Genetics of non-nodulation in groundnut (Arachis hypogaea L.) (1)

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Summary. — Non-nodulating groundnut plants were identified in the crosses of a rust resistant Peruvian cultivar, PI 259747, with two Virginia cultivars, NC 17 and NC Ac 2731. Segregation in the F_2 and F_3 progeny rows of the cross PI 259747 \times NC 17 indicated that a pair of independent duplicate genes controls nodulation. The genetic constitution of the non-nodulating plant could be inferred to be $n_1 n_2 n_1 n_2$.

INTRODUCTION

The host-rhizobium interaction in legumes is well documented [Voorhees, 1915; Nutman, 1954; Caldwell, 1966; Hubell and Elkan, 1967a, b and Vest and Caldwell, 1972]. The genetic basis of non-nodulation has been described in soybean [Williams and Lynch, 1954 and Weber, 1966], red clover [Nutman, 1949] and peas [Holl, 1975]. However, there is only one recent instance of non-nodulation occuring in the cultivated groundnut, Arachis hypogaea L. [Gorbet and Burton, 1979]. In this study Gorbet and Burton [1979] observed non-nodulating plants in an F₃ population in a breeding nursey and these observations were confirmed in subsequent generations. However, the authors could only conclude from their studies that non-nodulation is not conditioned by a single simple recessive gene.

In 1978 it was observed that in a rust screening nursery at the ICRISAT research farm at Patancheru, near Hyderabad in India, F2 progenies were segregating for plant colour. Plants were either normal green or yellow in colour, indicating severe nitrogen deficiency. On examination the plants with yellow foliage were found to be devoid of nodules. This first paper reports the results of the genetics of non-nodulation based on data from a number of F2 plants, and a full study on their individual F3 progenies.

MATERIALS AND METHODS

PI 259747 is a Valencia genotype (A. hypogaea subsp. fastigiata var. fastigiata) of Peruvian origin and has been found to possess a high level of resistance to rust (Puccinia arachidis). It has been used as a parent in many crosses in breeding programs at ICRI-SAT. Non-nodulating plants were observed in segregating F₂ progenies of the crosses, NC 17 × PI 259747 and NC Ac 2731 \times PI 259747. NC 17 and NC Ac 2731 are Virginia cultivars (A. hypogaea subsp. hypogaea var. hypogaea).

 F_2 progenies from individual F_1 plants in the cross $NC 17 \times PI 259747$ were planted in rows 75 cm apart and spaced at 15 cm apart within the row during the rainy season of 1978. Seeds obtained from each F2 plant were again progeny rowed to produce the F₃ generation during the postrainy season, 1978-79. Each individual F, plant was scored during the podding phase for green or yellow foliage. At harvest, F, plants were individually scored as nodule-bearing or non-nodulating (Fig. 1).

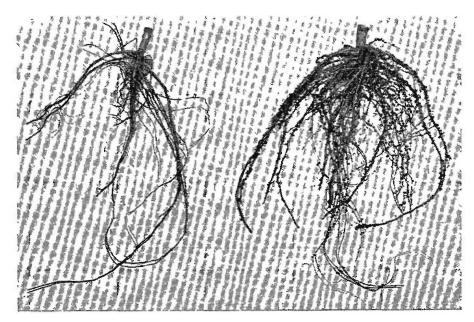


FIG. 1. — Non-nodulating (left) and nodulating (right) groundnut plants.

Groundnut Improvement Program, International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), ICRISAT Patancheru P. O., Andhra Pradesh 502 324, India. Submitted as J. A. No. 139.
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Data on segregation for nodulation of 19 progeny rows of the cross NC 17 \times PI 259747 were examined both at F_2 and F_3 for the possible hypotheses of genetic control of nodulation using the chi-square test.

RESULTS AND DISCUSSION

When the F_2 data on the 19 progeny rows (Table I) were examined on the leaf colour-nodulation 2×2 contingency table, it was found that these two factors are highly associated. The data when pooled over the progeny row gave the following observed frequencies:

	Nodulating green	1 198
********	Nodulating yellow	100
	Non-nodulating green	32
******	Non-nodulating yellow	72
	Total	1 402

The x^2 test for the Null hypothesis «nodulation is independent of leaf colour» was significant (332.9) at 1 p. 100 level thus rejecting it. Hence, further analyses were based on nodulation data alone.

The F_2 data (Table I) clearly pointed to a 15:1 ratio for nodulating to non-nodulating plants both for most of the 19 individual progeny rows and when analysed overall. This suggests a pair of independent duplicate genes controlling nodulation. This result was based on samples of 19 to 207 plants in individual progeny rows and on 1 402 plants for the cross NC 17 \times PI 259747. The genes can thus be symbolised as N_1 and N_2 with n_1 n_1 n_2 n_2 being the non-nodulating

genotype. Such an analysis was not done for the cross NC 2731 \times PI 259747 in F₂.

Based on the two duplicate gene hypothesis, the F_3 data were examined for segregation with respect to nodulation in two ways. Firstly, only families which segregated for nodulation in F_3 were considered. The F_2 genotypes which would give rise to F_3 families segregating for nodulation would be

$$\frac{N_1 N_2}{n_1 n_2}$$
, $\frac{N_1 n_2}{n_1 N_2}$, $\frac{N_1 n_2}{n_1 n_2}$ and $\frac{n_1 N_2}{n_1 n_2}$ only.

The segregation ratio for nodulating: non-nodulating would then be 27:5 in the F_3 generation. The test of significance of deviation from this ratio was provided by X^2B . Secondly, if we consider all the F_3 families descending from all possible F_2 plants, it is apparent that we get a 1:1 ratio for segregating to non-segregating families in F_3 , which was tested by X^2C .

A remarkable fit to the expected ratios was obtained in F_3 in both cases (Table I). Since the fit to expected ratios was adequate in most of the progeny rows, as well as overall, by three tests (X²A, X²B and X²C), and as the samples are fairly large in each progeny row and adequately large over the cross, NC 17 × PI 259747, the genetic constitution of the non-nodulating plant could be inferred to be $\frac{n_1 n_2}{n_1 n_2}$. This was well-supported by the data on the F_3 generation of the other cross, NC 2731 × PI 259747 (N = 2146; NN = 397; X²B = 0). However, the frequency of segregating to non-segregating families in F_3 did not fit to the expected ratio and this can almost

certainly be attributed the loss of several F3 families

TABLE I Status of nodulation in the cross NC 17 imes PI 259747

due to disease.

Identity	Observed frequency plants in \mathbb{F}_2		$ m X^2A$	Observed frequency plants in segregating F ₃		X²B	Observed frequency families in F ₃		X ² C
	N	NN		N	NN		SG	NS	
17-1	104	7	0	651	113	0.36	49	54	0.24
17-2	88	4	0.57	584	103	0.18	49	40	0.91
17-3	63	10	6.91 *	527	101	0.11	35	35	0
17-4	89	12	5.47 *	826	152	0.01	54	40	2.09
17-5	63	5	0.15	458	92	0.50	38	28	1.52
17-6	45	3	0	186	35	0	22	27	0.51
17-7	94	5	0.24	558	91	1.17.	53	34	4.15
17-8	193	14	0.09	1 060	218	1.92	91	93	0.02
17-9	112	4	1.55	935	169	0.06	57	50	0.46
17-10	114	6	0.32	706	144	1.08	60	57	0.08
17-11	74	7	0.79	396	58	0.41	35	42	0.64
17-12	141	15	3.02	851	154	0.07	66	66	0
17-13	24	1	0.22	143	24	0.18	10	9	0.05
17-14	11	0	+	39	6	0.17	3	8	+
17-15	7	0	+	62	13	0.10	4	2	+
17-16	12	2	+	125	35	4.74 *	9	$\begin{array}{c} 4 \\ 20 \\ 16 \\ 5 \end{array}$	1.92
17-17	40	5	1.82	312	71	2.39	24		0.37
17-18	37	4	0.86	327	66	0.49	25		1.98
17-19	17	2	0.59	102	69	77.58 *	13		3.56
Total	1 298	104	3.26	8 848	1 724	3.72	697	630	3.38

N: Non-nodulating.

SG: Segregating. NS: Non-segregating.

 X^2 A: For deviation from 15:1 ratio. X^2 B: For deviation from 27:5 ratio. X^2 C: For deviation from 1:1 ratio.

^{*:} Significant at 5 p. 100 level. +: Too few observations for testing a ratio.

The genetic control of non-nodulation has been welldocumented in peas [Holl, 1975]. In the case of a cross, Trapper (nodulated) × Afghanistan (non-nodulated), a 3:1F2 segregation was obtained, indicating a single gene control for non-nodulation. However, the nitrogen fixing ability (NFA), as measured by acetylene reduction, was found to be controlled by two complementary genes, Trapper being the parent with high NFA. Evidence has been obtained in this study that non-nodulation is itself under the control of two duplicate genes in Arachis hypogaea.

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RÉSUMÉ

Mécanisme génétique de la non-nodulation chez l'arachide (Arachis hypogaea L.) N. NIGAM, V. ARUNACHALAM, R. W. GIBBONS, A. BANDYOPADHYAY, et P. T. C. NAMBIAR, Oléagi-

neux, 1980, 35, No 10, p. 453-455.

Des plants d'arachides sans nodulations ont été repérés dans Des plants d'arachides sans nodulations ont ête reperes dans des croisements entre un cultivar péruvien résistant à la rouille, le PI 259747, et deux cultivars Virginia, les NC 17 et NC Ac 2731. La disjonction dans les lignées F_2 et F_3 des descendances du croisement PI 259747 \times NC 17 indique que la nodulation est contrôlée par une paire de gènes doubles indépendants. La constitution génétique de la plante sans produlation pouvreit être par la partie de la plante sans produlation pouvreit être par la partie de la plante sans produlation pouvreit être par la partie de la plante sans produlation pouvreit être par la partie de la plante sans produlation pouvreit être par la partie de la plante sans produlation pouvreit être par la partie de la plante sans produlation pouvreit être par la partie de la plante sans partie de la plante sans produlation pouvreit être par la partie de la plante sans produlation pouvreit être par la partie de la plante sans production pouvreit être par la partie de la plante sans production pouvreit être par la partie de la plante sans production pouvreit être par la partie de la plante sans production pouvreit être par la partie de la plante sans production pouvreit être par la partie de la plante sans production pouvreit être partie par nodulation pourrait être $n_1 n_2 n_1 n_2$.

RESUMEN

Mecanismo genético de la falta de nodulación en el maní (Arachis hypogaea L.)
S. N. NIGAM, V. ARUNACHALAM, R. W. GIBBONS, A. BANDYOPADHYAY y P. T. C. NAMBIAR, Oléagineux, 1980, 35, N° 10, p. 453-455.

Plantones de maní sin nodulaciones han sido localizados en cruzamientos entre un cultivar peruano resistente a la roya, el PI 259747, y dos cultivares Virginia, los NC 17 y NC Ac 2731. La disyunción en las líneas F_2 y F_3 de las descendencias del cruzamiento PI 259747 \times NC 17 muestra que la nodulación queda controlada por un par de genes duplicados independientes. La constitución genética de la planta sin nodulación podrío con para la participa de la planta sin nodulación podría ser $n_1 n_2 n_1 n_2$.

