



## Morphological traits as variety descriptors of *Arachis pinto*

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**ABSTRACT** - *Arachis pinto* is outstanding in the present agricultural scenery for adapting well to varied environments and in view of its high yield of quality fodder. It is therefore used as forage crop in different countries. In the last 15 years, more than ten cultivars were released in different countries; none of them is protected in Brazil. To protect a cultivar the minimum descriptors of the species must be determined. In this study,  $F_2$  populations of *A. pinto* were evaluated by the number of bristles on the petiole, number of bristles on the basal and distal leaflets, length and width of internodes, length and width of basal and distal leaflets, and flower color. The objective was the determination of morphological traits for variety identification of forage peanut. The performance of the  $F_2$  progenies was trait-dependent. The heritability of all traits was high, indicating that a great part of the variation observed in these genotypes is genetic. This reinforces the usefulness of these traits as variety descriptors of forage peanut.

**Key words:** forage peanut, heritability, bristles, leaflets, flower color.

### INTRODUCTION

One of the nine sections that compose the genus *Arachis*, *Caulorrhizae*, is outstanding as pasture and soil cover, mainly due to the adaptation to different environments and for producing forage of excellent quality (Ladeira et al. 2002). The species *A. pinto* and *A. repens* constitute this section, characterized by rooting nodes that form stolons.

In the study of different descriptors, the following were identified as discriminatory in the differentiation of the two species of the section: leaflets size and shape and bristle presence or absence on the petioles and/or leaflet underside (Krapovickas and Gregory 1994). Intermediate forms between the extremes considered

typical of each species are found in the available germplasm. A larger set of accessions was detected closer to *A. pinto*. Due to the variability in leaflet size and bristle distribution on petioles and leaflets, these traits are potential morphological descriptors of *A. pinto* cultivars.

Since 1990, more than ten commercial varieties of *A. pinto* have been released in different countries. The descriptions of these cultivars include leaflet size and bristle distribution on the plant. The type specimen of *A. pinto*, accession GKP 12787, was considered as reference (Paganella and Valls 2002).

All *A. pinto* cultivars released to date have yellow flowers, the color that prevails in the section

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*Caulorrhizae*. Several collecting expeditions for forage peanut germplasm identified additional accessions with cream, orange and white flowers. In artificial crosses involving genotypes with distinct flower colors, yellow flowers occurred in the F<sub>1</sub> generation and were dominant over cream, orange and white flowers (Oliveira and Valls 2003).

The adoption of easily identifiable descriptors with a low genotype-environment interaction is fundamental to protect, maintain, multiply and trade the cultivars released on the market (CIMMYT 1999). This study aimed to identify morphological traits with potential as forage peanut variety descriptors.

## MATERIAL AND METHODS

The genotypes evaluated here are constituents of the *Arachis* genebank that is maintained by Embrapa Recursos Genéticos e Biotecnologia, in Brasília, Distrito Federal, Brazil. F<sub>2</sub> populations of intraspecific crosses of *A. pinto* (Table 1) were obtained from seed harvested in October 1999, from hybrids developed by M. P. Oliveira in 1996 and 1997 (Oliveira and Valls 2003). The F<sub>2</sub> seeds were germinated in chambers under controlled humidity and temperature conditions, according to the procedures recommended for *A. hypogaea*. The seedlings were planted in 5 l pots with sterilized soil, in a greenhouse of Embrapa Recursos Genéticos e Biotecnologia.

The F<sub>2</sub> populations (Table 1) were transplanted to an experimental field of Embrapa Cerrados, Planaltina,

DF, in December 2001, in a completely randomized design. One month later, the plants were uniformly cut and three stolons in each plant were randomly marked. The flower color of each genotype was evaluated at flowering. Forty-eight days after cutting, the thickness of the marked stolons was measured by an electronic caliper (in mm), between the third and the fourth node (from stolon top to base), as well as the internode length, using a ruler. The stolons were pressed and dried and the number of bristles was counted on the lower half of the central vein of each previously measured leaflet and on the petiole of the respective leaf by a stereoscopic microscope.

The experimental data of the evaluated F<sub>2</sub> populations were submitted to Pearson's simple correlation analysis and to variance analysis (Table 2), to estimate variance components, heritability and genetic gain with selection for the above-mentioned traits.

The genetic gain with selection ( $G_s$ ) was estimated by:

$$G_s = sd(h_a^2)$$

$$sd = \bar{Y}_s - \bar{Y}_o$$

where:

sd = selection differential;

$\bar{Y}_s$  = mean of selected genotypes;

$\bar{Y}_o$  = general mean of original F<sub>2</sub> population;

$h_a^2$  = broad-sense heritability.

The analyses were run using the statistical package SAS (SAS Institute Inc. 1990).

**Table 1.** Morphological characterization of parents involved in crosses that originated the F<sub>2</sub> segregating populations of *Arachis pinto* evaluated on an experimental field in Planaltina, DF, Brazil. Traits: flower color (F), bristle number on petiole (BNP) and on basal (BNBL) and distal (BNDL) leaflets, internode length (IL) and thickness (IT), length of basal (LBL) and distal (LDL) leaflets, width of basal (WBL) and distal (WDL) leaflets

Cross: 13338 x 12787 - Number of evaluated F <sub>2</sub> genotypes: 56										
Collector <sup>r</sup>	F	BNP	BNBL	BNDL	IL	IT	LBL	LDL	WBL	WDL
V13338	cream	6.67	10.33	0	1.60	0.23	1.67	2.17	1.03	1.20
GKP12787	yellow	66.33	44.33	10.33	1.76	0.26	1.48	1.82	1.12	1.35
Cross: 13167 x 12787 - Number of evaluated F <sub>2</sub> genotypes: 76										
Collector	F	BNP	BNBL	BNDL	IL	IT	LBL	LDL	WBL	WDL
V13167	orange	0	0	0	1.02	0.22	1.32	2.05	0.98	1.20
GKP12787	yellow	66.33	44.33	10.33	1.76	0.26	1.48	1.82	1.12	1.35
Cross: 13167 x 6791-wf - Number of evaluated F <sub>2</sub> genotypes: 36										
Collector	F	BNP	BNBL	BNDL	IL	IT	LBL	LDL	WBL	WDL
V13167	orange	0	0	0	1.02	0.22	1.32	2.05	0.98	1.20
V6791-wf	white	3	2.33	2.67	1.29	0.24	3.47	3.60	1.60	2.00

<sup>r</sup> V = J. F. M. Valls; G = W. C. Gregory; K = A. Krapovickas; P = Pietrarelle

**Table 2.** Analysis of variance, with sources of variation (SV), degrees of freedom (df), mean squares (MS), expected mean squares [E(MS)], estimate of genetic variances (EGV) and broad-sense heritability ( $h_a^2$ )

SV	df	MS	E(MS)	EGV	$h_a^2$
F <sub>2</sub> populations	(g - 1)	MS1	$\sigma^2 + r\sigma_g^2$	$\sigma_g^2 = (MS1 - MS2)/r$	$h_a^2 = \sigma_g^2 / [\sigma^2 + (\sigma_g^2/r)]$
Residue	(g - 1)(r - 1)	MS2	$\sigma^2$	$\sigma^2 = MS2$	
Total	n - 1				

g = number of F<sub>2</sub> genotypes  
 r = number of stolons analyzed per plant;  
 n = total number of data;

Selection pressures of 5% and 20% were adopted to strengthen or weaken each evaluated trait. The correlated response to selection (CR<sub>s</sub>) was evaluated to understand how selection for genotypes with different flower colors (cream in F<sub>2</sub> of cross 13338 x 12787, orange in F<sub>2</sub> of 13167 x 12787, and orange and white in F<sub>2</sub> of 13167 x 6791-wf) could affect the other traits (bristle number on petiole and basal and distal leaflets, internode length and thickness, and length and width of basal and distal leaflets), following the generic expression proposed by Vencovsky and Barriga (1992):

$$CR_{s(2,1)} = sd_{(2,1)} \cdot h_m^2(2),$$

where:

$h_a^2(2)$  = heritability coefficient of a certain trait (2);

$sd_{(2,1)}$  = selection differential in trait (2), when selection focuses on the main trait (1).

$sd_{(2,1)} = \bar{Y}_{s(2,1)} - \bar{Y}_{o(2)}$ , in which:

$\bar{Y}_{s(2,1)}$  = trait mean (2) in populations selected for trait (1);

$\bar{Y}_{o(2)}$  = general mean of trait (2), of the F<sub>2</sub> progeny studied.

## RESULTS AND DISCUSSION

The results show that analysis of variance was significant for all traits in the three populations, except for number of bristles on distal leaflet (Table 3) and width of basal and distal leaflets (Table 4) in F<sub>2</sub> of cross 13167 x 6791-wf. This result can be explained by the similarity of accessions V 13167 and V 6791-wf regarding these traits (Table 1).

Broad-sense heritability estimates were higher than 0.80 for all traits in the three F<sub>2</sub> populations evaluated, except in the cases where variance was not significant (Tables 3, 4 and 5). All F<sub>2</sub> populations presented distinct performance, according to the traits studied; differences among parents involved in the crosses support these results (Table 1).

All evaluated populations proved promising for breeding programs. The variability degree indicates these F<sub>2</sub> as potential gene donors for gene transgression in cultivar development. Tables 6 and 7 show the genetic gains under selection pressures of 5 and 20% in the F<sub>2</sub> populations to increase or reduce each evaluated trait. The means obtained in the selected F<sub>2</sub> population 13167 x 12787 at a selection pressure of 5% to increase the traits (Table 6), show that this progeny can be considered a gene source for increases in bristle number on petiole and basal and distal leaflets, internode thickness, length of distal leaflet, width of basal and distal leaflet. At the same time, at a selection pressure of 5% to reduce these traits, F<sub>2</sub> population 13167 x 12787 can be considered a gene source for reductions in bristle number on petiole and distal leaflet length (Table 7). On the other hand, F<sub>2</sub> of 13338 x 12787 stands out as gene donor to reduce internode length and thickness and basal and distal leaflet width (Table 7). Finally, F<sub>2</sub> of 13167 x 6791-wf has great potential to increase internode length (Table 6) and to reduce bristle number on basal leaflet (Table 7).

Leaflet size and bristle number have frequently been used as descriptors of *A. pintoii* cultivars (Argel and Villarreal 1998). The variability in bristle number in the different plant structures as well as in leaflet size permits the use of these traits in cultivar development. However, the positive association found between the number of bristles on basal and distal leaflets and in the petiole (Table 8) makes it difficult to develop lines that diverge in bristle number, in different plant structures. Likewise, while one of the traits involved in leaflet size was selected, the other associated traits, i.e., length or width of basal and distal leaflets, were changed in the same direction (Table 8). These results justify the description used in released cultivars, which

**Table 3.** Analysis of variance of F<sub>2</sub> populations of the crosses 13338 x 12787 (1), 13167 x 12787 (2) and 13167 x 6791-wf (3), with sources of variation (SV), degrees of freedom (df), mean squares (MS), F test, general mean, coefficient of variation (C.V.), estimates of genetic (s<sub>g</sub><sup>2</sup>) and residual variations (σ<sup>2</sup>) and broad-sense heritability (h<sub>a</sub><sup>2</sup>), of number of bristles on petiole and basal and distal leaflets

SV	number of bristles																				
	petiole									basal leaflet						distal leaflet					
	df			MS			F			MS			F			MS			F		
	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3
F <sub>2</sub>	55	75	34	527.04	1442.37	254.79	4.13*	4.48*	2.39*	83.39	123.03	14.34	2.59*	2.92*	3.09*	9.23	11.01	0.02	1.81*	5.96*	0.89
Residue	84	144	73	127.59	322.08	106.45				32.19	42.19	4.64		5.11	1.85	0.03					
Total	139	219	107																		
F <sub>2</sub> progeny				1	2	3				1	2	3				1	2	3			
General mean				63.45	46.25	37.23				19.20	15.73	1.43				1.55	1.61	0.03			
C.V. (%)				17.80	38.80	27.71				29.55	41.29	150.34				145.8	84.60	636.87			
s <sub>g</sub> <sup>2</sup>				484.51	1334.67	219.31				72.66	108.96	12.79				7.52	10.39	0.01			
s <sup>2</sup>				127.59	322.08	106.42				32.19	42.19	4.63				5.11	1.84	0.02			
h <sub>a</sub> <sup>2</sup>				0.92	0.93	0.86				0.87	0.89	0.89				0.82	0.94	0.67			

\*statistically significant, P ≤ 0.05

**Table 4.** Analysis of variance of F<sub>2</sub> populations of the crosses 13338 x 12787 (1), 13167 x 12787 (2), 13167 x 6791-wf (3), with sources of variation (SV), degrees of freedom (df), mean squares (MS), F test, general mean, coefficient of variation (C.V.), estimates of genetic (s<sub>g</sub><sup>2</sup>) and residual (s<sup>2</sup>) variance and broad sense heritability (h<sub>a</sub><sup>2</sup>) of width of basal leaflet and length and width of distal leaflet

SV	number of bristles																				
	basal leaflet									distal leaflet											
	df			width						length						width					
	1	2	3	MS			F			MS			F			MS			F		
	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3
F <sub>2</sub>	55	75	34	40.19	0.24	0.06	2.70*	4.48*	1.13	0.24	0.53	0.14	2.04*	5.26*	2.15*	0.22	0.41	0.07	2.45*	4.99*	1.15
Residue	84	144	73	0.07	0.06	0.05				0.12	0.10	0.07				0.09	0.08	0.06			
Total	139	219	107																		
F <sub>2</sub> progeny				1	2	3				1	2	3				1	2	3			
General mean				1.27	1.38	1.31				2.20	2.19	2.46				1.53	1.66	1.60			
C.V. (%)				20.98	18.25	17.53				15.50	14.56	10.55				19.47	17.27	15.11			
s <sub>g</sub> <sup>2</sup>				0.17	0.22	0.03				0.19	0.50	0.12				0.18	0.37	0.04			
s <sup>2</sup>				0.07	0.06	0.05				0.12	0.10	0.06				0.08	0.08	0.05			
h <sub>a</sub> <sup>2</sup>				0.88	0.92	0.67				0.84	0.94	0.86				0.87	0.93	0.72			

\*statistically significant, P ≤ 0.05

**Table 5.** Analysis of variance of F<sub>2</sub> populations of the crosses 13338 x 12787 (1), 13167 x 12787 (2), 13167 x 6791-wf (3), with sources of variation (SV), degrees of freedom (df), mean squares (MS), F test, general mean, coefficient of variation (C.V.), estimates of genetic (σ<sub>g</sub><sup>2</sup>) and residual (σ<sub>r</sub><sup>2</sup>) variance and broad sense heritability (h<sub>a</sub><sup>2</sup>), of length and thickness of internode and length of basal leaflet

SV	df	internode						basal leaflet					
		length			thickness			length			thickness		
		MS	F	MS	F	MS	F	MS	F	MS	F		
	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3		
F <sub>2</sub>	55 75 34	1.32 6.37* 6.17*	3.10* 0.005 0.005	0.003 5.43* 4.04*	1.97* 0.32 0.42	0.20 4.77* 4.34*	2.06* 0.07 0.09	0.09					
Residue	84 144 73	0.21 0.27 0.23	0.001 0.001 0.001										
Total	139 219 107												
F <sub>2</sub> progeny		1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3	1 2 3			
General mean		2.19 2.51 3.12	0.26 0.28 0.28			1.95 1.98 2.27							
C.V. (%)		20.75 20.73 15.44	11.46 12.43 13.99			13.23 15.75 13.78							
s <sub>g</sub> <sup>2</sup>		1.24 1.57 0.64	0.001 0.001 0.002			0.29 0.39 0.17							
s <sub>r</sub> <sup>2</sup>		0.21 0.27 0.23	0.001 0.001 0.001			0.07 0.09 0.09							
h <sub>a</sub> <sup>2</sup>		0.95 0.95 0.89	0.93 0.92 0.83			0.94 0.93 0.85							

\*statistically significant, P ≤ 0.05.

are denoted glabrous or waxy. Glabrous leaves are always related to the presence of smaller leaflets than the type specimen, GK 12787 (Paganella and Valls 2002).

Besides, the possibility of creating divergent lines for these traits can lead to the generation of one genotype that presents, for instance, glabrous leaflets and bristly petioles, or longer and narrower leaflets, through artificial crosses between these lines. However, this genetic correlation must be due to linkage among the different genes responsible for these traits, and not to pleiotropy (Falconer 1981). On the other hand, the lack of association between leaflet size and bristle number in leaflets and petiole allows the development of cultivars that can be distinguished according to the different combination of these traits.

In the evaluated F<sub>2</sub> populations, the coefficients of variation in bristle number in the distal leaflet were high (Table 3). It should be emphasized that accessions used as parents of the populations evaluated here do not vary largely in bristle number in the distal leaflet. It would be necessary to evaluate populations of crosses between divergent accessions to draw sound conclusions on the possibility of using this trait as variety descriptor.

Stolon-related characteristics have been studied in depth in breeding programs of white clover, mainly due to the positive associations between internode length and pasture persistence (Collins et al. 1997) and between internode length and stolon density (Annicchiarico and Piano 1995). Besides the associations with traits of agronomic interest, these traits are not much influenced by the environment (Collins et al. 1997), featuring them as potential variety descriptors. The variability in F<sub>2</sub> populations is sufficient to develop divergent lines in both internode traits evaluated (Table 6 and 7).

The flower color in the accessions used as F<sub>1</sub> parents varied (Table 1). Preliminary results showed dominance of yellow flower over the other colors. In crosses between accessions of distinct colors, as for example orange x cream flower, the flowers of F<sub>1</sub> hybrids were always yellow (Oliveira and Valls 2003). In the F<sub>2</sub> progeny, derived from a selfed F<sub>1</sub> hybrid with yellow flowers (which was however originated by parents with different and not-yellow flower colors) some plants with

**Table 6.** Means of original F<sub>2</sub> populations ( $\bar{Y}_0$ ) and selected genotypes ( $\bar{Y}_s$ ), and genetic gain with selection (G<sub>s</sub>) to increase the traits bristle number on petiole (BNP) and basal (BNBL) and distal (NBBL) leaflets, internode length (IL) and thickness (IT), length of basal (LBL) and distal (LDL) leaflets, width of basal (WBL) and distal (WDL) leaflets, under selection pressures of 5% and 20% in F<sub>2</sub> populations of the intraspecific crosses of *Arachis pintoii*, 13338 x 12787 (1), 13167 x 12787 (2) and 13167 x 6791-wf (3)

Trait	$\bar{Y}_0$			5%						20%					
	$\bar{Y}_s$			$G_s$			$\bar{Y}_s$			$G_s$					
	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3
BNP	63.45	46.25	37.0	85.79	87.03	50.83	20.55	37.92	11.89	79.16	74.76	43.29	14.48	26.51	5.41
							(32.39%)*	(81.99%)	(32.14%)				(22.82%)	(57.32%)	(14.62%)
BNBL	19.20	15.73	1.64	32.75	33.80	7.5	11.79	16.08	5.22	26.3	26.42	2.88	6.29	9.51	1.10
							(61.4%)	(102.2%)	(318.3%)				(32.76%)	(60.46%)	(67.07%)
BNDL	1.55	1.61	0.02	6.58	8.60	0.16	4.12	6.57	0.09	4.01	5.43	0.04	2.03	3.59	0.01
							(265.81%)	(408.1%)	(450%)				(130.9%)	(222.9%)	(50%)
IL	2.19	2.51	3.12	3.50	3.81	4.22	1.24	1.24	0.98	3.0	3.52	3.80	0.77	0.96	0.61
							(56.62%)	(49.40%)	(31.41%)				(35.16%)	(38.25%)	(19.55%)
IT	0.26	0.28	0.28	0.33	0.35	0.33	0.07	0.07	0.04	0.30	0.33	0.31	0.04	0.05	0.02
							(26.92%)	(25.0%)	(14.29%)				(15.38%)	(17.86%)	(7.14%)
LBL	1.95	1.98	2.27	2.51	2.60	2.73	0.53	0.58	0.39	2.30	2.44	2.61	0.33	0.43	0.29
							(27.18%)	(29.29%)	(17.18%)				(16.92%)	(21.72%)	(12.77%)
LDL	2.20	2.19	2.46	2.69	2.87	2.84	0.41	0.64	0.33	2.51	2.67	2.74	0.26	0.45	0.24
							(18.64%)	(29.22%)	(13.41%)				(11.81%)	(20.55%)	(9.76%)
WBL	1.27	1.38	1.31	1.64	1.90	1.65	0.33	0.48	0.23	1.55	1.71	1.53	0.39	0.30	0.15
							(25.98%)	(34.78%)	(17.56%)				(30.71%)	(21.74%)	(11.45%)
WDL	1.53	1.63	1.60	1.97	2.26	1.90	0.41	0.59	0.28	1.84	2.09	1.80	0.27	0.43	0.19
							(26.79%)	(36.19%)	(17.5%)				(17.65%)	(26.38%)	(11.87%)

\*In parentheses: genetic gain in percentage of original mean

**Table 7.** Means of original F<sub>2</sub> populations ( $\bar{Y}_0$ ) and selected genotypes ( $\bar{Y}_s$ ), and genetic gain with selection (G<sub>s</sub>) to reduce the traits bristle number on petiole (BNP) and basal (BNBL) and distal (BNDL) leaflets, internode length (IL) and thickness (IT), length of basal (LBL) and distal (LDL) leaflets, width of basal (WBL) and distal (WDL) leaflets, under selection pressures of 5% and 20% in F<sub>2</sub> populations of the intraspecific crosses of *Arachis pintoii*, 13338 x 12787 (1), 13167 x 12787 (2) and 13167 x 6791-wf

Trait	$\bar{Y}_0$			5%						20%					
	$\bar{Y}_s$			$G_s$			$\bar{Y}_s$			$G_s$					
	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3
BNP	63.45	46.25	37.0	36.38	2.03	25.67	-24.90	-41.12	-9.74	45.97	8.47	29.75	-16.08	-35.14	-6.24
							(-39.24%)	(-88.91%)	(-26.32%)				(-25.34%)	(-75.98%)	(-16.86%)
BNBL	19.20	15.73	1.64	8.25	16.20	0	-9.53	0.42	-1.46	12.03	14.59	0.13	-6.24	-1.01	-1.34
							(-49.63%)	(2.67%)	(-89.02%)				(-32.52%)	(-6.42%)	(-81.71%)
BNDL	1.55	1.61	0.02	0	0	0	-1.27	-1.51	-0.13	0	0	0	-1.27	-1.51	-0.13
							(-89.93%)	(-93.79%)	(-650.0%)				(-81.94%)	(-93.79%)	(-650.0%)
IL	2.19	2.51	3.12	0.73	1.09	2.25	-1.39	-1.35	-0.77	1.05	1.49	2.53	-1.08	-0.97	-0.53
							(-63.47%)	(-53.78%)	(-24.68%)				(-49.31%)	(-38.65%)	(-16.99%)
IT	0.26	0.28	0.28	0.16	0.20	0.21	-0.09	-0.07	-0.06	0.19	0.22	0.23	-0.07	-0.06	-0.04
							(-34.62%)	(-25.0%)	(-21.43%)				(-26.92%)	(-21.43%)	(-14.28%)
LBL	1.95	1.98	2.27	1.0	1.03	1.83	-0.89	-0.88	-0.38	1.36	1.38	1.93	-0.55	-0.56	-0.29
							(-45.62%)	(-44.44%)	(-16.74%)				(-28.21%)	(-28.28%)	(-12.77%)
LDL	2.20	2.19	2.46	1.34	0.91	2.04	-0.72	-1.20	-0.36	1.66	1.55	2.18	-0.45	-0.60	-0.24
							(-32.73%)	(-54.79%)	(-14.63%)				(-20.45%)	(-27.39%)	(-9.76%)
WBL	1.27	1.38	1.31	0.60	0.66	1.12	-0.59	-0.66	-0.13	0.81	0.95	1.15	-0.40	-0.39	-0.13
							(-46.46%)	(-47.83%)	(-9.92%)				(-31.50%)	(-28.26%)	(-9.92%)
WDL	1.53	1.63	1.60	0.65	0.67	1.32	-0.76	-0.89	-0.26	0.98	1.03	1.40	-0.48	-0.56	-0.19
							(-49.67%)	(-54.60%)	(-16.25%)				(-31.37%)	(-34.35%)	(-11.87%)

\*In parentheses: genetic gain in percentage of original mean

**Table 8.** Pearson's simple correlation analysis among the traits bristle number on petiole and basal and distal leaflets, internode length and thickness, basal and distal length and width. Joint data analysis of F<sub>2</sub> populations of intraspecific crosses of *Arachis pintoi* (13338 x 12787, 13167 x 12787 and 13167 x 6791-wf). Analysis based on means of three observations per plant

	petiole bristle	basal leaflet bristle	distal leaflet bristle	internode length	internode thickness	basal leaflet length	distal leaflet length	basal leaflet width	distal leaflet width
petiole bristle	1	0.53**	-0.04	-0.03	0.14	0.09	0.11	-0.02	0.11
basal leaflet bristle		1	0.23**	0.02	0.03	0.05	0.11	0.09	0.07
distal leaflet bristle			1	-0.03	-0.03	-0.03	0.01	-0.02	0.06
internode length				1	0.71**	0.67**	0.64**	0.43**	0.73**
internode thickness					1	0.62**	0.64**	0.43**	0.73**
basal leaflet length						1	0.88**	0.59**	0.73**
distal leaflet length							1	0.45**	0.82**
basal leaflet width								1	0.55**
distal leaflet width									1

\*\*statistically significant, P < 0.01

\*statistically significant, P < 0.05

the flower color of the parents of the F<sub>1</sub> hybrid are found, although most flowers are yellow. A good example is the F<sub>2</sub> progeny of 13167 x 6791-wf, with orange x cream flowers. The F<sub>1</sub> derived from this cross has yellow flowers. However, some plants in the F<sub>2</sub> population had white, others orange and a high proportion of genotypes had yellow flowers. The size of the F<sub>2</sub> populations evaluated in this study is still small; the elucidation of this genetic inheritance is therefore not complete, although the proportions confirm the dominance of the yellow over the other colors.

The variation in flower color found in the F<sub>2</sub> populations makes it possible to develop cultivars that diverge in this trait. The correlated responses to selection of F<sub>2</sub> plants with cream-colored flowers of cross 13338 x 12787 show a reduction in the overall mean of the traits evaluated (Table 9). The responses to selection for orange flowers in F<sub>2</sub> of 13167 x 12787 was also negative in all traits evaluated, except in bristle number on distal leaflet. However, in the F<sub>2</sub> progeny of 13167 x 6791-wf, selection for orange flowers did not affect internode thickness. The responses were negative for all other traits evaluated, apart from distal leaflet width, in which the mean of the selected population increased slightly. Selection for flower color further resulted in glabrous distal leaflets but no variation in internode thickness. The basal leaflet length decreased slightly, opposite to the slight increase in the other traits (Table 9).

The results suggest that selection for cream, orange or white flowers result in a reduction of number of bristles on petiole and basal and distal leaflets. The morphological characterization of interspecific hybrids (*A. pintoi* x *A. repens*), and intraspecific hybrids of *A. pintoi* showed that the presence of bristles is genetically inherited (Oliveira and Valls 2003), suggesting dominance of bristle presence over absence. The correlated response to flowers of cream, orange or white colors shows an association between these colors and reduction of number of bristles that can limit the development of cultivars with non-yellow flowers and high bristle density.

It is important to emphasize that genetic gains with selection were high for all traits under study, in the increases as much as decreases of a given trait. It is therefore possible to obtain rapid advances in selection in both directions (Collins et al. 1997). Likewise, the high heritability of all traits evaluated shows that a relevant part of the variation in genotypes of the F<sub>2</sub> populations is genetic (Annicchiarico 1993). This underpins the use of these traits as variety descriptors, though the correlations between these traits must be taken into consideration.

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**Table 9.** Correlated response (CRs) in traits bristle number on petiole (BNP) and basal (BNBL) and distal (BNDL) leaflets, internode length (IL) and thickness (IT), length of basal (LBL) and distal (LDL) leaflets, width of basal (WBL) and distal (WDL) leaflets, for selection according to flower color (cream in F<sub>2</sub> progeny of the 13338 x 12787, orange in F<sub>2</sub> progeny of 13167 x 12787 and orange or white in F<sub>2</sub> of 13167 x 6791-wf), under selection pressures of 5% and 20%

Trait	F <sub>2</sub> 13338 x 12787			F <sub>2</sub> 13167 x 12787			F <sub>2</sub> 13167 x 6791-wf					
	Cream flower selection			orange flower selection			orange flower selection			white flower selection		
	$\bar{Y}_{0*}$	$\bar{Y}_{S**}$	CRs	$\bar{Y}_0$	$\bar{Y}_S$	CRs	$\bar{Y}_0$	$\bar{Y}_S$	CRs	$\bar{Y}_0$	$\bar{Y}_S$	CRs
BNP	63.45	56.08	-6.78 (-10.68%)***	46.25	46.19	-0.06 (-0.13%)***	37.0	30.33	-5.74 (-15.51%)***	37.0	41.56	3.92 (10.59%)***
BNBL	19.20	18.50	-0.61 (-3.17%)	15.73	14.92	-0.72 (-4.58%)	1.64	0	-1.46 (-89.02%)	1.64	0.33	-1.16 (-70.73%)
BNDL	1.55	1.40	-0.12 (-7.74%)	1.61	1.95	0.32 (19.88%)	0.02	0	-0.01 (-50%)	0.02	0	-0.01 (-50%)
IL	2.19	1.88	-0.29 (-13.24%)	2.51	2.42	-0.08 (-3.19%)	3.12	3.20	0.07 (-2.24%)	3.12	3.25	0.12 (3.85%)
IT	0.26	0.24	-0.02 (-7.69%)	0.28	0.27	-0.01 (-3.57%)	0.28	0.28	0	0.28	0.28	0
LBL	1.95	1.76	-0.18 (-9.23%)	1.98	1.95	-0.03 (-1.52%)	2.27	2.23	-0.03 (-1.32%)	2.27	2.36	0.08 (-3.52%)
LDL	2.20	2.06	-0.12 (-5.45%)	2.19	2.14	-0.05 (-2.28%)	2.46	2.40	-0.05 (-2.03%)	2.46	2.53	0.06 (2.44%)
WBL	1.27	1.16	-0.09 (-7.09%)	1.38	1.23	-0.14 (-10.14%)	1.31	1.29	-0.01 (-0.76%)	1.31	1.33	0.01 (0.76%)
WDL	1.53	1.42	-0.09 (-5.88%)	1.63	1.58	-0.05 (-3.07%)	1.60	1.62	0.018 (1.13%)	1.60	1.61	0.01 (0.63%)

\* = original mean of F<sub>2</sub> progeny.\*\* = trait mean when occurred selection for flowers of the colors: cream, in F<sub>2</sub> progeny of 13338 x 12787; orange, in F<sub>2</sub> of 13167 x 12787; orange or white in F<sub>2</sub> of 13167 x 6791-wf.

\*\*\*inside parenthesis, response correlated to selection in percentage of the original mean

## Caracteres morfológicos com potencial de uso como descritores varietais de *Arachis pintoi*

**RESUMO** - *Arachis pintoi* tem tido destaque no cenário agrícola mundial principalmente em função da sua adaptação a diversos ambientes. Mais de dez cultivares foram lançadas nos últimos quinze anos, nenhuma destas protegidas. Para proteger uma cultivar é necessário primeiramente estabelecer os descritores mínimos da espécie. No presente trabalho, progênies F<sub>2</sub> de *A. pintoi* foram caracterizadas quanto ao número de cerdas no pecíolo, folíolos basal e distal, comprimento e espessura do entrenó, comprimento e largura dos folíolos basal e distal e cor das flores, com o objetivo de identificar caracteres morfológicos com potencial de uso como descritores varietais. As progênies F<sub>2</sub> apresentam comportamentos distintos de acordo com o caráter em estudo. A herdabilidade de todos os caracteres foi alta, mostrando que, grande parte da variação observada entre os genótipos das F<sub>2</sub> é genética, o que sustenta a adoção destas características como descritores varietais.

**Palavras-chave:** amendoim forrageiro, herdabilidade, cerdas, folíolos, cor de flor.

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