($\mu D' + \mu E'$) and F' values indicated that both the donor parents had high genetic affinity with NDLH 1938 (P_1) and presence of favourable alleles in MCU 5 (P_2) for both the characters. Hence,

NDLH 1938 need to be improved for both the quality traits and improved parent can be used to get target cross with high seed cotton yield along with good quality fibre.

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