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Ranking contrasting genotypes of forage peanut based on nutritive value and fermentation kinetics

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ABSTRACT

The objective of this study was to evaluate the nutritional divergence of perennial peanut genotypes through chemical characteristics as well as *in vitro* fermentation and degradation kinetics. The experiment was conducted at The Brazilian Agricultural Research Corporation (Embrapa Cerrados). The treatments consisted of 10 accessions of *Arachis* spp., 6 accessions of *A. pintoi* (Ap 8, Ap 19, Ap 20, Ap 24, Ap 31, Ap 65) and the cultivar Belmonte, 2 accessions of *Arachis repens* (Ar 5, Ar 26) and an interspecific hybrid (Ap × Ar) 9. The experimental design was a completely randomised block with four replications. Forage evaluations were made at a stubble height of 5 cm from the soil surface with fixed cutting intervals of 42 days during the rainy season. Nutritional divergence was assessed using canonical variate analysis and hierarchical agglomerative clustering including the variables crude protein, neutral detergent fibre, lignin(sa), potential DM degradation at 48 h, the insoluble but potentially degradable DM fraction and the degradation rate of the insoluble but potentially degradable DM fraction. Variables with higher contribution to discrimination of accessions were: rate of degradation, crude protein and potential DM degradation at 48 h. Four distinct nutritional groups were identified: Group I (Ap 8, Ap 19, Ap 31, cv. Belmonte), Group II (Ap 20, Ap 24, Ap 65), Group III (Ar 5. Ar 26) and Ggroup IV (Ap × Ar 9). The nutritional divergence of the *Arachis* evaluated show great variability relative to the parameters analysed, which may impact genetic improvement programs which focus on chemical composition and *in vitro* fermentation characteristics. Group IV (hybrid Ap × Ar 9) had the highest nutritional quality as ruminant feeds.

1. Introduction

Legumes of the genus *Arachis* occur naturally in South America where approximately 80 species exist, 68 of which are in Brazil. The species *Arachis pintoi*, *Arachis repens* and *Arachis glabrata* are also known as forage peanut, and are the most common species used in pastures (Valls and Pizarro, 1994). These species have been recommended for animal feeding due

Abbreviations: ADF, acid detergent fibre; ADICP, AD insoluble CP; *B*, insoluble but potentially degradable DM fraction; *b*, potential DM degradation; C1, degradation rate of NFC; C2, degradation rate for FC; DM, dry matter; EE, ether extract; FC, fibrous carbohydrates; IVDMD, *in vitro* DM digestibility; kd, degradation rate of fraction B; L, lag phase before digestion begins; NDF, neutral detergent fibre; NFC, non-fibre carbohydrates; TC, total carbohydrates; Vf1, maximum volume of gases from NFC; Vf2, maximum volume of gases from FC; WDS, water disposition in the soil.

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Table 1
Average climate data for December 2008 to January 2009 in Planaltina, Federal District, Brazil.

Year	Month	Precipitation (mm)	Temperature (°C)		WDS
			Max.	Min.	Proportion
2008	Dec	149.3	31.3	16.2	0.78
2009	Jan	159.1	30.9	16.3	0.81
2009	Fev	129.5	31.0	15.5	0.84

WDS = water disposition in the soil.
Max. = maximum; Min. = minimum.

Table 2
Average values of pH, aluminum (Al^{3+}), phosphorus (P), potassium (K), calcium (Ca^{2+}), magnesium (Mg^{2+}), hydrogen plus (H + Al) and organic matter (OM), according to depth, in soil at experimental field area in Planaltina.

Depth (cm)	pH (in H_2O)	Al^{3+} (cmolc/dm^3)	P (mg/dm^3)	K (mg/dm^3)	Ca^{2+} (cmolc/dm^3)	Mg^{2+} (c molc/dm^3)	H + Al (cmolc/dm^3)	OM (g/kg)
0–20	5.19	0.12	5.83	63.0	1.33	0.64	4.42	212

to their versatility in utilisation, as they can be fed as cut fresh forage, hay or silage. They have satisfactory productivity, persistency in grass consortiums, and also provide excellent nutritive value (Lascano, 1994). Dry matter (DM) productivity varying from 7000 to 16,000 kg/ha/year, as well as the capacity of these forage legumes to form persistent consortiums with runner growth habit grasses, such as those of the genus *Brachiaria* and *Panicum* species, have been reported (Andrade et al., 2006; Valentim et al., 2001).

Ladeira et al. (2002) evaluated *A. pintoi* using an *in vivo* digestibility essay and demonstrated its superior nutritional value compared to other tropical forage legumes such as stylosanthes (*Stylosanthes guianensis*), perennial soybeans (*Glycine wightii*), leucaena (*Leucaena leucocephala*) and alfalfa (*Medicago sativa*).

Determination of the genetic divergence in accessions of *Arachis* ssp, with the objective of evaluating and selecting forage peanut genotypes based on establishment speed as well as forage and crude protein (CP) production capacity were studied by Valentim et al. (2003). However, studies aiming at differentiating the nutritional value of forage peanut genotypes used in ruminant feeding are scarce. Multivariate analysis has been used to evaluate nutritional divergence in forage species (Azevêdo et al., 2003; Freitas et al., 2006). Among the several multivariate techniques, principal component analysis and use of canonical variables (including Euclidian distance), were recommended by Cruz et al. (2004).

Our objective was to rank different accessions of forage peanut based on chemical composition and *in vitro* DM digestion kinetics.

2. Material and methods

2.1. Location, sampling and treatments

The experiment was conducted at the Brazilian Agriculture Research Institute (Embrapa Cerrados) located at 15° 35′ 30″ latitude south, 47° 42′ 30″ longitude west, from December 2008 to February 2009. The climate is characterised as 'Aw' according to the Köppen classification, denominated as tropical savannah with a 5 months dry season and average annual precipitation of 1577 mm, average annual temperature of 20.4 °C and altitude of approximately 1000 m above sea level (Table 1). The soil in the area is classified as an alic to moderate dark-red Latosol, very clayey texture (LVef), Cerrado phase (*Typic haplustox*) and flat to mildly hilly relief (EMBRAPA, 1999). Soil samples were collected at 0–20 cm and these parameters are in Table 2. Levels of nutrients and pH in the soil were considered satisfactory and no fertilisation was applied before or during the experiment.

The experiment began in December 2007, as a randomised block experimental design with four field replicates. Individual field replicates were obtained from three consecutive forage cuttings. The treatments consisted of 10 accessions of *Arachis spp*. from Embrapa/Acre State (Brazil), constituting 6 accessions of *A. pintoi* (Ap 8, Ap19, Ap 20, Ap24, Ap31, Ap 65) and the cultivar Belmonte, 2 accessions of *A. repens* (Ar 5, Ar 26) and an interspecific hybrid (Ap × Ar 9), all part of the "Embrapa perennial peanut breeding program" (Project No SEG 02.10.07.006.00). The plots were constituted by four lines of 2 m in length, with 0.5 m spacing between lines and 0.25 m between plants, with a usable area of 1 m^2. Planting was with rooted seedlings produced from vegetative material (*i.e.*, stolons). Forage evaluations were at a stubble height of 5 cm from the soil surface, with fixed cutting intervals of 42 days, on 12/04/2008, 1/15/2009 and 2/26/2009, during the rainy season.

After cutting, forage samples were weighed, dried in a forced air circulation oven at 55 °C, ground in a mill to pass a 1 mm mesh screen, and kept in identified plastic containers for later laboratory analyses.

2.2. Chemical analyses and in vitro experiments

The following methods of AOAC, 1990) were used: method 934.01 for DM, method 990.03 for N, method 920.39 for ether extract (EE), method 973.18 for lignin(sa), and ash was determined as the gravimetric residue after heating to 550 °C for 8 h.

Method 973.18 was used for acid detergent fibre (ADF). Neutral detergent fibre (NDF) was assayed using the procedure of Van Soest et al. (1991) without use of α-amylase and sodium sulfite. NDF was expressed inclusive and exclusive of residual ash. ADF was expressed inclusive of residual ash. The AD insoluble CP (ADICP) was assayed according to Licitra et al. (1996). Non-fibre carbohydrates (NFC) were calculated as:

$$\text{NFC} = 1000 - (\text{CP} + \text{NDFom} + \text{EE} + \text{ash})$$

where NDFom represents neutral detergent fibre corrected for ash and the other variables as previously described.

In vitro DM digestibility (IVDMD) was determined by the two-stage method of Tilley and Terry (1963). Gas production and degradability used the *in vitro* semi-automatic gas production technique of Maurício et al. (1999) using inocula collected from ruminally cannulated Holstein cows fed a 700:300 (DM) forage:concentrate diet. Pressure readings were at pre-established intervals of 2, 4, 6, 8, 10, 12, 15, 19, 24, 30, 34, 48, 72 and 96 h by means of a pressure transducer. These values were converted into gas volume through the equation defined by Maurício et al. (2003).

Fermentation residues were obtained through filtration of the fermentation bottles in crucibles (*i.e.*, porosity 1, 100–160 μm) at 12, 24, 48, 72 and 96 h. Results obtained were used to calculate IVDMD.

For mathematical description of ruminal fermentation kinetics obtained from the *in vitro* gas production technique, the two-pool logistic model of Schofield and Pell (1994) was used, adjusted to the cumulative production curves of the gases as:

$$V = \frac{\text{Vf1}/(1 + \exp(2 - 4 * \text{C1} * (t - L))) + \text{Vf2}}{(1 + \exp(2 - 4 * \text{C2} * (t - L)))}$$

where Vf1 is equivalent to the maximum volume of gases from NFC; C1, to the degradation rate (/h) of NFC; Vf2, to the maximum volume of gases from FC; C2, to the degradation rate (/h) of FC; and t and L, to the incubation times (h) and to the lag time (h), respectively.

For evaluation of degradation kinetics using gravimetric techniques an exponential model was used, corrected for the latency period, as described by Snedecor and Cochran (1989) as:

$$Y = b' - B * \exp(-c * t)$$

where Y is the DM residue at time t; b', potential DM degradation; B, the insoluble but potentially degradable DM fraction which will be degradable as a function of time at degradation rate c; c, the degradation rate of fraction B (/h); and t, the incubation time. At 48 h, 3 bottles/replicate were taken out for filtration to estimate potential degradability (PD48, g/kg DM).

2.3. Statistical analyses

Data were subjected to univariate statistical analysis and means were compared by Tukey's test at the 0.05 probability level. Then, multivariate variance analysis with the canonical variate analysis (CANDISC of SAS, 2011) and hierarchical agglomerative clustering by the complete linkage method using the computational resources of MINITAB (2006), adopting standardised mean Euclidean distance as a basic measure of dissimilarity were applied. Mean variables of the groups used in cluster analysis were subjected to Tukey's test at the 0.05 probability level. The univariate and multivariate analyses (*i.e.*, canonical variate analysis) were made through SAS (2011). The non-linear models used to determine the *in vitro* DM kinetics parameters (*i.e.*, potential DM degradation, insoluble but potentially degradable DM fraction and degradation rate of insoluble but potentially degradable DM fraction were fitted using NLIN of SAS (2011).

3. Results

3.1. Chemical composition

Dry matter, ash, CP, ADICP, EE, ADF, and lignin(sa) differed ($P<0.05$) among genotypes (Table 3). The content of DM and ash varied from 221 to 291 g/kg and from 89 to 136 g/kg DM, respectively. The accessions had CP concentrations of 184–250 g/kg DM. Concentrations of EE in the DM varied from 8 to 18 g/kg. Average contents of ADF and lignin(sa) among genotypes were 281 and 76 g/kg DM, respectively. There were no differences in NDF and NFC among genotypes. The content of NDF and NFC varied from 538 to 578 and 112 to 173 g/kg DM, respectively.

3.2. In vitro gas fermentation, PD48 and IVDMD

The potentially degradable DM fraction (b) and the insoluble but potentially degradable DM fraction (B) ranged from 545 to 663 and from 351 to 580 g/kg DM, respectively. Degradation rates (kd) averaged 0.061/h (Table 3).

Lag time (L) varied from 2.6 to 4.3 h (Table 4) which are similar to values for other tropical grasses (Bueno et al., 2005; Maurício et al., 2003). Degradation rates of NFC (C1) varied from 0.069 to 0.085/h. Gas production relative to the fermentation of FC (Vf2) varied from 68.9 to 96.6 ml. The *in vitro* potential degradability at 48 h (PD48) varied from 536 to 639 g/kg DM. There were no differences among genotypes for IVDMD, which varied from 657 to 721 g/kg DM.

Table 3
Content of dry matter (DM, g/kg), ash (g/kg DM), crude protein (CP, g/kg DM), ether extract (EE, g/kg DM), acid detergent insoluble CP (ADICP, g/kg DM), total carbohydrates (TC, g/kg DM), neutral detergent fiber (NDF, g/kg DM), non-fibrous carbohydrate (NFC, g/kg DM), acid detergent fiber (ADF, g/kg DM) and lignin(sa) (g/kg DM) relative to the genotypes of forage peanut.

	Genotype										SEM	LSD
	(Ap × Ar) 9	Ap 8	Ap 19	Ap 20	Ap 24	Ap 31	Ap 65	Ar 5	Ar 26	cv. Belm.		
DM	289	221	233	225	263	268	291	257	254	229	9.3	47.5
Ash	92	116	108	107	123	101	136	89	112	102	7.3	37.5
CP	198	213	225	207	184	210	191	234	250	221	5.0	25.4
EE	9.0	17.9	10.9	8.0	8.4	11.3	11.9	10.4	12.1	12.1	0.69	3.5
ADICP	44	43	40	37	38	58	41	44	49	47	1.5	8.0
TC	701	654	656	678	684	677	661	666	626	665	9.7	79.6
NDF	544	542	543	546	578	578	538	563	562	557	11.7	59.3
NFC	173	144	137	156	147	129	141	152	112	151	12.2	61.7
ADF	229	312	275	296	294	285	289	265	278	287	8.6	43.5
Lignin (sa)	63	82	79	75	73	83	72	78	82	77	3.3	16.7

cv. Belm. = cultivar Belmonte.
LSD obtained by Tukey test at the 0.05 probability level.

Table 4
Average of adjusted parameters relative to *in vitro* degradation kinetics of DM and gas production kinetics of non-fibre carbohydrates (NFC) and of fibre carbohydrates (FC), *in vitro* DM digestibility (IVDMD, g/kg DM) and potential DM degradability at 48 h incubation (PD48, g/kg DM) relative to the genotypes of forage peanut.

	Genotypes										SEM	LSD
	(Ap × Ar) 9	Ap 8	Ap 19	Ap 20	Ap 24	Ap 31	Ap 65	Ar 5	Ar 26	cv. Belm.		
In vitro degradation kinetics												
b (g/kg DM)	645	560	545	630	646	602	590	663	641	608	16.7	81.2
B (g/kg DM)	580	351	370	410	389	476	429	389	384	448	24.2	117.9
kd (/h)	0.095	0.065	0.078	0.066	0.060	0.057	0.066	0.041	0.045	0.060	0.0048	0.020
Gas production kinetics												
L (h)	2.8	4.0	3.1	3.2	3.0	3.8	3.0	2.9	3.3	4.3	0.13	0.68
Vf1 (ml)	133.6	117.5	115.5	120.6	121.9	120.2	110.3	134.4	117.7	125.4	3.11	15.7
C1 (/h)	0.083	0.069	0.070	0.083	0.084	0.073	0.083	0.082	0.085	0.069	0.0015	0.008
Vf2 (ml)	92.3	68.9	71.5	96.6	81.2	89.2	74.0	86.5	87.4	83.1	3.42	17.3
C2 (/h)	0.025	0.022	0.023	0.024	0.025	0.024	0.024	0.024	0.025	0.022	0.0007	0.002
PD48	639	545	536	612	590	571	572	604	600	583	17.3	92.3
IVDMD	717	677	687	721	687	657	666	706	702	713	1.7	91.2

b = potential DM degradation; *B* = insoluble but potentially degradable DM fraction; kd = degradation rate of fraction B; Vf1 = maximum volume of gases from NFC; C1 = degradation rate of NFC; *L* = lag time; Vf2 = maximum volume of gases from FC; C2 = degradation rate of FC; PD48 = potential DM degradation at 48 h; IVDMD = *in vitro* DM digestibility.
cv. Belm. = cultivar Belmonte
LSD obtained by Tukey test at the 0.05 probability level.

3.3. Multivariate analyses

A canonical variate analysis was used to reduce the dimensionality of the data (*i.e.*, number of variables), and was mostly employed in relation to analysis of main components due to the presence of samples with repeated observations. Use of this technique allowed evaluation of the simultaneous effect of the original features (*i.e.*, DM, Ash, CP, EE, ADIP, TC, lignin(sa), NDF, ADF, *b*, *B*, kd, *L*, Vf1, C1, Vf2, C2, PD48, IVDMD) and thus captures variations not detected when using the original features alone.

The first three canonical variables (*i.e.*, CV1 = 0.51; CV2 = 0.24 and CV3 = 0.20) explain 0.96 of total variance, thus being used for identification of characters with greater importance to discriminate the genotypes based on nutritional parameters (Table 5).

The relative importance of the nutritional characteristics evaluated (*i.e.*, variables) were quantified by the magnitude of the standardised canonical coefficients in the canonic variables, where the chemical composition and *in vitro* data of lowest importance were those for which the canonical coefficients had greater magnitude, in absolute value, in the last canonical variables. All variables in this study were used initially but, among the variables, those with low contribution for distinction of the accessions were discarded (*i.e.*, DM, Ash, EE, ADIP, TC, NDF, *b*, *L*, Vf1, C1, Vf2, C2, IVDMD). Variables kd, CP and PD48 were considered important for discrimination of genotypes since these had higher canonical coefficients in the first canonical variables. Variable kd had the highest canonical coefficient (1.40) in the canonical variable of highest eigenvalue (0.51 of total variance), presenting itself as the main discriminating factor among genotypes (Table 5).

For the hierarchical clustering procedure the 6 discriminatory variables indicated by the analysis of canonical variables (kd, CP, PD48, ADF, lignin(sa), B) were used, since they had greater discriminatory power in distinguishing accessions. The

Table 5
Estimates of eigenvalues (λ), of accumulated variance and of the relative importance of characters in the canonic variables (CV), obtained based on 6 variables, in 10 genotypes of forage peanut.

Canonic variables	λ	Accumulated variance (proportion)	Canonical coefficients					
			CP	ADF	Lignin(sa)	PD48	B	kd
CV1	14.4211	0.51	−0.0363	−0.2387	−1.2614	0.6478	−0.2176	1.4013
CV2	6.8139	0.76	1.0036	−0.4365	0.1401	0.4788	−0.3783	0.2865
CV3	5.6125	0.96	−0.2575	0.3777	0.1567	0.9992	−0.6631	−0.4951
CV4	0.9189	0.99	0.2576	0.6469	−0.5434	0.2180	−0.7361	0.7016
CV5	0.2807	0.99	0.1640	0.5513	0.1801	0.1906	0.6606	0.0360
CV6	0.0262	1.00	−0.1698	−0.1796	0.7357	0.1911	−0.2145	0.2463

CP = crude protein; ADF = acid detergent fibre; PD48 = potential DM degradation at 48 h; *B* = insoluble but potentially degradable DM fraction and kd = degradation rate of fraction *B*.
The positive and negative values represent the coordinates of the original variables in the canonical axes.

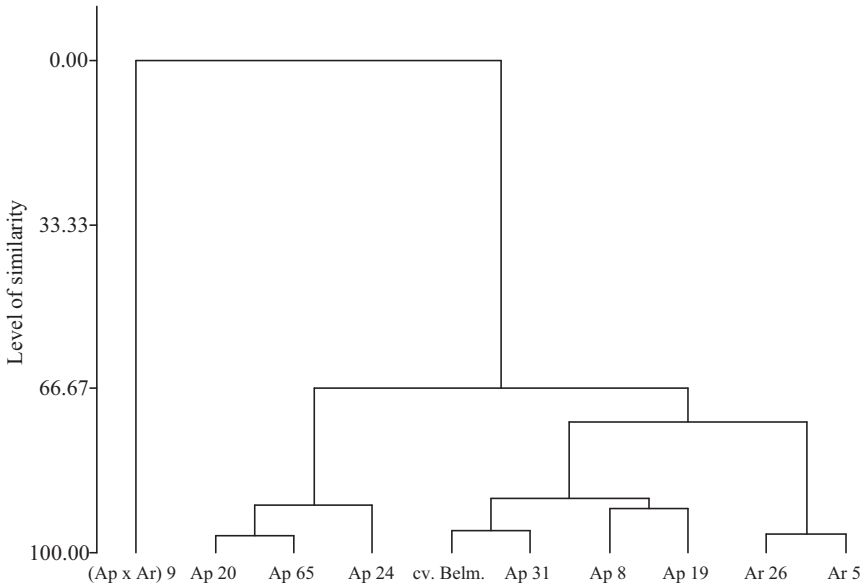

Fig. 1. Similarity dendrogram for the nutritional value of the 10 genotypes of forage peanut.

complete linkage method, based on the maximum distance of similarity between genotypes, and standardised average Euclidean distance, were used to form the dendrogram.

At a level of 80% similarity, four distinct groups formed. Group I was totally dissimilar to the other groups with the hybrid (Ap × Ar) 9 as its single component. Group II (Ap 20, Ap 65, Ap 24) and group III (Ap 8, Ap 19, Ap 31, cv. Belmonte) displayed similarities of 90 and 89%, respectively. Group IV (Ar 5, Ar 26) displayed the highest similarity (96%) among the groups formed, showing great nutritional similarity among genotypes (Fig. 1).

In addition, Tukey's test demonstrated differences ($P<0.05$) for the variables among groups (Table 6). Group I (hybrid Ap × Ar 9) was higher than the other groups, since it had the highest values for PD48, kd, and the lowest for ADF and lignin(sa) ($P<0.05$). Group IV (Ar 5, Ar 26) had similarities in chemical composition and degradation kinetic parameters. This group had the highest ($P<0.05$) CP content, lowest values for ADF and fraction B, and elevated PD48. However, it had the lowest ($P<0.05$) kd.

Group II (Ap 20, Ap 24, Ap 65) had elevated values of PD48 and fraction *B*, low lignin(sa) and high kd. Group III (Ap 8, Ap 19, Ap 31, cv. Belmonte) had the lowest ($P<0.05$) PD48.

4. Discussion

This study evaluated 10 genotypes of forage peanuts using chemical composition and *in vitro* DM digestion kinetic parameters in order to select the most promising accessions by multivariate analysis to be used in animal feeding. The study concentrated on the main nutritional characteristics which impact animal production. The accessions (Ap × Ar) 9, Ap 20, Ap 24 and Ap 65 demonstrated promising nutritive value and will be used in peanut breeding programs at Embrapa. The main limitation of our study was the lack of measures of products of digestion such as volatile fatty acids, ammonia N, as well as

Table 6
Groups of genotypes of forage peanut obtained by the complete linkage method and the average of the variables in each group.

	Groups				SEM	LSD
	I	II	III	IV		
	(Ap × Ar) 9	Ap 20	Ap 8	Ar 5		
	–	Ap 24	Ap 19	Ar 26		
	–	Ap 65	Ap 31	–		
	–	–	cv. Belm.	–		
Averages						
CP (g/kg DM)	198	194	217	242	4.7	18.2
ADF (g/kg DM)	229	293	290	271	6.9	26.8
Lignin(sa) (g/kg DM)	63	73	80	80	2.1	6.8
PD48 (g/kg DM)	639	591	559	602	6.9	26.5
B (g/kg DM)	580	409	411	386	15.2	59.2
kd (/h)	0.095	0.064	0.065	0.043	0.0042	0.014

cv. Belm. = cultivar Belmonte.
CP = crude protein; ADF = acid detergent fibre; PD48 = potential DM degradation at 48 h; *B* = insoluble but potentially degradable DM fraction and kd = degradation rate of fraction B
LSD obtained by Tukey test at the 0.05 probability level.

microbial protein and methane production. Recently, methane emission by ruminants has received attention (Thorpe, 2009; Steinfeld et al., 2010; Key and Tallard, 2009). Linking forage nutritive value to plant breeding programs to identify which genotypes might lend to an improvement in efficiency of animal production in the future. Other limitations of our study were the absence of estimates of CP digestibility and condensed tannin analyses.

4.1. *Arachis* chemical composition

In regards to NDF, the values were lower than 578 g/kg DM for all genotypes. According to Van Soest (1994), NDF concentration in the DM would not limit its intake if lower than 550–600 g/kg DM. Paulino et al. (2009) showed that concentrations of EE, ADF and lignin(sa) in the forage peanut DM were higher (20; 390 and 93 g/kg DM, respectively) than values in the 10 genotypes we evaluated (13, 271, 73 g/kg DM, respectively). The lower IVDMD found by Paulino et al. (2009) compared to our results demonstrates the importance of chemical composition on nutritive value of forages (Chaves et al., 2006a,b).

4.2. *In vitro* gas fermentation parameters, PD48 and IVDMD

The *in vitro* DM digestibility of these forage peanut genotypes are adequate to allow them to be fed to ruminants as tropical forages without affecting performance/intake, considering that diet digestibility values lower than 660 g/kg DM would reduce feed intake due to physical limitations in the rumen (Conrad et al., 1964). In addition, the highest degradation rate (0.095/h) by the hybrid (Ap × Ar) 9 was probably due to the lower content of ADF (229 g/kg DM) and higher NFC (173 g/kg DM), resulting in a higher amount of fermentable substrate at any time. These results are in agreement with others studies where kd for tropical legumes ranged from 0.02 to 0.1/h (Velásquez et al., 2009; Carvalho et al., 2008; Katsuki et al., 2006).

The volume of gas produced *in vitro* can be correlated with DM intake and animal growth (Blümmel and Ørskov, 1993). Due to higher gas production, the genotypes (Ap × Ar) 9, Ap 5 or Ap 20 should be further tested *in vivo* to quantify intake as well as animal performance. Among the genotypes tested, degradation rates of NFC (0.07–0.08/h) were similar to results of Detmann et al. (2009) with four tropical grasses (0.04–0.08/h).

4.3. Multivariate analyses

The genus *Arachis* includes several species that are also known as forage peanut. The species *A. pintoi*, *A. repens* and *A. glabrata* are the most widely used as ruminant feeds in the Americas. Several cultivars are available for this purpose, obtained through selection of native species and by genetic breeding by means of intra and interspecies breeding. A wide variation in the chemical composition and digestibility occurs in genotypes from this genus, which could be an intrinsic characteristic, or variations existing due to soil and climatic conditions, and to the maturity of the plants evaluated. In our study, 10 genotypes were evaluated and classified under the same environmental conditions. They were planted, developed and harvested in the same location to avoid effects related to environment and plant age.

Multivariate analyses were used to represent the genotype groups and the interrelationships between them as a function of their chemical composition and degradation characteristics. Among the variables selected by the multivariate analysis (*i.e.*, CP, ADF, lignin(sa), DP48, *B*, kd) the variables kd, CP and DP48 had more discriminating power to compose the groups. It is notable that the same variables had high correlations with the nutritional value of feedstuffs and animal performance (Barnes et al., 2007).

The genotype Ap × Ar 9, obtained by crossing *A. pintoi* and *A. repens* species, stood out dramatically from the remaining genotypes. The two accessions of *A. repens* occupied the same group, depicting nutritional and chemical characteristics peculiar and distinct from those of genotypes *A. pintoi* and of the hybrid Ap × Ar 9. The elevated CP content and the lower DM degradation rates of *A. repens* accessions suggest that these may have secondary compounds which resulted in a lower nutrient availability per unit time, since NDF content was similar to the other genotypes. Lascano (1994) reported that even though *A. pintoi* genotypes had low contents of condensed tannins (25 g/kg), they had lower CP degradation rates compared to species that had high contents of soluble CP and trivial levels of tannins (*i.e.*, <2 g/kg) such as Centrosema.

Nutritional information on *A. repens* genotypes are scarce since the majority of studies with this purpose used accessions of *A. pintoi* and *A. glabrata*. However a few studies based on agronomic characteristics have demonstrated differences between *A. pintoi* and *A. repens* species, including DM yield and accumulation rate, N fixation, establishment period and macronutrient accumulation (Valentim et al., 2003; Assis et al., 2008; Soares et al., 2006; Miranda et al., 2003).

Arachis genetic diversity needs to be studied further, given the wide variety of existing genotypes with distinct nutritional characteristics. This study contributes to selection of this species, not only due to agronomic characteristics, commonly applied, but also due to the nutritional value of the forage.

5. Conclusions

Accessions of *Arachis* evaluated had substantial variability in chemical composition and *in vitro* DM digestion kinetics. Based on multivariate analyses, accessions of *Arachis pintoi* ranked in order for nutritive value: hybrid (Ap × Ar) 9 > Ap 20 = Ap 24 = Ap 65. However the hybrid (Ap × Ar) 9 stood out nutritionally among the genotypes evaluated and it will be considered for further *in vivo* evaluations. Multivariate analyses, chemical composition and *in vitro* digestion kinetics should be integrated in genetic improvement programs with the aim of developing cultivars with higher nutritional value for the animals which will consume them.

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