Genetic Studies of Peanut Proteins and Oils

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ABSTRACT

Six peanut cultivars (Chico, Argentine, Tennessee Red, Florunner, F334A-B-14, and Florida Jumbo) and their F_2 seed populations were used to determine the inheritance of protein and oil contents. The results suggested that both protein and oil contents were quantitatively inherited. Calculated correlation coefficients between protein and oil contents were negative and varied from nonsignificant to highly significant in both parental and F_2 populations. Three F_2 populations, F334 x Tennessee Red, Florida Jumbo x Chico, and F334 x Argentine, plus their parents were studied for genetic behavior of amino acid and fatty acid compositions. The results indicate that these traits also were inherited quantitatively, and the peanuts had the capacity to give a transgressive segregation with some of the amino acids and fatty acids. Correlations among 18 amino acids plus 8 fatty acids suggested a complex system of genetic control among amino acid and fatty acid compositions within each of the peanut cultivars and their F_2 progenies.

INTRODUCTION

The peanut (*Arachis hypogaea* L.) has a relatively high protein content and is an important source of plant protein for human consumption. Holley and Hammons (1) reported differences in protein and oil among genotypes, and Young and Hammons (2) reported a range of 22.7-29.3% protein among 105 genotypes of peanuts. Protein levels varied significantly among individual seeds from a plant which produced peanuts with a range from mature to immature (3). Considerable variation in amino acid composition of peanut meal among cultivars has been reported (4,5). No inheritance studies of protein content or amino acid composition of peanuts have been reported.

Worthington and Hammons (6) studied the genotypic variation in fatty acid composition and stability of *A. hypogaea* L. oil and found that linoleic acid varied among genotypes from ca. 14-40%. In general, the large seeded Virginia (subsp. *hypogaea*) cultivars were lower while the Spanish (subsp. *fastigiata* var. *vulgaris*) types were higher in linoleic acid. Worthington, et al., (7) reported that the ranges in fatty acid levels (each expressed as % total fatty acids) among 82 genotypes was: palmitic (16:0) 7.4-12.9%, stearic (18:0) 1.6-5.3%, oleic (18:1) 35.7-68.5%, linoleic (18:2) 14.0-40.3%, arachidic (20:0) 0.9-2.2%, eicosenoic (20:1) 0.6-2.0%, behenic (22:0) 1.3-5.1%, and lignoceric (24:0) 0.6-2.0%. Holley and Hammons (1) and Worthington and

Hammons (6) found a strong negative correlation (r = -.99) between 18:1 and 18:2, significant positive correlations between 18:2 and 16:0, 22:0 and 24:0, and a negative correlation between 18:2 and 18:0.

Tai (8) and Tai, et al., (9) investigated the inheritance of oleic:linoleic (O:L) acid ratio in peanuts and found that the cultivars varied widely. They reported that there was no consistent evidence to support a hypothesis of maternal influence on the O:L ratio in peanuts, and that inheritance of the O:L ratio is controlled by quantitative genes.

Holley and Hammons (1) reported a tendency for high protein strains to be low in oil, and vice versa, but exceptions were common enough in 26 strains to invalidate an absolute reciprocal relationship between oil and protein. In fat free peanut meals, 18 amino acids were found (4), but of the 7 essential amino acids, only leucine and phenylalanine were nutritionally adequate in all cultivars examined.

The objectives of this study were to investigate the inheritance of protein and oil contents of peanuts and of their amino acid and fatty acid compositions as a basis for improving the nutritional value and oil quality of peanuts. The quantitative relationships among the 18 amino acids and the 8 fatty acids also were examined.

MATERIALS AND METHODS

Six peanut cultivars, representing three botanical varieties and 4 commercial types (Table I), were studied. Both Tennessee Red (TR) and Florida Jumbo (FJ) were reported to have high protein and high lysine content (4). Argentine (AR) had a moderately high content of protein and lysine, whereas, both Chico (CH) and Florunner (FR) had relatively low protein content. F334A-B-14 had the lowest protein content among these 6 cultivars. According to Worthington (R.E. Worthington, unpublished data, 1972), Florida Jumbo had the highest oleic acid (66.0%) and lowest linoleic acid content (16.6%), whereas, F334 had the lowest oleic acid (41.4%) and highest linoleic acid content (39.8%) among these 6 cultivars. The oleic and linoleic acid content of the other 4 cultivars were between those of F334 and Florida Jumbo.

All possible reciprocal infraspecific crosses were attempted by hand pollination among these 6 cultivars in the early spring of 1973, but F_1 seeds were obtained in 11 combinations only (Tables II and III). Because most of the F_1 seeds were not fully matured, chemical analysis of these seeds could not be conducted. The F_1 plants were field grown at the USDA Plant Introduction Station at Experi-

TABLE I

Peanut (*Arachis hypogaea* L.) Cultivars Selected for Genetic Studies of Protein and Oil Content

Cultivar	Code	Botanical subspecies and variety	U.S. commercial type
Tennessee Red	TR	*fastigiata - fastigiata*	Valencia
F334A-B-14[a]	F334	*hypogaea*	Runner
Chico[b]	CH	*fastigiata vulgaris*	Spanish
Argentine[a]	AR	*fastigiata vulgaris*	Spanish
Florunner[a]	FR	*hypogaea*	Runner
Florida Jumbo[c]	FJ	*hypogaea - hypogaea*	Virginia

[a]Advanced selections from breeding programs using infraspecific hybridization, and, therefore, not strict *hypogaea* botanical varieties.

[b]See Ref. 23.

[c]A large seeded, non-commercial peanut employed in breeding research.

TABLE II

Frequency Distributions and Statistical Summary of Protein of Parents and F2's from
Single Seeded Analyses and Heritability (H)[a]

Population[b]	Class centers (%)								n[c]	Mean ± s.d.	H
	21.0	23.0	25.0	27.0	29.0	31.0	33.0	35.0			
Parents											
CH			1	6	4	3	1		15	28.72 ± 2.16	-
AR				2	3	6	1		12	30.18 ± 1.80	-
TR			2	5	4	1			12	27.91 ± 1.79	-
F334		1	4	4	2				11	26.54 ± 1.91	-
FR	1	3	3	3					10	24.60 ± 2.17	-
FJ			3	6	7	4			20	28.04 ± 1.86	-
Pooled	1	4	13	26	20	14	2		80	27.75 ± 2.49	-
F2 generation											
CH x AR				8	19	6	3		36	29.23[d] ± 1.82	0
AR x CH				5	16	10	4		35	29.89[d] ± 1.81	0
CH x F334			1	6	12	11	5		35	29.74[e] ± 2.02	0
CH x FJ			8	7	6	6	8		35	28.93[e] ± 2.91	53
FJ x CH		1	2	8	6	8	9		34	29.76[e] ± 2.80	44
AR x FR		2	1	5	10	9	6	3	36	29.87[e] ± 2.89	53
FJ x AR		1	3	11	8	10	3		36	28.84[e] ± 2.51	47
F334 x TR		1	3	21	23	17	7		72	28.94[d] ± 2.12	24
F334 x AR	1	5	7	8	5	6	2		34	27.21[e] ± 3.21	67
FR x CH	3	2	7	6					18	24.98[e] ± 2.27	10
CH x F334		1	2	5	9	2	1		20	28.20[e] ± 2.33	35
Pooled	4	13	34	90	114	85	48	3	391	28.88 ± 2.70	-

[a]H = ([VF₂ - (VP₁ · VP₂)^{1/2}]/VF₂) x 100.

$$^aH = ([VF_2 - (VP_1 \cdot VP_2)^{1/2}]/VF_2) \times 100.$$

[b]CH = Chico; AR = Argentine; TR = Tennessee Red; FR = Florunner; FJ = Florida Jumbo.

[c]n = Number.

[d]Not significantly different from mean of either parent (P>0.05).

[e]Significantly different from mean of 1 parent (P<0.05).

TABLE III

Frequency Distributions and Statistical Summary of Oil Content of Parents and F2's from Single Seeded Analyses,
Heritability (H), and Correlation Coefficients (r) between Protein and Oil

Population[a]	Class center (%)										n[b]	Mean ± s.d.	H	r
	41	43	45	47	49	51	53	55	57	59				
Parents														
CH				3	3	4	2	2	1		15	51.11 ± 3.11	-	-.655[f]
AR	1			2	2	2	5				12	50.03 ± 3.48	-	-.623[f]
TR		1			4	2	5				12	50.55 ± 2.71	-	-.822[g]
F334					1	5	2	3			11	52.38 ± 2.22	-	-.652[f]
FR					1	4	4		1		10	52.39 ± 2.15	-	-.412
FJ	1	2	5	6	4	2					20	46.72 ± 2.64	-	-.587
Pooled	2	3	5	111	15	19	18	5	2		80	50.00 ± 3.47	-	
F2 generation														
CH x AR			2	3	10	12	8	1			36	50.41[c] ± 2.37	0	-.621[g]
AR x CH		1		4	4	14	8	3		1	35	51.14[c] ± 2.71	0	-.522[g]
CH x F334				3	4	15	8	4	1		35	51.44[c] ± 2.34	0	-.465[g]
CH x FJ			2	6	7	3	11	5	1		35	50.93[d] ± 3.14	17	-.736[g]
FJ x CH	1		1	1	4	8	8	7	4		34	51.96[d] ± 3.50	33	-.660[g]
AR x FR			1	2	5	7	13	6	2		36	52.07[d] ± 2.60	0	-.364[f]
FJ x AR		1	1	3	8	11	6	4	2		36	50.91[d] ± 3.07	3	-.555[g]
F334 x TR	2	3	13	19	18	14	3				72	47.64[e] ± 2.72	19	-.184
F334 x AR			3	10	9	6	3	3			34	49.29[d] ± 2.83	4	-.423[f]
FR x CH				2	5	7	2	2			18	50.67[c] ± 2.23	0	-.748[g]
FJ x F334		1		1	3	11	3	1			20	50.46[d] ± 2.52	0	-.177
Pooled	3	5	24	54	77	108	73	36	10	1	391	50.42 ± 3.12	--	

[a]CH = Chico; AR = Argentine; TR = Tennessee Red; FR = Florunner; FJ = Florida Jumbo.

[b]n = Number.

[c]Nonsignificantly different from mean of either parent (P>0.05).

[d]Significantly different from mean of 1 parent (P<0.05).

[e]Significantly different from both parental means at (P<0.05).

[f](P<0.05).

[g](P<0.01).

ment, Georgia, in 1973. At harvest, fruits were dried under forced air at room temperature, hand shelled, and fully matured seeds were selected for chemical analyses.

The samples for chemical analyses were on an individual seed basis (3). The dried peanut seeds were crushed with a glass pestle and extracted with diethyl ether. The extracted oil was dried and weighed. Fat free peanut meals were used for the determination of protein by the macro-Kjeldahl method (10). Percent protein was calculated as % nitrogen x 5.46 (11,12). Both oil and protein contents were calculated to whole peanut on an oven dry basis.

Three F2 populations, F334 x TR, FJ x CH and F334 x AR, and their parents were selected for studies of the amino acid and fatty acid compositions. Due to technical difficulties, only 30 individual seeds from each F2 population and 10 individual seeds of each of the parents were

TABLE IV

Frequency Distributions for 8 Essential Amino Acids in 5 Parents and 3 F_2 Populations of Peanuts, Means and Standard Deviations[g]

Threonine (Thr)

Population[h]	2.575	2.625	2.675	2.725	2.775	2.825	2.875	2.925	2.975	Mean ± s.d.
TR			2	5	2	1				2.73bc ± .05
F334					2	5	3			2.83e ± .03
CH		2	2	5	3	1				2.74bc ± .04
AR		3	3	3	3					2.74bc ± .05
FJ	2	6	6	10	13					2.65a ± .05
F334 x TR	4	5	3	3	8	4	1			2.75c ± .04
FJ x CH		7	7	8	11	2	2	1		2.71b ± .08
F334 x AR		1	1	8	11	7	6	2	1	2.79d ± .06
Pooled	6	7	24	34	42	20	6	0	1	2.47 ± .16

Cystine (Cys)

Population[h]	0.65	0.75	0.85	0.95	1.05	1.15	1.25	1.35	Mean ± s.d.
TR	2	2	2	2	2	3			1.06c ± .16
F334	2	3	3	1		2			.84a ± .13
CH	1	4	4	2	1				.91ab ± .08
AR	2	2	4	4	1				.83a ± .13
FJ	1	3	4	2	2				.96abc ± .11
F334 x TR		2	4	9	6	4	2		1.02bc ± .16
FJ x CH	6	10	4	4	3	2			.94ab ± .16
F334 x AR	2	1	8	11	3	1	1		.95abc ± .14
Pooled	7	16	32	40	19	15	9	2	.94 ± .25

Valine (Val)

Population[h]	3.55	3.65	3.75	3.85	3.95	4.05	4.15	4.25	4.35	4.45	4.55	Mean ± s.d.
TR			1	1	1	3	1	2	1			4.09de ± .17
F334		2			1	3	1	2	3			4.18ef ± .13
CH		2	4	1	1	3	1					3.92bc ± .16
AR			2	1	3	2						3.87b ± .15
FJ	4		3	13	10	3						3.66a ± .12
F334 x TR		3	3	1	7	5	5	3	1			3.90b ± .10
FJ x CH				1	4		3	11	8	3	2	4.03cd ± .24
F334 x AR	4	7	17	19	27	19	11	18	13	3	2	4.24f ± .15
Pooled												3.99 ± .34

Methionine (Met)

Population[h]	0.65	0.75	0.85	0.95	1.05	1.15	1.25	1.35	1.45	Mean ± s.d.
TR				3	4	2	1			1.06c ± .08
F334			3		6	4				1.08c ± .06
CH		6	4	4	2	1				.97b ± .08
AR		3	4	3						.83a ± .11
FJ	4	3	4	3						.85a ± .09
F334 x TR				1	7	13	8	1		1.16d ± .07
FJ x CH			1	3	12	5	7	1		1.12cd ± .12
F334 x AR	0		1	4	7	16	2		1	1.10c ± .08
Pooled		9	13	18	38	41	18	2	1	1.02 ± .34

Isoleucine (Ile)

	2.75	2.85	2.95	3.05	3.15	3.25	3.35	
TR			1	2	3	3	1	3.18de ± .12
F334				2	3	4	1	3.19e ± .09
CH			5	2	3			3.03bc ± .10
AR	1		4	3	1	1		3.01b ± .12
FJ	4	3	2	1				2.87a ± .10
F334 x TR		3	12	15	3			3.01b ± .12
FJ x CH	1	1	4	11	6	4		3.10cd ± .14
F334 x AR	1		7	10	9		3	3.22e ± .11
Pooled	7	7	35	46	28	12	5	3.08 ± .31

Leucine (leu)

	5.675	5.725	5.775	5.825	5.875	5.925	5.975	6.025	6.075	6.125	6.175	6.225	
TR								2	7		1		6.08e ± .04
F334								2	2	2	3	1	6.12e ± .06
CH							2	6	2				6.00d ± .07
AR					2	4	4						5.92c ± .09
FJ	1	5	3	1									5.74a ± .04
F334 x TR	2	3	7	7	7	4							5.82b ± .07
FJ x CH	2	1		1	1	1	9	5	8	1	1		6.00d ± .10
F334 x AR								4	12	9	5		6.09e ± .08
Pooled	5	9	10	9	10	9	15	19	31	12	10	1	5.97 ± .24

Lysine (lys)

	3.2	3.3	3.4	3.5	3.6	3.7	3.8	3.9	4.0	4.1	
TR			2	4	2	1	1				3.56ab ± .12
F334				1	4	3	2				3.65bc ± .10
CH				3	2	2	3				3.66bc ± .13
AR				2	3	3	2				3.73c ± .16
FJ				1	2	2	4	1			3.72c ± .12
F334 x TR				1	10	5	8	3	2	1	3.74c ± .15
FJ x CH	2	4	10	6	5	1	1				3.47a ± .16
F334 x AR	1	5	5	9	7	2	1				3.49a ± .14
Pooled	3	9	17	27	35	19	21	6	2	1	3.60 ± .18

Phenylalanine (Phe)

	5.4	5.6	5.8	6.0	6.2	6.4	6.6	
TR		1	6	3				5.85ab ± .11
F334			7	2	1			5.93b ± .12
CH					4	5	1	6.17c ± .22
AR					2	6	2	6.38de ± .16
FJ					1	6	3	6.45e ± .10
F334 x TR				10	17	2	1	6.23cd ± .15
FJ x CH	1	10	7	4	5	3		5.87b ± .28
F334 x AR	7	6	10	5	2			5.74a ± .26
Pooled	8	17	30	24	30	24	7	6.05 ± .30

a-f Means followed by same letter are not significantly different at the 5% level of probability.

g Ten seeds from each of the parents and 30 seeds from each of the F_2's were analyzed.

h TR = Tennessee Red; CH = Chico; AR = Argentine; FJ = Florida Jumbo.

analyzed. About 125 mg fat free peanut meal was hydrolyzed in 20 ml 6 N HCl for 15 hr at 110 C, pH adjusted to 2.0-2.2 with 12 N NaOH, diluted to 50 ml, centrifuged on a Beckman microfuge and analyzed (4). Amino acid analyses were performed by the ion exchange chromatography technique of Spackman, et al., (13), with a Durrum Model D-500 Amino Acid Analyzer using a 1.75 mm (internal diameter (ID) x 48 cm length column, packed with the Durrum high resolution cation exchanger (bead diameter, 8 ± 2 microns). Running time was 60 min including regeneration of column. Tryptophan data were not provided by the procedure.

Fatty acid composition was determined by gas liquid chromatography (GLC) according to the procedure reported by Worthington, et al., (7). One drop of peanut oil was transesterified with 5 ml methanol:benzene:sulfuric acid (2:1:3) at 80 C for 2 hr. The fatty acid composition of oil was calculated as % total fatty acids. Duplicate samples were used for all amino acid and fatty acid analysis.

Means and standard deviations (s.d.) were calculated for each of the parental and F_2 populations. The analysis of variance for each of the amino acids and fatty acids was based on the combined data of all parental and F_2 populations (14). Broad sense heritabilities (H) for protein and oil contents were estimated using the formula of Mahmud and Kramer (15).

Correlation coefficients (r) were computed for all possible combinations of the 26 variables (18 amino acids + 8 fatty acids) for each of the parental and F_2 populations.

RESULTS AND DISCUSSION

The levels of protein and oil content, and the corresponding frequency distributions of the 6 parents and F_2 populations of 11 combinations of these parents, are shown in Tables II and III, respectively. Argentine was highest (30.18%) and Florunner lowest (24.60%) in protein content. Five F_2 populations (CH x AR, AR x CH, AR x FR, FJ x AR, and F334 x AR) had average protein contents that were between the 2 parents. Five other populations (CH x F334, CH x FJ, FJ x CH, F334 x TR, and FJ x F334) averaged higher than the parents and gave a transgressive segregation toward high protein content. Only 1 F_2 population, FR x CH, exhibited transgressive segregation toward low protein content. Among the 11 F_2 populations, F334 x AR showed the widest range of distribution, while both CH x AR and its recirpocal cross gave the narrowest range of distribution.

The F334 and Florunner parents had the highest oil content, whereas, Florida Jumbo had the lowest. As with protein, oil content showed a wide range of distribution in most of the 6 cultivars examined (Table III). The oil content of F_2 populations appeared to have a normal distribution in all crosses except FJ x CH, CH x FJ, and F334 x TR. The range for CH x FJ and its reciprocal cross indicated transgressive segregation toward high oil content. The F_2 population of F334 x TR on the other hand, showed transgressive segregation toward low oil content.

These results show that most parental and F_2 populations were less variable in oil content than in protein content. From the F_2 populations examined, the inheritance of protein and oil contents appeared to be controlled by quantitative genes. The differences in mean and frequency distribution indicated that numerous genes were operative in some parents and their F_2 populations, but that only a few genes were involved in others.

Tables II and III show the heritabilities for protein and oil content, respectively, in all 11 crosses. Heritability estimates for protein content varied from 0-67. F334 x AR produced the highest value, while CH x F334 showed no appreciable value for the protein heritability from parents to F_2 progenies. Only 5 of the 11 F_2 populations showed

TABLE V

Statistical Summary of Nonessential Amino Acids of Fat Free Meal of 5 Parents and 3 F_2 Populations of Peanuts

Amino acid	Population[a] (mean ± s.d.)								
	TR	F334	CH	AR	FJ	F334 x TR	FJ x CH	F334 x AR	Pooled
Aspartic acid[b]	11.50 ± .16	11.57 ± .13	11.68 ± .27	11.87 ± .12	11.93 ± .24	11.69 ± .11	11.88 ± .19	11.73 ± .17	11.73 ± .19
Serine[b]	5.21 ± .10	5.37 ± .11	5.31 ± .06	5.32 ± .09	5.11 ± .01	5.28 ± .06	5.26 ± .10	5.27 ± .09	5.26 ± .10
Glutamic acid[b]	20.65 ± .15	20.28 ± .27	20.48 ± .20	20.35 ± .19	20.38 ± .23	19.94 ± .23	20.55 ± .23	20.30 ± .19	20.32 ± .31
Proline[b]	4.84 ± .19	4.61 ± .14	4.35 ± .32	4.66 ± .29	4.60 ± .20	4.69 ± .16	4.96 ± .27	5.12 ± .31	4.73 ± .33
Glycine[b]	5.11 ± .15	5.60 ± .15	5.42 ± .11	5.35 ± .26	5.10 ± .19	5.13 ± .23	5.24 ± .25	5.34 ± .18	5.28 ± .25
Alanine[b]	4.03 ± .04	4.10 ± .07	4.10 ± .06	4.10 ± .03	4.01 ± .08	4.10 ± .11	4.18 ± .08	4.13 ± .08	4.09 ± .09
Tyrosine[b]	3.93 ± .05	4.08 ± .06	4.17 ± .13	4.23 ± .09	4.30 ± .06	4.05 ± .08	3.91 ± .15	3.89 ± .11	4.06 ± .29
Histidine[b]	2.93 ± .04	3.02 ± .06	3.11 ± .11	3.13 ± .13	3.16 ± .11	3.16 ± .08	2.99 ± .15	2.95 ± .09	3.06 ± .14
NH3[b]	1.78 ± .02	1.73 ± .04	1.72 ± .04	1.63 ± .03	1.69 ± .03	1.74 ± .04	1.73 ± .06	1.72 ± .07	1.72 ± .06
Arginine[b]	12.57 ± .13	12.23 ± .16	12.43 ± .14	12.37 ± .23	12.88 ± .26	12.82 ± .42	12.41 ± .23	12.16 ± .24	12.48 ± .37

[a] Ten seeds from each of the parents and 30 seeds from each of the F_2's were analyzed. TR = Tennessee Red; CH = Chico; AR = Argentina; FJ = Florida Jumbo.
[b] Significant difference among all (8) populations at the 5% level of probability.

TABLE VI

Frequency Distributions for 8 Fatty Acids in 5 Parents and 3 F_2 Populations of Peanuts[g]

16:0

Population[h]	7.50	8.50	9.50	10.50	11.50	12.50	13.50	Mean ± s.d.
TR				5	5			11.20c ± .54
F334					6	3		11.60c ± .98
CH						2	5	12.80e ± .81
AR					3	10		12.58de ± .22
FJ	7	3						7.94a ± .46
F334 x TR			1	7	20	3		11.45c ± .54
FJ x CH		1	12	13	4			10.24b ± .79
F334 x AR					15	13	2	12.16d ± .67
Pooled	7	4	13	25	53	31	7	11.20 ± .95

18:0

Population[h]	1.90	2.30	2.70	3.10	3.50	3.90	4.30	4.70	Mean ± s.d.
TR				5	5			1	3.32e ± .43
F334	8	2							2.00a ± .16
CH			2	8					2.98d ± .17
AR				4	5				3.30e ± .23
FJ			3	5		4		1	2.89f ± .40
F334 x TR	8	12	7	3			2		2.41b ± .39
FJ x CH		7	22	1					2.63c ± .22
F334 x AR	7	16	5	2			3		2.29b ± .34
Pooled	23	37	39	23	10	4	3	1	2.86 ± .79

18:1

Population[h]	37.50	40.50	43.50	46.50	49.50	52.50	55.50	58.50	61.50	64.50	67.50	Mean ± s.d.
TR	8	5	4	1								42.73bc ± 1.72
F334	8	2										37.63a ± 1.25
CH		6	9	1								41.71bc ± 1.49
AR		9										44.14c ± 0.87
FJ								1		5	4	65.12e ± 3.55
F334 x TR	7	16	6	1								40.92b ± 2.43
FJ x CH			1	5	11	4	4	4	1			51.62d ± 4.55
F334 x AR		10	13	9	11	4	5					41.36b ± 2.47
Pooled	23	39	37	23	10	4	4	5	5	5	4	45.72 ± 3.87

18:2

Population[h]	15.50	18.50	21.50	24.50	27.50	30.50	33.50	36.50	39.50	42.50	Mean ± s.d.
TR							2	4	4		35.95de ± 1.87
F334									4	10	41.47g ± 0.38
CH						2		8			35.23cd ± 0.85
AR						1	9				33.31c ± 0.86
FJ	4	5	1								17.33a ± 2.77
F334 x TR							1	6	16	7	38.53f ± 2.24
FJ x CH			1	7	4	6	6	1			29.03b ± 3.75
F334 x AR				7	4	1	14	12	3		37.50ef ± 1.93
Pooled	4	5	1	7	4	9	21	33	32	30	33.55 ± 2.75

20:0

	1.05	1.15	1.25	1.35	1.45	1.55	1.65	1.75	1.85	Mean
TR	1			2	2	3	1	1	1	1.55c ± .16
F334		5		1			1			1.20a ± .09
CH			3	3	4	2	1			1.46b ± .07
AR					6	3	1	2		1.51bc ± .08
FJ					1	2	4		1	1.65c ± .12
F334 x TR	2	5	13	6	2	2	2			1.28a ± .12
FJ x CH	1	1	2	10	7	6	1	1		1.44b ± .20
F334 x AR	4	8	5	9	2	1				1.27a ± .16
Pooled	8	19	23	31	24	19	10	4	2	1.42 ± .25

20:1

	0.65	0.75	0.85	0.95	1.05	1.15	1.25	1.35	1.45	1.55	Mean
TR		1	3	1	4	1					.95bc ± .12
F334				1		4	2	2	1		1.21d ± .12
CH				5	2	1					.89b ± .05
AR	2	4	2								.75a ± .07
FJ	1	2	4								.82ab ± .10
F334 x TR			4	2	1	6	7	2	1	4	1.19d ± .21
FJ x CH		1	5	8	5	3	1	1	1		1.02c ± .14
F334 x AR			5	6	9	5	2	2	1		1.06c ± .17
Pooled	3	8	23	24	31	20	12	7	4	4	.98 ± .37

22:0

	2.20	2.40	2.60	2.80	3.00	3.20	3.40	3.60	Mean
TR	1				4	2	2		3.05cd ± .32
F334		1		2	1	2	4	1	3.22de ± .27
CH			1	1		2	5	2	3.33e ± .24
AR						4	2	1	3.24de ± .24
FJ		7	1	1	3				2.42a ± .30
F334 x TR	1	3	4	9	8	3	1		2.82b ± .31
FJ x CH	2	4	4	8	8	3	1		2.80b ± .31
F334 x AR	1	1	4	10	6	4	3	1	2.94bc ± .31
Pooled	6	16	14	31	30	20	18	5	2.98 ± .46

24:0

	0.75	1.05	1.35	1.65	1.95	2.25	Mean
TR		4	5	1			1.27bc ± .20
F334			3	5	2		1.65d ± .18
CH			4	5		1	1.62d ± .48
AR			5	5			1.18ab ± .18
FJ	4	6					1.00a ± .07
F334 x TR	1	6	12	10	1		1.39c ± .25
FJ x CH	2	14	13	12	1		1.20b ± .21
F334 x AR	1	5	11			1	1.26b ± .26
Pooled	8	35	53	38	5	1	1.55 ± .59

a-fMeans followed by same letter are not significantly different at the 5% level of probability.

gTen seeds from each of the parents and 30 seeds from each of the F₂'s were analyzed.

hTR = Tennessee Red; CH = Chico; AR = Argentine; FJ = Florida Jumbo.

TABLE VII

Correlation Between 8 Essential Amino Acids and Fat Free Peanut Meal of
5 Parents and 3 F_2 Populations of Peanuts

Correlation between[a]	TR[c]	F334	CH[c]	AR[c]	FJ[c]	F334 x TR	FJ x CH	F334 x AR
1-2	-.63[b]	.01	.02	-.25	-.41	-.57	-.59	-.06
1-3	.63	-.03	.16	.28	.26	.43	.77	.16
1-4	-.09	.54	-.03	.65	-.41	.11	.45	.53
1-5	.62	-.08	.15	.06	.22	.19	.43	.12
1-6	.06	-.11	.19	-.18	-.31	.01	.41	-.00
1-7	.36	.03	.14	.22	.56	.48	-.17	.15
1-8	.90	.79	.61	.91	.95	.67	-.07	.62
2-3	-.45	-.81	-.25	-.72	-.61	-.20	-.53	-.27
2-4	.55	.04	.32	-.32	.58	.26	-.12	.14
2-5	-.51	-.75	-.17	-.71	-.65	-.19	-.41	-.37
2-6	.12	-.38	.12	-.43	-.36	-.34	-.44	-.26
2-7	-.67	-.33	-.04	.04	-.79	-.62	.18	-.09
2-8	-.69	-.19	.21	-.36	-.57	-.59	.10	-.10
3-4	.21	-.10	-.81	.34	-.50	-.07	.41	.20
3-5	.99	.93	.98	.95	.99	.83	.83	.86
3-6	.55	.14	.65	.39	.72	.34	.68	.63
3-7	-.01	.41	-.47	.08	.45	-.06	-.44	-.65
3-8	.81	.32	-.30	.38	.38	.11	-.36	-.14
4-5	.11	-.26	-.83	.23	-.50	-.25	.44	.00
4-6	.36	-.49	-.67	-.11	-.42	-.56	.23	-.06
4-7	-.70	-.23	.18	.16	-.57	.08	-.29	-.26
4-8	-.14	.37	.29	.79	-.42	.25	.34	.21
5-6	.51	.33	.62	.60	.77	.46	.78	.71
5-7	.08	.22	-.37	-.14	.46	-.24	-.67	-.32
5-8	.82	.29	-.20	.18	.35	.05	-.20	.12
6-7	-.69	-.37	-.59	-.83	.14	-.27	-.79	-.55
6-8	.07	-.29	-.47	-.25	-.17	-.39	-.48	-.25
7-8	.47	.30	-.74	.38	.65	.68	.40	.68

[a]1 = Threonine; 2 = cystine; 3 = valine; 4 = methionine; 5 = isoleucine; 6 = leucine; 7 = phenalanine; 8 = lysine.

[b]Significance for (parents) 8 d.f. .63 (5%), and for (F_2's) 28 d.f. .36 (5%).

[c]TR = Tennessee Red; CH = Chico; AR = Argentine; FJ = Florida Jumbo.

measurable values of heritability for oil content. These values were somewhat lower than those reported by Patil (16) and Martin (17).

Parents and F_2 populations differed in the degree of correlation between protein and oil contents and ranged from nonsignificant to highly significant. All of the correlations were negative. Holley and Hammons (1) also pointed out that a recirpocal relationship between oil and protein did not occur in all strains of peanuts.

The statistical summary of the amino acids of fat free peanut meals of parents and F_2 populations and their frequency distributions are shown in Tables IV and V. Mean and standard deviation varied significantly for each amino acid. Analysis of variance for each of the amino acids also showed that there were significant genetic differences among the combined populations of all parents and F_2's. There were also differences in the degree of variability among the 18 amino acids. Cystine and methionine had the highest variability, while glutamic acid had the lowest.

Eight essential amino acids were selected for further examination of frequency distributions and resulting data are shown in Table IV. No attempt was made to examine the frequency distributions of the nonessential amino acids in this paper. Among the combined populations of all parents and F_2's, Florida Jumbo was lowest in threonine, valine, isoleucine, and leucine, and highest in phenylalanine. Argentine was lowest for cystine and methionine, but relatively high in phenylalanine and lysine. F334 had the highest average in both threonine and leucine in all populations examined. With most of the essential amino acids, the frequency distributions of the F_2 populations gave a wider range of variability than the parent populations. The F_2 population of F334 x TR had a fairly normal distribution in both threonine and cystine, but transgressive segregations toward low values occurred for valine, isoleucine, and leucine, and a transgressive segregation toward high values for methionine, lysine, and phenylalanine. In FJ x CH and F334 x AR, the F_2 populations showed that, except threo-

nine and cystine, there was a similar pattern of distribution in the 8 essential amino acids. Valine, methionine, and isoleucine exhibited a transgressive segregation toward high values, while both lysine and phenylalanine showed transgressive segregation toward low values. Leucine had a normal distribution in these 2 F_2 populations.

The statistical summary of the fatty acid composition of parental and F_2 populations and their frequency distributions are shown in Table VI. Analysis of variance for each of the fatty acids indicated that there was significant ($P<0.05$) genetic difference among the combined populations of all parents and F_2's. The means from all populations showed that Florida Jumbo was the lowest in 16:0, 18:2, 22:0, and 24:0, but highest in 18:0, 18:1, and 20:0, whereas, F334 was the lowest in 18:0, 18:1, and 20:0, but highest in 18:2, 20:0, and 24:0. Chico was the highest in 16:0 and 22:0. The oleic and linoleic acid content of Florida Jumbo and F334 showed the same pattern as those obtained earlier by Worthington (unpublished data, 1972). As with essential amino acids, most of the frequency distributions of the fatty acids of the F_2 populations had a wider range of variability than their parents. Most of the F_2 means of the 8 fatty acids were between the means of their respective parents. All 3 F_2 populations of 16:0 and 24:0 appeared to have a normal distribution. The frequency distribution of 18:0 skewed toward the low range in the F_2 populations, F334 x TR and F334 x AR. The frequency distribution of 18:2, however, skewed toward the high range. FJ x CH appeared to have a normal distribution of these two fatty acids in the F_2 populations. Transgressive segregations of the F_2 populations were also detected in 20:0, 20:1, and 22:0. Results indicate that, in the F_2 populations, each of the 8 fatty acids in peanuts was inherited quantitatively and controlled by multiple genes. The genetic system for controlling the amount of each fatty acid in peanuts does not appear as simple as has been reported in maize (18) and safflower (19-21). The results, however, suggested that peanuts had the capacity to give a

TABLE VIII

Correlation Between 8 Fatty Acids of Oil of 5 Parents and 3 F_2 Populations of Peanuts

Correlation between[a]	TR[c]	F334	CH[c]	AR[c]	FJ[c]	F334 x TR	FJ x CH	F334 x AR
1-2	-.44[b]	.15	-.14	.19	.38	.13	.15	-.07
1-3	-.81	-.89	-.77	-.01	-.82	-.51	-.85	-.50
1-4	.83	-.08	.71	-.18	.78	.40	.82	.20
1-5	-.63	.27	-.08	-.30	-.12	-.10	.02	.01
1-6	-.44	-.39	.33	-.31	-.80	-.35	-.33	-.03
1-7	-.75	.55	-.28	.02	-.10	-.35	.24	-.09
1-8	-.77	-.03	-.03	-.38	-.89	-.17	-.29	-.06
2-3	.14	-.22	.45	-.53	-.46	-.11	-.22	.65
2-4	-.35	-.12	-.26	.43	.29	.09	.18	-.68
2-5	.67	.76	.71	.56	.74	.87	.48	.83
2-6	-.12	-.54	-.12	-.40	-.55	-.87	-.33	-.88
2-7	.56	.20	-.18	-.38	-.39	-.47	.09	-.32
2-8	.32	-.58	-.17	-.59	-.43	-.61	-.15	-.78
3-4	-.97	-.27	-.78	-.87	-.97	-.97	-.99	-.87
3-5	.62	-.34	.37	-.47	-.22	-.04	-.17	.42
3-6	.28	.18	-.43	.11	.90	.14	.19	-.58
3-7	.37	-.83	-.05	.06	-.13	.11	-.44	-.24
3-8	.49	.07	-.10	.14	.77	.07	.10	-.51
4-5	-.77	-.25	.06	.26	.08	.06	.09	-.49
4-6	-.18	.20	.61	-.27	-.88	-.12	-.25	.64
4-7	-.49	.36	-.07	-.45	.20	-.20	.34	.03
4-8	-.52	-.16	-.33	-.33	-.74	-.18	-.15	.47
5-6	.17	-.06	.27	.34	-.17	-.65	.45	-.63
5-7	.56	.36	-.08	.23	-.18	-.41	.37	-.23
5-8	.30	-.59	-.59	-.07	-.02	-.58	.01	-.76
6-7	.35	.16	-.14	.69	.07	.49	.32	.23
6-8	.17	.17	-.56	.43	.82	.60	.33	.70
7-8	.72	.03	.55	.71	.42	.71	.32	.64

[a]1 = 16:0; 2 = 18:0; 3 = 18:1; 4 = 18:2; 5 = 20:0; 6 = 20:1; 7 = 22:0; 8 = 24:0.

[b]Significance for (parents) 8 d.f. .63 (5%), and for (F_2's) 28 d.f. .36 (5%).

[c]TR = Tennessee Red; CH = Chico; AR = Argentine; FJ = Florida Jumbo.

transgressive segregation with some of the amino acids and fatty acids.

Correlations among 8 essential amino acids of fat free peanut meal of 5 parents and 3 F_2 populations are summarized in Table VII. The correlation coefficients varied among the parental and F_2 populations between any 2 amino acids and also among the paired amino acids within each of these populations. Valine-isoleucene, valine-leucine, and isoleucine-leucine had a positive correlation, and cystine-valine and cystine-isoleucine showed a negative correlation in all 5 parents and their F_2 populations. Correlations for other pairs of amino acids were inconsistent as to sign. The correlation between valine and isoleucine was the strongest (r = .83-.99) among all pairs of the 8 essential amino acids examined.

Table VIII shows the correlation among 8 fatty acids of the oil of parent and F_2 populations. High negative correlation coefficients between oleic and linoleic acid were obtained in all populations except F334, which had r = -.27. This parent was low in 18:1 and high in 18:2. Among all correlation coefficients calculated for the 8 fatty acids of the 5 parents, only 7 pairs (16:0-18:1, 16:0-24:0, 18:0-20:0, 18:0-20:1, 18:1-18:2, and 18:2-24:0) had a coefficient with consistent sign. Six of 7 pairs (except 18:2-24:0) also appeared to have correlations in the F_2 populations consistent in sign with their respective parents. The simple correlation coefficients between pairs of fatty acids in inbred lines and varieties of sunflower also showed that there was inconsistency in sign for some of the fatty acids (22).

Correlations between individual amino acids and fatty acids were also examined but most of the relationships were low and inconsistent.

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