

Branching Pattern in Successive Generations of Peanuts *Arachis hypogaea* L.

C. Harkness* and D. J. Wright¹

ABSTRACT

Variation in branching pattern was studied in six Virginia group peanut cultivars (ssp. *hypogaea* var. *hypogaea*). Lines with genetically distinct branching patterns differing from the normal pattern were readily found in two of the cultivars. These variable lines showed no yield advantage over the normal lines. It was concluded that there is considerable genetic variation for branching pattern in Virginia peanuts. The variation could be ascribed to a range of modifier genes which can change the normal pattern of branching. There were indications of a strong environmental effect on branching pattern and of a genotype by environment interaction.

Key Words: Peanut, branching pattern, heritability, variability.

The branching pattern in peanuts (*Arachis hypogaea* L.) has been described by designating the main axis N, the axes developing from it becoming N + 1 branches, with N + 2 branches arising from them (4). In Virginia cultivars, (ssp. *hypogaea* var. *hypogaea*), N + 2 branches generally alternate with two vegetative branches followed by two reproductive branches (2). This pattern is repeated on N + 2 and the higher order vegetative branches. Perry (3) reported radiation mutations in Virginia peanuts which departed from this general pattern. Some had more vegetative N + 2 branches than normal, while others had fewer. It was evident, that, in Nigerian peanuts (ssp. *hypogaea* var. *hypogaea*), there is similar variation in branching pattern among plants within several cultivars. Some cultivars had more individuals differing from a strictly alternate pattern than others. Wynne (5) discussed inheritance of branching pattern in crosses between the peanut subspecies where a side range of patterns appeared. He was not able to postulate any simple genetic models and thought that branching pattern was a quantitative trait.

None of the Nigerian material described in the present work is known to have resulted from sub-specific crosses, and the variation in branching pattern was tentatively ascribed to natural variation within ssp. *hypogaea* var. *hypogaea*. This paper examines whether pattern variants within a cultivar could be isolated by selection and also investigates pattern differences between cultivars. The effect of branching pattern variation on yield was also investigated.

¹Addresses of authors:

C. Harkness, Institute for Agricultural Research, P. M. B. 1044, Zaria, Nigeria.

D. J. Wright, Operational Research Department, Sussex University, Brighton, U. K.

Materials and Methods

The work was carried out at Mokwa Agricultural Research Station, Nigeria (9°19'N, 5°0'E) from 1963 to 1966. Trials were planted about 2nd May in 1964 and 1966 but not until 20th May in 1965 due to late rains in that year.

Six contrasting alternately branched peanut cultivars (ssp. *hypogaea* var. *hypogaea*) of local Nigerian origin were used. Samaru 38 was an old pure line cultivar which had been a standard in yield trials. It was bulked in 1938 from three progeny rows derived from a single plant. The other cultivars were not pure lines, each one comprising a bulk of plants selected in 1959 or 1960 from a plot of a local cultivar. The cultivars, with their groups (1) and original numbers of plants, were as follows: Samaru 38 (Castle Cary Bunch, 1), UBU 591 (Samaru Bunch, 500), TBU 5913 (Ilorin Bunch, 6), VBU 593 (Matevere Bunch, 9), GBS 601 (Kongwa Runner, 150) and GBS 592 (Zaria Runner, 9). In all trials where branching pattern was recorded the peanuts were grown as spaced, single plants 22.9 cm. apart on 0.91m ridges.

In 1963, 0.1 hectare plots of each cultivar were grown. Ten undamaged, typical plants with good yield were taken from each (for TBU 5913, Samaru 38 and GBS 592 twenty plants were taken). The branching pattern of the individual plants was not a criterion for selection. In 1964, progeny of the selected plants were grown in nonreplicated rows containing 40 to 150 plants. At harvest the branching pattern of all the plants in each row, with the exception of damaged ones and those next to missing stands was recorded. The recording was limited to the position of the first set of reproductive branches on the two N + 1 cotyledonary branches, referred to as branches 1, 2 in this paper, and on the two next N + 1 order branches above them, branches 3, 4. The first set of reproductive branches on N + 1 branches was chosen for recording because they are important contributors to yield and are easy to score.

In a normal alternate branching pattern the first set of reproductive branches are at nodes 3 and 4 along an N + 1 branch, while there are vegetative branches at nodes 1, 2 and 5, 6. This pattern is designated 34. Other patterns were for example, 23, 345, 45, etc. Recording stopped on each branch after the position of the first set of reproductive branches was noted and a vegetative branch occurred. The first reproductive branch along the N + 1 branch was frequently solitary and followed by a vegetative branch. The position of such a branch was recorded but for this paper all solitaries were given the classification "S". Any missing or damaged branches were noted but not used in the analysis. Branches 1 and 2 were classified to fall into one of ten categories: 34, 345, 3456, 23, 234, 123, 12, 45, 456, S. Branches 3 and 4 were similarly but not identically classified: 34, 345, 23, 234, 123, 12, 45, 56, S. The difference in categories was due to the very low frequency of 56 on branches 1 and 2 and of 3456 and 456 on branches 3 and 4. For the branches 1, 2, 3 and 4 those having 34 were regarded as normal. Those with 12, 123, 23, 234, 345, 3456 were regarded as variable and, perhaps, advantageous, since they have more reproductive branches formed earlier and may therefore set more pods than normal patterns. Branches 1, 2, 3, and 4 which had the variable classifications were also given the general classification "A" indicating possible advantageous arrangements of flowering nodes. The terms variable and normal are used below to refer to the 1964 parents and their progeny, whilst the classification "A" indicates a possible branching pattern of those progeny.

In 1964 there were 10 progeny rows grown for GBS 601, UBU 591, VBU 593 and 20 rows for the other three cultivars. Parent progeny rows were selected on the basis of percents of plants in the row with branches 1, 2, 3, and 4 having normal 34 patterns and "A" patterns. For each cultivar the most normal row and the most variable row were selected. The significance of the differences between the percents of "A" patterns was calculated for each branch using an unpaired t-test. Seed from the whole rows was harvested and mixed and a sample taken to plant the next generation.

In 1965 there were two lines, one normal and one variable from each cultivar. They were planted in a randomized block with three replications and a plot size of two 0.91m ridges x 7.28 m. At harvest, primary branches 1, 2, 3, and 4 were recorded as in 1964 on about 50 plants per plot excluding those opposite or adjacent to gaps in the row. All seeds of each line were picked and mixed and a sample taken for planting in 1966.

Two trials were planted in 1966, one a replica of the 1965 layout with slightly larger plots (two 0.91m ridges x 9.14m) and one a yield trial of the 12 lines. Seed for both trials was taken from the same source. Branching pattern in the 1966 replica trial was recorded as in 1965, but more plants per plot (about 70) were recorded. The yield trial was a latin square with the six cultivars as main treatments and plots split for normal and variable lines. Sub-plot size was four 0.91m. ridges x 4.75m and planting was two seeds per hole at 22.9cm spacing as per locally recommended practice. Paired t-tests were used to indicate whether the yield differences were significant.

The data were analysed as follows. First, a contingency Chi Square test was applied to each branch of each cultivation 1965 and 1966 to test whether there was an overall relationship between branching pattern and parentage. Second an unpaired t-test was applied to test whether the differences between the rates of occurrence of each branching pattern between the progeny of variable and normal parents was significant. This test was applied only when the difference was in the direction expected for all patterns except "S". This pattern "S" to some extent accounts for any residual differences, and so the t-test was applied to it independent of the direction of the difference.

An hypothesis that 75% of all branches would have the pattern 34 was checked using another unpaired t-test for each year 1964-1966.

Results and Discussion

Relation Between Branching Pattern and Parentage

The results of the Chi Square tests (Table 1) indicate, in most cases, a highly significant degree of dependence between branching pattern and parentage. The branching patterns that give rise to this dependence may, however be different for different branches, years and varieties. To explore this point and also the question of how much difference there was between the branching patterns of the progeny of variable and normal parents we proceed to the results of our t-tests (Table 2). Branching patterns which occurred infrequently have been omitted from the table.

The most important result was the significant differences between branching patterns of group "A" since this was the basis for selection of the parent lines in 1964. The results for the "A" and the 34 patterns of GBS 601 and Samaru 38 indicate that there are highly significant differences be-

Table 1. Significance of Chi-Square values for dependence between branching pattern and parentage.

	GBS 601	Samaru 38	VBU 593	TBU 5913	UBU 591	GBS 592
	'65 '66	'65 '66	'65 '66	'65 '66	'65 '66	'65 '66
Branch 1	** **	**	** **	** **	**	**
Branch 2	** **	**	• ** *	** *	** **	** **
Branch 3	** **	** **	• *	** **	** **	** **
Branch 4	** **	* **	** **	** •	** **	** **

*, ** Significant at the 0.05 and 0.01 levels respectively, blank indicates non-significant according to Chi-Square test.

tween progeny of variable and normal parent lines in the direction expected in 1965 and 1966. For VBU 593, TBU 5913 and UBU 591 there are significant differences in 1965 but not in 1966 except for branch 3 of VBU 593. For GBS 592 there were several significant differences between variable and normal lines for percents of the 34 pattern but not for the "A" patterns, except for branch 2 in 1966. These results suggest that there are clear genetic differences between the normal and variable lines in GBS 601 and Samaru 38 but not in the other cultivars. However, the differences between the variable and normal parent lines in 1964 also depended on the cultivar (Table 3). The parents were highly significantly different in branches 1 and 2, except for UBU 591 where the differences were almost significant at the 0.05 level.

Effect of Environment

The branching patterns of the lines differed considerably between 1965 and 1966 (Table 2). For branches 1 and 2 of all the normal lines there were more "A" patterns in 1966 than in 1965, and in most cases the percents about doubled. Also for branches 1 and 2 and patterns 34 and "A", the normal lines of GBS 601 and Samaru 38 changed in the same direction and so did the variable lines. The changes were notably large in the latter. The solitary reproductive branch "S" occurred less frequently in 1966 than 1965 on nearly all branches of nearly all lines. Similarly there were fewer 45 (and 456) patterns on branches 1 and 2 in all lines. These instances of regularity in the differences in results between 1965 and 1966 are indications of an environmental effect.

Genotype and environment interaction

There are indications of interaction between the genotype and environment from comparisons between the 1965 and 1966 results for 34 and "A" patterns (Table 2, Totals all branches). The variable lines of VBU 593 and GBS 592 differed the most from one another in response while the normal and variable lines of GBS 601 also showed marked differences. Heterozygosity may have contributed to apparent interaction but most lines had

Table 2. Percent of plants with various branching patterns from selected parental populations of six peanut cultivars.

BRANCHING PATTERN	GBS601		Samaru 38		VBU 593		TBU 5913		UBU 591		GBS 592		
	1965	1966	1965	1966	1965	1966	1965	1966	1965	1966	1965	1966	
	V N	V N	V N	V N	V N	V N	V N	V N	V N	V N	V N	V N	
Branch 1	34	25 45**	17 47**	64 72	42 77**	57 72*	67 64	55 58	70 61	54 54	60 64	50 69**	47 59*
345	43 21**	26 32	14 7*	25 9**	18 10	14 23	17 11	18 15	5 2	14 12	16 14	35 25	
3456	18 11	54 16**	4 1	21 3**	5 2	4 8	5 1*	4 6	1 0	2 1	2 3	11 7*	
23	2 4	1 1	1 2	5 3	4 3	9 1**	4 1	4 2	1 1	4 8	3 0*	1 4	
234	1 6	1 2	1 0	3 1	5 1*	1 1	2 1	1 1	1 0	2 0	0 0	2 2	
45	7 4	1 1	5 8	1 2	4 8	2 1	8 25	1 8	28 26	16 14	21 1**	2 1	
A	66 42**	83 51**	20 10*	56 17**	33 17**	29 34**	29 13**	28 26	10 3*	21 22	22 17	49 39	
S	1 6**	0 0	8 10	1 2	1 1	1 1	6 4	1 0	6 15	1 0	1 12**	1 0	
Branch 2	34	32 42	14 50**	64 67	53 70**	62 74*	69 65	60 61	68 59	51 54	68 70	53 66*	47 66**
345	37 22**	28 30	15 11	24 14**	16 12	12 21	10 9	14 12	11 2**	4 6	13 12	29 22	
3456	18 9	50 14**	1 1	8 4	4 2	5 5	3 1	6 9	1 0	0 1	4 3	14 5**	
23	2 4	2 2	1 1	9 8	4 2	10 2**	4 0*	4 6	5 1*	7 9	0 1	4 5	
234	1 5	6 2	0 1	3 0*	5 1	1 1	0 1	2 0	2 0	1 1	0 1	1 2	
45	5 6	0 1	8 6	1 3	6 7	2 3	6 19	2 7	28 25	15 9	23 2**	3 1*	
A	58 41*	85 48**	17 13	44 26**	29 16*	29 30	19 11*	28 29	20 3**	12 19	17 16	48 33**	
S	2 8*	0 1	10 12	1 1	2 2	0 0	14 7	1 1	1 18**	0 1	3 14**	0 1	
Branch 3	34	29 57**	25 75**	63 72	69 84**	46 71**	74 86**	71 85**	81 81	70 70	85 82	92 66	76 81
345	4 1	23 8**	1 1	9 2**	0 3	7 7	0 0	4 5	2 0	7 2*	0 1	12 8	
23	48 25**	30 10**	21 11*	13 11	40 14**	14 5**	13 3**	13 10	17 7**	5 12	4 8	7 6	
234	4 1	18 5**	1 1	3 1*	0 2	1 0	1 0	1 1	1 0	0 0	1 1	1 1	
A	62 30**	73 24**	25 12**	29 14**	46 19**	25 13**	17 4**	18 17	21 7**	12 15	5 12	21 16	
S	8 11	0 0	12 16	0 1	7 10	1 0	11 11	1 1	9 23**	0 0	2 20**	2 2	
Branch 4	34	28 58**	40 83**	50 51	72 58	40 75**	80 85	60 85**	82 88	75 69	81 84	90 56	81 88*
345	1 1	9 4	3 1	6 1**	1 1	3 6	0 0	7 6	2 1	3 1	0 2	8 5	
23	38 19**	36 11**	29 15**	14 38	40 14**	12 8	19 5**	9 3	17 3**	15 11	2 11	7 6	
234	9 4	13 2**	1 1	3 1	4 1	0 1	4 0*	0 1	1 1	0 1	0 2	0 1	
A	60 27**	59 17**	35 20**	27 40	54 16**	17 14	25 6**	16 10	20 4**	17 14	2 15	16 11	
S	12 14	1 1	15 28**	1 1	6 9	0 1	13 9	1 1	5 26**	1 1	5 30**	3 0**	
All Branches	34	28 50**	24 64**	60 65	59 72**	50 73**	72 75	61 72*	75 72	62 62	73 75	71 64	63 72
A	61 35**	75 35**	24 16	38 24**	40 17**	25 23	22 8**	22 20	18 4**	15 17	12 15	33 25	
No. of plants	151 145	178 177	159 155	200 213	112 132	201 180	160 163	200 207	154 149	190 214	140 150	178 216	

A indicates possibly advantageous branching patterns

S indicates a solitary branching pattern

*, ** indicate differences between variable, V, and normal, N, lines significant at 0.05 and 0.01 levels according to an unpaired t - test.

appeared stable from 1964 to 1966 (Table 4).

Genetic Control

It was common for 34 branches and non 34 branches to occur on the same plant, while individuals with all four branches having non 34 patterns were rare. A consideration of the numbers of plants bearing nil, one, two, three or four non 34

branches did not suggest any simple genetic models.

A measure of the normality of branching pattern is given by the percent of 34 branches in the population (Table 4). From these figures it could be suggested that 75% is normal and that modifiers occur to change this. The significance of differences from 75% is indicated in the table and it is clear

Table 3. Percent of 1964 plants with branching patterns in group "A".

	GBS 601		Samaru 38		VBU 593		TBU 5913		UBU 591		GBS 592	
	V	N	V	N	V	N	V	N	V	N	V	N
Branch 1	53	12**	43	8**	20	0**	44	6**	17	6	49	11**
Branch 2	57	15**	35	4**	50	0**	35	6**	16	4	51	14**
Branch 3	57	12**	39	38	20	0**	6	0	11	4	2	4
Branch 4	68	8**	4	11	20	3	0	0	2	0	0	7
No. of plants	28	65	23	26	10	34	52	46	63	46	49	28

*, ** significant at the 0.05 and 0.01 levels, respectively according to an unpaired t - test.

Table 4. Percents of 34 branching pattern over all N+1 branches, 1964-1966, with test of whether these percents are significantly different from 75.

	GBS 601		Samaru 38		VBU 593		TBU 5913		UBU 595		GBS 592	
	V	N	V	N	V	N	V	N	V	N	V	N
1964	33**	86*	65	78	65	82	78	92**	72	75	72	86
1965	28**	50**	60**	65**	51**	73	61**	72	63**	62**	71	64**
1966	24**	64**	59**	72	72	75	75	72	73	75	63**	72

*, ** indicate significance of difference from 75% at the 0.05 and 0.01 levels respectively, using an unpaired t - test.

that GBS 601 variable and normal lines are significantly different in each year 1964-1966. Most lines deviate from 75% 34 branches in 1965 perhaps due to the late rains that year. The variable lines of Samaru 38 and GBS 592 differed significantly from 75% 34 branches in 1966 but not in 1964.

A separate unpaired t-test showed that in only two lines was there a significant difference at the 0.05 level between the percent of 34 branches in 1964 and in 1966. These were the GBS 601 and the TBU 5913 normal lines. Both had significantly less 34 branches in 1966 than in 1964 but also both had had exceptionally high percents of 34 branches in 1964. This change could indicate heterozygosity in the 1963 single plant parents or mutation or outcrossing during the course of the experiment. The very high percents of 34 branches present in 1964 may have indicated modification of a normal situation in the other direction.

The sources of the genetic variation selected in GBS 601 and Samaru 38 are not known. In the case of GBS 601, the original bulk contained 150 plants and different genotypes were likely to have been present when the parent plants were selected. It is interesting that from only 10 plants selected, two of them gave rise to lines with different branching patterns.

For Samaru 38 the situation was different since

the cultivar came from a single plant. The original plant may have been heterozygous, while outcrossing, mutation or both could well have occurred over the years. Lines differing in branching pattern were obtained from only 20 single plants. It appears therefore that there is considerable genetic variation for branching pattern present in Virginia peanut cultivars.

Effect of Branching Pattern on Yield

There were no significant differences in yield between the variable and normal lines for five of the cultivars. In TBU 5913, the normal line significantly outyielded the variable line at the 0.05 level. Yields were in the range 2100 to 2500 kg. ha⁻¹ pods.

Conclusions

From the cultivars GBS 601 and Samaru 38, genetically distinct lines were selected with different arrangements of reproductive branches at the proximal end of the four first formed N + 1 branches. The lines represented in each cultivar a normal arrangement for Virginia peanuts and a variable arrangement. The latter showed longer sequences of reproductive branches and their appearance at lower nodes than usual.

In four of the cultivars normal and variable lines did not appear to be distinctly different. However, over all cultivars and branches there was a general dependence of branching pattern on parentage.

There was evidence of a strong environmental effect on branching pattern from comparisons between 1965 and 1966. The latter also showed an interaction between genotype and environment.

The variable lines showed no yield advantage over the normal lines.

The data collected on branching pattern provided a basis for speculation on genetical interpretations of branching behavior. No simple genetic models were apparent. It was thought that there may be several genes which can modify the normal branching pattern in various ways. There is evidently a considerable amount of genetic variation for branching pattern present in Virginia peanut cultivars.

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