Arunachalam, V., Bandyopadhyay, A., Nigam, S.N. and Gibbons, R.W. Some Basic Results of Applied Value in Groundnut Breeding.

Proc. National Seminar on the Application of Genetics to Improvement of Groundnut. Coimbatore, India. July 16-17 (1980): 1-19.

NATIONAL SEMINAR

ON

THE APPLICATION OF GENETICS TO IMPROVEMENT OF GROUNDNUT

JULY 16 – 17, 1980

SCHOOL OF GENETICS

SOME BASIC RESULTS OF APPLIED VALUE IN GROUNDNUT BREEDING

V.Arunachalam, A.Bandyopadhyay, S.N.Nigam and R.W.Gibbons

Breeding strategies for enhancing productivity in groundnut in India have mainly been based on one of the following:

a) Simple re-selection of alien germplasm in native environments

b) Pure lines derived from single crosses

c) Mutation breeding for specific attributes like large seed size, high oil content and others.

The success in breeding for pure line derivatives was, however, not commensurate with the efforts in terms of space, time and labour and also with the rate and magnitude of improvement in yield. One of the inferences could be that the potential of single crosses, which might have been identified in any generation, could not be sustained to the logical end of obtaining a productive homozygous derivative. Yet there are no specific reports bringing to light the reasons for the low success. It may be that groundnut, with possible tetrasomic inheritance, may require non-traditional breeding approaches, based on a right understanding of all the relevant factors which can be physiological, genetical, biochemical or microbiological in nature.

A start was made in 1978 in a national project on basic genetic studies on groundnut to understand the nature of genetic divergence among Spanish, Valencia and Virginia types and to relate it to the heterotic potential of single

crosses. It was felt desirable to identify any possible association of the combining ability components of parents and crosses with realised heterosis. Based on the results it was felt worthwhile to frame possible short-term approaches of broadening the initial genetic base so as to enhance the scope of breeding for pure lines with greater success.

The results of these studies are discussed in this paper.

MATERIALS AND METHODS

160 varieties, consisting of 40 each (20 Exotic and 20 Indian) of Spanish (SP), Valencia (VL), Virginia Bunch (VB) and Virginia Runner (VR) groups from a cross-section of the germplasm maintained at ICRISAT were grown during Summer, 1978 in a randomised blocks design. One Spanish variety failed to germinate. They were evaluated for genetic divergence using Mahalanobis' D^2-statistic on 17 characters spanning the seedling to harvest phase of the plant. They were: Days to first flowering (FT); Seedling Height (SH); Number of leaves (NL); Shoot-root dry weight ratio (SR); Seedling vigour (dry weight of plant) (SV); Number of primary branches (PB); No.of aerial pegs (AP); Number of mature pods (MP); Number of immature pods (IP); Weight of mature pods (WM); Shelling percent (SP): Maturity Index (as % of mature pods to total pods) (MI); Recovery percent (as % of mature pods to total pods and aerial pegs) (RP); 100-kernel weight (TW) and oil percent (OP). Based on seedling characters measured before flowering, namely, SH, NL, R and SV, each of the 20 varieties in sub-groups (like

Spanish exotic, Spanish Indian etc.) were allotted a High or Low status on a total score over the characters.

Assuming M to be the mean of 20 varieties in a sub-group for a character and s, the standard error of mean based on the analysis of variance, 3 classes - I. varietal mean falling /and M+S and III. Varietal mean falling below M-s above M + s, II. varietal mean falling between M - s/were identified and respective scores equal to + 1, 0 and - 1 were given. The same procedure was followed for every character, thus providing a score for each variety and character. The scores were totalled over characters providing a final score to each variety. The mean of final scores, GM was computed. Those varieties getting a final score greater than or equal to GM were allotted a High (H) and the rest a Low (L) status.

A sample of 48 varieties, was chosen from the 160 varieties to contain 12 varieties in each of the SP, VL, VB and VR groups. Each of these 12 varieties consisted, in turn, of 6 exotic and 6 Indian ones, each of which was again made up of 3 High and 3 Low varieties. These varieties were grouped into clusters based on their genetic divergence.

The second experiment was conducted in collaboration with ICRISAT. It consisted of two full diallels with reciprocals - one based on 15 representative parents (15 DL) selected for their productivity, in general and the other on 10 parents (10 DL) representing various land races and degrees of resistance to rust, leaf spot etc. They were evaluated in their F_1 generation at ICRISAT in a randomised blocks design

during Summer, 1979, on 15 characters - FT, SH, Leaf area (LA) NL, Specific leaf weight (SL), PB, No. of secondary branches (SB), Mean number of seeds in pod (MS), Variance of the no.of seeds in pods measured in log scale (VS), MI, RP, SP, TW, PY and SY. The combining ability analysis was done based on Griffing (1956). The parents and crosses were classified as High or Low on the basis of tested general combining ability (gca) and specific combining ability (sca) effects following the method proposed by Arunachalam and Bandyopadhyay (1979). The cross means were tested for significant difference from their respective superior parent means. When the difference was significant at 5% level, heterosis was calculated as

h = (C-P) x 100/P where C = cross mean and P = superior parent mean, taking into account the desirable direction of each character. When the difference (C-P) was not significant, heterosis was taken to be absent. Heterosis was calculated both for direct and reciprocal crosses.

RESULTS

The clustering pattern of the 48 varieties (Table 1) showed no overlapping between bunch and runner varieties. A Virginia Bunch and 2 Valancia varieties formed a single cluster (Cluster XII). Such overlapping could be observed only with Virginia Bunch in 3 out of 16 distinct clusters in the experiment with 160 varieties. No overlapping of Virginia Bunch with Runner varieties was observed in clusters in the experiment with 48 varieties in contrast to 5 overlapping clusters noted in the experiment with 160 varieties.

No distinction between Exotic and Indian entries could be made in terms of genetic divergence as they freely overlapped in many clusters both when 48 or when 160 varieties were considered

On the other hand, 2 clusters included only High and 2 only Low genotypes. Taking into account the 4 single variety clusters (XIII to XVI) also, there was ample evidence to support the meaning and validity of High-Low classification. However, the remaining 4 clusters included both High and Low genotypes (Table 1). This may not be out of place since the High-Low classification was based only on 4 early characters, being a diagnostic study (see also discussion).

Yet the extent of divergence among Spanish and Valencia groups (taken singly or together) was substantial if one considered that as high as 6 (of which 2 contained only Spanish and 1 only Valencia varieties) out of 16 clusters were formed out of them. Parallel results were observed in the divergence among 160 varieties also.

The utility of early characters in inferring the final status of a variety was checked by comparing the status given by the 4 early characters with the final status (Table 2). The tally was quite good in Spanish and Valencia followed by Virginia. An overall tally of 46 and 71% could be obtained for High and Low respectively. It could be speculated from earlier studies on Brassica and Pennisetum that the tally would improve with the inclusion of more early phase characters.

An examination of the status of the parents of the diallels based on an overall score of the gca effects over the 15 characters (Table 3) showed that 3 parents could not obtain a status in 15-DL since the gca effect was non-significant for every character in those cases. When the final status was compared with that defined by early characters (which were again four, viz., SH, NL, LA, SL, an overall tally of 70 and 90% was obtained in the case of 15-DL and 10-DL, respectively. The tally was equally good when right detection of High or Low status was considered (Table 3). The tally here was better as compared to the one obtained in the divergence experiment with 48 varieties.

A good range of heterosis (Table 4) was recorded for various component characters in 15-DL and 10-DL, except for mean number of seeds per pod, flowering time, percentage of nature pods and shelling percent. Heterosis was not frequent in 15-DL as compared to 10-DL. Only a few crosses recorded heterosis in the upper range.

The divergence among the parents of diallels (Table 5) provided a clue to the range and magnitude of F_1 heterosis. Though it was not possible, as expected, to establish a one-to-one correspondence between magnitude of divergence and frequency and magnitude of heterosis, the relatively lower range of divergence in 15-DL could explain the relatively inferior magnitude and frequency of heterosis as compared to 10-DL.

A study of the frequency of heterotic crosses in relation to the combining ability status (Table 6) revealed that crosses between parents of High and Low gca provided the largest frequency of heterotic crosses, both for one or 2 characters. In 15-DL heterosis was found only for 2 characters at the most and that too in only 2 crosses while in 10-DL, heterosis was realised for a maximum of 6 characters (Table 5). It may again be noted that, even in 10-DL, crosses that were heterotic for 4 to 6 components characters simultaneously were only 8 out of the 65 heterotic crosses. It was interesting that as many as 15 heterotic crosses on the whole showed heterosis with non-significant sca for every character.

DISCUSSION

Exhaustive attempts have been made to classify groundnut varieties on the basis of plant habit, branching pattern, kernel size, kernel colour and a number of pod characteristics (Bunting, 1955, 1958; Smartt, 1961; Gibbons, Bunting and Smartt, 1972). Such classifications did not attempt to take into account dependent components related to yield. However, bunch forms differ quite distinctly from runners, which, in turn, is reflected in the yield components as well. This may, perhaps, be one reason why a majority of groundnut breeders prefer, even today, to start with Virginia x Spanish or Virginia x Valencia crosses. The classification attempted in this study was quantitative in which environmental modification of the values of characters could, to an extent, be taken care of, through proper field designs. The logic behind

classifying varieties based on genetic divergence measured by D^2-statistic allows differentiation within groups like Spanish, Valencia or Virginia which is not the objective of the earlier classifications. Hence, the divergence analysis could bring to focus possibilities of starting breeding programmes with Spanish x Valencia, Spanish x Spanish or Valencia x Valencia crosses. The horizon of operational base for breeding pure lines can then get widened. Further, these crosses can lead to compact derivatives with a higher number of productive pegs around basal nodes of primary and secondary branches, permitting also a dense population per unit area, and an advantage of reasonably short maturity. However, these advantages are to be weighed against the frequency of deriving such productive pure lines down the pedigree line when compared to Virginia x Spanish, Virginia x Valencia and Virginia x Virginia crosses. One of the studies published in detail involved a 6-parent diallel consisting 2 parents each of Spanish, Valencia and Virginia (Wynne, Emery and Rice, 1970), in which Valencia x Spanish crosses not only showed heterosis for a number of component characters but the magnitude was parallel to that obtained in Virginia x Valencia or Virginia x Spanish crosses. Unlike the only Spanish x Spanish cross, the only Valencia x Valencia cross showed a good degree of heterosis.

While the heterosis reported in that study was based on the value of the hybrid expressed as a percentage of mid-parental value, studies reported here used a stringent and

practical measure. It is hence likely that many crosses reported to be heterotic by Wynne, Emery and Rice (1970) may turn out to be non-heterotic by the norms of this study. Yet all the crosses in 10-DL between a Spanish bunch variety constituting cluster II showed heterosis for 1 to 3 characters. Of the 11 crosses that showed heterosis for 1 character in 15-DL, a Spanish Bunch variety was involved in producing the maximum of 5 heterotic crosses, of which one was a Spanish x Spanish cross.

The low frequency and magnitude of Heterosis registered by 15-DL could be explained by the high magnitude of error variance, among other causes. This, in turn, would imply the presence of greater degree of genetic heterogeneity within varieties over the replications. This can be expected in groundnut with alleged non-disomic inheritance as "polysomic inheritance exaggerates the inflexibility and discontinuity in variation in connection with autogamy" (Mac Key, 1970). Unless a high frequency and magnitude of heterosis can be obtained with single crosses to allow for possibilities of derivatives becoming inferior or being at par to the check when made genetically homogeneous, multiple crosses may be a better alternative, since the broader genetic base will have more chances of locating transgressive segregants in later generations holding high genetic variability, when compared to starting with a single cross base.

One of the salient results of this study in this connection, is the heterotic potential of High -x Low crosses (Table 6 which has earlier been upheld in some other crops as well Arunachalam, 1980). When varieties or germplasm accessions are the starting point and when complete homozygosity cannot be ensured within lines, a strategy is needed for making High x Low crosses. If a plant is identified as High or Low; on the basis of all observations including post-harvest ones, then it becomes necessary to genetically duplicate it to enable the cross to be made next season. This will not be possible unless the plant is a pure homozygote. Such instances could be possible unless the plant is a pure homozygote. Such instances could not be high in groundnut with possible inheritance other than disomic.

A viable alternative was provided by early characters observed before flowering. The high tally obtained between the early and final status in both the divergence (Table 2) and gca (Table 3) studies would suggest identification of a High or Low plant based on early characters before flowering and using it the same season to make H x L crosses. The same logic would apply if one want to use an identified H x L cross as female and another H x L cross as male parent to produce a 4-way cross. The method could then be used successfully for making any level of multiple crosses, whatever be the genetic nature of the parents, be they homozygotes or heterozygotes.

Reports are available which suggest that it will be necessary to use physiological (and for that matter, microbiological, biochemical and other relevant) components for assessing the potential of a parent or variety (Wynne and Emery 1974; Bhagsari and Brown, 1976). Our studies have included physiological components measurable in the early growth phase which also proved to be potent in predicting final status. However, early generation testing has been found to be of limited use in selecting for yield though it may be useful as a breeding procedure for some pod characters (Wynne, 1976a Breeders would, in general, tend to concur with this view. However, it remains to be seen how useful indirect yield components including physiological ones will be in selecting for yield in F_2 and other segregating generations. Unless a relationship is found between F_1 heterosis and advanced generation performance, it will be difficult to programme any fruitful breeding procedure. The study by Wynne (1976a) could not provide any clue in this regard since genetic relationship was not preserved down the generations while carrying forward the material through bulks (See also Wynne, 1976b).

The need is urgent to collect basic information on all parameters covering the entire growth phase from seeding to harvest which necessarily should include the influence of diseases, insects, root development, photosynthetic mechanisms and energy balance (Young, Cox and Martin, 1976) in order to conceptualise breeding strategies suited to

specific conditions. Simultaneous effort in this direction along with breeding programmes based on genetic divergence and genetic components governing F_1 heterosis would go a long way in synthesising repeatable concepts and achieving commensurate yield advance in groundnut.

SUMMARY

Results of two experiments - one on evaluation of genetic divergence in 160 varieties from Spanish, Valencia, Virginia Bunch and Virginia Runner groups and the other on analysis of combining ability and heterosis of two full diallels were evaluated for their applied value. The classification based on genetic divergence upheld the distinct differences between Spanish and Valencia on the one hand and Virginia on the other. The divergence among Spanish and Valencia varieties was substantial enough to suggest Spanish x Spanish or Valencia x Valencia crosses as possible starting points of breeding programmes. Parents of diallel were classified as High (H) or Low (L) on the basis of their gca over 15 characters spanning the entire growth phase of the plant. H x L crosses were found to contain the highest frequency of heterotic crosses. Several crosses were heterotic with non-significant sca for every character. Early characters were found to perdict the status of a parent or a variety based on all the characters to a good degree of accuracy. This result was used to suggest methods to produce H x L or multiple crosses. Parental divergence could explain to a good extent the frequency and magnitude of realised heterosis. The high range of heterosis was

not commensurate with the low number of crosses responsible for it. Causes for the lack of heterosis and the need to start breeding programmes on broad multiple cross genetic base were underlined in the light of recent published information.

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Table 1. Clustering pattern of 48 varieties of groundnut

Cluster	SP				VL				VB				VR			
	GO		ST		GO		ST		GO		ST		GO		ST	
	E	I	H	L	E	I	H	L	E	I	H	L	E	I	H	L
I	1	-	-	1	-	3	-	3								
II	2	-	-	2	1	-	1	-								
III	2	1	-	3												
IV	1	4	3	2												
V	-	1	1	-	2	1	-	3								
VI					1	2	-	3								
VII									4	-	3	1				
VIII					-	4	4	-								
IX													3	-	1	2
X													1	2	3	-
XI													2	3	3	2
XII	2	-	-	2	1	-	1	-								
XIII					1	-	1	-								
XIV					-	1	1	-								
XV					-	1	1	-								
XVI									-	1	1					

GO = Geographic origin; ST = Status; E = Exotic; I = Indian;
H = High; L = Low.

Table 2. Tally of final status with that defined by early characters in 160 varieties of groundnut

Group	No. of lines	FS		ES		PA		
		H	L	H	L	H	L	T
SP	39	15	24	13	26	47	79	67
VL	40	2	38	13	27	100	71	73
VB	40	35	5	13	27	37	100	45
VR	40	30	10	22	18	53	40	50
Overall	159	82	77	61	98	46	71	58

FS = Final status; ES = Status defined by early characters; PA = Percentage agreement when compared to FS; H = High L = Low; T = Total; SP = Spanish Bunch; VL = Valencia Bunch; VB = Virginia Bunch; VR = Virginia Runner.

Table 3. Potential of Early characters in detecting final gca status in groundnut

	15-DL	10-DL	Overall
Parents getting a final status	13	10	23
Parents getting a status based on E	10	10	20
Right detection of High by E	5/7	4/5	9/12
Right detection of Low by E	4/6	5/5	9/11
Right detection	9/13	9/10	18/23
Wrong detection	1/10	1/10	2/20

E = Early characters-

Table 4. Range of heterosis realised for component characters in groundnut

Character	F		T	
	r	n	r	n
FT	-	-	12-23	2
SH	44	1	25-106	7
LA	-	-	29-70	17
NL	-	-	17-30	10
SL	30	1	31-39	3
PB	58	1	53-118	7
SB	-	-	46-293	13
MS	-	-	-	-
VS	111	1	49-105	5
MP	-	-	29	1
RP	71-151	5	38-138	16
SP	71	1	-	-
TW	89	1	27-113	11
PY	148-163	3	51-320	19
SY	258	1	46-344	16

F = 15 x 15 diallel; T = 10 x 10 diallel; r = range of heterosis.
n = no. of crosses involved.

Table 5. Parental divergence and heterosis in 15 x 15 and 10 x 10 diallel in groundnut

			I	II	III	IV	V	VI
I	F	D	3.3	6.1	5.1	6.3	7.7	7.1
		n	-	-	1^a	-	-	2^a
	T	D	7.7	9.8	14.1	9.3	13.7	11.3
		n	$2^a3^b3^c1^f$	4^a5^b	$2^a1^b1^c1^d$	3^a1^b	$1^b2^c1^d2^e$	5^a1^d
II		D	6.7		6.0	8.3	8.5	7.2
	F	n	-		2^a1^b	-	2^a1^b	1^a
		D	4.9		18.5	12.3	17.1	10.4
	T	n	2^a		1^a2^b	2^a2^b	3^a2^b	3^a2^c
		D			4.2	6.7	6.0	7.0
III	F	n			1^a	-	-	-
		D	-		13.4	14.8	15.6	
	T	n	-		-	1^e	2^a	
		D			-	6.0	8.0	
IV	F	n			-	-	-	
		D			-	12.4	13.7	
	T	n			-	1^a	1^a	
		D			-	8.0		
V	F	n			-	2^a		
		D			-	19.6		
	T	n			-	1^a1^d		

D = Inter-cluster distance; n = no. of heterotic crosses;
a, b, c, d, e, f = heterosis for 1, 2, 3, 4, 5, 6, characters.

Table 6. Heterosis in relation to gca and sca in 15 - and 10 -LL

g	s	fh a	fh b	C	T
HH	H	-	2	-	5	7
	L	1	1	-	2	4
	N	-	-	-	2	2
	T	1	3	-	9	13
HL	H	3	9	1	4	17
	L	-	6	-	-	6
	N	3	6	-	-	9
	T	6	21	1	4	32
LL	H	1	1	-	1	3
	L	1	7	-	3	11
	N	2	-	1	-	3
	T	4	8	1	4	17
Total		11	32	2	17	62

g = gca status of parents; s = sca status; N = Non-significant for every character; T = Total; a = 15-DL; b = 10-DL; fh = frequency of heterotic crosses; C = No. of characters.