Indian Journal of Agricultural Sciences **88** (3): 504–8, March 2018/Article

Identification of donor parents containing favourable alleles for improving target American cotton hybrid (*NA 1325 × L 604*)

BALAKRISHNA B[1], CHENGA REDDY V[2], K V SIVA REDDY[3], Y SATISH[4] and K BAYYAPU REDDY[5]

All India Co-ordinated Cotton Improvement Project, Regional Agricultural Research Station, Acharya N G Ranga Agricultural University, Lam, Guntur, Andhra Pradesh 522 034

Received:006 July 2017 ; Accepted: 06 December 2017

ABSTRACT

The present study was conducted during *kharif* 2013, *kharif* 2014 and *kharif* 2015 at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh, India. The aim of the present investigation was to evaluate four American cotton genotypes and to determine which have the greatest relative values of favourable alleles for the improvement of number of bolls/plant, boll weight (g), 2.5% span length (mm), bundle strength (g/tex), seed cotton yield/plant (g) and lint yield/plant (g) in the elite single cross cotton hybrid (NA 1325 × L 604). Based on the estimates of $\mu G'$ values the genotype Surabhi was noted with positive high $\mu G'$ value and may be used as source of favourable alleles for improving elite hybrid with respect to quality traits like bundle strength ($\mu G'$=1.830*) and 2.5% span length ($\mu G'$=1.325*). This improvement may be possible by transferring favourable alleles from Surabhi to NA 1325 through back crossing as it had high genetic affinity with NA 1325. For number of bolls/plant RAH 1004 ($\mu G'$=3.230*) and HYPS 152 ($\mu G'$=0.302*) for boll weight and both the donors for seed cotton yield/plant ($\mu G'_{RAH\ 1004}$=13.915*and $\mu G'_{HYPS\ 152}$=23.972*) may be used as donors as they recorded significant and positive $\mu G'$ estimates.

Key words: American cotton, Donors, Elite hybrid, Favourable alleles

Cotton (*Gossypium* spp.) popularly called as White Gold is a major fibre crop of global importance and it is the major fibre crop of India and contributing up to 75% of total raw material needs of textile industry and provides employment to about 60 million people (Manickam *et al*. 2010). It is well documented that intra-hirsutum cotton hybrids are a way to achieve quantum jump in quality and quantity of cotton. Likewise hybrid vigour/heterosis have been exploited in many of the crops and also inspired the cotton breeders to explore the benefits of heterosis in cotton (Singh *et al*. 1980 and Davis 1978). The demand for raw cotton is ever increasing and the Indian Cotton Mills Federation has projected the cotton requirement for 2025 at 600 lakh bales (Deshpande *et al*. 2008). Apart from these, the widespread use of high speeds pinning technology in the textile mills has increased the demand for raw cotton fibre with higher strength and length. Hence, cotton fibre productivity and quality must be improved to remain competitive with synthetic fibres and to meet the needs of news pinning and weaving methods (Kohel 1999).

The present fibre quality and quantity requirement changing scenario is limiting the period of cultivation of cotton hybrids. Therefore, they have to be replaced by new hybrids that will exceed the existing ones in their yield performance along with textile mills required fibre qualities with resistance to biotic and abiotic stresses. Ultimately, one of the objectives in cotton hybrid breeding is to improve different traits in the already existing hybrid(s) as well as to improve agronomic traits of parental component without negative effects on lint yield of elite single cross(s). One of the methods of the development of new hybrids is the improvement of existing hybrids, i.e. the improvement of one or both parental lines of the elite hybrid. For which older cultivars, lines etc. may serve for the improvement of existing cotton hybrids as the donors of the favorable alleles. The procedure involves the introduction of favorable alleles into the existing parental lines, which would be manifested through better agronomic properties of future hybrids. Hence, the present investigation was under taken to identify the donor parents with favourable alleles for improving elite single cross cotton hybrid, i.e. NA 1325 × L 604.

MATERIALS AND METHODS

Four cotton donor lines (Surabhi, RAH 1004, HYPS-152 and MCU 5) were selected for improvement of elite single cross NA 1325 × L-604 for important quantitative and qualitative characters.

The two parental lines of target cross were crossed with four donor lines excluding reciprocals during *kharif* 2012

[1]Teaching Associate (e mail: balubreeder@gmail.com), [2]Former Principal Scientist (Cotton). (e mail: vcreddyagri@gmail.com), [3,4,5] Scientist (e mail: kvsivareddy@yahoo.co.in, tej.satish1@gmail.com, drkaipu3@gmail.com)

and obtained F_1 seed for conducting the experiment for forthcoming season and crossing was done in every season for conducting the experiment in the next season. The plant material, i.e. 6 lines and 9 crosses (including target cross) was evaluated in randomized complete block design with 4 replications during *kharif* 2013, *kharif* 2014 and *kharif* 2015 at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh. The parents and F_1 crosses were sown in 10 lines for each entry with 105 cm × 60 cm spacing. The package of practices recommended for cotton production were applied throughout the growing season in each year. The data was recorded on 5 randomly selected competitive plants from all the parents and F_1 crosses for each treatment in replication for the characters, viz. number of bolls/plant, boll weight (g), 2.5% span length (mm), bundle strength (g/tex), seed cotton yield/plant (g) and lint yield/plant (g).

For any three homozygous lines, only eight classes of loci exist, viz. A to H (Table 1). Consider an elite single cross $P_1 \times P_2$, and a third line P_w, which might be used to improve either P_1 or P_2 for the production of a new hybrid superior to $P_1 \times P_2$. Among the eight classes of loci A and H indicates all three lines are homozygous, i.e. either + or – type of alleles. The most interest class is G, because for this class, P_w contains favourable alleles which are not present in either P_1 or P_2. Let A, B, C, D, E, F, G and H be the number of loci in their respective classes. Let the genotypic values of the three possible genotypes (++, +–, – –) at a single locus be μ, aμ and – μ, respectively (Comstock and Robinson 1948).

Dudley (1984a), under the assumptions of complete dominance (a=1) μ constant for all loci, $\mu A - \mu H = 0$ and $z = -\mu$ obtained estimators for μB, μC…., μG. If $\mu A \neq \mu H$ and $z \neq \mu$, then the expectations of μB,…., μG as estimated. Dudley (1987b) describes estimators (designated *lplμ*) for *lplμ* that are free of the assumption that $z = -\mu$ and A=H. If estimates of μG (e.g. μG') are obtained using the estimator *lplμ* then μG' – μG where μG is calculated. By adding or subtracting, as appropriate the μB',…μF' values obtained.

Table 1 Genetic status of classes of loci possible for three homozygous lines.

Class of loci	Line		
	P_1	P_2	P_w
A	+	+	+
B	+	+	–
C	+	–	+
D	+	–	–
E	–	+	+
F	–	+	–
G	–	–	+
H	–	–	–

+ = Loci homozygous for favourable allele,– = Loci homozygous for unfavourable allele, A, B,…. H = Number of loci in their respective classes.

A positive value μG' shows that line (Pw) has favorable alleles on loci where parental lines (P_1 and P_2) have unfavorable alleles. Value μB' gives relative number of loci where P_1 and P_2 have favorable alleles, μC' gives relative number of loci where P_1 and P_w have favorable alleles and P_2 does not, and μE' gives to the relative number of loci where P_2 and P_w have favorable alleles and P_1 does not. Values μD' and μF' show that P_1 or P_2 have favorable alleles at the loci where other two lines do not have favorable alleles. The sum of μC' and μF' gives relative number of loci where P_1 and P_w have the same (+ or -) alleles, while μD' + μE' give relative number of loci where P_2 and P_w have the same (+ or -) alleles. If: 1. μC' + μF' > μD' + μE' – line P_w is more closely related to P_1 and is used for the improvement of parent P_1. 2. μC' + μF' < μD' + μE' – donor line Pw is more closely related to P_2 and is used for the improvement of parent P2. Evaluation of parentage of donor (P_w) with elite hybrid parents (P_1 and P_2) can be performed by using the following formulae $[(P_2 \times P_w) - (P_1 \times P_w) + (P_1 - P_2)/2]$. Positive value points to the parentage between P_1 and P_w, while negative value points to the parentage between P_2 and P_w. Depending on which parent is being improved, P_1 or P_2, the founding initial population for selection is determined by comparing values μD' or μF' with value μG'. If parent P_1 is improved, there are three possibilities: 1. μD' = μG'; the probability that the new line will have more loci with favorable alleles in class D and G than either P_1 or P_w is maximum. Then the approach will be hybrid self-fertilization ($P_1 \times P_w$). 2. μD' > μG'; suggests the back crossing of hybrids (P1 × Pw) with parent P1. 3. μD' < μG'; back crossing of hybrids ($P_1 \times P_w$) with donor Pw is recommended.

The standard error (SE) of the estimators for μB' to μG' 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 identification of favourable alleles present in the donor lines (μG') but not in the hybrid to be improved for no. of bolls/plant, boll weight, 2.5% span length, fibre strength, seed cotton yield/plant and lint yield/plant was carried out by using Dudley (1987b) model over environments (pooled) and presented in Table 2. The various parameters to represent the different classes and the relationship of the donors of the cross concerned are presented in Tables 3 to 8.

For no. of bolls/plant, in pooled analysis over environments, among the four lines studied only one genotype, i.e. RAH 1004 had recorded significant positive μG' estimates. This indicates the existence of favourable alleles for further improvement of the target hybrid.μG' estimates could not be obtained for the donors HYPS 152 and MCU 5, respectively. The reasons may be due to the failure of the assumptions of complete dominance or epitasis (Dudley 1988). The cross L 604 ×P_w recorded high *per se* performance and higher μF' values (class where P_1 and P_w

Table 2 Estimates of μG' in the donors for different quantitative and qualitative traits in cotton over different environments when the hybrid NA 1325 × L 604 (target cross) was designated as the hybrid to be improved

Parent	μG'					
	No. of bolls/ plant	Boll weight (g)	Fibre length (mm)	Fibre strength (g/tex)	Seed cotton yield/ plant (g)	Lint yield/ plant (g)
Surabhi	1.005	0.022	1.325[c]*	1.830[c]*	5.285[b]*	1.572[b]*
RAH 1004	3.230[c]*	0.132	N	-0.120	13.915[b]*	N
HYPS 152	N	0.302[a]*	N	0.895[c]*	23.972[b]*	N
MCU 5	N	N	N	0.470	N	N
SE a		0.071				
SE b					2.492	0.767
SE c	0.603		0.367	0.256		
SE d						

N= μG' values not obtained, *Larger than 2 × SE; a = q_{j0}, q_{kl}, b = q_{j1}, q_{k0} c = q_{j0}, q_{j1}, d = q_{k0}, q_{k1}

have unfavourable alleles and P_2 has favourable alleles) indicating for further improvement of the target cross for this trait can be possible through replacement of P_1 with the donor line if other traits of elite hybrid remain unaltered. On the other hand, if the improvement of this cross is sought *via* parental improvement the genotype RAH 1004 can be used as donor for recycling as it showed high μG' values compared with other donors.Considering the parameters (μC'+μF') and (μD'+μE'), the donor has genetic affinity with NA 1325 and it may be summarized that enhancement of NA 1325 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.

Among the four donors studied the genotype HYPS 152 had significant positive μG' positive value for boll weight. This indicates for further improvement of target cross for this character possibly by using HYPS 152 as a donor line as it has favourable alleles for boll weight. It is interesting to note that L 604 × P_w had high per se performance along with significant and positive μF' values (class where P_1

Table 3 Estimates of μB'…… μG' for no. of bolls/plant in four donor lines when NA 1325× L 604 is the target hybrid to be improved

Donors	μB'	μC'	μD'	μE'	μF'	μG'	μC+F'	μD+E'	Genetic affinity with	Mean per se of NA 1325 × Donor	Mean per se of L 604 × Donor
Surabhi	-0.705	0.200	0.200	0.885	0.540	1.005	0.740	1.085	L 604	36.00	36.68
RAH 1004	-0.350	0.200	0.200	-1.245	2.670*	3.230*	2.870*	-1.045	NA 1325	36.19	41.13
HYPS 152											
MCU 5											

Target cross (NA 1325 × L 604) mean=35.07

Table 4 Estimates of μB'…… μG' for boll weight in four donor lines when NA 1325× L 604 is thetarget hybrid to be improved

Donors	μB'	μC'	μD'	μE'	μF'	μG'	μC+F'	μD+E'	Genetic affinity with	Mean per se of NA 1325 × Donor	Mean per se of L 604 × Donor
Surabhi	0.083	0.158	0.083	0.083	0.113	0.022	0.270	0.165	NA 1325	3.91	3.97
RAH 1004	0.227*	0.163	0.078	0.078	0.118	0.132	0.280*	0.155	NA 1325	4.12	4.20
HYPS 152	0.113	0.198	0.042	0.042	0.153*	0.302*	0.350*	0.085	NA 1325	4.39	4.61
MCU 5											

Target cross (NA 1325 × L 604) mean=4.09

Table 5 Estimates of μB'…… μG' for 2.5% span length in four donor lines when NA 1325 × L 604 is the target hybrid to be improved

Donors	μB'	μC'	μD'	μE'	μF'	μG'	μC+F'	μD+E'	Genetic affinity with	Mean per se of NA 1325 × Donor	Mean per se of L 604 × Donor
Surabhi	0.245	-0.385	-0.385	-0.055	0.880	1.325*	0.495	-0.440	NA 1325	30.54	33.07
RAH 1004											
HYPS 152											
MCU 5											

Target cross (NA 1325 × L 604) mean=29.65

Table 6 Estimates of µB'…… µG' for bundle strength in four donor lines when NA 1325× L 604 is the target hybrid to be improved

Donors	µB'	µC'	µD'	µE'	µF'	µG'	µC+F'	µD+E'	Genetic affinity with	Mean per se of NA 1325 × Donor	Mean per se of L 604 × Donor
Surabhi	0.630*	-0.105	-0.105	-0.425	0.570	1.830*	0.465	-0.530	NA 1325	23.96	25.31
RAH 1004	-0.955	-0.105	-0.105	-0.060	0.205	-0.120	0.100	-0.165	NA 1325	20.79	21.41
HYPS 152	-0.200	-0.105	-0.105	-0.335	0.480	0.895*	0.375	-0.440	NA 1325	22.27	23.44
MCU 5	-0.905	-0.105	-0.105	0.015	0.130	0.470	0.025	-0.090	NA 1325	22.12	22.59

Target cross (NA 1325 × L 604) mean=21.44

Table 7 Estimates of µB'…… µG' for seed cotton yield/plant in four donor lines when NA 1325× L 604 is the target hybrid to be improved

Donors	µB'	µC'	µD'	µE'	µF'	µG'	µC+F'	µD+E'	Genetic affinity with	Mean per se of NA 1325 × Donor	Mean per se of L 604 × Donor
Surabhi	-2.045	0.825	16.360*	13.600*	0.825	5.285*	1.650	29.960	L 604	157.16	126.09
RAH 1004	14.220*	2.325	14.860*	12.100*	2.325	13.915*	4.650	26.960*	L 604	171.42	146.35
HYPS 152	13.247*	5.483*	11.703*	8.943*	5.483*	23.972*	10.965*	20.645*	L 604	185.22	172.78
MCU 5											

Target cross (NA 1325 × L 604) mean=148.24

Table 8 Estimates of µB'…… µG' for lint yield/plant in four donor lines when NA 1325 × L 604 is the target hybrid to be improved

Donors	µB'	µC'	µD'	µE'	µF'	µG'	µC+F'	µD+E'	Genetic affinity with	Mean per se of NA 1325 × Donor	Mean per se of L 604 × Donor
Surabhi	-0.788	0.012	3.797*	2.517*	0.012	1.572*	0.025	6.315*	L 604	51.01	43.44
RAH 1004											
HYPS 152											
MCU 5											

Target cross (NA 1325 × L 604) mean=47.89, * Larger than 2 × SE.

and P_w have unfavourable alleles and P_2 has favourable alleles). It revealed that replacement of P_1 with HYPS 152 in target cross can give better alternative for getting high boll weight when the other superior traits of target hybrid remain unaltered. For enhancing the cross NA 1325 × L 604 through parental improvement, NA 1325 possessed genetic affinity with this donor, hence improvement of the cross NA 1325 × L 604 might be anticipated *via* recycling of the parent NA 1325 using HYPS 152 as donor.Bayyapu Reddy (2015) also identified donor genotypes in American cotton for improving boll weight.

Significant and positive µG' value for 2.5% span length was recorded by the donor Surabhi and therefore this line would be the best donor for favourable alleles. Estimates of (µC'+µF') and (µD'+µE') indicated that donor line had high genetic affinity with parental line NA 1325. This revealed that improvement of elite hybrid NA 1325 × L 604 for 2.5% span length may be possible by improving line NA 1325 through back crossing. Bayyapu Reddy (2015) also reported Surabhi as donor for favourable for improving 2.5% span length in cotton.

The donor Surabhi had recorded highest significant and positive µG' value followed by HYPS 152 for bundle strength. These results revealed that Surabhi was a potential donor for improving elite hybrid with respect to this character. The cross P_2 × P_w had recorded high *per se* performance and at the same time it had also recorded high µF' value indicating increased bundle strength in elite hybrid, P_1 may be replaced by the donor line Surabhi or otherwise improvement of elite hybrid may be possible through improving the parental line NA 1325 (P_1) through back crossing with Surabhi as the donor has genetic affinity with NA 1325.

For seed cotton yield/plant, in combined analysis, three out of four donors, viz. Surabhi, RAH 1004 and HYPS 152 gave significant positive µG' estimates, of which HYPS 152 recorded the highest positive µG' estimate followed by RAH 1004 and Surabhi indicating their worth in transferring favourable alleles. The cross P_1× P_w had recorded high *per se* performance along with high positive significant µD' value along with significant and positive µF' estimates and revealing that P_2 cannot be completely replaced by the donor line for further improvement of this trait.So parental improvement is desired, considering the parameters (µC' +

$\mu F'$) and ($\mu D' + \mu E'$) donor has genetic affinity with L 604. Therefore, further improvement of seed cotton yield/plant in elite hybrid may be possible *via* back crossing [(L 604 × P_w) × L 604)].

Out of four donors studied only one, i.e. Surabhi recorded with significant and positive $\mu G'$ estimates for lint yield/plant and exhibiting its ability to transfer favourable alleles for its traits to elite hybrid for further improvement. $P_1 \times P_w$ recorded high *per se* performance and high significant and positive $\mu D'$ value indicating further improvement of elite hybrid with respect to this trait may be through replacing of P_2 with donor line. If improvement in elite hybrid sought through the parental line improvement then P_2 may be improved for favourable alleles with donor line *via* back crossing as it has genetic affinity with Surabhi. The present results also substantiate the usefulness of the $\mu G'$ estimates besides assessing the other biometrical parameters. Similarly several workers (Dudley 1984a, 1988) used this model for inbred improvement and several workers (Dudley 1987a, Dudley *et al.* 1996, Kumar *et al*. 2003, Reddy *et al*. 2003, 2004, 2005, Naik 2012 and Todorovic *et al*. 2012) in maize and Drazic *et al*. (2010) in tobacco used this model for selecting donor genotypes with significant favourable alleles for different traits.

The genotype Surabhi can be selected as the donor of favourable alleles for improving parents of elite single cross hybrid NA 1325 × L 604 with respect to 2.5% span length and bundle strength. This line has new alleles for these two traits not present in elite hybrid. Based on the parentage of Surabhi with hybrid parents, the improvement for two quality traits should be carried out by improving the parental line NA 1325. RAH 1004 for number of bolls/plant and HYPS 152 for boll weight and both the donors for seed cotton yield/plant recorded significant and positive $\mu G'$ estimates. These genotypes may be used as donors for favourable alleles for improving said traits and ultimatelythe seed cotton yield/plant of elite hybrid NA 1325 × L 604.

REFERENCES

AICCIP. 2015. *Annual Report 2014-15*. All India Coordinated Cotton Improvement Project. Coimbatore, Tamilnadu.

Bayyapu Reddy K. 2015. 'Genetic analysis of fibre quality traits in intra-specific hybrids of cotton (*Gossypium hirsutum* L.)'. Ph D thesis, Acharya N G Ranga Agricultural University, Hyderabad.

Comstock R E and Robinson H F. 1948. The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. *Biometrics*. **4**: 254–66.

Davis D D. 1978. Hybrid cotton: Specific problems and potentials. *Advances in Agronomy* **30**: 129–57.

Deshpande N P, Dheva N G, Potdukhe N R, Parmar J N and Wadodkar M B. 2008. Combining ability study for yield and morphological traits in inter-specific crosses between *G. hirsutum* L. and *G. barbadense* L. *International Journal of Plant Sciences* **3**: 158–62.

Drazic S, Prodanovic S and Zivanovic T. 2010. Identification of donor lines containing favorable alleles for quantitative traits in burley tobacco (*Nicotiana tabacum* L.). *Genetika* **42**(2): 287–97.

Dudley J W.1984a. A method of identifying population containing favorable alleles not present in elite germplasm. *Crop Science* **24**: 1053–4.

Dudley J W. 1987a. Modification of methods for identifying populations to be used for improving parents of elite single crosses. *Crop Science*. **27**: 940–7.

Dudley J W. 1987b. Modification of methods for identifying inbred lines useful for improving parents of elite single crosses. *Crop Science* **27**: 944–7.

Dudley J W. 1988. Evaluation of maize population as sources of favorable alleles. *Crop Science*. **28**: 486–91.

Dudley J W, Lamkey K R and Geadelmann J L. 1996. Evaluation of populations for their potential to improve three maize hybrids. *Crop Science* **36**: 1553–9.

Kohel R J. 1999. Cotton germplasm resources and the potential for improved fibre production and quality. (*In*) *Cotton Fibres*, pp 167-82. Basra A S (Eds). The Haworth Press, Inc., New York, USA.

Malvar R A, Cartea M E, Revilla P, Soengas P and Ordas A. 2004. Verification of predictions from estimators of favorable alleles to improve yield of sweet corn hybrids. *Maydica* **49**: 49–55.

Manickam S, Gururajan K N and Gopalakrishnan N. 2010. Development of isogenic restorer line in extra long staple cotton variety suvin. *Electronic Journal of Plant Breeding* **1**(4): 632–6.

Kumar M V N, Venkatesh S and Satyanarayana E. 2003. Comparison of methods to identify donor inbreds with favourable alleles for the improvement of elite maize single cross hybrids. *Indian Journal of Genetics andPlant Breeding* **63**(3): 212–4.

Reddy D M, Ahuja V P and Mukherjee B K. 2003.Identification of favourable alleles in inbred parents for the improvement of single cross hybrids in maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding* **63**(3): 253–4.

Reddy D M, Ahuja V P and Mukherjee B K. 2004. Selection of recycled inbreds through identification of favourable alleles for the improvement of an elite single cross hybrid in maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding* **64**(1): 31–4.

Reddy D M, Ahuja V P and Mukherjee B K. 2005.Comparison of various statistics for identification of maize inbreds with favourable alleles useful for the improvement of single cross hybrid in maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding* **65**(4): 253–6.

Naik V S. 2012. Genetic studies for improvement of single cross hybrids of maize (*Zea mays* L.) through identification of elite inbreds with favourable alleles for yield and yield components. Ph D thesis, Acharya N G Ranga Agriculture University, Hyderabad.

Singh T H, Chahal G S, Bhardwaj H and Tikku P l. 1980. Exploitation of heterosis in cotton -A review. *Journal of Indian Society for Cotton Improvement* **5**(2):46–56.

Todorovic G, Secanski M, Zivanovic T, Protic R, Kostic M, Jovanovic S and Bozovic D. 2012. Inbred lines of different cycles of selectio-donors of favourable alleles for the improvement of the kernel row number of F_1 maize hybrids. *Turkish Journal of Field Crops* **17**(2): 198–202.