Inheritance of a One-Seeded Pod Trait in Peanut

WILLIAM D. BRANCH

From the Department of Crop and Soil Sciences, University of Georgia, Coastal Plain Experiment Station, Tifton, GA 31793-0748.

Address correspondence to W. D. Branch at the address above, or e-mail: wdbranch@uga.edu.

Normally, the cultivated peanut (Arachis hypogaea L.) has predominantly 2 seeds per pod or more. Two seeds per pod are predominantly found in A. hypogaea L. subsp. hypogaea (the botanical classification of the US runner and virginia market types) and in subsp. fastigiata var. vulgaris (the US spanish market type); whereas, predominantly 3 or more seeds per pod are found in subsp. fastigiata var. fastigiata (the US valencia market type), peruviana (not marketed in the United States), and aequatoriana (not marketed in the United States), and in subsp. hypogaea var. hirsuta (not marketed in the United States). However, recently, predominantly 1 seed per pod selections were found within a Georgia cross population. Crosses involving the 1-seeded pod selection were made to determine its inheritance. The F1, F2, and F3 data indicated that any 2 of 3 duplicate recessive genes designated, osp1, osp2, and osp3, control the 1-seeded pod trait in peanut.

During 2001, highly unusual predominantly one seed per pod selections were found in the F4 cross population between Georgia Browne (Branch 1994) × an advanced Georgia breeding line, GA 962540. Both of these parents have the predominantly normal 2 seeds per pods. GA 962540 originated from a prior cross between PI 203396 × Georgia Browne. Pedigree selection of these plants was practiced through the F4:5 and F4:6 generations. The 1-seeded pod trait bred true to type and resulted in an advanced pure-line genetic selection. Since then, this unusual pod trait has also been observed in the segregating populations from other unrelated cross combinations as well. The objective of this study was to determine the mode of inheritance for this atypical 1-seeded pod trait in peanut.

Materials and Methods

Crosses were made in the greenhouse between the 1-seeded pod genetic selection and the normal 2 seeds per pod peanut cultivars, Georgia Green (Branch 1996) and Georgia-02C (Branch 2003). Georgia Green is from the same cross combination as Georgia Browne (Southern Runner [Gorbet et al. 1987] × Sunbelt Runner [Mixon 1982]); whereas, Georgia-02C is from a cross between Southern Runner and a Georgia high–oleic fatty acid selection derived by γ-irradiation induced mutation from seed of Georgia Runner (Branch 1991). All of the parents in these pedigrees have the normal 2 seeds per pod.

The F1, F2, and F3 cross populations were space planted during 2004, 2005, and 2006, respectively, in field nursery plots at the agronomy research farm near the University of Georgia, Coastal Plain Experiment Station, Tifton, GA. Phenotypic classification was based on individual plants after digging, and segregation data were analyzed by the chi-square A (CHISQA) computer program (Hanna et al. 1978). The CHISQA computer program has periodically been updated to test goodness-of-fit of observed data with >50 different theoretical genetic ratios (Hanna WW, personal communication).
Results and Discussion

The number of seeds per pod of each F1 plant for both cross combinations was classified as normal with 2 seeds per pod. This indicates that the 1-seeded pod trait is recessive to the normal 2 seeds per pod.

The F2 plant segregation from each cross fit a 54 normal, 2 seeds per pod:10 one seed per pod (Table 1). Total, pooled, and homogeneity chi-square values also fit a 54:10 ratio. These results suggest that any 2 of 3 duplicate recessive genes control the 1-seeded pod trait in peanut.

Individual F2 plant selections were made within the Georgia Green/C2 1-seeded pod selection cross combination for subsequent progeny row testing in the F3 generation. The number of seeds per pod from normal F2 plants ranged 78–91% two seeds per pod and 9–22% one seed per pod; whereas, the number of seeds per pod from the plants with the 1-seeded pod trait ranged 5–28% two seeds per pod and 72–95% one seed per pod.

Segregation among F2:3 progeny from a relatively small number of 30 F2 plants with normal 2 seeds per pod did not fit an expected 44 (segregating):10 (nonsegregating) ratio ($\chi^2 = 6.548, P < 0.05$). However, F3 progeny from 15 F2 plants with the 1-seeded pod trait bred true to type. These F3 results still strongly support the F2 findings for trigenic inheritance because other similar ratios (225:31, 55:9, and 13:3) would each result in F3 segregation among F2 plants with the 1-seeded pod trait.

The data from this genetic study indicate that any 2 of 3 duplicate recessive genes control the 1-seeded pod trait. The symbols, osp1, osp2, and osp3, are proposed for the genes controlling this unusual 1-seeded pod trait recently found in the cultivated peanut.

### Table 1. F2 plant segregation for number of seed per pod among 2 peanut cross combinations

<table>
<thead>
<tr>
<th>Cross combination</th>
<th>Number of families</th>
<th>Normal</th>
<th>One (54:10)</th>
<th>$\chi^2$</th>
<th>P</th>
<th>range</th>
</tr>
</thead>
<tbody>
<tr>
<td>Georgia Green × 1-seeded pod selection</td>
<td>3</td>
<td>309</td>
<td>49</td>
<td>1.020</td>
<td>0.25–0.50</td>
<td></td>
</tr>
<tr>
<td>Georgia-02C × 1-seeded pod selection</td>
<td>2</td>
<td>208</td>
<td>38</td>
<td>0.006</td>
<td>0.90–0.95</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
<td>1.026</td>
<td>0.50–0.75</td>
<td></td>
</tr>
<tr>
<td>Pooled</td>
<td></td>
<td>517</td>
<td>87</td>
<td>0.683</td>
<td>0.25–0.50</td>
<td></td>
</tr>
<tr>
<td>Homogeneity</td>
<td></td>
<td></td>
<td></td>
<td>0.343</td>
<td>0.50–0.75</td>
<td></td>
</tr>
</tbody>
</table>

References


