GENETIC ANALYSIS OF ROOT LENGTH, ROOT VOLUME AND FRUIT WEIGHT OF PEANUT

Arachis Hypogaea L.

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TABLE OF CONTENTS

Page

PART III

LIST OF TABLES

Table | Page

PART I

Table Page

PART II

PART III

Table Page

Table Page

LIST OF FIGURES

Figure Page

PART III

PART I

DIALLEL ANALYSIS OF ROOT LENGTH, ROOT VOLUME, AND FRUIT WEIGHT OF FOUR PEANUT GENOTYPES AND THEIR F_1 HYBRIDS

ABSTRACT

Peanut (Arachis hypogaea L.) genotypes representing each botanical type (spanish, valencia, and virginia) were crossed in a diallel mating system to produce F_1's. The 12 F_1's and the four parents were evaluated for root length, root volume, and fruit weight in a replicated greenhouse and field test. The data were subjected to a combining ability analysis. General (GCA) and specific (SCA) combining ability effects were estimated. The results showed that both root length and fruit weight were controlled largely by nonadditive genetic effects. For root volume, both additive and nonadditive genetic effects were important. Estimates of general combining ability (GCA) for UF 77318 and PI 405915 were high for root length. Other genotypes with high GCA were Chico and PI 355993 for root volume and UF 77318 for fruit weight. Positive SCA effects were identified for root length. PI 405915 X PI 355993 had a significant positive SCA effect for root volume. UF 77318 X Chico and its reciprocal showed a significant positive SCA effect for fruit weight. Positive associations between root length and root volume, and root volume with fruit weight should result in progenies with longer root lengths, and higher root volumes coupled with increased yields.

INTRODUCTION

Peanut (Arachis hypogaea L.) is one of the leading oil seed crops in the world and is a rich source of edible oil and protein (Sangha and Labana, 1982).

Researchers have investigated the genetic variation of fruit yield and seed characters in peanut (Dwivedi, Thendapani, and Nigam, 1989), but little work has been conducted on root characteristics.

The characteristics of the root system that might be of use in breeding for the ability to avoid physiological drought depend on whether supplies of moisture are likely to be available at greater soil depths. Where moisture reserves exist at depth, ability to produce a deep extensive rooting system which responds positively to declining soil moisture is advantageous. Although efficiency of extraction of water seems to be less at greater depths, the rate of water uptake by roots deep in the soil is reportedly greater than shallow ones (Frey, 1981). Researchers have reported that peanuts have greater root densities at deeper soil depths in dry areas (Pandy et al., 1984.).

Ketring (1984) suggested that peanut genotypes with extensive root systems could prove valuable for developing cultivars with improved drought tolerance. In his and other studies, peanut genotypes differed significantly in root volume and root length (Ketring, et al. 1982).

In practice the most useful root system over a range of environments appears to be one with the ability to produce deep roots (Wilson, 1981) and high root volume (Ketring, 1984). This trait combination with an efficient soil water extraction system in the surface layers, where most nutrients are concentrated, as well as deep in the soil profile for water (Erickson, et al., 1991) can provide a highly effective root system. An important mechanism of drought avoidance exists in peanut roots by their ability to extract water from deep soil profiles and continuously maintain adequate water uptake (Pandey et al., 1984; Erickson et al., 1991). High yielding peanut cultivars with large root volumes and long root lengths are desirable for drought-prone areas. Improved high yielding virginia type cultivars have shown a trend for more extensive root systems (Ketring, et al., 1982).

The objectives of this study were to (i) characterize the nature of gene action controlling root length, root volume, and fruit weight characters, and (ii) determine the potential of individual parents in producing superior lines.

MATERIALS AND METHODS

Parental genotypes used in this study were chosen from each peanut botanical type (spanish, valencia, and virginia). Included were Chico, breeding line UF 77318, and plant introductions PI 355993 and PI 405915. Only four parental lines were used in these studies because: 1) each flower producing a fruit requires a single hand pollination compared to 25 to 30 pollinations per head for crops such as wheat; 2) flowers available for pollination on a daily basis per plant are few; 3) and a maximum of four to five pollinations were attempted per plant for an overall total of 57 to 60 pollinations. 4) These parental lines represent the maximum diversity found in root length and root volume. Morphological traits of the four lines are shown in Table 1. These traits were measured from greenhouse evaluations (Ketring et al. 1982, Ketring, 1984). The four lines, each represented by two plants, were crossed in a complete diallel with reciprocals. The crossing method was similar to that used by Banks, 1976. Pollen parents were grown in a fiberglass greenhouse at 21 to 29 C. The maternal parents were grown in growth chambers with a 12 hour, 21 C night and 12 hour, 29 C day regime. The day and night schedules began at 4:30 p.m. and 4:30 a.m., CST, respectively. This reverse regime results in flower buds which are near optimum for emasculation during the morning hours. Between 8:00 a.m. and 9:30 a.m., plants were removed from the chamber, emasculated, and immediately pollinated with pollen from flowers taken from greenhouse plants.

Root chambers containing PVC tubes measuring 10.2 cm in diameter and 76.2 cm in length were used to evaluate the root systems (Ketring 1984). Fritted clay was sieved in a 14-mesh stainless steel screen and placed in each PVC tube to about 2.54 cm from the top of the tube.

F_1 and parental seeds were placed in 9 cm-diameter glass petri plates containing Whatman No. 5 filter paper and 15 ml of distilled water. Petri plates containing the seeds were placed in an incubator at 30C for 24 hours. The imbibed seeds were gently wrapped in moist germination paper and placed upright (radicle tip down for straight taproot growth) and returned to the incubator for 18 hours. Seedlings of uniform radicle length (1-2 cm) were planted about 2.54 cm deep in each of 192 PVC tubes (12 tubes per parent, 12 tubes per F_1 and 12 tubes per reciprocal F_1 hybrids) containing fritted clay. Two to three extra seedlings of each genotype were planted in order to replace any seedlings that did not emerge during the first week after planing. The seedlings were planted in PVC tubes on May 21, May 22, and May 23, 1985. The plants were transplanted to the field on June 25, June 26, and June 28, 1985. The process of imbibition and planting of seeds was done over three consecutive days in order to stagger harvest dates for root measurements and transplanting to the field.

The third transplanting to the field was delayed one day because of rain.

A drip irrigation system was used to water each PVC tube individually. The plants were watered one or two times per day for two minutes. Watering frequency was adjusted to maintain well watered plants due to either sunny or overcast days. The watering system provided about 500 ml per two minutes and the amount supplied at each watering was checked by use of beakers connected to a drip tube for each root chamber.

Ten days after planting, 100 ml of modified Hoagland's nutrient solution (Ketring 1984) was applied to each plant. Thereafter, 150 ml of Hoagland's solution was applied to each plant, twice weekly. One week prior to root measurements and transplanting, watering was stopped to aid separation of the fritted clay from the roots.

Thirty-five days after planting, root length and root volume were measured. The plants were removed from each PVC tube and the root system washed free of the fitted clay with water. The taproot was measured from the cotyledonary node to the tip with a meter stick. Root volume was measured by water displacement (Ketring, 1984). These measurements of the root system are rapid, nondestructive, and allow recovery of the hybrids (Heinzman, et al., 1977). Each plant was then gently wrapped in moist paper towels and shaded until transplantation in the field. Sixty-four plants were measured and transplanted to the field during each of two consecutive days with the third measurement and transplanting delayed one day because of rain. Seedlings were transplanted to 20.32 cm dia X 45.72 cm deep predrilled holes in the field. Both greenhouse and field experiments were in randomized complete block designs with 16 genotypes and 12 replications (12 F_1's and 4 parents). The plants were grown in the field for pod yields and recovery of F_2 generation seeds. Obvious selfs found in the field were accounted for in the analysis.

Diallel analysis was performed on F_1, reciprocal F_1, and parents using Griffing's Method I, Model I (Griffing, 1956). The appropriate linear model was $X_{ij} = u + g_i + g_j + s_{ij} + r_{ij} + 1/bckl\ (EEejkl)$, where X_{ij} is the observed value of the hybrid resulting from crossing the ith and jth parents, u is the population mean, g_i and g_j are the general combining ability (GCA) effect for the ith (jth) parents, s_{ij} is the specific combining ability (SCA) effect for the cross between the ith and jth parents such that $s_{ij} = s_{ji}$, r_{ij} is the reciprocal effect involving the reciprocal crosses between the ith and jth parents such that $r_{ij} = -r_{ji}$, and eijkl is the environmental effect associated with the ijklth individual observation. The following restrictions are imposed on the combining ability elements: Eigi = 0 and Eisij = 0 (for each j).

RESULTS AND DISCUSSION

Root Length

Analysis of variance for root length showed genotypes and SCA to be highly significant (Table 2).

The means for root length of parents (diagonal) and their F_1's are presented in Table 3. Parental means for root length ranged from 84.16 cm to 94.08 cm. UF 77318 and PI 405915 showed significantly longer root length than PI 355993 and Chico. First generation crosses showed a range of 92.69 cm to 98.32 cm for root length with PI 405915 X PI 355993, UF 77318 X PI 405915, and PI 355993 X UF 77318 showing the longest root lengths.

Largely nonadditive genetic effects are indicated for root length as shown by highly significant SCA effects in Table 2.

The estimates of GCA effects of each parental line and the SCA effects of their crosses are presented in Table 4. Positive values indicate a long root contribution while negative values represent a short root contribution. Progenies from crosses involving UF 77318 or PI 405915 generally had longer root lengths.

Selection for longer root length may not be effective in early generation due to the predominatly nonadditive genetic effects and should be deferred to later generations. However, highly significant mean squares for SCA for root length indicate that some progeny had higher root length than expected on the basis of the GCA of the two parents involved.

Positive SCA effects were high for PI 355993 X UF 77318 and PI 355993 X PI 405915.

Root Volume

Analysis of variance for root volume showed genotypes, GCA, SCA, and reciprocal x GCA to be highly significant, while SCA x reciprocal was significant at the 0.05 level (Table 5).

The means for root volume of parents (diagonal) and their F_1's are presented in Table 6. Parental means for root volume ranged from 10.12 ml to 12.45 ml. Chico had the highest root volume among parents. PI 355993 and PI 405915 had intermediate root volume, while UF 77318 had the lowest root volume. First generation crosses showed a range of 12.71 ml to 23.98 ml for root volume with PI 355993 X Chico, PI 355993 X UF 77318, PI 355993 X PI 405915, UF 77318 X Chico, UF 77318 X PI 355993, and PI 405915 X PI 355993 showing significantly higher root volumes than all other crosses. UF 77318 X Chico had the highest root volume.

Both additive and nonadditive genetic effects were significant for root volume.

The estimates of GCA effects of each parental line and the SCA effects of their crosses are presented in Table 7. Chico and PI 355993 had positive GCA effects. Progenies from crosses involving Chico or PI 355993 were generally higher in root volume.

Highly significant mean squares for SCA for root volume indicate that certain progeny had higher or lower root volume than expected on the basis of the GCA of the two parents involved. The combination PI 405915 X PI 355993 exhibited a significant positive S_{ij} effect. This parental combination also showed long root length.

The largely additive genetic effects for root volume indicate that selection for higher root volume should be effective in early generations.

Fruit Weight

All seedlings survived after transplanting.

Analysis of variance for fruit weight showed genotypes, SCA, reciprocal X GCA, and SCA X reciprocal to be highly significant (Table 8).

The means for fruit weight of parents (diagonal) and their F_1's are presented in Table 9. Parental means for fruit weight ranged from 4.95 gm to 11.62 gm per plant. UF 77318 and PI 405915 had the highest fruit weights, while PI 355993 and Chico had the lowest fruit weights. First generation crosses showed a range of 9.62 gm to 63.00 gm per plant for fruit weight with PI 355993 X UF 77318 and UF 77318 X Chico showing significantly higher fruit weights than all other crosses. UF 77318 X Chico and its reciprocal had high fruit weights. Nonadditive genetic effects are important for fruit weight as shown by highly significant SCA effects in Table 8. Similar results were reported by Dwivedi, et al., 1989.

The estimates of GCA effects of the four parents and the SCA effects of their crosses are shown in Table 10. The estimates of GCA for fruit weight was highest for the Virginia type, UF 77318. Progenies from crosses involving UF 77318 were generally higher in fruit weight. The spanish, virginia, and valencia lines, Chico, PI 405915 and PI 355993, respectively were lowest in GCA for fruit weight.

Significant SCA effects were seen in two crosses. The combinations of UF 77318 X Chico and its reciprocal showed a significant positive S_{ij} effect. These high SCA effects indicate that crosses do deviate from GCA expectations and early generation selection for fruit yield may be impossible (Wynne, et al., 1975). However, highly significant mean squares for SCA indicate that certain progeny had higher fruit weight than expected based on GCA of the two parents involved.

Based on our study, we believe that additive effects of genes are important in determining high root volume in the progeny. Nonadditive effects were found to be more important for root length and fruit weight. The number of significant SCA effects can often be associated to random variation. Thus, the importance of SCA in determining progeny improvement in root length, root volume, and fruit weight, while less important than GCA, should not be dismissed. Use of a recurrent selection scheme with progeny evaluation for high root volume in the F_3 or F_4 should effectively utilize the additive effects of genes among these parents.

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TABLE 1

Phenotypic Descriptions of Peanut Entries used in the Growth Chamber Crossing Trials

Botanical Type	Entry	Shoot Trait	Taproot[1] Length (cm) after 55 days	Root Volume (ml) after 49 days	No. of Laterals at 1M[2]
Spanish	Chico	Small, compact	153.7	20.6[3]	1.2
Valencia	PI 355993	Large, bushy	161.8[4]	32.4	3.0[5]
Virginia A	UF 77318	Runner	186.6	37.2[3]	4.9
Virginia B	PI 405915	Bunch	156.0	19.4	4.0

[1] Taproot length and root volume were measured in separate experiments.

[2] Number of strong downward growing lateral roots at 1 meter after 55 days.

[3] Root volume after 46 days.

[4] Taproot length after 47 days.

[5] Number of strong downward growing lateral roots at 1 meter after 47 days.

TABLE 2

Diallel Analysis of Variance for
Peanut Root Length (cm)

Source	df	Sum of Squares	Mean Square	F	Pr>F
Reps	11	1631.72	148.33	2.50**	0.0065
Genotype	15	2669.26	177.95	3.00**	0.0003
GCA	3	221.24	73.74	1.24	0.2958
SCA	6	2282.95	380.49	6.42**	0.0001
Reciprocal	1	3.63	3.63	0.06	0.8049
R X GCA	2	135.85	67.92	1.15	0.3207
SCA X R	3	40.97	13.65	0.23	0.8751
Error	149	8831.60	59.27		
Total	175	13147.99			

**Significant at the 0.01 probability level.

TABLE 3

Mean Root Length (cm) of Four Peanut Genotypes (diagonal) and their F_1 Crosses Grown for 35 days in PVC Tubes in a Fiberglass Greenhouse

	Parents (Males)			
Parents (Females)	UF 77318	PI 405915	PI 355993	Chico
UF 77318	94.08[1]a	97.58 a	95.66 a	95.00 a
PI 405915	93.08 a	94.00 a	98.32 a	93.91 a
PI 355993	97.15 a	96.58 a	85.08 b	94.08 a
Chico	92.69 a	93.49 a	93.79 a	84.16 b

[1]Means followed by different letters across all rows and columns were significantly different ($p < 0.05$) as determined by Duncan's multiple range test.

TABLE 4

Estimates of GCA Effects (in parenthesis), SCA Effects (above and below diagonal) for Peanut Root Length

Parents	UF 77318	PI 405915	PI 355993	Chico
UF 77318	(1.24)	-1.03	0.03	-2.52
PI 405915	0.65	(1.45)	2.77	-0.97
PI 355993	5.44	6.48	(-0.44)	2.97
Chico	1.45	1.31	1.54	(-2.25)

SE (g_i) = 2.36

SE $(g_i - g_j)$ = 3.85 (i not equal to j)

SE (S_{ij}) = 4.30 (i not equal to j)

SE $(S_{ij} - S_{jk})$ = 6.67 (i not equal to j, k; j not equal to k)

TABLE 5

Diallel Analysis of Variance for
Peanut Root Volume (ml)

Source	df	Sum of Squares	Mean Square	F	Pr>F
Reps	11	325.03	29.54	1.44	0.1593
Genotypes	15	2929.89	195.32	9.54**	0.0001
GCA	3	952.26	317.42	15.51**	0.0001
SCA	6	1209.19	201.53	9.84**	0.0001
Reciprocal (R)	1	49.76	49.76	2.43	0.1211
R X GCA	2	506.87	253.43	12.38**	0.0001
SCA X R	3	210.06	70.02	3.42*	0.0189
Error	149	3050.31	20.47		
Total	175	6303.51			

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.

TABLE 6

Mean Root Volume (ml) of Four Peanut Genotypes (diagonal) and their F_1 Crosses Grown for 35 days in a Fiberglass Greenhouse

Parents (females)	Parents (Males)			
	Chico	PI 355993	PI 405915	UF 77318
Chico	12.45[1]f-h	14.38 e-h	16.06 d-f	14.48 e-h
PI 355993	19.89 b-d	11.13 g-h	22.07 a-b	20.37 a-c
PI 405915	16.35 c-f	19.28 b-d	11.13 g-h	12.71 f-h
UF 77318	23.98 a	17.53 c-d	14.70 e-g	10.12 h

[1]Means followed by different letters across all rows and columns were significantly different ($P<0.05$) as determined by Duncan's multiple range test.

TABLE 7

Estimates of GCA Effects (in parenthesis), SCA Effects (above and below diagonal) for Peanut Root Volume

Parents	Chico	PI 355993	PI 405915	UF 77318
Chico	(0.21)	-0.05	-0.98	2.04
PI 355993	0.77	(0.93)	4.31	2.58
PI 405915	1.31	5.78*	(-0.61)	-1.18
UF 77318	3.51	3.23	-2.01	(-0.53)

*Significant at the 0.10 probability level.

SE (g_i) = 1.39

SE $(g_i - g_j)$ = 2.27

SE (S_{ij}) = 2.53 (i not equal to j)

SE $(S_{ij} - S_{jk})$ = 3.92 (i not equal to j, k; j not equal to k)

TABLE 8

Diallel Analysis of Variance for Peanut Fruit Weight (gm per plant)

Source	df	Sum of Squares	Mean Square	F	Pr>F
Reps	11	11878.39	1079.85	4.32**	0.0001
Genotypes	15	35971.61	2398.10	9.59**	0.0001
GCA	3	1756.56	585.52	2.34	0.0756
SCA	6	26431.72	4405.28	17.63**	0.0001
Reciprocal (R)	1	690.74	690.74	2.76	0.0986
R X GCA	2	4370.61	2185.30	8.74**	0.0003
SCA X R	3	3943.14	1314.38	5.26**	0.0018
Error	145	36241.63	249.94		
Total	171	85312.83			

*, ** Significant at the 0.05 and 0.01 probability levels, respectively.

TABLE 9

Mean Fruit Weight (gm per plant) of Four Peanut Genotypes (diagonal) and their F_1 Crosses

	Parents (Males)			
Parents (Females)	UF 77318	PI 405915	PI 355993	Chico
UF 77318	11.62[1]d-f	26.51 b-d	18.31 c-f	63.00 a
PI 405915	25.30 b-e	10.51 d-f	16.91 c-f	17.91 c-f
PI 355993	38.63 b	15.23 c-f	6.14 f	16.91 c-f
Chico	30.86 b-c	17.30 c-f	9.62 e-f	4.95 f

[1]Means followed by different letters across all rows and columns were significantly different (P<0.05) as determined by Duncan's multiple range test.

TABLE 10

Estimates of GCA Effects (in parenthesis), SCA Effects (above and below diagonal) for Peanut Fruit Weight (gm per plant)

Parents	UF 77318	PI 405915	PI 355993	Chico
UF 77318	(7.62)	0.75	3.32	21.78*
PI 405915	13.00	(-3.08)	3.17	4.70
PI 355993	12.40	0.003	(-4.62)	-2.80
Chico	18.62**	-10.71	-15.05	(0.08)

*, ** Significant at the 0.05 and 0.10 probability levels, respectively.

SE (g_i) = 4.84

SE $(g_i - g_j)$ = 7.9

SE (S_{ij}) = 8.84 (i not equal to j)

SE $(S_{ij} - S_{ik})$ = 13.69 (i not equal to j, k; j not equal to k)

PART II

HERITABILITY OF ROOT LENGTH, ROOT VOLUME AND FRUIT WEIGHT IN TWO PEANUT POPULATIONS

ABSTRACT

Improved drought tolerance and seed yield in peanut (*Arachis hypogaea* L.) may result from selection to increase the root length and/or root volume of the crop. To investigate that possibility, broad-sense heritabilities of root length, root volume and fruit weight were estimated for two F_2 peanut populations. One population was derived from a cross of UF 77318 X Chico (long root length, low root volume and high fruit weight, UF 77318, and short root length, high root volume and low fruit weight, Chico). The second population was derived from the reciprocal of population one. Both populations, their F_1's and parents were grown in a greenhouse. The root length and root volume measurements were determined for individual plants. Then these same plants were transplanted to the field. The fruit weights at harvest were recorded for individual plants. Broad-sense heritability estimates of root length ranged from 0.24 to 0.37. Estimates for root volume ranged from 0.05 to 0.33. Estimates for fruit weight ranged from 0.34 to 0.57. There was a nonsignificant positive correlation for all traits. These results suggest that improving drought tolerance in peanut is feasible through selection based on root length and/or root volume. Selection for high seed

yield may result in the identification of plants with long root length and/or high root volume.

INTRODUCTION

Peanut (*Arachis hypogaea* L.) is one of the world's important food and oil-seed crops. The principle peanut production areas are located in arid and semi-arid regions where drought is a contributing factor in peanut losses (Boote et al., 1982). In even the most productive agricultural regions, periodic or prolonged droughts can occur during the growing season, resulting in injury and reduced plant yield (Barton et al., 1983). Drought not only reduces yield, but also causes poor seed quality and germination, and increases the incidence of aflatoxins (Boote et al., 1982).

Wilson (1981) suggested characteristics of the root system that might be of use in breeding for ability to avoid drought depend on whether supplies of moisture are likely to be available at greater depths. Where deep water reserves exist, the ability to produce a deep extensive rooting system which responds positively to declining soil moisture is advantageous (Wilson, 1981).

New supplies of water become available to the plant either from water supplied by irrigation, precipitation, or by the extension of the plant root system (Mitchell, 1977).

Development of good agronomic lines with vigorous, deep growing, highly branched root systems may allow fuller utilization of the stored water resource and enhance the drought resistance of the crop (Jordan et al., 1983).

Peanuts appear to have a genetic ability for deep rooting (Ketring et al., 1982) and deep water extraction if grown in a barrier-free soil (Boote et al., 1982). Such a trait would postpone desiccation during extended droughts (Boote et al., 1982).

High root volume indicates the ability to explore a larger volume of soil and theoretically have more water-gathering potential for growth and survival (Abd-Ellatif, et al., 1978).

Selections for extensive root systems should extract more soil water from greater soil volumes than selections without extensive root systems. The former should be able to develop and maintain a larger leaf area during drought periods (Ketring, et al., 1982).

The objective of this research was to estimate the broad-sense heritabilities of root length, root volume and fruit weight to determine the heritability of selection in peanut for enhanced drought tolerance and yield.

MATERIALS AND METHODS

These experiments were conducted in the Spring and Summer of 1986. Experiment 1 was conducted in a greenhouse at the USDA-ARS Plant Science Research Laboratory, Stillwater, Ok.. Nine root chambers were used to evaluate the root systems. Each chamber contained 24 PVC tubes measuring 10.2 cm in diameter and 76.2 cm in length. Fritted clay was sieved in a 14-mesh stainless steel screen and placed in each PVC tube to about 2.54 cm from the top of the tube.

In the Spring of 1986, experiment 1 contained the following peanut plants:

33 P_1 (parental) plants,

33 P_2 (parental) plants,

12 F_1 plants (derived from the cross of P_1 X P_2),

12 F_1 plants (derived from the cross of P_2 X P_1),

59 F_2 plants (derived from the cross of P_1 X P_2),

and 61 F_2 plants (derived from the cross of P_2 X P_1).

Experiment 1 contained the parental lines UF 77318 (a virginia breeding line) and Chico (a spanish cultivar). The F_1 and F_2 progeny were derived from a cross of UF 77318 (with long root length, low root volume, and high fruit weight) X Chico (with short root length, high root volume, and low fruit weight) and their reciprocal crosses.

Four to 21 F_1, F_2, and parental seeds were placed in 9 cm diameter glass petri plates containing Whatman No. 5 filter paper and 7 to 30 ml of distilled water, depending on the number of seeds. Petri plates containing the seeds were placed in an incubator at 30 C for 24 hours. Then the imbibed seeds were gently wrapped in moist germination paper and placed upright (radicle tip down for straight taproot growth) and returned to the incubator for 18 hours. Seedlings of uniform radicle length (1-2 cm) were planted about 2.54 cm deep in each of 72 PVC tubes containing fritted clay. Up to four extra seedlings of each genotype were planted in order to replace any tubes where seedlings did not emerge during the first week after planting. The process of imbibition and planting of seeds was done over three consecutive days in order to stagger harvest dates for root measurements and transplanting to the field.

A drip irrigation system was used to water each PVC tube individually. The plants were watered one or two times per day for two minutes. Watering frequency was adjusted to maintain well-watered plants due to either sunny or overcast days. The watering system provided about 500 ml per two minutes and the amount supplied at each watering was checked by the use of beakers connected to a drip tube for each root chamber.

Ten days after planting, 100 ml of modified Hoagland's nutrient solution (Ketring, 1984) was applied to each plant. Thereafter, 150 ml of Hoagland's solution was applied to each plant, once weekly. One week prior to root measurements and transplanting, watering was stopped to aid separation of the fritted clay from the roots.

Thirty-four days after planting, root length, and root volume were measured. The plants were removed from each PVC tube and the root system washed free of the fritted clay with water. The taproot was measured from the cotyledonary node to the tip with a meter stick. Root volume was measured by water displacement (Ketring, 1984). These measurements of the root system are rapid, nondestructive, and allow recovery of the plants (Heinzman, 1977). Each plant was then gently wrapped in moist paper towels, and shaded until transplanted in the field. Seventy-two plants were measured and transplanted to the field during each of three consecutive days corresponding to planting date of the seeds. Seedlings were transplanted to 20.32 cm diameter X 45.72 cm deep predrilled holes in the field.

Experiment 2 was conducted in the summer of 1986 at the Oklahoma State University Agronomy Research Station at Perkins, Oklahoma. The F_1, F_2 and parental plants were transplanted to the field. Both greenhouse and field experiments were complete randomized designs. These plants were harvested 147 to 155 days after planting for pod yields and recovery of F_3 generation seeds. Broad-sense heritability estimates were calculated by the procedure described by Simmonds (1979), which utilizes the parental lines and F_1's of an F_2 population to estimate environmental variance, according to the formula:

$$h^2 = (VF_2-[(VP_1 + VP_2 + VF_1)/3]VF_2 = Vg\backslash Vp$$

where;

h^2 = broad-sense heritability,

VF_2 = variance of the F_2,

VP_1 = variance of parent 1,

VP_2 = variance of parent 2,

VF_1 = variance of the F_1,

Vg = genotypic variance, and

Vp = phenotypic variance.

Broad-sense heritabilities were calculated for root length, root volume, and fruit weight.

RESULTS AND DISCUSSION

Root Length

The analysis of variance for root length is shown in Table 1.

Significant differences were observed between entries for root length (Table 2). The virginia type parent, UF 77318, had significantly longer root lengths than the spanish type parent, Chico. Similar results were reported by Morris et al., (In review). The F_2's with UF 77318 as a female parent tended to have longer root lengths than the F_2's with Chico as a female parent.

A comparison of entry means for root length indicated that both F_2 crosses produced progeny with similar root lengths that resembled UF 77318.

Root Volume

The analysis of variance for root volume is shown in Table 3.

Significant differences were attained between genotypes for root volume (Table 4). The spanish type parent, Chico, had similar root volumes as the virginia type parent, UF 77318. The F_2's with UF 77318 as a female parent had higher root volumes than the F_2's with Chico as a female parent, but not significantly different. The F_2's of UF 77318 X Chico had significantly higher root volumes than either parent. The F_2's of its reciprocal cross (Chico X UF 77318) also had higher root volumes than either parent.

Fruit Weight

The F2 cross of UF 77318 X Chico and its reciprocal both had higher fruit weights than either parent, but not significantly different (Table 5).

The entry means for fruit weight revealed that the F_2 for UF 77318 X Chico produced progeny with the highest fruit weight (Table 6).

The F_2 cross combination of UF 77318 X Chico and its reciprocal had a nonsignificant correlation coefficient of 0.17 and 0.10 respectively between root length and fruit weight. Increases in root length are therefore positively associated with increases in fruit weight. Ketring et al., (1982) indicated that improved root length may contribute to increased peanut yields.

The F_2 cross combination of UF 77318 X Chico and its reciprocal had a nonsignificant correlation coefficient of 0.23 and 0.26, respectively between root volume and fruit weight. These same F_2 cross combinations had a nonsignificant correlation coefficient of 0.01 and 0.22, respectively between root length and root volume. Root volume increases are positively associated with increases in root length and fruit weight.

Heritability

Broad-sense estimates of heritability are reported in Table 7. The F_1 data are shown also because their variances were used in calculating the heritability estimates. Heritability for root length was moderate (0.37) for Chico X UF 77318, while its reciprocal cross revealed a low heritability estimate of 0.24. The smaller heritability estimate for this cross resulted from little total F_2 variance for root length. Although little variability existed among the progeny of UF 77318 X Chico for this trait, the means for root length indicated that the progeny, though not significantly different from UF 77318, tended to be more like the long root length parent (UF 77318). Heritability for root volume was moderate (0.33) for Chico X UF 77318. The reciprocal F_2 Cross (UF 77318 X Chico) showed a low heritability estimate of 0.05. The very small heritability estimate attained for this cross resulted from the small total F_2 variance for root volume. Although small variability existed among the progeny of UF 77318 X Chico for high root volume, the means for this trait indicated that the progeny tended to be significantly higher than either parent. The heritability estimates attained indicate some improvement in root volume should be possible by selection within some of the F_2 crosses tested.

Estimates of heritability for fruit weight was moderate (0.34) for Chico X UF 77318, but its reciprocal had a high heritability estimate of 0.57. Improvement of root length beyond that attained in the F_2's of crosses UF 77318 X Chico would not be expected from selection because the heritability estimate was low (Table 7).

All these traits (except for root volume in the cross UF 77318 X Chico) have intermediate to high heritability values, and progress in a selection program for any one of them (with the one exception) should be possible.

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TABLE 1

Analysis of Variance for Peanut
Root Length (cm)

Source	df	Sum of Squares	Mean Square	F	Pr>F
Genotype	5	4410.27	882.05	6.14**	0.0001
Error	204	29316.80	143.70		
Total	209	33727.07			

** Significant at the 0.01 probability level.

TABLE 2

Mean Root Length (cm) of Two Peanut Genotypes, and their F_1 and F_2 Crosses

Population	Genotype	Root Length (cm)
F_1	UF 77318 X Chico	90.00[1]a
F_1	Chico X UF 77318	87.33 a-b
F_2	UF 77318 X Chico	84.93 a-b
F_2	Chico X UF 77318	81.47 b
P_1	UF 77318	85.36 a-b
P_2	Chico	73.33 c

[1]Means followed by different letters within columns were significantly different ($P<0.05$) as determined by Duncan's multiple range test.

TABLE 3

Analysis of Variance for Peanut
Root Volume (ml)

Source	df	Sum of Squares	Mean Square	F	Pr>F
Genotype	5	828.51	165.70	9.48**	0.0001
Error	204	3565.46	17.47		
Total	209	4393.98			

** Significant at the 0.01 probability level.

TABLE 4

Mean Root Volume (ml) of Two Peanut Genotypes, and their F_1 and F_2 Crosses

Population	Genotype	Root Volume (ml)
F_1	UF 77318 X Chico	22.16[1]a
F_1	Chico X UF 77318	14.33 c
F_2	UF 77318 X Chico	17.03 b
F_2	Chico X UF 77318	16.32 b-c
P_1	UF 77318	13.84 c
P_2	Chico	14.12 c

[1]Means followed by different letters within columns were significantly different ($P<0.05$) as determined by Duncan's multiple range test.

TABLE 5

Analysis of Variance for Peanut Fruit Weight (gms)

Source	df	Sum of Squares	Mean Square	F	Pr>F
Genotype	5	3588.19	717.63	1.43	0.2150
Error	204	102412.75	502.02		
Total	209	106000.94			

TABLE 6

Mean Fruit Weight (gms) of Two Peanut Genotypes, and their F_1 and F_2 Crosses

Population	Genotype	Fruit Weight (gms)
F_1	UF 77318 X Chico	20.97[1]a
F_1	Chico X UF 77318	17.86 a
F_2	UF 77318 X Chico	26.00 a
F_2	Chico X UF 77318	20.02 a
P_1	UF 77318	14.31 a
P_2	Chico	16.80 a

[1]Means followed by different letters within columns were significantly different ($P<0.05$) as determined by Duncan's multiple range test.

TABLE 7

Broad-sense Heritability Estimates for Root Traits, and Fruit Weight in Two Peanut F_2 Populations

	Broad-sense Heritability Estimates		
F_2 Genotype	Root Length	Root Volume	Fruit Weight
UF 77318 X Chico	0.24	0.05	0.57
Chico X UF 77318	0.37	0.33	0.34

PART III

GENETIC ADVANCE FOR FRUIT YIELD OF PEANUT

ABSTRACT

Over 50% of the world's peanut (Arachis hypogaea L.). acreage is grown in the semiarid tropics and is often subject to low rainfall and water deficits. Development of improved peanut germplasm that is productive over a range of soil moisture conditions is a major objective of peanut breeding worldwide. Heritable genetic variation is needed for genetic progress in a breeding program. Genetic variability among breeding lines declines in some crop species as water is reduced. Neither this relationship nor the genetic responses at different irrigation regimes have been studied in peanut. Therefore, different irrigation regimes were used in this study to evaluate their effect on important genetic parameters. Fruit yield was measured on populations of peanut grown in three experiments under field irrigation regimes. The means, genetic variances, broad-sense heritabilities, and genetic advance from selection declined for fruit yield as drought increased in population 1 (UF 77318 X Chico families). The genetic variances in Experiment 3 for population 1 increased at Intermediate Irrigation and declined at Minimum Irrigation. However, the genetic variances, broad-sense heritabilities, and genetic advance from selection in population 2 (Chico X UF 77318 families) increased for fruit yield as drought increased.

Gains due to selection were more rapid if selection was made at full rather than Intermediate Irrigation for population 1 (UF 77318 X Chico). However, genetic gains were better if selections were made at Intermediate rather than Full Irrigation for population 2 (Chico X UF 77318). Thus, selection for heritable drought tolerance traits in peanut requires a range of water regimes to test genetic populations. Population 2 would be better for further evaluations for drought tolerance.

INTRODUCTION

Peanut response to drought is of worldwide importance, because over 50% of the world's peanut acreage is grown in the semiarid tropics and is often subject to low rainfall and water deficits. India produces almost one-third of the world's peanuts usually under water deficit conditions. Sudan, Senegal, and Nigeria each have equal peanut acreage equal to the U.S.A., but production is much lower because of drought (Boote and Ketring, 1990).

High yielding peanut cultivars with large root systems (Ketring et al., 1982) and early maturity are desirable for use in the drought prone production areas of the world. The spanish genotype, Chico represents a source of early maturity, but it has small root traits (Ketring 1984 and Ketring et al., 1982) and is lower yielding than the virginia type. It would be advantageous to develop high root volume and/or long rooting, and high yield (Morris et al.), in early maturing peanut cultivars by crossing virginia and spanish types (Chiow and Wynne, 1983).

Although little research has been conducted with peanuts to alter genetic responses to drought, progress has been reported for other crops. Genetic variances and heritability estimates for yield in crop species have been reported for wheatgrass [_Agropyron_ _desertorum_ (Fisch. ex

Link) Schult] (Asay et al., 1990; Rumbaugh et al., 1984) and peanut (Chiow and Wynne, 1983). Rumbaugh et al., (1984) showed that means, genetic variances, broad-sense heritabilities, and predicted genetic gains from selection, declined for wheatgrass seedling establishment characters as drought increases. Asay et al., 1990 reported sufficient genetic stability for forage dry matter yield in crested wheatgrass at water levels above the target level. Chiow and Wynne, (1983) found high heritability estimates for yield.

The line-source sprinkler system (Hanks et al., 1976) is very useful to apply various levels of irrigation to experiments. Hanks et al. suggested that this method may be useful in breeding programs for evaluating genetic responses to water stress.

Hanks et al., 1980 suggested there were limitations of statistical analysis and data interpretation from experiments utilizing the line-source sprinkler system. However, they pointed out that irrigation levels are not imposed in random fashion for each plot. In our tests genotypes were randomized within each water level. Our objectives were to evaluate the effect of irrigation regimes on genetic variances, heritability approximations, and genetic gains for peanut.

MATERIALS AND METHODS

Three experiments were conducted to investigate breeding for resistance to drought stress of peanut by utilizing different irrigation regimes. These experiments were conducted in field nurseries. Experiment 1 included F_3 families of a peanut hybrid UF 77318 X Chico and the reciprocal hybrids. Experiment 2 included F_4 families from the peanut hybrids in experiment one. Experiment 3 used F_6 lines of the peanut hybrid UF 77318 X Chico.

Experiment 1

The families tested were in the F_3 generation from the cross between UF 77318 X Chico (population 1), and its reciprocal cross (population 2). The virginia entry, UF 77318, a breeding line from the University of Florida, is late maturing, high yielding, and produces large seeds. The spanish entry, Chico, is small seeded and early maturing.

Eight families from the cross of UF 77318 X Chico (population 1) and 8 families from its reciprocal cross (population 2) in the F_3 generation, were traced to a separate selected F_2 plant. In 1987, the 16 families and the two parents were evaluated at two sprinkler irrigation regimes at the Oklahoma State University Agronomy Research Station, Perkins, Oklahoma. Plants were grown on a Teller sandy loam soil (fine, mixed, thermic, Udic Argiutolls).

The plots were arranged in a modified split plot design with the two water levels as whole plots and the 16 families plus parents as subplots. Families and parents were randomized within each water level. The design was replicated three times. Each plot consisted of one 0.91, 1.52, or 1.83 m long row depending on the number of F_3 seed available for planting. The spacing between rows was 0.91 m and within row spacing was approximately 0.10 m. Irrigation water was applied by a line-source sprinkler system (Hanks et al., 1976). The line of sprinklers was adjacent to the edge of the plots and parallel to the row direction. The system had eight sprinklers spaced at 6.1 m intervals, which gave an overall useable plot of 12.2 by 15.3 m. The sprinklers were operated at approximately 3 bars pressure (45 psi) and produced a wetted radius of approximately 15 m. Using row distance from the line source, two irrigation levels were selected for this study. The wettest level (closest to the line source), which received the maximum amount of water, was designated 'Full Irrigation' and the next lower level was designated 'Intermediate Irrigation'. Irrigation amounts and rainfall were monitored by rain gauges in the plots. Mean amounts of irrigation water plus rainfall received by Full Irrigation and Intermediate Irrigation were 29.1, and 25.2 mm., respectively, on aweekly basis. The plots consisting of early maturing spanish segregates and the plots of the late maturing virginia F_3 segregates were harvested at 131 and 142 days, respectively. Fruit yields were recorded in grams per plot and converted to kilograms per hectare.

Data were subjected to analysis of variance. The following variance components were calculated:

σ^2_G = a genetic component arising from genetic differences among families.

σ^2_{GI} = a component arising from interactions of families and irrigation regimes.

σ^2_E = error variance.

The total phenotypic variance (σ^2_{PH}) for progeny means was calculated as:

$\sigma^2_{PH} = \sigma^2_G + \sigma^2_{GI}/I + \sigma^2_E/RI$

where R, and I are the numbers of replications, and irrigation regimes, respectively. In the computation of the variance components, irrigation regimes were considered random effects. Families were considered fixed effects because they were derived from selected plants.

Broad-sense heritabilities were estimated according to the formulae as (Chiow and Wynne, 1983):

$h^2 = \sigma^2_G / \sigma^2_{PH}$

The genetic gain in fruit weight was calculated for the F_3 families evaluated in the field by Allard's (1960) formula using a 1% selection intensity:

$Gs = (k)\ (\sigma_A)\ (h^2)$

where:

Gs = expected genetic advance under selection.

k = selection differential.

σ_A = phenotypic standard deviation of the mean yields.

h^2 = heritability coefficient.

Experiment 2

The procedures used were the same as those described for Experiment 1.

Fourteen families from the cross of UF 77318 X Chico (population 1) and ten families from its reciprocal cross (population 2) in the F_4 generation, traced to a separate selected F_2 plant. In 1988, the 24 families and the two parents were evaluated at two irrigation regimes (Full Irrigation and Intermediate Irrigation) as described above for Experiment 1. Mean amounts of irrigation water plus rainfall received by Full Irrigation and Intermediate Irrigation were 28.2 and 26.4 mm, respectively on a weekly basis. Each plot consisted of one row at 0.91-m in length. Spacing between and within rows was the same as in Experiment 1. Plots of the early maturing spanish and late maturing virginia segregates were harvested at 111 and 135 days, respectively. The fruit yield data were converted to kg/ha, and analyzed in the same way as the data from Experiment 1.

Experiment 3

Two family lines from the cross of UF 77318 X Chico in the F_6 generation, each tracing to a separate selected F_2 plant, were evaluated in this experiment. In 1990, these 2 families, Spanco (a spanish cultivar), and Okrun (a virginia cultivar) were evaluated. These genotypes were planted in four row plots at 6.1 m in length. Spacing between and within rows was the same as in Experiments 1 and 2. In addition to Full and Intermediate Irrigation regimes, a third water amount, designated Minimum Irrigation, was used in this experiment. Mean amounts of irrigation plus rainfall received by Full Irrigation, Intermediate Irrigation, and Minimum Irrigation were 24.3, 21.8, and 15.1 mm, respectively, on a weekly basis. Two rows from each plot were harvested 119 and 133 days after planting for Test 1. Two rows from each plot were harvested 126 and 140 days after planting for Test 2. The fruit yield data were processed, and analyzed in the same way as the data from Experiment 1.

RESULTS AND DISCUSSION

Experiment 1

Peanut fruit yield closely reflected the amount of water received by the plots for population 1 (UF 77318 X Chico families), but not for population 2 (Chico X UF77318 families) (Figure 1). Mean fruit yield ranged from 1834 to 1691 kg/ha for population 1 (UF 77318 X Chico) and from 1864 to 1991 kg/ha for population 2 (Chico X UF 77318). Highly significant ($P < 0.01$) differences were found among the 16 peanut F_3 families and parents at both irrigation regimes (Table 1). The sum of squares due to linear regression of fruit yield on irrigation regimes was significant ($P < 0.01$). The decline in fruit yield in population 1, and the increase in population 2 was linear as indicated by the significant ($P < 0.01$) linear interaction effect (Table 1).

Extremely good opportunities are present in these peanut breeding populations to make substantial genetic progress in fruit yield. Significant differences were obtained between the two parents and between the parents and the hybrid progeny for fruit yield at Full Irrigation (Table 2) and at intermediate irrigation (Table 3). The progenies differed significantly for fruit yield indicating that substantial amounts of variability existed for this trait. Similar results were observed by Chiow and Wynne, 1983.

Parameters associated with genetic advance (genetic variance among the F_3 families from population 1 and broad-sense heritability values) declined as water application decreased (Table 4). The ranges in fruit yield for population 1 (UF 77318 X Chico families) were 2430 and 1760 kg/ha at Full Irrigation and Intermediate Irrigation, respectively. A similar trend in genetic variances was also observed with a decline from a maximum of 592,163 at Full Irrigation to 467,037 at Intermediate Irrigation. Broad-sense heritability values declined from 0.31 at Full Irrigation to 0.26 at Intermediate Irrigation.

The experimental error, as reflected by the coefficients of variation (CV) values were slightly higher under drier conditions than at the Full Irrigation regime (Table 4). The CV values were approximately 9 to 10% for Full and Intermediate Irrigation.

Expected genetic advance among the F_3 families from population 2 (Chico X UF 77318) increased as water application decreased (Table 5). The ranges in fruit yield for population 2 were 1114 and 1972 kg/ha at Full Irrigation and Intermediate Irrigation, respectively. Genetic variances increased substantially from 356,494 at Full Irrigation to 1,052,639 at Intermediate Irrigation. Broad-sense heritability values increased from 0.27 at Full Irrigation to 0.43 at Intermediate Irrigation.

The CV values were constant at both irrigation regimes (Table 5).

Genetic gains from selection (1% selection intensity) for fruit yield are given in Table 6. The genetic gains for population 1 were 1127 and 914 kg/ha at Full Irrigation and Intermediate Irrigation, respectively. The genetic gains observed indicated that single plant selection under Full Irrigation was superior to single plant selection at Intermediate Irrigation for population 1. These results support earlier findings with other crop species (Asay et al., 1990; Frey 1964; and Rumbaugh et al., 1984) that selection can be effective at irrigation regimes above the target level.

Genetic gains from a 1% selection intensity for population 2 were 939 and 1770 kg/ha at Full Irrigation and Intermediate Irrigation, respectively (Table 6). Thegenetic gains observed indicated that single plant selection under Intermediate Irrigation was superior to single plant selection at Full Irrigation for population 2. These results indicated the Intermediate Irrigation regime differentiated the adaptive reaction of peanuts better than the Full Irrigation regime for population 2.

Experiment 2

Peanut fruit yield reflected the amount of water received by the plots for population 1 and 2 (Figure 2). Mean fruit yield ranged from 869 to 616 kg/ha for population 1 and from 1207 to 809 kg/ha for population 2. Highly significant ($P < 0.01$) differences were found among the 24 peanut F_4 families and parents at both irrigation regimes (Table 7). The sum of squares due to linear regression of fruit yield on irrigation regimes was significant ($P < 0.01$). The decline in fruit yield was linear as indicated by the significant ($P < 0.01$) linear interaction effect (Table 7).

Excellent opportunities exist in these populations to make substantial genetic progress in fruit yield. Significant differences were found between the parents and between the parents and the hybrid progeny for fruit yield at Full Irrigation (Table 8) and at Intermediate Irrigation (Table 9). The progenies differed significantly for fruit yield indicating a large amount of variation existing for this trait.

Genetic variance among the F_4 families from population 1 and broad-sense heritability values declined as water levels decreased (Table 10). The ranges in fruit yield for population 1 were 2228 and 1724 kg/ha at Full Irrigation and Intermediate Irrigation, respectively. Genetic variances declined from 1,143,483 at Full Irrigation to 883,932 at Intermediate Irrigation. Broad-sense heritability values also declined slightly from 0.53 at Full Irrigation to 0.47 at Intermediate Irrigation.

The CV values were higher under drier conditions than at the Full Irrigation regime (Table 10). The CV values were 33% at Full Irrigation, increasing to 47% at Intermediate Irrigation.

Genetic variance among the F_4 families from population 2 increased as water application decreased (Table 11). The ranges in fruit yield for population 2 were 2284 and 1196 kg/ha at Full and Intermediate Irrigation, respectively. Genetic variances increased substantially from 395,385 at Full Irrigation to 701,488 at Intermediate Irrigation. Broad-sense heritability values increased from 0.25 at Full Irrigation to 0.38 at Intermediate Irrigation.

The CV values increased from 18% at Full Irrigation to 27% at Intermediate Irrigation (Table 11).

Genetic gains from a 1% selection intensity for fruit yield are given in Table 12. The genetic gains for population 1 (UF 77318 X Chico families) were 2055 and 1710 kg/ha at Full and Intermediate Irrigation, respectively.

These genetic gains in fruit yield indicate that single plant selection under Full Irrigation was superior to single plant selection at Intermediate Irrigation. These results are similar to Experiment 1.

Genetic gains from a 1% selection intensity for population 2 were 824 and 1370 kg/ha at Full and Intermediate Irrigation, respectively (Table 12). These genetic gains indicate that single plant selection at Intermediate Irrigation was superior to single plant selection at Full Irrigation for population 2 (Chico X UF 77318 families) (Table 12). These results for population 2 are similar to Experiment 1. Genetic progress in peanut was more effective at Full Irrigation for population 1. Asay et al., 1990 observed higher heritable genetic variation at more optimum moisture levels.

Experiment 3

Peanut fruit yield in 1990 for harvest Test 1 [119 and 133 days after planting, (DAP)] (Figure 3) and Test 2 (126 and 140 DAP) (Figure 4), closely reflected the amount of water received by the plots. Mean fruit yield ranged from 2495 to 1601 kg/ha in Test 1. Test 2 revealed mean fruit yields ranging from 2380 to 1451 kg/ha. Highly significant ($P < 0.01$) differences were found among the three irrigation regimes and among the 2 peanut F_6 families and cultivars at all irrigation regimes in Test 1 (Table 13) and Test 2 (Table 14). The sum of squares due to linear regression of fruit yield on irrigation regimes was significant ($P < 0.01$)

for Test 1 (Table 13). The decline in fruit yield was linear as indicated by the significant ($P < 0.01$) linear interaction effect, although the quadratic interaction effects also were significant ($P < 0.01$) in Test 1 (Table 13). There also was a significant quadratic effect in Test 2 (Table 14). This was apparently due to the sharper decline in fruit yield from Intermediate Irrigation to Minimum Irrigation than from Full Irrigation to Intermediate Irrigation (Figure 3).

Genetic progress for fruit yield exists in this population. Significant differences were found between the cultivars and between the cultivars and the hybrid progeny for fruit yield at: Full Irrigation in Test 1 (Table 15), and Test 2 (Table 16); Intermediate Irrigation in Test 1 (Table 17) and Test 2 (Table 18); and Minimum Irrigation in Test 1 (Table 19) and Test 2 (Table 20). Significant variation for fruit yield exists in these hybrid progenies.

Genetic variance among the F6 lines increased as water amounts decreased from Full to Intermediate Irrigation in both Tests 1 and 2 (Tables 21 and 22). But remained the same or decreased from Intermediate Irrigation to Minimum Irrigation in Test 1 amd 2, respectively (Tables 21 and 22). The range between minimum and maximum fruit yield were 354, 27, and 271 kg/ha at Full, Intermediate, and Minimum Irrigation, respectively for Test 1. The range between minimum and maximum fruit yield for Test 2 were 68, 285, and 298 kg/ha at Full, Intermediate, and Minimum Irrigation, respectively. Genetic variances increased from 79,609 at

Full Irrigation to 89,915 at Intermediate Irrigation in Test 1. Also, genetic variances increased from 53,406 at Full Irrigation to 93,572 at Intermediate Irrigation in Test 2. The genetic variance for minimum irrigation remained similar in Test 1 and declined in Test 2. Broad-sense heritability values remained constant at 0.04 for all three irrigation regimes in Test 1. The heritability values increased from 0.03 at Full Irrigation to 0.05 at Intermediate Irrigation and then declined to 0.04 at Minimum Irrigation in Test 2. This indicates that optimum selection is best at intermediate irrigation in both Tests 1 and 2. However, selection could be effective under any of the three irrigation regimes in Test 1. Selection at intermediate irrigation is most effective in Test 2. These differences in variances could be due to differences in harvest dates.

The CV values for fruit yield were slightly larger under drought stress (Minimum Irrigation) than at higher irrigation amounts in both Test 1 (Table 21) and Test 2 (Table 22). The CV values ranged from 6 to 9% (Table 21) and 4 to 7% (Table 22). The experimental error was slightly higher at the driest condition than at the wettest condition.

The genetic gains from a 30% selection intensity for fruit yield were constant at 69 kg/ha across all irrigation regimes in Test 1. However, genetic gains in Test 2 increased from 48 kg/ha at Full Irrigation to 80 kg/ha at Intermediate Irrigation and then declined to 64 kg/ha at Minimum Irrigation. These results indicate that selections under any of the three irrigation regimes are of equal value in Test 1. Selections under Intermediate Irrigation are superior to selections under both Full and Minimum Irrigation, and selections under Minimum Irrigation are superior to selections under Full Irrigation in Test 2. These results suggest heritable genetic variation conducive to genetic progress at lower irrigation regimes. However, low heritability values in both Tests 1 and 2 indicate equal peanut adaptation to nonstress and stress environments. Heritabilities for fruit yield in the F_3 and F_4 were close to the predicted value in the F_2 (Morris et al.,).

Two breeding strategies are used by breeders working to develop cultivars that yield well in a water deficit environment (Quisenberry, 1982). These strategies are to develop cultivars that are highly adapted only to a water stress environment or to breed cultivars with adaptation to a wide range of environmental conditions. Frey (1964) suggested the latter strategy would be most effective.

The means, genetic variances, broad-sense heritabilities, and genetic advance from selection declined for fruit yield as drought increased in population 1. However, the genetic variances in Experiment 3 increased at Intermediate Irrigation, and declined at Minimum irrigation in both Test 1, and Test 2. The genetic variances, broad-sense heritabilities, and genetic advance from selection increased for fruit yield as drought increased in population 2. Only the means in Experiment 1 increased as drought increased. In general, these results indicate quicker genetic progress would occur if selections were made under intermediate drought conditions than under nondrought stress.

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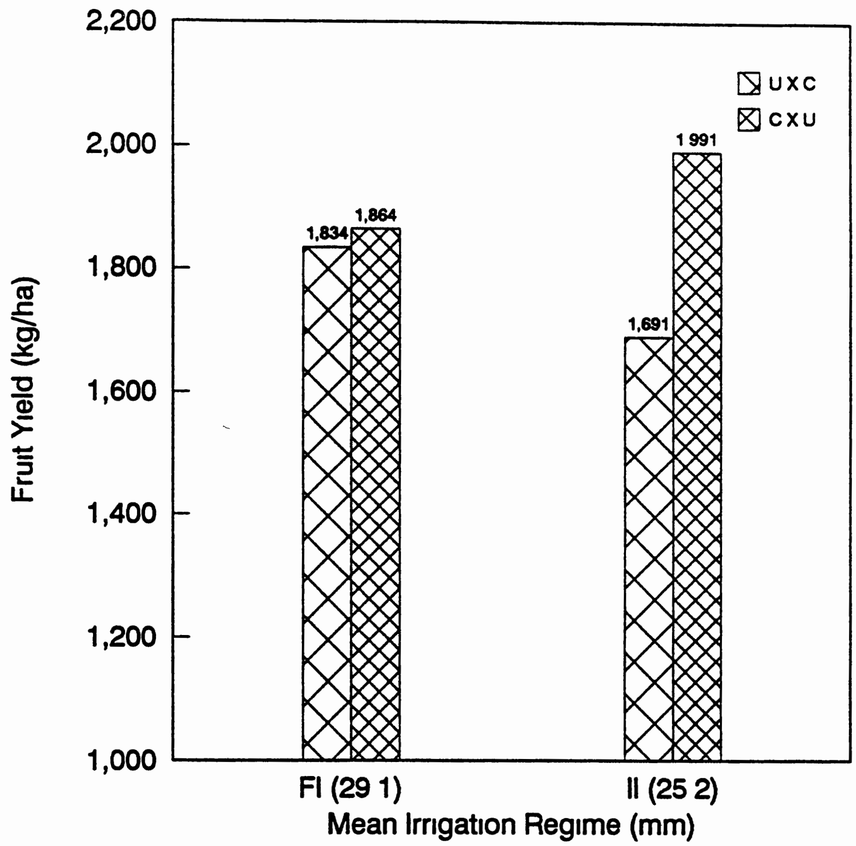

Fig. 1 Mean 1987 yield of 8 peanut F_3 families from the cross of UF 77318 X Chico (population 1) and 8 F_3 families from its reciprocal cross (population 2) at two irrigation regimes. Mean amounts of irrigation water plus precipitation were 29 1 and 25.2 mm for full irrigation (FI) and intermediate irrigation (II), respectively.

TABLE 1

Analysis of Variance for 1987 Fruit Yield of 16 Peanut F_3 Families and 2 Parents at Two Irrigation Regimes

Source	df	Sum of Squares	Mean Squares	F
Among whole units	5	1,785,378.1	357,075.6	0.84
Reps	2	850,113.3	425,056.7	1.00
Irrigation	1	84,991.6	84,991.6	0.20
Linear	1	84,991.5	84,991.5	0.20
Error a (R X I)	2	850,273.2	425,136.6	
Within whole units	102	70,254,709.6	688,771.7	1.60
Genotypes	17	32,475,173.8	1,910,304.3	4.40**
I X G	17	7,992,352.1	470,138.4	1.10
IL X G	1	7,992,352.2	7,992,352.2	18.20**
Error b (Residual)	68	29,787,183.7	438,046.8	
Total	108	72,040,087.7	667,037.8	

**Significant at the 0.01 probability level.

TABLE 2

Differences Between 1987 Mean Yield (kg/ha) in 16 Peanut F_3 Families and 2 Parents at Full Irrigation

	U[a] 3277	UC D[b] 3038	UCF 2517	CU D[c] 2506	UCG 2485	CUA[d] 2071	CUE 2007	UCC 1953	CUB 1953	CUC 1845	CUF 1682	C[e] 1606	UCA 1519	UCB 1519	CUA 1456	CUB 1392	UCA 1031
UCE 608	2669[f] **	2430 **	1910 **	1899 **	1877 **	1463 **	1400 **	1345 **	1345 **	1237 **	1074 **	998 *	911 *	911 *	848 *	785 *	423
UCA 1031	2246 **	2007 **	1487 **	1476 **	1454 **	1040 **	977 *	922 *	922 *	814 *	651	575	488	488	425	362	
CUB 1392	1884 **	1646 **	1125 **	1114 **	1092 **	678	615	561	561	452	289	213	127	127	63		
CUA 1456	1821 **	1582 **	1062 **	1051 **	1029 **	615	552	497	497	389	226	150	63	63			
UCB 1519	1758 **	1519 **	998 *	987 *	966 *	552	488	434	434	326	163	87	0 1				
UCA 1519	1758 **	1519 **	998 *	987 *	966 *	552	488	434	434	326	163	87					
C 1606	1671 **	1432 **	911 *	901 *	879 *	465	401	347	347	239	76						

TABLE 2 CONTINUED

		U [a]	UC D [b]	UCF	CU D [c]	UCG	CUA [d]	CUE	UCC	CUB	CUC	CUF	C [e]	UCA	UCB	CUA	CUB	UCA
		3277	3038	2517	2506	2485	2071	2007	1953	1953	1845	1682	1606	1519	1519	1456	1392	1031
CUF	1682	1595[f] **	1356 **	836 *	825 *	803 *	389	326	271	271	163							
CUC	1845	1432 **	1194 **	673	662	640	226	163	109	109								
CUB	1953	1324 **	1085 **	564	553	532	118	54	0									
UCC	1953	1324 **	1085 **	564	553	532	118	54										
CUE	2007	1269 **	1031 **	510	499	477	63											
CUA	2071	1206 **	968 *	447	436	414												
UCG	2485	792 *	553	33	22													

TABLE 2 CONTINUED

	U[a]	UCD[b]	UCF	CUD[c]	UCG	CUA[d]	CUE	UCC	CUB	CUC	CUF	C[e]	UCA	UCB	CUA	CUB	UCA
	3277	3038	2517	2506	2485	2071	2007	1953	1953	1845	1682	1606	1519	1519	1456	1392	1031
CUD 2506	770[f]	532	11														
UCF 2517	759*	521															
UCD 3038	239																

[a] UF 77318

[b] UF 77318 X Chico

[c] Chico X UF 77318

[d] A - G = Family representative

[e] Chico

[f] Average of three replications The LSD values for comparing two genotypes under full irrigation is 764 2 kg/ha and 1016 4 kg/ha at the 0 05 and 0 01 probability levels, respectively *,** Significant at the 0 05 and 0 01 probability levels, respectively

TABLE 3

Differences Between 1987 Mean Yield (kg/ha) in 16
Peanut F_3 Families and 2 Parents
at Intermediate Irrigation

		CUF	UCG	U [a]	CUA	UC D [b]	CU D [c]	CUA [d]	CUB	CUE	UCC	UCF	UCA	C [e]	UCB	UCA	CUB	CUC
		3220	2606	2485	2405	2293	2246	1926	1826	1799	1703	1660	1573	1508	1474	1374	1260	1248
UCE	846	[f] 2374**	1759**	1638**	1559**	1447**	1400**	1080**	980*	953*	857*	814*	727	662	628	528	414	401
CUC	1248	1973**	1358**	1237**	1559**	1045**	998*	678	579	552	456	412	326	260	226	127	12	
CUB	1260	1961**	1346**	1225**	1145**	1033**	986*	666	567	540	444	400	313	248	214	115		
UCA	1374	1846**	1231**	1110**	1031**	919*	872*	552	452	425	329	286	199	134	100			
UCB	1474	1747**	1132**	1011*	931*	819*	772*	452	353	326	230	186	99	34				
C	1508	1712**	1098**	977*	897*	785*	738	418	318	291	195	152	65					
UCA	1573	1647**	1032**	911*	832*	720	673	353	253	226	130	87						

TABLE 3 CONTINUED

	CUF 3220	UCG 2606	U[a] 2485	CUA 2405	UC D[b] 2293	CU D[c] 2246	CUA[d] 1926	CUB 1826	CUE 1799	UCC 1703	UCF 1660	UCA 1573	C[e] 1508	UCB 1474	UCA 1374	CUB 1260	CUC 1248
UCF 1660	1560[f] **	946 *	825 *	745	633	586	266	166	139	43							
UCC 1703	1517 **	902 *	781 *	702	590	543	222	123	96								
CUE 1799	1421 **	806 *	685	606	494	447	127	27									
CUB 1826	1394 **	779 *	658	579	467	420	99										
CUA 1926	1295 **	680	559	479	367	320											
CUD 2246	975 *	360	239	159	47												
UCD 2293	928 *	313	192	112													

TABLE 3 CONTINUED

	CUF 3220	UCG 2606	U[a] 2485	CUA 2405	UC D[b] 2293	CU D[c] 2246	CUA[d] 1926	CUB 1826	CUE 1799	UCC 1703	UCF 1660	UCA 1573	C[e] 1508	UCB 1474	UCA 1374	CUB 1260	CUC 1248
CUA 2405	815[f]	201	80														
U 2485	736*	121															
UCG 2606	615																

[a] UF 77318

[b] UF 77318 X Chico

[c] Chico X UF 77318

[d] A-B = Family representative

[e] Chico

[f] Average of three replications The LSC values for comparing two genotypes under intermediate irrigation is 764 2 kg/ha and 1016 4 kg/ha at the 0 05 and 0 01 probability levels, respectively *,** Significant at the 0 05 and 0 01 probability levels, respectively

TABLE 4

Summary of 1987 Fruit Yield Data from 8 UF 77318 X Chico F_3 Families (Population One) at Two Irrigation Regimes

Statistic	Irrigation Regime: Full Irrigation	Irrigation Regime: Intermediate Irrigation
	kg/ha	kg/ha
Mean	1834.00	1691.00
Range		
Min	608.00	846.00
Max	3038.00	2606.00
Genetic Variance[a]	592,163.00	467,037.00
Heritability[b]	0.31	0.26
CV, %	9.00	10.00

[a]Genetic variance = component arising from genetic differences among families.

[b]Heritability = computed in the broad sense.

TABLE 5

Summary of 1987 Fruit Yield Data from 8 Chico X UF 77318 F_3 Families (Population Two) at Two Irrigation Regimes

Statistic	Irrigation Regime: Full Irrigation	Irrigation Regime: Intermediate Irrigation
	kg/ha	
Mean	1864.00	1991.00
Range		
Min	1392.00	1248.00
Max	2506.00	3220.00
Genetic Variance[a]	356,494.00	1,052,639.00
Heritability[b]	0.27	0.43
CV, %	9.00	9.00

[a]Genetic variance = component arising from genetic differences among families.

[b]Heritability = computed in the broad sense.

TABLE 6

Genetic Gain in 1987 Fruit Yield with a 1% Selection Intensity Among 2 F_3 Peanut Populations Grown Under Two Irrigation Regimes

	Irrigation Regime	
Population	Full Irrigation	Intermediate Irrigation
	kg/ha	
UF 77318 X Chico	1127	914
Chico X UF 77318	939	1770

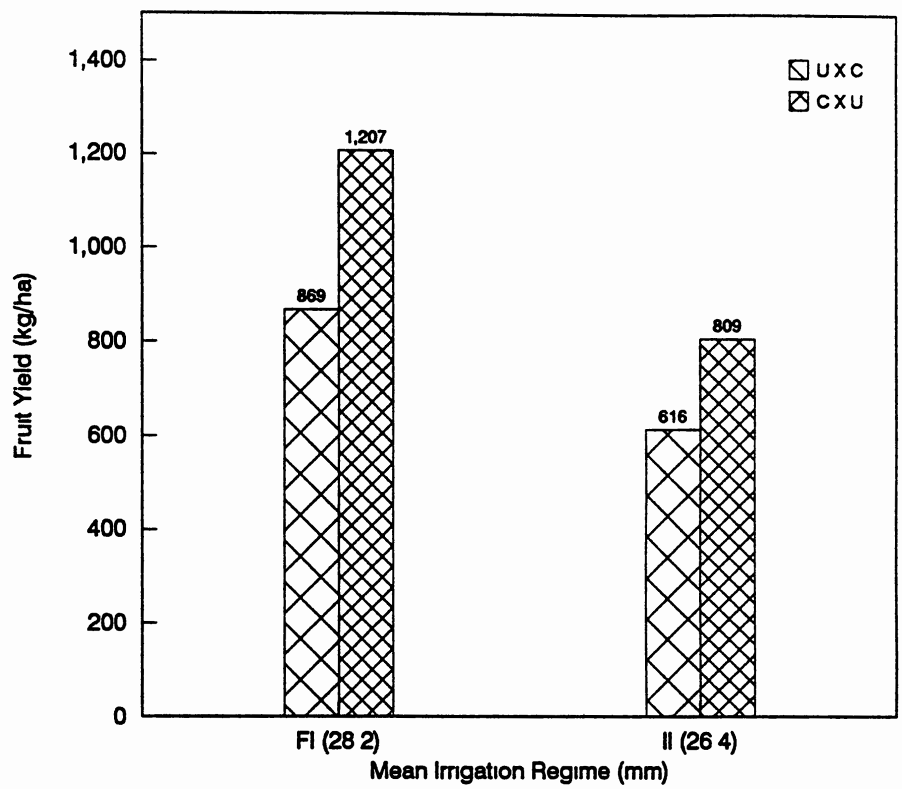

Fig. 2 Mean 1988 yield of 24 peanut F_3 families from the cross of UF 77318 X Chico (population 1) and 10 F_3 families from its reciprocal cross (population 2) at two irrigation regimes Mean amounts of irrigation water plus precipitation were 28 2 and 26 4 mm for full irrigation (FI) and intermediate irrigation (II), respectively

TABLE 7

Analysis of Variance for 1988 Fruit Yield of 24 F_4 Peanut Families and 2 Parents at Two Irrigation Regimes

Source	df	Sum of Squares	Mean Squares	F
Among whole units	9	28,745,526.6	3,193,947.4	2.7
Reps	4	17,827,846.6	4,456,961.7	3.8
Irrigation	1	6,182,494.8	6,182,494.8	5.2
Linear	1	6,182,495.0	6,182,495.0	5.2
Error a (R X I)	4	4,735,185.2	1,183,796.3	
Within whole units	250	278,632,529.1	1,114,530.1	1.6**
Genotype	25	111,824,915.4	4,472,996.6	6.2**
I X G	25	23,529,419.1	941,176.8	1.3
IL X G	1	23,529,421.0	23,529,421.0	32.8**
Error b (Residual)	200	143,278,194.6	716,391.0	
Total	259	307,378,055.7	1,186,787.9	

**Significant at the 0.01 probability level.

TABLE 8

Differences Between 1988 Mean Yield (kg/ha) in 24 Peanut F_4 Families and 2 Parents at Full Irrigation.

	a C 3068	b CU 3b 2551	c UC 7a 2382	d CU1c 2309	UC7b 1884	UC7c 1754	CU3a 1616	CU1b 1364	CU3c 1295	UC4a 1255	UC6 1074	CU4 954	e U 907	UC4f 691	UC1a 682	CU5b 622	CU5a 549	CU1a 541	UC4g 492	UC4b 433	UC4d 418	UC4c 411	UC4e 282	CU5c 267	UC1b 258
UC4h 153	2915 **	2398 **	2229 **	2156 **	1731 **	1601 **	1463 **	1211 **	1142 **	1102 **	921 *	801 *	754 *	538	529	469	396	388	339	280	265	258	129	114	105
UC1b 258	2810 **	2293 **	2124 **	2051 **	1626 **	1496 **	1358 **	1106 **	1037 **	997 **	816 *	696	649	433	424	364	291	283	234	175	160	153	24	9	
CU5c 267	2801 **	2284 **	2115 **	2042 **	1617 **	1487 **	1349 **	1097 **	1028 **	988 **	807 *	687	640	424	415	355	282	274	225	166	151	144	15		
UC4e 282	2786 **	2269 **	2100 **	2027 **	1602 **	1472 **	1334 **	1082 **	1013 **	973 *	792 *	672	625	409	400	340	267	259	210	151	136	129			
UC4c 411	2657 **	2140 **	1971 **	1898 **	1473 **	1343 **	1205 **	953 *	884 *	844 *	663	543	496	280	271	211	138	130	81	22	7				
UC4d 418	2650 **	2133 **	1964 **	1891 **	1466 **	1336 **	1198 **	946 *	877 *	837 *	656	536	489	273	264	204	131	123	74	15					
UC4b 433	2635 **	2118 **	1949 **	1876 **	1451 **	1321 **	1183 **	931 *	862 *	822 *	641	521	474	258	249	189	116	108	59						
UC4g 492	2576 **	2059 **	1890 **	1817 **	1392 **	1262 **	1124 **	872 *	803 *	763 *	582	462	415	199	190	130	57	49							
CU1a 541	2527 **	2010 **	1841 **	1768 **	1343 **	1213 **	1075 **	823 *	754 *	714	533	413	366	150	141	81	8								

TABLE 8 CONTINUED

	C[a] 3068	CU 3b[b] 2551	UC 7a[c] 2382	CU1c[d] 2309	UC7b 1884	UC7c 1754	CU3a 1616	CU1b 1364	CU3c 1295	UC4a 1255	UC6 1074	CU4 954	U[e] 907	UC4f 691	UC1a 682	CU5b 622	CU5a 549	CU1a 541	UC4g 492	UC4b 433	UC4d 418	UC4c 411	UC4e 282	CU5c 267	UC1b 258
CU5a 549	2519[f] **	2002 **	1833 **	1760 **	1335 **	1205 **	1067 **	815 *	746 *	706	525	405	358	142	133	73									
CU5b 622	2446 **	1929 **	1760 **	1687 **	1262 **	1132 **	994 **	742	673	633	452	332	285	69	60										
UC1a 682	2386 **	1869 **	1700 **	1627 **	1202 **	1072 *	934 *	682	613	573	392	272	225	9											
UC4f 691	2377 **	1860 **	1691 **	1618 **	1193 **	1063 **	925 *	673	604	564	383	263	216												
U 907	2161 **	1644 **	1475 **	1402 **	977 **	847 *	709	457	388	348	167	47													
CU4 954	2114 **	1597 **	1428 **	1355 **	930 *	800 *	662	410	341	301	120														
UC6 1074	1994 **	1477 **	1308 **	1235 **	810 *	680	542	290	221	181															
UC4a 1255	1813 **	1296 **	1127 **	1054 **	629	499	361	109	40																
CU3c 1295	1773 **	1256 **	1087 **	1014 **	589	459	321	69																	
CU1b 1364	1704 **	1187 **	1018 **	945 *	520	390	252																		
CU3a 1616	1452 **	835 *	766	693	268	138																			

TABLE 8 CONTINUED

	C[a] 3068	CU 3b[b] 2551	UC 7a[c] 2382	CU1c[d] 2309	UC7b 1884	UC7c 1754	CU3a 1616	CU1b 1364	CU3c 1295	UC4a 1255	UC6 1074	CU4 954	U[e] 907	UC4f 691	UC1a 682	CU5b 622	CU5a 549	CU1a 541	UC4g 492	UC4b 433	UC4d 418	UC4c 411	UC4e 282	CU5c 267	UC1b 258
UC7c 1754	1314[f] **	797 *	628	555	130																				
UC7b 1884	1184 **	667	498	425																					
CU1c 2309	759 *	242	73																						
UC7a 2382	686	169																							
CU3b 2551	517																								

[a] Chico

[b] Chico X UF 77318

[c] UF 77318 X Chico

[d] 1a-7c = Family representative

[e] UF 77318

[f] Average of five replications The L.S.D values for comparing two genotypes under full irrigation is 743 kg/ha and 978 kg/ha at the 0.05 and 0.01 probability levels respectively * ** Significant at the 0.05 and 0.01 probability levels respectively

TABLE 9

Differences Between 1988 Mean Yield (kg/ha) in 24 Peanut F_4 Families and 2 Parents at Intermediate Irrigation

	C[a] 2764	UC 7c[b] 1842	CU 3c[c] 1521	UC7b 1520	UC7a 1494	CU5c 1340	CU3a 1241	UC4f 929	CU5a 870	CU3b 862	UC4e 728	U[d] 722	CU1b 652	CU1c 497	CU1a[e] 394	CU4 388	UCb 341	UC4c 328	CU5b 325	UC4b 265	UC4a 262	UC4h 261	UC4g 209	UC1b 195	UC1a 125
UC4d 118	2646[f] **	1724 **	1403 **	1402 **	1376 **	1222 **	1123 **	811 *	752 *	744 *	610	604	534	379	276	270	223	210	207	147	144	143	91	77	7
UC1a 125	2639 **	1717 **	1396 **	1395 **	1369 **	1215 **	1116 **	804 *	745 *	737	603	597	527	372	269	263	216	203	200	140	137	136	84	70	
UC1b 195	2569 **	1647 **	1326 **	1325 **	1299 **	1145 **	1046 **	734	675	667	533	527	457	302	199	193	146	133	130	70	67	66	14		
UC4g 209	2555 **	1633 **	1312 **	1311 **	1285 **	1131 **	1032 **	720	661	653	519	513	443	288	185	179	132	119	116	56	53	52			
UC4h 261	2503 **	1581 **	1260 **	1259 **	1233 **	1079 **	980 **	668	609	601	467	461	391	236	133	127	80	67	64	4	1				
UC4a 262	2502 **	1580 **	1259 **	1258 **	1232 **	1078 **	979 **	667	608	600	466	460	390	235	132	126	79	66	63	3					
UC4b 265	2499 **	1577 **	1256 **	1255 **	1229 **	1075 **	976 **	664	605	597	463	457	387	232	129	123	76	63	60						
CU5b 325	2439 **	1517 **	1196 **	1195 **	1169 **	1015 **	916 *	604	545	537	403	397	327	172	69	63	16	3							
UC4c 328	2436 **	1514 **	1193 **	1192 **	1166 **	1012 **	913 *	601	542	534	400	394	324	169	66	60	13								

TABLE 9 CONTINUED

	C[a] 2764	UC 7c[b] 1842	CU 3c[c] 1521	UC7b 1520	UC7a 1494	CU5c 1340	CU3a 1241	UC4f 929	CU5a 870	CU3b 862	UC4e 728	U[d] 722	CU1b 652	CU1c 497	CU1a[e] 394	CU4 388	UCb 341	UC4c 328	CU5b 325	UC4b 265	UC4a 262	UC4h 261	UC4g 209	UC1b 195	UC1a 125
UCb 341	2423[f] **	1501 **	1180 **	1179 **	1153 **	999 **	900 *	588	529	521	387	381	311	156	53	47									
CU4 388	2376 **	1454 **	1133 **	1132 **	1106 **	952 *	853 *	541	482	474	340	334	264	109	6										
CU1a 394	2370 **	1448 **	1127 **	1126 **	1100 **	946 *	847 *	535	476	468	334	328	258	103											
CU1c 497	2267 **	1345 **	1024 **	1023 **	997 **	843 *	744 *	432	373	365	231	225	155												
CU1b 652	2112 **	1190 **	869 *	868 *	842 *	688	589	277	218	210	76	70													
U 722	2042 **	1120 **	799 *	798 *	772 *	618	519	207	148	140	6														
UC4e 728	2036 **	1114 **	793 *	792 *	766 *	612	513	201	142	134															
CU3b 862	1902 **	980 **	659	658	632	478	379	67	8																
CU5a 870	1894 **	972 *	651	650	624	470	371	59																	

TABLE 9 CONTINUED

	C[a] 2764	UC 7c[b] 1842	CU 3c[c] 1521	UC7b 1520	UC7a 1494	CU5c 1340	CU3a 1241	UC4f 929	CU5a 870	CU3b 862	UC4e 728	U[d] 722	CU1b 652	CU1c 497	CU1a[e] 394	CU4 388	UCb 341	UC4c 328	CU5b 325	UC4b 265	UC4a 262	UC4h 261	UC4g 209	UC1b 195	UC1a 125
UC4f 929	1835[f] **	913 *	592	591	565	411	312																		
CU3a 1241	1523 **	601	280	279	253	99																			
CU5c 1340	1424 **	502	181	154																					
UC7a 1494	1270 **	348	27	26																					
UC7b 1520	1244 **	322	1																						
CU3c 1521	1243 **	321																							
UC7c 1842	922 *																								

a Chico

b UF 77318 X Chico

c Chico X UF 77318

d UF 77318

e 1a-7c = Family representative

f Average of five replications The L.S.D values for comparing two genotypes under intermediate irrigation is 743 kg/ha and 978 kg/ha at the 0.05 and 0.01 probability levels, respectively *,** Significant at the 0.05 and 0.01 probability levels, respectively

TABLE 10

Summary of 1988 Fruit Yield Data from 14 UF77318 X Chico F_4 Families (Population One) at Two Irrigation Regimes

Statistic	Irrigation Regime: Full Irrigation	Irrigation Regime: Intermediate Irrigation
	kg/ha	
Mean	869.00	616.00
Range		
Min	153.00	118.00
Max	2,381.00	1,842.00
Genetic variance[a]	1,143,483.00	883,932.00
Heritability[b]	0.53	0.47
CV, %	33%	47%

[a]Genetic variance = component arising from genetic differences among families.

[b]Heritability = computed in the broad sense.

TABLE 11

Summary of 1988 Fruit Yield Data from 10 Chico X UF 77318 F_4 Families (Population Two) at Two Irrigation Regimes

Statistic	Irrigation Regime: Full Irrigation	Irrigation Regime: Intermediate Irrigation
	kg/ha	
Mean	1207.00	809.00
Range		
Min	267.00	325.00
Max	2551.00	1,521.00
Genetic variance[a]	395,385.00	701,488.00
Heritability[b]	0.25	0.38
CV, %	18%	27%

[a]Genetic variance = component arising from genetic differences among families.

[b]Heritability = computed in the broad sense.

TABLE 12

Genetic Gain in 1988 Fruit Weight with a 1% Selection Intensity Among 2 F_4 Peanut Populations Grown Under Two Irrigation Regimes

Population	Irrigation Regime	
	Full Irrigation	Intermediate Irrigation
	kg/ha	
UF 77318 X Chico	2055	1710
Chico X UF 77318	824	1370

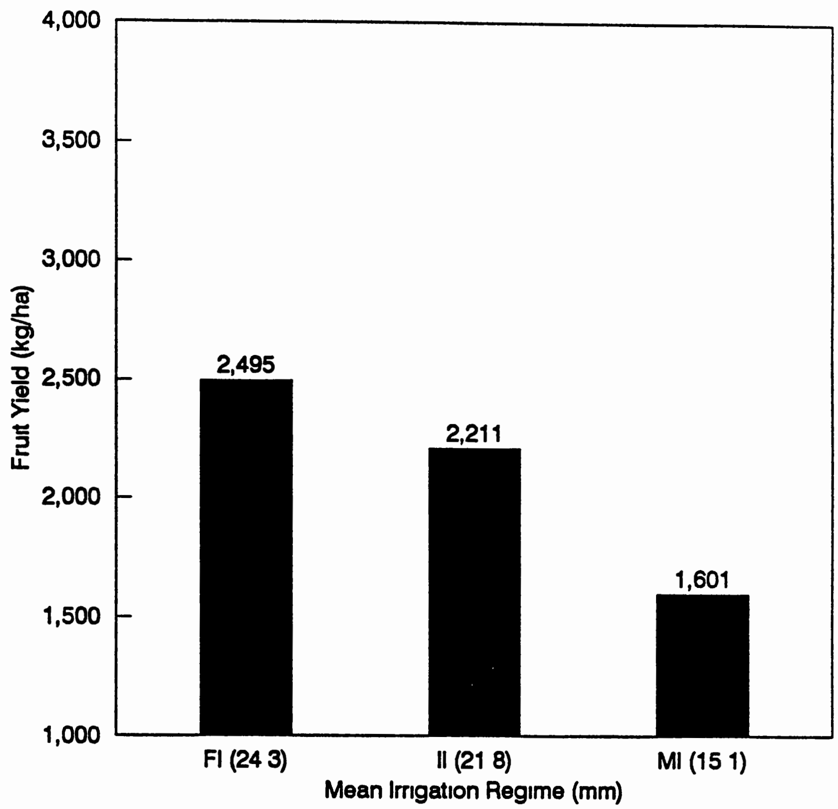

Fig 3 Mean 1990 yield of 2 peanut F_6 lines from the cross of UF 77318 X Chico at three irrigation regimes for test 1. Mean amounts of irrigation water plus precipitation were 24.3, 21 8, and 15.1 mm for full irrigation (FI), intermediate irrigation (II), and minimum irrigation (MI), respectively

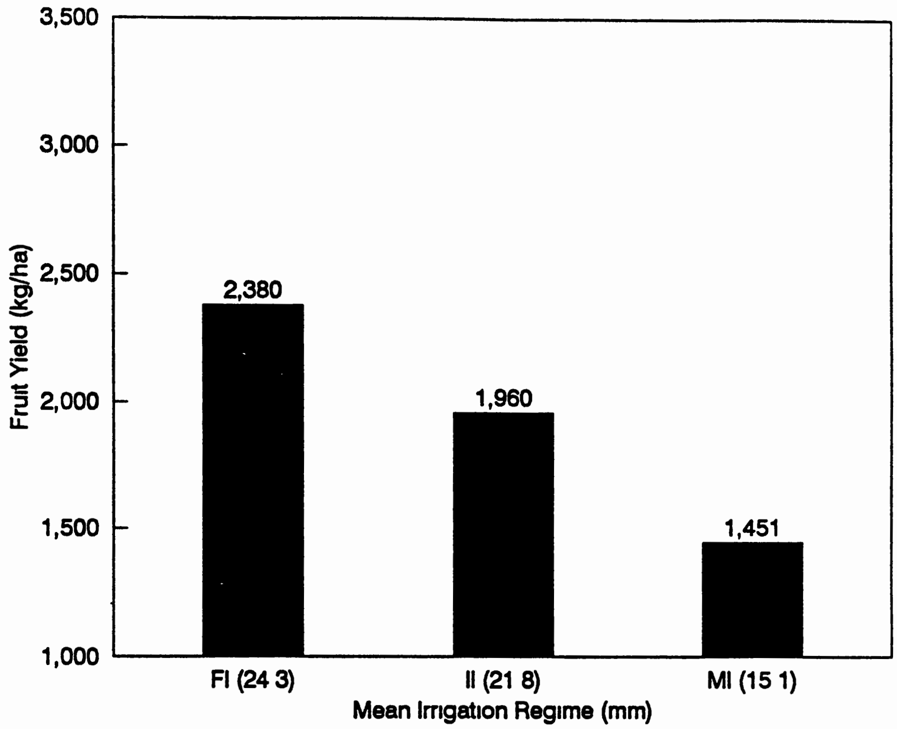

Fig 4 Mean 1990 yield of 2 peanut F_6 lines from the cross of UF 77318 X Chico at three irrigation regimes for test 2. Mean amounts of irrigation water plus precipitation were 24 3, 21.8, and 15 1 mm for full irrigation (FI), intermediate irrigation (II), and minimum irrigation (MI), respectively.

TABLE 13

Analysis of Variance for 1990 (Harvest Date 1) Fruit Yield of 2 F_6 Peanut Lines and 2 Cultivars at Three Irrigation Regimes

Source	df	Sum of Square	Mean Square	F
Among whole units	8	7,149,125.8	893,640.7	16.1**
Reps	2	970,286.9	485,143.5	8.7*
Irrigation (A)	2	5,956,466.6	2,978,233.3	53.6**
Linear, A	1	5,757,207.2	5,757,207.2	103.6**
Quadratic, A	1	199,259.3	199,259.3	3.6
R X I (Error a)	4	222,372.3	55,593.0	
Within whole unit	27	6,035,027.9	223,519.6	7.9**
Genotype (B)	3	5,184,584.1	1,728,194.7	61.0**
I X G	6	340,157.2	56,692.9	2.0
IL X G	1	181,133.6	181,133.6	6.4*
I Quad X G	1	159,023.6	159,023.6	5.6*
Residual (Error b)	18	510,286.6	28,349.2	
Total	35	13,184,153.7	376,690.1	

*,**Significant at the 0.05 and 0.01 probability levels, respectively.

TABLE 14

Analysis of Variance for 1990 (Harvest Date 2) Fruit Yield of 2 F_6 Peanut Lines and 2 Cultivars at Three Irrigation Regimes

Source	df	Sum of Squares	Mean Square	F
Among whole units	8	6,261,197.3	782,649.7	193.4**
Reps	2	913,260.2	456,630.1	112.8**
Irrigation, A	2	5,331,746.2	2,665,873.1	658.6**
Linear, A	1	5,254,423.4	5,254,423.4	1298.1**
Quadratic, A	1	77,322.8	77,322.8	19.1*
R X I (Error a)	4	16,190.9	4047.7	
Within whole units	27	3,897,041.8	144,334.9	4.9**
Genotype, B	3	3,259,105.2	1,086,368.4	36.8**
I X G	6	106,216.7	17,702.8	2.6
IL X G	1	43,585.7	43,585.7	1.5
I Quad X G	1	62,630.9	62,630.9	2.1
Residual (Error b)	18	531,719.9	29,540.0	
Total	35	10,158,239.1	290,235.4	

*,** Significant at the 0.05 and 0.01 probability levels, respectively.

TABLE 15

Differences Between 1990 (Harvest Date 1) Mean Yield (kg/ha) in 2 Peanut F_6 Lines and 2 Cultivars at Full Irrigation

	Spanco 3635	Okrun 2862	UC 2 2672
UC 1 2318[a]	1317 **[c]	544 **	354 **
UC 2 2672[b]	963 **	190 *	
Okrun 2862	773 **		

[a] UF 77318 X Chico line 1.

[b] UF 77318 X Chico line 2.

[c] Average of 3 replications. The LSD values for comparing two genotypes under full irrigation is 166.8 kg/ha and 228.5 kg/ha at the 0.05 and 0.01 probability levels, respectively. *, ** Significant at the 0.05 and 0.01 probability levels, respectively.

TABLE 16

Differences Between 1990 (Harvest Date 2) Mean Yield (kg/ha) in 2 Peanut F_6 Lines and 2 Cultivars at Full Irrigation

	Spanco 3079	Okrun 2726	UC 2 2414
UC 1[a] 2346	732 **[c]	380 **	68
UC 2[b] 2414	665 **	312 **	
Okrun 2726	353 **		

[a] UF 77318 X Chico line 1.

[b] UF 77318 X Chico line 2.

[c] Average of 3 replications. The L.S.D. values for comparing two genotypes under full irrigation is 170.2 kg/ha and 233.1 kg/ha at the 0.05 and 0.01 probability levels, respectively. ** Significant at the 0.01 probability level.

TABLE 17

Differences Between 1990 (Harvest Date 1) Mean Yield (kg/ha) in 2 Peanut F_6 Lines and 2 Cultivars at Intermediate Irrigation

	Spanco 3011	Okrun 2726	UC 2 2224
UC 1[a] 2197	814 **[c]	529 **	27
UC 2[b] 2224	787 **	502 **	
Okrun 2726	285 **		

[a] UF 77318 X Chico line 1.

[b] UF 77318 X Chico line 2.

[c] Average of 3 replications. The L.S.D. values for comparing two genotypes under intermediate irrigation is 166.8 kg/ha and 228.5 kg/ha at the 0.05 and 0.01 probability levels, respectively. ** Significant at the 0.01 probability level.

TABLE 18

Differences Between 1990 (Harvest Date 2) Mean Yield (kg/ha) in 2 Peanut F_6 Lines and 2 Cultivars at Intermediate Irrigation

	Spanco 2658	Okrun 2509	UC 2 2102
UC 1[a] 1817	841 **[c]	692 **	285 **
UC 2[b] 2102	556 **	407 **	
Okrun 2509	149		

[a] UF 77318 X Chico line 1.

[b] UF 77318 X Chico line 2.

[c] Average of 3 replications. The L.S.D. values for comparing two genotypes under intermediate irrigation is 170.2 kg/ha and 233.1 kg/ha at the 0.05 and 0.01 probability levels, respectively. ** Significant at the 0.01 probability level.

TABLE 19

Differences Between 1990 (Harvest Date 1) Mean Yield (kg/ha) in 2 Peanut F_6 Lines and 2 Cultivars at Minimum Irrigation

	Spanco 2360	Okrun 2007	UC 2 1736
UC 1 1465 [a]	895 [c] **	543 **	271 **
UC 2 1736 [b]	624 **	271 **	
Okrun 2007	353 **		

[a] UF 77318 X Chico line 1.

[b] UF 77318 X Chico line 2.

[c] Average of 3 replications. The L.S.D. values for comparing two genotypes under minimum irrigation is 166.8 kg/ha and 228.5 kg/ha at the 0.05 and 0.01 probability levels, respectively. ** Significant at the 0.01 probability level.

TABLE 20

Differences Between 1990 (Harvest Date 2) Mean Yield (kg/ha) in 2 Peanut F_6 Lines and 2 Cultivars at Minimum Irrigation

	Spanco 2102	Okrun 1817	UC 2 1600
UC 1[a] 1302	800 **[c]	515 **	298 **
UC 2[b] 1600	502 **	217 *	
Okrun 1817	285 **		

[a] UF 77318 X Chico line 1.

[b] UF 77318 X Chico line 2.

[c] Average of 3 replications. The L.S.D. values for comparing two genotypes under minimum irrigation is 170.2 kg/ha and 233.1 kg/ha at the 0.05 and 0.01 probability levels, respectively. *,** Significant at the 0.05 and 0.01 probability levels, respectively.

TABLE 21

Summary of 1990 (Harvest Date 1) Fruit Yield Data from 2 UF 77318 X Chico F_6 Lines at Three Irrigation Regimes

Statistic	Irrigation Regime		
	Full Irrigation	Intermediate Irrigation	Minimum Irrigation
	kg/ha		
Mean	2495.00	2211.00	1601.00
Range			
Min	2318.00	2197.00	1465.00
Max	2672.00	2224.00	1736.00
Genetic Variance[a]	79,609.00	89,915.00	89,953.00
Heritability[b]	0.04	0.04	0.04
CV, %	6.00	6.00	9.00

[a]Genetic variance = component arising from genetic differences among families.

[b]Heritability = computed in the broad sense.

TABLE 22

Summary of 1990 (Harvest Date 2) Fruit Yield Data from 2 UF 77318 x Chico F_6 Lines at Three Irrigation Regimes

Statistic	Irrigation Regime		
	Full Irrigation	Intermediate Irrigation	Minimum Irrigation
	kg/ha		
Mean	2380.00	1960.00	1451.00
Range			
Min	2346.00	1817.00	1302.00
Max	2414.00	2102.00	1600.00
Genetic Variance[a]	53,406.00	93,572.00	67,353.00
Heritability[b]	0.03	0.05	0.04
CV, %	4.00	5.00	7.00

[a]Genetic variance = component arising from genetic differences among families.

[b]Heritability = computed in the broad sense.

VITA 2

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Doctor of Philosophy

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