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Nutritional divergence in genotypes of forage peanut

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ABSTRACT - The objective of this study was to evaluate the nutritional divergence between ten genotypes of forage peanut, based on chemical composition as well as fermentation and *in vitro* degradation kinetic characteristics. Treatments consisted of ten genotypes of *Arachis pintoi*, namely eight accessions (31135, 30333, 15121, 31828, 15598, 31534, 13251 and 31496) and two cultivars (cv. Belmonte and cv. Amarillo). The genotypes were harvested in each plot at a height of 3 cm from the ground, in 42-day intervals, during the time of heaviest rainfall. For the multivariate analysis the following variables, the following were used: crude protein, neutral detergent fiber, potential degradation in 48 hours, degradation rate of insoluble potentially degradable fraction and degradation rate of non-fibrous carbohydrate. The application of the hierarchical clustering analysis, using the Euclidian distances matrix of standardized averages allowed for the identification of five homogeneous groups. Among them, the accessions 31828, 31534, 15121 and cv. Belmonte stood out nutritionally among the remaining genotypes evaluated, depicting as promising for the utilization in ruminant feeding.

Key Words: chemical composition, gas production, multivariate analysis

Introduction

The biggest Brazilian differential in the production of beef at competitive costs is the fact that climatic conditions allow for the use of pastures year round. Within this tropical environment favorable to pasture growth, the challenge is to fulfill the nutritional requirements of grazing animals, since animal production is a direct response of the quantity and quality of the feed consumed (Minson, 1982).

Leguminous plants are forages that play a relevant role in animal production, exerting an important function due to their high protein content and to their capacity of biologically fixating atmospheric nitrogen. These characteristics enable a qualitative and a quantitative increase in forage production. Studies done in different Brazilian ecosystems (Pizarro et al., 1992; Carneiro et al., 2000) identified accessions of *Arachis pintoi* with superior yield and quality to the cultivar Amarillo, the most disseminated among Central and South America producers.

Agronomical evaluations based on productivity, occurrence of pests and diseases, seed production, compatibility with forage grass and arboreal species as well as perennial shrubs and, above all, resistance to grazing have been used in recommendations of promising *Arachis* genotypes in the production systems of grazing cattle (Valentim et al., 2003). However, little is known about the differences in the nutritional potential among genotypes of forage peanut (*Arachis pintoi*) for ruminants.

Azevedo et al. (2003), adapting the term genetic divergence to nutritional divergence, showed that it is possible to identify within a group of tropical forage varieties, one which is more nutritionally promising, using as a basis, the simultaneous evaluation of important discriminatory variables for ruminant nutrition. The evaluation of nutritional divergence in forage peanut genotypes presents potential to aid in the selection of superior genotypes, since nutritional value directly influences animal performance.

Within this context, the objective here was to evaluate the nutritional divergence of ten genotypes of *Arachis pintoi*, aiming at identifying promising genotypes for ruminant feeding.

Material and Methods

In the experimental field station of Animal Science of the Extreme South (ESSUL) belonging to the Executive Commission for the Cocoa Culture Plan (CEPLAC), located

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at Itabela (16 º 39' S and 39 º 30' W), in the extreme south of Bahia, an experiment was implemented in order to evaluate the adaptability and productivity of *Arachis* genotypes using a randomized block design, with four repetitions (Ruiz & Santana, 2004).

The area is under the domain of the ecosystem "Mata Atlântica" and the local climate is a transition between the Af and Am types, according to the Köppen classification, with annual rainfall of 1,312 mm and average temperature of 23 ºC, with no defined dry season. The soil is a sandy (>700 g of sand/Kg) Ultisol (Typical Paleudult fine-loamy, kaolinitic, isohyperthermic), in the superficial 20 cm. Its average chemical characteristics, when the experiment was implemented were: pH in H_2O = 4.9; P = 1 mg/dm^3; Ca, K and Al = 0.6, 0.5 and 0.1 meq/100 g, respectively.

At set up, the soil was plowed at 0.20 m, conveniently harrowed and furrowed. At the bottom of the furrow, 40 kg/ha of P_2O_5 were applied, using the fertilizer superphosphate (18% of P_2O_5) as a source for this nutrient. The planting was done with vegetative material (stolons). One year after sampling had begun, for determination of dry matter (DM) production, fertilizer replenishment was done with 40 kg/ha of P_2O_5.

Plots were set up with an area of 7.5 m^2 (3 × 2.5 m), in 5 rows, at a 0.50- × 0.50-m spacing.

For biomass sampling, the genotypes were harvested in each plot at a height of 3 cm from the ground, in 42-day intervals. The experimental period comprehended the time of heaviest rainfall, corresponding to the months between December, 2000 and April, 2001.

Climatic data relative to the experimental period were obtained from the Animal Husbandry Experimental Station of the Extreme South (ESSUL), located in the municipality of Itabela – BA (Table 1).

Ten genotypes of *Arachis pintoi* were used in this experiment, namely eight accessions (31135, 30333, 15121, 31828, 15598, 31534, 13251 e 31496) and two cultivars (cv. Belmonte and cv. Amarillo).

After collection and weighing of the green forage from the usable area (2 m^2), the material was dried in an forced ventilation oven at 55 ºC for 72 hours, ground in a Willey type mill with 1-mm mesh sieve and packaged in polyethylene jars for posterior analysis.

Analysis were performed in order to determine the contents of dry matter (DM), ash, ether extract (EE), crude protein (CP), acid detergent insoluble protein (ADIP), and the concentrations of neutral detergent fiber (NDF), acid detergent fiber (ADF) as described by Silva & Queiroz (2002). Total carbohydrate (TC) was calculated through the formula TC = 100 - (%CP + %EE + %Ash) and non-fibrous carbohydrate (NFC), from the formula: NFC = 100 - (%CP + % NDFap + %EE + %Ash), according to Hall (2000), where NDFap represents neutral detergent fiber corrected for ash and protein and the other variables, as previously described.

The genotypes were further evaluated by the *in vitro* semi-automatic gas production technique (Mauricio et al., 1999) at the gas production laboratory from the Faculty of Veterinary Medicine at UFMG. For this evaluation, one gram of sample from these materials was incubated in glass flasks with capacity for 160 mL, to which 10 mL of ruminal inoculate and 90 mL of culture media were manually added, according to Theodorou et al. (1994). The flasks were sealed with rubber corks (14 mm). The ruminal inoculate was collected from a Jersey steer fitted with a ruminal cannula, kept under a diet of corn silage and 1 kg/day of commercial concentrate with 22% CP. The pressure readings were taken at 2, 4, 6, 8, 10, 12, 14, 17, 20, 24, 28, 34, 48, 72 and 96 hours after inoculation. Pressure results were used for the calculation of gas volume, using the equation described by Mauricio et al. (2003).

Fermentation residues were obtained through the filtration of residue from the fermentation flasks in filtering crucibles (porosity 1). These residues were dried at 105 ºC down to a constant weight and the results were used for the calculation of *in vitro* degradability of DM.

Table 1 - Monthly climatic data average in the period between October 2000 and April 2001 in Itabela, Bahia

Year	Month	Precipitation	Temperature (Cº)			Evaporation	Relative air humidity (%)
		(mm)	Max.	Min.	Avg.	(mm)	(%)
2000	October	27.7	29.7	19.0	23.4	5.4	79.5
2000	November	282.5	29.5	20.6	24.2	4.9	84.2
2000	December	200.3	29.7	21.8	24.9	5.4	80.6
2001	January	218.1	30.1	21.4	24.9	5.0	83.1
2001	February	120.6	31.1	21.4	25.0	5.9	82.4
2001	March	217.1	30.0	21.2	24.6	4.8	86.5
2001	April	315.2	28.5	21.1	23.8	3.7	88.8

Max. - maximum; Min. - minimum; Avg. - average.

For the evaluation of degradation kinetics (gravimetric technique), the model proposed by Sampaio et al. (1995) was used:

$Y = A – B * exp (-c*t)$

where: Y is the DM residue at time t; A, the potential degradation of the DM fraction; B, the insoluble potentially degradable fraction; exp, the base of neperian logarithms; c, the degradation rate of fraction B by unit of time (/h); and t, the incubation time.

For ruminal fermentation kinetics, obtained by the gas production technique, the kinetic variables for fibrous carbohydrate (FC) and non-fibrous carbohydrate (NFC) were estimated by the two-pool logistic model proposed by Schofield et al. (1994), adjusted to the gas cumulative production curves, as described:

$V = Vf1 / (1 + exp(2 - 4*C1*(T - L))) + Vf2 / (1 + exp(2 - 4*C2*(T - L)))$

where: Vf1 is equivalent to the maximum volume of gases in the NFC fraction; C1, to the degradation rate (/h) of the NFC fraction; Vf2, to the maximum volume of gases in the FC fraction; C2, to the degradation rate (/h) of the FC; and T and L, to the incubation times (h) and to the latency (h), respectively.

The nonlinear models used to describe the degradation profiles obtained by gravimetric and metabolic pathways were fitted by the iterative algorithm of Gauss-Newton.

Univariate statistical analysis was performed through the program SAEG (System for Statistical and Genetic Analysis, version 9.1). Means were compared using the Tukey test at 5% probability. Multivariate analysis was performed using the computational resources of the Minitab 16 program, where the agglomerative hierarchical cluster analysis took place, by the complete linkage method, with the standardized average Euclidean distance as a basic measure of dissimilarity.

Results and Discussion

No differences were observed for DM, ADICP, ADF, EE or NFC ($P>0.05$), with mean values of 16.8; 13.0; 38.6; 1.6 and 19.8%, respectively (Table 2).

Mean values relative to variables ash, CP, NDF, TC and Deg48 differed between the treatments evaluated. CP contents were elevated, with average value of 24.8%. Average values for NDF, ADF and TC ranged from 50.2 to 55.5; 36.3 to 41.8 and from 68.7 to 72.3%, respectively. The greatest CP and TC contents were found for genotypes 30333 and cv. Belmonte, respectively, while the lowest NDF content was found for accession 31496. Crude protein, NDF and ADF contents described by Silva et al. (2009), while evaluating forage peanut with cutting age of 60 days, were inferior to those observed in this study. However, superior values were observed for EE (1.9%), TC (78.9%) and NFC (26.5%) contents.

Similar results for CP and inferior ones for ADF were found by Affonso et al. (2007), after studying the effect of cutting management (1, 2, 3, 4 or 5 cuttings) during spring-summer, on the nutritional value of this forage. These authors report concomitant elevation of CP (18 to 26%) and reduction of ADF (26 to 31%) contents as cutting frequency increased.

Dry matter and ash contents obtained were relatively low when compared with those reported in the literature (Silva et al., 2009; Valadares Filho et al., 2006; Staples et al., 1997). Low DM and ash contents were due to the fact that the genotypes evaluated were harvested at a lower cutting interval (42 days), when compared with the studies cited (60 to 183 days). According to Nascimento Júnior & Vilela (1995), the cutting represents a moment of stress for the plant, characterized by a drop in reserve carbohydrate content, interruption in root growth and a decrease in nutrient absorption.

The differences observed relative to chemical composition are mainly due to variations in edaphoclimatic factors in the regions where the evaluations took place, favoring a greater or lower speed in development and, consequently, early or late maturation of the forages; genotype choice, given the intrinsic variation in chemical composition between them; and the cutting intervals employed.

Nascimento et al. (2010) evaluated the effect of cutting management (21, 42, 63 and 84 days) on the quality of forage obtained from forage peanut. They observed an increase in the amount of NDF and ADF contents and a reduction of CP content and *in vitro* digestibility as cutting intervals increased, as a consequence of the relationship leaf and petiole per stem. These authors reported that the best response for nutritional value was obtained in the cutting at 42 days of plant growth.

Lenzi et al. (2009), studying production and quality of coastcross pasture (*Cynodon dactylon*) intercropped with peanut forage or not, reported that, regardless of the season, there was no difference in the chemical and *in vitro* digestibility of *Arachis pintoi*, demonstrating the ability of this legume to maintain good nutrition throughout the year.

Deg48 values ranged from 43.1 to 53.1%, showing differences only between cultivars cv. Amarillo and cv.

Belmonte; however, the remaining genotypes did not differ (Table 2). In the present study, high levels of NDF were negatively correlated (r = -0.73) with Deg48. According to Van Soest (1994), the lower the fiber content of a forage, the higher its digestibility, since most of the indigestible components of a feed are found in this fraction.

High positive correlation (r = 0.72) was also found between the levels of CP and acid detergent insoluble protein (ADIP), indicating that higher levels of CP tend to increase the protein fraction bound to ADF, which represents the unavailable fraction.

For the adjusted parameters of dry matter *in vitro* degradation kinetics (Table 3), the values for insoluble potentially degradable fraction (B) and for potential degradation of the DM fraction (A) ranged from 33.2 to 51.5 and 46.7 to 52.2%, respectively. Cultivar Amarillo had the lowest average value and cv. Belmonte had the highest one for potential degradation, while the highest values for fraction B were observed for accession 31534. Degradation rates (kd) were high, with overall average of 0.066/h for the genotypes evaluated.

Evangelista et al. (2002) studied the *in situ* degradability of 15 alfalfa cultivars, and found similar mean values for fraction B (38.0 to 44.4%) and higher for kd rate (0.078 to 0.124/h) and potential degradation (78.4 to 81.6%). Veloso et al. (2006) evaluated *in situ* DM degradation for the follicles of tropical legumes leucena (*Leucaena leucocephala*) and guandu (*Cajanus cajan*) as well as for the leaves of manioc (*Manihot sculenta*). These authors reported higher values for fraction B (62.9, 43.4 and 73.0%) and Kd rates (0.060, 0.039 and 0.106/h) for the forages, respectively.

The latency (L) ranged from 4.4 to 5.5 hours, showing relatively low and desirable values (Table 4) compared with those reported by Sá et al (2011) for *Brachiaria brizantha* (12.9 to 14.6 h), with ages ranging from 28 to 54 days, and by Campos et al. (2000) for corn silage (6.2 to 9.1 h) in a period of 48 hours. The fiber fraction is directly related to most of the events involved in this parameter.

The larger gas volumes produced for the rapid degradation fraction (VF1) were obtained for cv. Belmonte, followed by accession 31534 and cv. Amarillo (Table 4). These high values for VF1 are due to the higher NFC content presented by these genotypes (Table 2), conferring greater availability of fermentable substrate and providing greater gas production for this fraction. Degradation rates for the rapidly degradable fraction (C1) were low, averaging 0.068/h, since reports of values from 0.1 to 0.2/h, are frequent (Cabral et al., 2003; Senger et al., 2007; Detmann et al., 2009). The highest gas productions from the fermentation of the slowly degradable fraction (VF2) were found for accessions 31828 and 31534.

Table 2 - Average contents of chemical composition, degradability and gas production as a function of the genotypes of *Arachis*

Item	Genotype										Average	CV
	31135	30333	15121	31828	15598	31534	13251	31496	cv. Bel	cv. Ama		
DM, %	16.6	16.8	15.9	17.0	16.1	17.9	16.5	16.1	16.9	18.0	16.8	7.9
Ash, %DM	2.9ab	3.1ab	3.2a	2.4ab	2.6ab	2.8ab	2.6ab	2.5ab	2.3b	2.7ab	2.7	10.2
CP, %DM	24.8ab	26.4a	24.6ab	25.1ab	23.6b	24.9ab	25.4ab	26.0ab	23.5b	23.7ab	24.8	3.8
ADICP, %CP	12.6	12.7	12.9	13.7	11.8	15.5	12.9	13.4	12.5	12.2	13.0	17.3
NDF, %DM	55.5a	52.6ab	53.2ab	53.8ab	54.4ab	55.3a	54.8ab	50.2b	53.0ab	54.2ab	53.7	3.0
ADF, %DM	38.7	36.3	41.1	38.2	41.6	37.2	38.9	38.2	36.7	38.8	38.6	5.9
EE, %DM	1.4	1.8	1.7	1.6	1.3	1.2	1.7	1.8	1.6	1.5	1.6	8.9
TC, %DM	70.5ab	68.7b	70.3ab	70.7ab	72.0a	70.5ab	70.1ab	69.7ab	72.3a	71.8a	70.7	2.3
NFC, %DM	18.8	17.5	19.7	19.6	19.9	20.0	18.5	20.3	22.3	21.1	19.8	10.1
Deg48, %	47.0ab	45.9ab	47.5ab	48.7ab	45.2ab	49.1ab	45.3ab	46.2ab	51.3a	43.1b	46.9	4.9

ADF - acid detergent fiber; EE - ether extract; TC - total carbohydrates; NFC - non-fibrous carbohydrates; Deg48 - *in vitro* digestibility in 48 hours of incubation; CV - coefficient of variation in %; cv. Bel - cv. Belmonte; cv. Ama - cv. Amarillo.
Means followed by different letters in each row differ statistically by the Tukey test at a 5% probability level.

Table 3 - Average of adjusted parameters relative to *in vitro* degradation kinetics of dry matter relative to the genotypes of *Arachis*

Item	Genotype										Average
	31135	30333	15121	31828	15598	31534	13251	31496	cv. Bel	cv. Ama	
A (%)	48.3	47.4	48.4	49.9	48.3	50.0	47.5	50.1	52.2	46.7	48.9
B (%)	34.0	36.8	41.7	44.9	35.7	51.5	36.1	33.2	44.2	34.8	39.3
Kd (/h)	0.055	0.071	0.082	0.075	0.051	0.087	0.064	0.045	0.081	0.047	0.066
R^2	0.885	0.882	0.889	0.891	0.938	0.903	0.913	0.906	0.938	0.852	-

A - potential degradation of the DM fraction; B - insoluble potentially degradable fraction; Kd - degradation rate of fraction B; cv. Belm. - cv. Belmonte and cv. Ama - cv. Amarillo.

Degradation rates for the slowly degradable fraction (C2) had a mean value of 0.018/h. The highest gas production for the rapidly degradable fraction obtained for the accessions evaluated had been predicted by Schofiled & Pell (1995), according to whom the contribution of gas production from the NFC fraction would be greater for legumes than for the grasses.

Campos et al. (2000), while evaluating alfalfa hay, found the following values for the fermentation kinetic parameters: VF1 = 95 mL; C1 = 0.17h^{-1}; L = 1.5 h; VF2 = 107 mL; C2 = 0.031h^{-1} and PG48 = 203 mL/g DM. For all kinetic parameters, superiority is observed for the alfalfa hay when compared with the genotypes of *Arachis* evaluated. This discrepancy can be attributed in part to differences in the chemical composition of these two legumes, since the referenced alfalfa hay had lower levels of CP (20.9%), NDF (33.8%) and ADF (25.8 %), which allows for the inference that alfalfa probably had a higher fibrous fraction degradability and a higher contribution of NFC for the production of gases.

The largest volumes of gas produced within a 24-hour fermentation period in the DM fraction were obtained for genotypes cv. Belmonte and 31534, with the respective values of 119.9 and 113.8 mL/g DM, while smaller volumes were observed for the accessions 30333 and 31496, with values of 85.7 and 94.9 mL/g DM, respectively (Figure 1).

After the of 48 hours of fermentation period, gas production of TC tended to stabilize, reaching values above 90% of total gas production for all genotypes. Gas production of NFC increased gradually until the period of 17 hours of fermentation, tending to stabilize after 24 hours of fermentation, while the highest gas production from FC occurred in the period between 24 and 36 hours of fermentation. The fermentation of cv. Belmonte and accession 31534 provided greater total gas production; therefore, it can be inferred that for these genotypes, the fiber fraction was more extensively degraded. The opposite can be observed for accession 30333, which provided a lower volume of gas (Figure 1).

According to Getachew et al. (2004), the amount of gases produced by incubating a feedstuff reflects the production of short chain fatty acids, which are the main source of energy for ruminants. The gases come directly from the microbial degradation of food, and indirectly from the reaction of the buffer with the acids generated as a result of fermentation.

In the evaluation of the nutritional divergence, all variables present in this study were used in order to carry out a cluster analysis, as a result of which, those with the highest power of discrimination were selected. Based on the transformation of discriminatory variables CP, NDF, Deg48, Kd and C1 with the highest contribution to the distinction of the accessions evaluated, the dendrogram of similarity was obtained. Thus, hierarchy levels were established and the ten genotypes of forage peanut were grouped in different homogeneous groups based on the similarity expressed by the standardized average Euclidean distance (Figure 2).

Proceeding to the analysis of the results of agglomerative hierarchical clustering, one can observe the formation of two large dissimilar groups (Figure 2). Group 1, consisting of the genotypes 31135, 13251, 15121, 31828, 31534 and cv. Belmonte, presenting 39% similarity between themselves and Group 2, composed of the genotypes 30333, 31496, 15598, and cv. Amarillo, with only 27% similarity.

Carrying out the partition of the dendrogram (Figure 2), done in a subjective way, assuming a 70% similarity, the formation of five subgroups was detected.

Subgroup I, represented by accessions 31135 and 13251, had 91% similarity, characterized by high levels of CP and NDF, high C1 rates and low Kd rates (Table 5). Subgroup II had accession 15121 as its single component and was the subgroup which distanced itself the most in relation to the remaining ones, with the largest average Euclidean distance (2.61) and greater degree of dissimilarity between the genotypes evaluated. The highest rates for Kd and C1 and the high level of Deg48 contributed to the formation of this isolated subgroup (Table 5).

Table 4 - Average of adjusted parameters relative to gas production kinetics of non-fibrous carbohydrate (NFC) and of fibrous carbohydrate (FC) in a 48 hour period relative to the genotypes of *Arachis*

Item	Genotype										Average
	31135	30333	15121	31828	15598	31534	13251	31496	cv. Bel	cv. Ama	
L (h)	4.8	4.8	4.4	5.0	5.5	4.9	4.5	4.8	4.9	4.7	4.8
VF1 (mL)	89.7	75.0	89.3	94.8	93.4	101.6	89.1	84.6	106.0	101.0	92.5
C1 (h^{-1})	0.070	0.069	0.074	0.066	0.067	0.065	0.071	0.066	0.068	0.063	0.068
VF2 (mL)	45.3	39.7	41.4	50.8	48.3	50.2	45.7	41.2	51.3	47.6	46.2
C2 (h^{-1})	0.018	0.017	0.019	0.018	0.018	0.018	0.018	0.017	0.018	0.017	0.018
R^2	0.989	0.920	0.912	0.982	0.994	0.988	0.985	0.911	0.997	0.995	-

VF1 - maximum volume of gases for the NFC fraction; C1 - degradation rate for the NFC fraction; L - latency; VF2 - maximum volume of gases for the FC fraction; C2 - degradation rate for the FC fraction; cv. Belm. - cv. Belmonte and cv. Ama - cv. Amarillo.

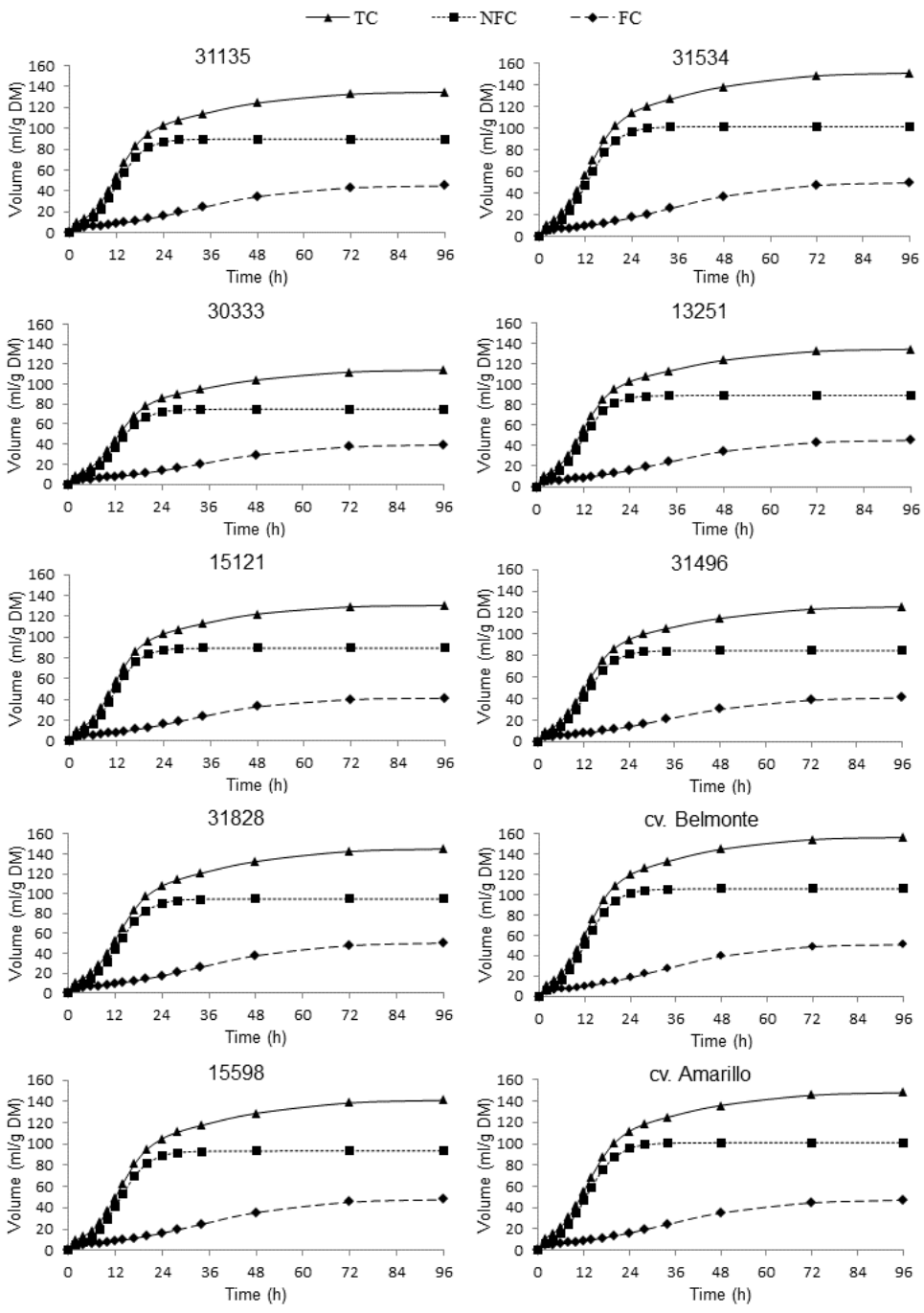

Figure 1 - Gas production curves for total carbohydrates (TC), non-fibrous carbohydrates (NFC) and fibrous carbohydrates (FC), relative to the genotypes of *Arachis*.

For subgroup III, consisting of accessions 31828, 31534 and cv. Belmonte, minimal similarity was obtained, at 72%, with the greatest similarity observed for accessions 31828 and 31534, which presented the lowest average Euclidean distance (1.30). This subgroup can be considered of higher nutritional value for presenting the highest values of Deg48 and Kd rates.

Accessions 30333 and 31496 formed subgroup IV, which showed 71% similarity and was characterized by higher contents of CP, lower NDF content and low Kd rates.

In contrast, subgroup V, consisting of accession 15598 and cv. Amarillo, showed similarity of 89%, demonstrating large nutritional similarity between these genotypes. However, this subgroup showed the highest contents of NDF, the lowest values of Deg48 and lower Kd rates, assessed as nutritionally inferior compared with the other subgroups (Table 5).

Table 5 - Groups of genotypes of forage peanut, average Euclidean distances and average variables in each group formed by the hierarchical agglomerative clustering method of Complete Linkage, based on standardized average Euclidean distance

Items	Groups				
	I	II	III	IV	V
Genotypes	31135	15121	31828	30333	15598
	13251	-	31534	31496	cv. Amarillo
	-	-	cv. Belmonte	-	-
Distances	1.89	6.80	6.02	6.08	2.40
CP (% DM)	25.0	24.6	24.5	26.2	23.6
NDF (% DM)	55.2	53.2	54.0	51.4	54.3
Deg 48 (%)	46.2	47.5	49.7	46.1	44.1
Kd (h^{-1})	0.060	0.082	0.081	0.058	0.049
C1 (h^{-1})	0.071	0.074	0.066	0.068	0.065

CP - crude protein; NDF - neutral detergent fiber; Deg48 - *in vitro* degradability within 48 hours of incubation; kd - degradation rate of insoluble potentially degradable fraction; C1 - degradation rate for the NFC fraction.

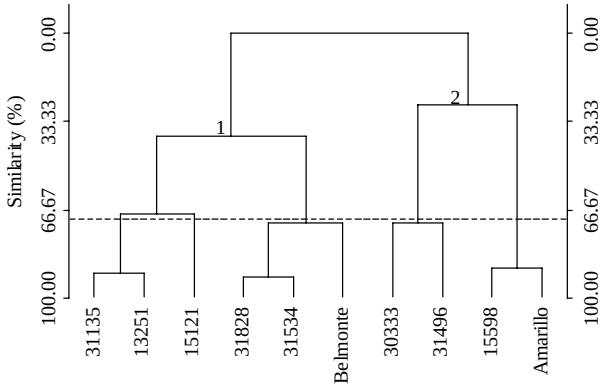

Figure 2 - Similarity dendrogram for the nutritional value of the ten genotypes of forage peanut.

Forages with high degradation potential indicate good nutritional value, since they can provide rapid and abundant availability of nutrients to the microorganisms in the rumen. But low rates of ruminal degradation may reduce DM intake and energy availability, which limits the productive performance of animals (Barnes et al., 2007). Khazaal et al. (1995), evaluating parameters of chemical composition, *in vitro* and *in situ* degradation as well as gas production in the prediction of voluntary intake, reported that consumption was significantly ($P<0.05$) related to the *in vitro* degradability at 48 hours ($r = 0.75$), and degradation rate ($r = 0.66$) of the forage.

Conclusions

The genotypes studied exhibit variations in the nutritional characteristics evaluated, and were grouped into distinct subgroups. Accessions 31828, 31534, 15121 and cv. Belmonte stood out nutritionally among the remaining genotypes evaluated, depicting themselves as promising for the utilization in ruminant feeding.

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