
Record no. D-41
Genetics of non-nodulation in groundnut
(Arachis hypogaea L.)

S. N. NIGAM, V. ARUNACHALAM (2), R. W. GIBBONS, A. BANDYOPADHYAY (2) and P. T. C. NAMBIAR

Summary. — Non-nodulating groundnut plants were identified in the crosses of a rust resistant Peruvian cultivar, PI 259747, with two Virginia cultivars, NG 17 and NC Ac 2731. Segregation in the F2 and F3 progeny rows of the cross PI 259747 × NG 17 indicated that a pair of independent duplicate genes controls nodulation. The genic constitution of the non-nodulating plant could be inferred to be n1 n2 n1 n2.

INTRODUCTION

The host-rhizobium interaction in legumes is well documented [Voorhees, 1915; Nutman, 1954; Caldwell, 1966; Hubbell 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 occurring in the cultivated groundnut, Arachis hypogaea L. [Gorbet and Burton, 1979]. In this study Gorbet and Burton [1979] observed non-nodulating plants in an F1 population in a breeding nursery 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. fastigiala var. fastigiala) 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 ICRISAT. Non-nodulating plants were observed in segregating F1 progenies of the crosses, NC 17 × PI 259747 and NC Ac 2731 × PI 259747. NC 17 and NC Ac 2731 are Virginia cultivars (A. hypogaea subsp. hypogaea var. hypogaea).

F2 progenies from individual F1 plants in the cross NC 17 × 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 F2 plant was scored during the podding phase for green or yellow foliage. At harvest, F2 plants were individually scored as nodule-bearing or non-nodulating (Fig. 1).

---

Fig. 1.—Non-nodulating (left) and nodulating (right) groundnut plants.
RESULTS AND DISCUSSION

When the F2 data on the 19 progeny rows (Table I) were examined on the leaf colour-nodulation 2 x 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 .................. 1198
- Nodulating yellow ................ 100
- Non-nodulating green ............ 32
- Non-nodulating yellow .......... 72

The x² test for the Null hypothesis «nodulation is independent of leaf colour» was significant (322.9) at 1 p. 100 level thus rejecting it. Hence, further analyses were based on nodulation data alone.

The F2 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 1402 plants for the cross NC 17 x PI 259747. The genes can thus be symbolised as N1 and N2 with n1n1 n2n2 being the non-nodulating genotype. Such an analysis was not done for the cross NC 2731 x PI 259747 in F2.

Based on the two duplicate gene hypothesis, the F2 data were examined for segregation with respect to nodulation in two ways. Firstly, only families which segregated for nodulation in F2 were considered. The F2 genotypes which would give rise to F3 families segregating for nodulation would be

\[
\frac{n_1 n_1 n_2 n_2}{n_1 n_2 n_1 n_2}
\]

The segregation ratio for nodulating : non-nodulating would then be 27 : 5 in the F2 generation. The test of significance of deviation from this ratio was provided by x² B. Secondly, if we consider all the F2 families descending from all possible F1 plants, it is apparent that we get a 1 : 1 ratio for segregating to non-segregating families in F3, which was tested by x² C.

A remarkable fit to the expected ratios was obtained in F2 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 (x² A, x² B and x² C), and as the samples are fairly large in each progeny row and adequately large over the cross, NC 17 x PI 259747, the genetic constitution of the non-nodulating plant could be inferred to be n1n2 n1n2.

This was well-supported by the data on the F3 generation of the other cross, NC 2731 x PI 259747 (N = 2146; NN = 397; X² B = 0). However, the frequency of segregating to non-segregating families in F2 did not fit to the expected ratio and this can almost certainly be attributed the loss of several F3 families due to disease.

TABLE I

<table>
<thead>
<tr>
<th>Identity</th>
<th>Observed frequency plants in F2</th>
<th>x² A</th>
<th>Observed frequency plants in segregating F3</th>
<th>x² B</th>
<th>Observed frequency families in F3</th>
<th>x² C</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>N</td>
<td>NN</td>
<td></td>
<td>N</td>
<td>NN</td>
<td>SG</td>
</tr>
<tr>
<td>17-1</td>
<td>104</td>
<td>7</td>
<td>0</td>
<td>651</td>
<td>113</td>
<td>0.36</td>
</tr>
<tr>
<td>17-2</td>
<td>88</td>
<td>4</td>
<td>0.57</td>
<td>584</td>
<td>103</td>
<td>0.18</td>
</tr>
<tr>
<td>17-3</td>
<td>63</td>
<td>10</td>
<td>0.91 *</td>
<td>527</td>
<td>131</td>
<td>0.11</td>
</tr>
<tr>
<td>17-4</td>
<td>89</td>
<td>12</td>
<td>5.47 *</td>
<td>828</td>
<td>152</td>
<td>0.01</td>
</tr>
<tr>
<td>17-5</td>
<td>63</td>
<td>5</td>
<td>0.15</td>
<td>458</td>
<td>92</td>
<td>0.50</td>
</tr>
<tr>
<td>17-6</td>
<td>45</td>
<td>3</td>
<td>0</td>
<td>186</td>
<td>35</td>
<td>0</td>
</tr>
<tr>
<td>17-7</td>
<td>94</td>
<td>5</td>
<td>0.24</td>
<td>558</td>
<td>91</td>
<td>1.17</td>
</tr>
<tr>
<td>17-8</td>
<td>153</td>
<td>14</td>
<td>0.09</td>
<td>1090</td>
<td>218</td>
<td>1.95</td>
</tr>
<tr>
<td>17-9</td>
<td>112</td>
<td>4</td>
<td>1.55</td>
<td>933</td>
<td>169</td>
<td>0.06</td>
</tr>
<tr>
<td>17-10</td>
<td>114</td>
<td>6</td>
<td>0.32</td>
<td>706</td>
<td>144</td>
<td>1.08</td>
</tr>
<tr>
<td>17-11</td>
<td>74</td>
<td>7</td>
<td>0.79</td>
<td>396</td>
<td>58</td>
<td>0.41</td>
</tr>
<tr>
<td>17-12</td>
<td>141</td>
<td>15</td>
<td>3.02</td>
<td>551</td>
<td>154</td>
<td>0.07</td>
</tr>
<tr>
<td>17-13</td>
<td>24</td>
<td>1</td>
<td>0.22</td>
<td>143</td>
<td>21</td>
<td>0.18</td>
</tr>
<tr>
<td>17-14</td>
<td>11</td>
<td>0</td>
<td>+</td>
<td>39</td>
<td>6</td>
<td>0.17</td>
</tr>
<tr>
<td>17-15</td>
<td>7</td>
<td>0</td>
<td>+</td>
<td>62</td>
<td>13</td>
<td>0.10</td>
</tr>
<tr>
<td>17-16</td>
<td>12</td>
<td>2</td>
<td>+</td>
<td>125</td>
<td>35</td>
<td>4.74 *</td>
</tr>
<tr>
<td>17-17</td>
<td>40</td>
<td>5</td>
<td>1.22</td>
<td>312</td>
<td>71</td>
<td>2.39</td>
</tr>
<tr>
<td>17-18</td>
<td>37</td>
<td>4</td>
<td>0.86</td>
<td>327</td>
<td>66</td>
<td>0.49</td>
</tr>
<tr>
<td>17-19</td>
<td>17</td>
<td>2</td>
<td>0.59</td>
<td>102</td>
<td>69</td>
<td>0.77 *</td>
</tr>
</tbody>
</table>

| Total | 1298 | 104 | 3.26 | 8848 | 1724 | 3.72 | 697 | 630 | 3.38 |

NN : Non-nodulating. NS : Non-segregating. X² B : For deviation from 27 : 5 ratio.
* : Significant at 5 p. 100 level. X² C : For deviation from 1 : 1 ratio.
+ : Too few observations for testing a ratio.
The genetic control of non-nodulation has been well-documented in peas [Holl, 1975]. In the case of a cross, Trapper (nodulated) x Afghanistan (non-nodulated), a 3:1 F$_2$ 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.

REFERENCES


RÉSUMÉ

Mecanisme génétique de la non-nodulation chez l'ara-chide (Arachis hypogaea L.)


Des plants d'arachides sans nodulations ont été repérés dans des croisements entre un cultivar pérévien résistant à la rouille, le PI 259747, et deux cultivars Virginia, les NC 17 et NC Ar 2731. La disjonction dans les lignées F$_2$ et F$_3$ des descendances du croisement PI 259747 x NC 17 indique que la nodulation est contrôlée par une paire de gènes doubles indépendants. La constitution génétique de la plante sans 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.)


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 Ar 2731. La disyunción en las líneas F$_2$ y F$_3$ de las descendencias del cruzamiento PI 259747 x NC 17 muestra que la nodulación queda controlada por un par de genes duplicados independientes. La constitución genética de la planta sin nodulación podría ser n$_1$ n$_2$ n$_1$ n$_2$.