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NUTRITIVE VALUES OF EIGHT GENOTYPES OF COWPEA WHOLE PLANTS AS FODDER

A.G. Mahala[1*], Aziza A. Elhussein[1]., S. M. Gasim[2] and A. A.Abdelmulla[2]

[1] University of Khartoum, Faculty of Animal Production, Dept. of Animal Nutrition
[2] University of Khartoum, Faculty of Agriculture, Dept. of Agronomy

ألمستخلص

تهدف هذه الدراسة لتقييم ثمانية طرز وراثية من لوبيا حلو كعلف للحيوان وذلك بتحديد المكون الكيميائى , معدل تكسر الكمادة الجافة والمادة العضوية و القيمة التغذوية النسبية للنباتات كاملة. لدراسة معدل التكسر تم تحضين العينات فى كرش العجول لمدة 16,8,4, 24, 48, 72, 96 ساعة باستخدام عجول بها ناسور كرشى. تم استخدام تصميم القطاعات كاملة العشوائية بثلاثث مكررات لتخطيط التجربة. تم تحليل المعلومات باستخدام معادلة الخط الستقيم. كانت هنالك فروق معنوية بالنسبة للمكون الكيميائى. كانت نسبة البروتين الخام والرماد عالية نسبيا. أعلى قيم (19.24% و 12.23%) للبروتين الخام و الرماد على التوالى قد سجلت للطراز الوراثى HSD2976. أما الألياف الخام وألياف المنظفات المتعادة و الحمضية كانت عالية فى معظم الطرز الوراثية (44.34%, 67.175 و50.05%) على التوالى حيث أدت الى انخفاض فى القيمة التغذوية النسبية . عموما كانت القيمة التغذوية النسبية فى المدى المقبول, تراوحت من 79.19% الى 80.51% وهذا يعزى الى النضج الكامل للنباتات مما يزيد من مستوى الألياف. بالنسبة للقيمة التغذوية النسبية فان الطرز الوراثى هوالأعلى فى الترتيب والطرز الوراثى HSD2966. HSD5132 له قيم عليا لتكسر المادة الجافة و العضوية (73% و 71%) بالتوالى. على الرغم من المستوى العالى للألياف فأن علف نباتات لوبيا حلو يمكنها دعم تغذية الحيوان وذلك بأعتبار ما تحتويه من مستوى عالى من البروتين ونسبة عالية من التكسر.

Abstract

The aim of this study was to evaluate eight cowpea genotypes as animal feed, by estimating the chemical composition, dry matter DM and organic matter OM degradability and relative feed value RFV of the whole plant. For degradability study, samples were incubated in rumen for 4,8,16,24,48,72 and 96 hrs using fistulated calves. The experiment was laid out in randomized complete block design with three replicates. Data were analyzed using general linear model. Significant

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[*] Corresponding author: E- mail ahmedgofoon9@yahoo.com

variations ($p<0.05$) were observed in the chemical composition. CP and ash content were relatively high. The highest values (19.24% and 12.23%) of CP and ash respectively, were obtained for genotype HSD2976. CF, NDF and ADF were high in most genotypes, 44.34%, 67.17% and 50.02% respectively, which resulted in low RFV. Generally RFVs were within the fair level, ranged from 70.19 to 80.51 this might be due to fully mature plants having high level of fiber. However according to RFV, cowpea genotypes HSD2966 ranked first and genotype HSD5132 had a high ($p<0.05$) DM and OM degradability 73% and 71% respectively, in spite of high level of fiber, cowpea fodder can maintain animal nutrition considering the high level of protein and relatively high degradability.

Key words: Cow pea, fodder, NDF, RFV, degradability.

Introduction

Cowpeas are heat-and drought-tolerant crops (Apata & Ologhobo, 1997), requiring low input costs and are well adapted to the arid agronomic areas (Nell et al., 1992). Cowpea was grown as a grain legume crop in Rabi season and grown as fodder in kharif season (Ullah et al., 1995). It produced 2.5 t ha^{-1} (Singh *et al.*,2003) fodder with an excellent source of essential nutrients with an average digestibility co-efficient of 74.35% of whole plant, 78.06% of crude protein, 72.42 of crude fiber, and 76.98% of nitrogen free extract (soluble carbohydrate) and 71.81% of ether extract. The green pod of cowpea contains 51.40%water, 22.5% protein, 10.1% crude fiber, 56.29%soluble carbohydrate, 2.10% fat and 9.0% minerals (Singh, 1979; Rahman et al.,1992). Feed constrain is the most important impediment to improved livestock production in the sub-Sahara Affrica (SSA) countries (Agyemang.,2002). The low level of productivity in the livestock industry is due to a combination of under feeding, disease and poor husbandry. Of immediate concern therefore in any development program for improvement of livestock productivity, is the need for improved management, especially nutrition. Nutrition is perhaps the most important consideration in livestock management. Inability to supply feed in adequate quality and quantity is responsible for the low livestock productivity in the sub-Saharan (SSA) countries (Agyemang., 2002). In Sudan cowpea is grown mainly for seeds production, farmers waiting up to late maturity of plants, this result in losing the leaves components and the plant remains as fibrous post harvesting residues. These practices necessitate increasing the wariness of farmers towards the plant value as fodder.

The objective of this study is to evaluate cowpea whole plant genotypes as animal feed.

Material and Methods

Plant material:

The plant material used consisted of eight genotypes of cowpea. They were kindly provided by Plant Genetic Resources Unit, Agricultural Research Corporation, Sudan. These genotypes differ mainly in pod length, pod color, leaf shape, leaf size, flowers color, seed size and seed color. They were designated as: HSD2966, HSD2967, HSD2976, HSD5130, HSD5131, HSD5132, HSD5670 and HSD5672. These genotypes were planted on the heavy craking clay soil of the Demonstration Farm, Faculty of Agriculture, university of Khartoum (Latitude15˚ 40 N, Longitude 32˚ 32E and Altitude 280m above Sea level). Genotypes were sown during the season (2011/2012) in a randomized complete block design with three replicates. The plot size was 2.1×6 m, consisting of three ridges, 70 cm apart, two seeds were planted per hole, the spacing was 40cm between holes along the ridge, the experimental plots were irrigated at an average interval of 14 days and weeding was carried out when ever needed.

Sampling

Samples of whole plant from 8 genotypes of sweet beans (cowpea) were collected after stage of fully maturity.

Nutritive values

To measure the nutritive values samples were weighted, dried over night for further chemical analysis, crude Protein (CP), crude fibre (CF), Ash and Ether extract (EE) were determined according to (AOAC, 1980).ADL; NDF and ADF in the samples were determined by the method described by VanSoest et al (1991), and relative feed values were calculated according to Stallings (2005) following the equation:

RFV= (DMD* DMI)/1.29

Where:

DMD=dry matter digestibility=88.9-(0.77*%ADF)

DMI=dry matter intake=120/%NDF

1.29= (the expected digestible dry matter intake as% of body weight for full-bloom cowpeas).

Degradability Study

DM and OM degradability were carried out using method described by (Mehrez and Orskov., 1977). Five grams of each plant sample were weighed into a nylon bag tied with nylon ribbon and introduced, using a plastic tube of 20-25 cm length, above the fistula level to ease the movement of the bag inside the rumen. The bags (3bags/bull/period) were incubated for 4, 8, 16,24,48,72, and 96

Animals

Three animals were individually housed and fed fresh *barseem* (*medigaco satavia*) sorghum hay and wheat bran. They had free access to drinking water and salt licks

Statistical analysis

The experiment was laid out in randomized complete block design (RCBD) with three replications. Analysis of variance was carried out using general linear model (GLM). Means were compared using Least Significant Different (LSD) test according to Gomez and Gomez, (1984).

Results and Discussion

Chemical composition of the cowpea plants of the different genotypes were shown in Table (1). Chemical composition were significantly ($P< 0.05$) varied among the genotypes. CP content of whole plant in this study was varied from 15.4% to 19.3%, this result is in agreement with (Canon and Carre, 1989) and similar to findings of Mahala *et al* (2012) who found 19% CP in *lablab purpureus* at mature stage, and Singh *et al* (2003) who found 17% - 18% CP in cowpea haulms.

The high ($p<0.05$) values of CF content were 44.3% , 43.7% and 43.6% found in genotypes HSD2966, HSD2967, HSD2976 respectively and the low values recorded for genotypes HSD5131, HSD5671 and HSD5670 were 36.6% , 36.3 and 36.1% respectively. Due to late stage of maturity these results were relatively higher than that reported by Mahala et al (2012) who reported 25%.

Regarding ash content legumes accumulate minerals more than grasses, therefore ash content of cowpea recorded relatively high values 9.97% in genotype HSD5130 closely followed by 10.12% in genotype HSD5132.

EE content in genotype HSD2976, was 3.95% which is significantly ($p<0.05$) higher when compared with other genotypes, and the lowest value was recorded for genotype HSD5132.

NDF and ADF were ranged from 60.16% to 67.12% and from 40.10% to 50.01% respectively Table (2), these results were higher compared to 41.09% - 50.77% for NDF and consistent to 43.295 - 47.61% for ADF in *Lablab purpureus* (Mahala et al (2012). These relatively high fiber will result in low calculated RFV, which ranged between 71.6 fair to 80.5% good, compared with very good 106 to prime 141that reported by Mahala et al (2012), these variations might be due to stage of maturity.

Table (1): Chemical composition of eight cowpea genotypes whole plant on DM basis.

Treat	**Cp%**	**Ash%**	**EE%**	**CF%**
HSD2966	17.8^{b}	11.2^{c}	3.2^{b}	44.3^{a}
HSD2967	19.3^{a}	12.2^{a}	2.9^{c}	43.7^{a}
HSD2976	16.5^{e}	10.7^{d}	3.9^{a}	43.6^{a}
HSD5130	17.8^{b}	9.9^{h}	2.7^{e}	37.8^{b}
HSD5131	15.4^{f}	10.7^{e}	2.8^{d}	36.6^{c}
HSD5132	15.4^{g}	10.1^{g}	2.5^{g}	37.4^{b}
HSD5670	16.8^{d}	10.4^{f}	2.6^{f}	36.1^{c}
HSD5671	17.2^{c}	11.5^{b}	2.7^{e}	36.3^{c}
SEM	0.013	0.015	0.013	0.38

^{a,b,c,} means in the same Column with different superscripts differ significantly ($p<0.05$). CP=Crude Protein, CF=Crude Fiber, EE=Ether extract, SEM=Standard Error of means

Table (2): NDF, ADF, ADL and RFV of eight cow pea genotypes whole plant on DM basis.

genotyes	NDF%	ADF%	ADL%	RFV%
HSD2966	59.7^{h}	47.5^{f}	18.4^{d}	80.5^{a}
HSD2967	60.2^{g}	48.1^{d}	18.9^{c}	79.3^{a}
HSD2976	66.2^{b}	47.9^{e}	19.5^{b}	72.4^{Bc}
HSD5130	67.1^{a}	46.8^{g}	19.5^{b}	72.3^{Bc}
HSD5131	65.9^{c}	48.4^{c}	21.0^{a}	72.2^{Bc}
HSD5132	64.8^{e}	49.0^{b}	18.5^{d}	72.7^{Bc}
HSD5670	65.8^{d}	40.1^{h}	18.0^{e}	73.7^{B}
HSD5671	64.7^{f}	50.0^{a}	17.7^{f}	71.6^{Bc}
SEM	0.0175	0.0195	0.0555	1.155

^{a,b,c,} means in the same Column with different superscripts differ significantly ($p<0.05$). NDF=neutral detergent fiber, ADF=acid detergent fiber, ADL= acid detergent lignin, RFV=relative feed value, SEM=Standard Error of Means

The degradation of dry matter in the plants of the 8 cowpea genotypes was shown in Table (3). Cowpea genotypes plants were varied significantly ($p<0.05$) in readily soluble fraction (a) the highest value (17.70) shown in genotype HSD2976. The degradable fraction (b) and rate of degradability (c) were varied among genotypes, fraction (b) was higher significantly ($p<0.05$) in genotype HSD5130 (70.0) and the lowest values in genotypes HSD2966 (46.65%). Rate of degradability, fraction (c) ranged from 0.041 to 0.109 for genotype HSD5670 and genotype HSD5130, respectively. The highest ($p<0.05$) value (73%) potential degradability (a + b) was recorded in genotype HSD5132 and HSD5670 and lower amount found in genotype HSD2966 (62.25%). These values were comparable with finding of Etela *et al* (2007), who found 58% DM degradability for 48 hours in cowpea plants while in this study incubated for 96 hours. This result of cowpea whole plants degradability was high in spite of high fiber levels; this might be due to high level of readily fermentable carbohydrates water soluble sugars and pectin in legumes (Ulyate *et al* 1973)

Table (3): DM Degradability parameters of eight cowpea genotypes, whole plants.

Genotypes	a	b	c	a+b
HSD2966	15.6^{d}	46.6^{h}	0.097^{b}	62.2^{g}
HSD2967	15.1^{e}	47.3^{g}	0.098^{b}	62.4^{f}
HSD2976	17.7^{a}	47.5^{f}	0.059^{d}	65.1^{e}
HSD5130	-18.0^{g}	70.0^{a}	0.109^{a}	68.2^{d}
HSD5131	12.8^{f}	55.6^{d}	0.07^{c}	68.4^{c}
HSD5132	16.5^{c}	56.5^{c}	0.042^{ef}	73.0^{a}
HSD5670	16.5^{c}	56.9^{b}	0.041^{f}	73.0^{a}
HSD5671	17.2^{b}	54.9^{e}	0.043^{e}	72.1^{b}
SEM	0.056	0.035	6.12e-04	0.083

(a) readily soluble fraction,(b) not soluble but degradable fraction,(c) rate of degradability /hour, (a+b) the effective degradable fraction

OM degradation parameters of the 8 genotypes cowpea whole plants were shown in Table (4). The readily soluble fraction (a) were significantly ($p<0.05$) varied among the genotypes. The high values were (15.5, 14.9 and 13.1) in genotypes HSD5132, HSD2976 and HSD5671 respectively, and the lowest value shown in genotype HSD5130 (-8.5). The degradable fraction (b) was higher ($p<0.05$) in genotype HSD5130 (73.7%) and effective OM degradability (a + b) ranged between 60.3% in genotype HSD2966 and 71.6% in genotype HSD5132. These values were agreed by Uchenna *et al* (2011), who found 58.5% – 80.2% OM degradability of cowpea plants.

Table (4): OM Degradability parameters of eight cowpea genotypes whole plants.

genotypes	A	b	c	a+b
HSD2966	9.6^{ab}	50.9^{e}	0.012^{d}	60.3^{e}
HSD2967	9.6^{ab}	50.6^{e}	0.012^{d}	60.3^{e}
HSD2976	14.9^{a}	50.3^{e}	0.062^{c}	65.2^{d}
HSD5130	-8.5^{c}	73.7^{a}	0.13^{a}	65.7^{d}
HSD5131	3.4^{b}	68.5^{b}	0.096^{b}	66.9^{c}
HSD5132	15.5^{a}	56.1^{d}	0.043^{c}	71.6^{a}
HSD5670	9.6^{ab}	58.1^{c}	0.056^{c}	67.7^{bc}
HSD5671	13.1^{a}	55.2^{d}	0.053^{c}	68.3^{b}
SEM	2.9	0.48	9.4-03	0.44

(a) readily soluble fraction, (b) not soluble but degradable fraction, (c) rate of degradability /hour, (a+b) the effective degradable fraction

Conclusion:

Cowpea genotypes plants had relatively higher CP content; therefore it may improve the quality of poor grasses particularly in the dry season.

The high levels of fiber in cowpea plants due to fully mature stage were effectively utilized by rumen microbes resulted in high degradability percentage.

Cowpea genotypes whole plants with high protein content and effectively degradable fiber could support animal nutrition

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