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CROP BREEDING AND
APPLIED BIOTECHNOLOGY

Morphological traits as variety descriptors of *Arachis pintoi*

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ABSTRACT - Arachis pintoi *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. pintoi *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. pintoi* and *A. repen*s 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. pintoi*. Due to the variability in leaflet size and bristle distribution on petioles and leaflets, these traits are potential morphological descriptors of *A. pintoi* cultivars.

Since 1990, more than ten commercial varieties of *A. pintoi* 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. pintoi*, accession GKP 12787, was considered as reference (Paganella and Valls 2002).

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

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_1 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 Brasilia, Distrito Federal, Brazil. F_2 populations of intraspecific crosses of *A. pintoi* (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_2 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_2 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_2 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:

$G_s = sd(h_a^2)$

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

where:

sd = selection differential;

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

$\overline{Y}_o$ = general mean of original F_2 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 parentals involved in crosses that originated the F_2 segregating populations of *Arachis pintoi* 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

Collector[r]	F	BNP	BNBL	BNDL	IL	IT	LBL	LDL	WBL	WDL
Cross: 13338 x 12787 - Number of evaluated F_2 genotypes: 56										
V 13338	cream	6.67	10.33	0	1.60	0.23	1.67	2.17	1.03	1.20
GKP 12787	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_2 genotypes: 76										
Collector	F	BNP	BNBL	BNDL	IL	IT	LBL	LDL	WBL	WDL
V 13167	orange	0	0	0	1.02	0.22	1.32	2.05	0.98	1.20
GKP 12787	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_2 genotypes: 36										
Collector	F	BNP	BNBL	BNDL	IL	IT	LBL	LDL	WBL	WDL
V 13167	orange	0	0	0	1.02	0.22	1.32	2.05	0.98	1.20
V 6791-wf	white	3	2.33	2.67	1.29	0.24	3.47	3.60	1.60	2.00

[1]* V = J. F. M. Valls; G = W. C. Gregory; K = A. Krapovickas; P = Pietrareli

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_2 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	σ^2	$\sigma^2 = MS2$	
Total	$n - 1$				

g = number of F_2 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_s) was evaluated to understand how selection for genotypes with different flower colors (cream in F_2 of cross 13338 x 12787, orange in F_2 of 13167 x 12787, and orange and white in F_2 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).

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

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

$\overline{Y}_{o(2)}$, = general mean of trait (2), of the F_2 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_2 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_2 populations evaluated, except in the cases where variance was not significant (Tables 3, 4 and 5). All F_2 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_2 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_2 populations to increase or reduce each evaluated trait. The means obtained in the selected F_2 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_2 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_2 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_2 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. pintoi* 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_2 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^2_g) and residual variations (σ^2) and broad-sense heritability (h^2_a), of number of bristles on petiole and basal and distal leaflets

										number of bristles											
				petiole						basal leaflet						distal leaflet					
SV	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_2	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_2 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^2_g				484.51	1334.67	219.31				72.66	108.96	12.79				7.52	10.39	0.01			
s^2				127.59	322.08	106.42				32.19	42.19	4.63				5.11	1.84	0.02			
h^2_a				0.92	0.93	0.86				0.87	0.89	0.89				0.82	0.94	0.67			

*statistically significant, $P \leq 0.05$

Table 4. Analysis of variance of F_2 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^2_g) and residual (s^2) variance and broad sense heritability (h^2_a) of width of basal leaflet and length and width of distal leaflet

				basal leaflet						distal leaflet											
				width						length						width					
SV	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_2	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_2 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^2_g				0.17	0.22	0.03				0.19	0.50	0.12				0.18	0.37	0.04			
s^2				0.07	0.06	0.05				0.12	0.10	0.06				0.08	0.08	0.05			
h^2_a				0.88	0.92	0.67				0.84	0.94	0.86				0.87	0.93	0.72			

*statistically significant, $P \leq 0.05$

Table 5. Analysis of variance of F_2 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^2_g) and residual (σ^2) variance and broad sense heritability (h^2_a), of length and thickness of internode and length of basal leaflet

				internode												basal leaflet					
				length						thickness						length					
	df			MS			F			MS			F			MS			F		
SV	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3	1	2	3
F_2	55	75	34	1.32	1.67	0.72	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*
Residue	84	144	73	0.21	0.27	0.23				0.001	0.001	0.001				0.07	0.09	0.09			
Total	139	219	107																		
F_2 progeny				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^2_g				1.24	1.57	0.64				0.001	0.001	0.002				0.29	0.39	0.17			
s^2				0.21	0.27	0.23				0.001	0.001	0.001				0.07	0.09	0.09			
h^2_a				0.95	0.95	0.89				0.93	0.92	0.83				0.94	0.93	0.85			

*statistically significant, P $\leq$ 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_2 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_2 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_1 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_1 hybrids were always yellow (Oliveira and Valls 2003). In the F_2 progeny, derived from a selfed F_1 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$_2$ populations ($\overline{Y}_O$) and selected genotypes ($\overline{Y}_S$), and genetic gain with selection (G$_s$) 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$_2$ populations of the intraspecific crosses of *Arachis pintoi*, 13338 x 12787 (1), 13167 x 12787 (2) and 13167 x 6791-wf (3)

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

*In parentheses: genetic gain in percentage of original mean

Table 7. Means of original F$_2$ populations ($\overline{Y}_o$) and selected genotypes ($\overline{Y}_s$), and genetic gain with selection (G$_s$) 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$_2$ populations of the intraspecific crosses of *Arachis pintoi*, 13338 x 12787 (1), 13167 x 12787 (2) and 13167 x 6791-wf

| Trait | $\overline{Y}_0$ | | | 5% | | | | | | 20% | | | | | |
| | | | | $\overline{Y}_8$ | | | G$_8$ | | | $\overline{Y}_8$ | | | G$_8$ | | |
	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 (-39.24%)	-41.12 (-88.91%)	-9.74 (-26.32%)	45.97	8.47	29.75	-16.08 (-25.34%)	-35.14 (-75.98%)	-6.24 (-16.86%)
BNBL	19.20	15.73	1.64	8.25	16.20	0	-9.53 (-49.63%)	0.42 (2.67%)	-1.46 (-89.02%)	12.03	14.59	0.13	-6.24 (-32.52%)	-1.01 (-6.42%)	-1.34 (-81.71%)
BNDL	1.55	1.61	0.02	0	0	0	-1.27 (-89.93%)	-1.51 (-93.79%)	-0.13 (-650.0%)	0	0	0	-1.27 (-81.94%)	-1.51 (-93.79%)	-0.13 (-650.0%)
IL	2.19	2.51	3.12	0.73	1.09	2.25	-1.39 (-63.47%)	-1.35 (-53.78%)	-0.77 (-24.68%)	1.05	1.49	2.53	-1.08 (-49.31%)	-0.97 (-38.65%)	-0.53 (-16.99%)
I T	0.26	0.28	0.28	0.16	0.20	0.21	-0.09 (-34.62%)	-0.07 (-25.0%)	-0.06 (-21.43%)	0.19	0.22	0.23	-0.07 (-26.92%)	-0.06 (-21.43%)	-0.04 (-14.28%)
LBL	1.95	1.98	2.27	1.0	1.03	1.83	-0.89 (-45.62%)	-0.88 (-44.44%)	-0.38 (-16.74%)	1.36	1.38	1.93	-0.55 (-28.21%)	-0.56 (-28.28%)	-0.29 (-12.77%)
LDL	2.20	2.19	2.46	1.34	0.91	2.04	-0.72 (-32.73%)	-1.20 (-54.79%)	-0.36 (-14.63%)	1.66	1.55	2.18	-0.45 (-20.45%)	-0.60 (-27.39%)	-0.24 (-9.76%)
WBL	1.27	1.38	1.31	0.60	0.66	1.12	-0.59 (-46.46%)	-0.66 (-47.83%)	-0.13 (-9.92%)	0.81	0.95	1.15	-0.40 (-31.50%)	-0.39 (-28.26%)	-0.13 (-9.92%)
WDL	1.53	1.63	1.60	0.65	0.67	1.32	-0.76 (-49.67%)	-0.89 (-54.60%)	-0.26 (-16.25%)	0.98	1.03	1.40	-0.48 (-31.37%)	-0.56 (-34.35%)	-0.19 (-11.87%)

*In parentheses: genetic gain in percentage of original mean

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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_2 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_1 hybrid are found, although most flowers are yellow. A good example is the F_2 progeny of 13167 x 6791-wf, with orange x cream flowers. The F_1 derived from this cross has yellow flowers. However, some plants in the F_2 population had white, others orange and a high proportion of genotypes had yellow flowers. The size of the F_2 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_2 populations makes it possible to develop cultivars that diverge in this trait. The correlated responses to selection of F_2 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_2 of 13167 x 12787 was also negative in all traits evaluated, except in bristle number on distal leaflet. However, in the F_2 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_2 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_2 progeny of the 13338 x 12787, orange in F_2 progeny of 13167 x 12787 and orange or white in F_2 of 13167 x 6791-wf), under selection pressures of 5% and 20%

Trait	F₂ 13338 x 12787 Cream flower selection			F₂ 13167 x 12787 orange flower selection			F₂ 13167 x 6791-wf orange flower selection			white flower selection		
	$\bar{Y}_{o*}$	$\bar{Y}_{S**}$	CRs	$\bar{Y}_o$	$\bar{Y}_S$	CRs	$\bar{Y}_o$	$\bar{Y}_S$	CRs	$\bar{Y}_o$	$\bar{Y}_S$	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_2 progeny.

**= trait mean when occurred selection for flowers of the colors: cream, in F_2 progeny of 13338 x 12787; orange, in F_2 of 13167 x 12787; orange or white in F_2 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_2 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_2 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_2 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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