Revolute-Leaf, a New Completely Dominant Mutant in Peanut

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ABSTRACT

A Revolute-Leaf mutant plant was discovered in an advanced Georgia peanut (Arachis hypogaea L.) breeding line, GA 112702. The mutant had leaf margins that curve downward on each of the four small light-green leaflets. Two cross combinations were used to determine the inheritance of this new mutant. F_1 , F_2 , and F_3 segregation data strongly supported a single completely dominant gene, designated Rev, controlling the inheritance of the Revolute-Leaf mutant. The $F_{2:3}$ homozygous revolute-leaf individual plants had shorter mainstem heights, narrower leaflet length and width, narrower canopy width, reduced pod and seed weights, but similar SMK percentages compared to the F_{2:3} homozygous normal leaf plants resulting from the same closely related cross combination (GA 112702 x Revoluted-Leaf mutant).

Key Words: groundnut, *Arachis hypogaea* L., genetic ratio, cross combination.

During 2012, an F_6 high-oleic peanut (*Arachis hypogaea* L.) preliminary yield trial was conducted at the Gibbs Farm near the University of Georgia, Coastal Plain Experiment Station Tifton Campus. The advanced Georgia breeding line, GA 112702, had an unusual looking mutant plant, designated Revolute-Leaf (Fig. 1A). GA 112702 originated from a cross between 'Georgia-06G' (Branch, 2007) and GA 032913 [a sister-line of 'Georgia-09B' (Branch, 2010)].

The Revolute-Leaf mutant has leaf margins that curve downward on each of the four small lightgreen leaflets. It differs from any previously reported dominant leaf mutants found in the literature (Hammons, 1973; Murthy and Reddy, 1993). The Revolute-Leaf mutant is very distinctive and readily apparent after 3-4 weeks from emergence compared to the normal leaf siblings. So, the objective of this study was to determine the inheritance of this new Revolute-Leaf mutant found in peanut.

Materials and Methods

Two cross combinations were made in the greenhouse between GA 112702 x Revolute-Leaf and 'OLin' (Simpson, et al., 2003) x Revolute-Leaf during 2013. F_1 , F_2 , and F_3 populations were grown during 2014, 2015, and 2017, respectively. GA 112702 is a runner market type belonging to subsp. *hypogaea* var. *hypogaea*; whereas, OLin is a spanish market type belonging to subsp. *fastigiata* var. *vulgaris*.

Each year, seed were space-planted 30.5 cm apart in two rows with variable length depending upon number of seed x 1.8 m wide beds on a Tifton loamy sand soil type (fine-loamy, siliceous, thermic, Plinthic Kandidult) at the Gibb's research farm near the University of Georgia, Coastal Plain Experiment Station, Tifton campus (latitude: 31.43°N and longitude: -83.59°W). Recommended cultural practices with irrigation were followed throughout the growing seasons.

Individual plants were harvested near optimum maturity based upon number of days after planting and above-ground plant appearance. After harvest, peanut pods were dried with forced warm air to approximately 6% moisture content before weighing and shelling.

Phenotypic classification was based on individual plants before digging and inverting. Segregation data was analyzed by chi-square analysis for goodness-of-fit (P \leq 0.05) to expected genetic ratios (Strickberger, 1968). Least significant difference (LSD) t-test was used to compare the ten plant average between F_{2:3} Revolute-Leaf and normal leaf homozygous genotypes for mainstem height, leaflet length and width, canopy width, pod weight, sound mature kernels (SMK), and 100 SMK weight.

Results and Discussion

Each F_1 plant from both crosses had the Revolute-Leaf trait (Fig. 1B). This indicated that the Revolute-Leaf trait is completely dominant to normal leaves.

Likewise, the F_2 segregation from the two cross combinations (GA 112702 x Revolute-Leaf and OLin x Revolute-Leaf) showed an acceptable fit for a 3 Revolute-Leaf to 1 Normal leaf expected ratio, respectively (Table 1). The total, summed, and

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Fig. 1. A) Shows a normal leaf shape (left) and the Revolute-Leaf mutant (right). B) Shows the completely dominant effect of the Revolute-Leaf plant in the F_1 generation. C) Shows the $F_{2:3}$ normal leaf progeny rows from the GA 112702 x Revolute-Leaf cross combination. D) Shows two (2-row) plots of Revolute-Leaf mutant plants color and size. E) Shows the whole plant differences among dug and inverted individual plants of normal leaf (left) and Revolute-Leaf (right). F) Shows the pronounced plant differences between Revolute-Leaf mutant (left) and the Spear-shaped Leaf mutant (right).

homogeneity chi-square values were each found acceptable for the 3:1 expected genetic ratio.

 F_3 results confirmed a single completely dominant inheritance model with a 2 segregating: 1 nonsegregating progeny row ratio from $F_{2:3}$ Revolute-Leaf plants ($\chi^2 = 1.785$, $\rho = 0.10 - 0.25$). The normal leaf plants bred true-to-type in the $F_{2:3}$ population from the GA 112702 x Revolute-Leaf cross combination as was expected (Fig. 1C). These $F_{2:3}$ homozygous Revolute-Leaf individual plants had shorter mainstems, smaller leaflet length and width, narrower canopy width, reduced pod and seed weight, but similar sound mature kernels (SMK) percentages as compared to

Table 1. F ₂ plant se	gregation for number	of Revolute-Leaf	and normal shap	ed leaf plants from	two cross combinations, 2015.
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	No. F_2	Plants		ρ	
Cross	Revolute	Normal	$\frac{\chi^2}{(3:1)}$		
GA 112702 x Revolute-Leaf	50	20	0.476	0.25 - 0.50	
OLin x Revolute-Leaf	96	38	0.806	0.25 - 0.50	
Total			1.282	0.50 - 0.75	
Summed	146	58	1.281	0.25 - 0.50	
Homogeneity			0.001	>0.99	

Table 2. Ten plant average comparison between F_{2:3} normal vs revolute-shaped leaf peanut genotypes from the GA 112702 x Revolute-Leaf cross combination, 2017.

Peanut Genotype	Mainstem Height	Leaflet Length	Leaflet Width	Canopy Width	Pod Weight	Sound Mature Kernels	SMK Weight
	(cm)	(mm)	(mm)	(cm)	(g)	(%)	(g/100)
Normal Leaf	17.0 a ^a	33.9 a	19.9 a	78.5 a	174.6 a	73.6 a	59.8 a
Revolute-Leaf	11.7 b	24.6 b	11.7 b	33.6 b	15.2 b	73.8 a	44.0 b

^aMeans within columns followed by the same letter are not significantly different at $P \le 0.05$.

the $F_{2:3}$ homozygous normal leaf plants at maturity resulting from this same closely related cross combination (Table 2).

These findings strongly suggest that the inheritance of the new peanut Revolute-Leaf mutant is controlled by a single completely dominant gene, designated *Rev*. The Revolute-Leaf mutant has a distinctive plant appearance with light-green color and small size (Fig. 1D). It also has shown a onegene completely dominant inheritance as the two other leaf-shape peanut mutants previously reported, Krinkle-leaf (Hammons, 1964) and Gujarat narrow leaf (Balaiah et al., 1977).

The pleiotropic affect between the Revolute-Leaf mutant morphology and associated phenotypic variation is quite pronounced (Fig 1E). The Revolute-Leaf mutant results in more of a whole plant difference in size, shape, color, pod, and seed compared to the Spear-shaped Leaf mutant (Fig. 1F) which was found recently within the Georgia-06G runner-type peanut cultivar (Branch, 2017).

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