# Food-Fodder Traits in Groundnut

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Groundnut (*Arachis hypogaea*) is one of the key crops of the semi-arid tropics. It is commonly cultivated as a food-feed crop that provides pods for human food and haulms for livestock feeding (Larbi et al. 1999, Omokanye et al. 2001). From farmer participatory studies in the Deccan plateau of India, Rama Devi et al. (2000) concluded that food from grain/pods and fodder from the crop residues almost equally contribute to livelihoods in mixed-crop livestock systems. It was because of this important dual-purpose usage of groundnut that the groundnut improvement group of the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) and livestock nutrition group of the International Livestock Research Institute (ILRI), Patancheru, India started to explore collaboratively the potential for improving pod yield and haulm quantity and quality. Successful inclusion of haulm fodder traits into groundnut improvement has three prerequisites:

1. Livestock-nutritionally important genotypic variation in haulm value (quantity and quality);
2. Laboratory infrastructure that can predict fodder quality in a large number of plant entries; and
3. No serious trade-off between pod and haulm traits.

The work reported here investigated haulms from 860 breeding lines and cultivars of groundnut considering these three prerequisites.

## Materials and methods

**Groundnut breeding lines and cultivars used.** The groundnut genotypes, 860 in all, were grown during the postrainy season 2001/02 at ICRISAT, Patancheru, using established ICRISAT protocols. The genotypes came from diverse spectra of groundnut improvement: medium duration, confectionery type, rust and late leaf spot resistant and aflatoxin resistant materials. Twelve cultivars (checks) were repeated in the 2002/03 postrainy season for the initial assessment of year-to-year effects.

**Haulm quality analysis.** Haulms were analyzed by a combination of conventional laboratory techniques and Near Infrared Spectroscopy (NIRS). The NIRS instrument used was a FOSS Forage Analyzer 5000 with software package WinISI II. From 860 haulm samples, 180 representative samples were selected based on their NIRS spectra for conventional analyses of haulm nitrogen content by Kjeldahl method and haulm in vitro organic matter digestibility (OMD) and metabolizable energy content as described by Menke and Steingass (1988). The selected set of 180 haulm samples was randomly divided into 2 subsets of 90 samples each, one for development of the NIRS calibration equations and the other for validation procedures after blind-predicting haulm nitrogen, in vitro OMD and metabolizable energy content. Relationships between blind-predicted and conventionally analyzed variables were described by $R^2$ and standard error of prediction (SEP).

## Results and discussion

**Haulm quality characteristics predictions by NIRS.** The statistical comparison of nitrogen content, in vitro OMD and metabolizable energy content of 90 haulm samples as blind-predicted by NIRS and as analyzed by conventional laboratory analysis is presented in Table 1.

There was very good agreement between NIRS predicted and measured values (Table 1). The $R^2$ for the relationships were well above 0.90, which is considered excellent particularly for biological methods like

**Table 1. Comparisons of NIRS blind-predicted nitrogen, in vitro organic matter digestibility (OMD) and metabolizable energy (ME) content with actually analyzed values in haulms of 90 groundnut genotypes**.

| NIRS blind-predicted trait | Agreement between NIRS predicted (y) and analyzed value (x) |
|---|---|
| Haulm nitrogen | $y = 0.18 + 0.9x$; $R^2 = 0.94$; SEP[1] = 0.06 |
| Haulm in vitro OMD | $y = 8.2 + 0.85x$; $R^2 = 0.92$; SEP = 0.88 |
| Haulm in vitro ME | $y = 0.5 + 0.93x$; $R^2 = 0.93$; SEP = 0.13 |

1. For assessments of standard error of prediction (SEP), see also mean and range in Table 2.

**Table 2. Means and ranges of nitrogen content, in vitro organic matter digestibility (OMD) and metabolizable energy (ME) content and their least significant difference (LSD) and probability values (*P*) for haulms of 860 groundnut genotypes.**

| Haulm trait | Mean | Range | LSD | *P* |
|---|---|---|---|---|
| Nitrogen (%) | 1.7 | 1.2–2.3 | 0.16 | <0.0001 |
| In vitro OMD (%) | 56.3 | 51.7–61.1 | 1.9 | <0.0001 |
| In vitro ME (MJ kg$^{-1}$) | 7.9 | 6.9–8.9 | 0.4 | <0.0001 |

**Table 3. Relationships between haulm and pod traits in groundnut.**

| Trait comparisons[1] | n | Relationship |
|---|---|---|
| Haulm N (x) versus pod yield (y) | 860 | y = 1427 + 1303x; r = 0.28; *P* <0.0001 |
| Haulm N (x) versus haulm yield (y) | 839 | y = –2911 + 3569x; r = 0.26; *P* <0.0001 |
| Haulm in vitro OMD (x) versus pod yield (y) | 860 | y = 2163 + 25.7x; r = 0.05; *P* = 0.13 |
| Haulm in vitro OMD (x) versus haulm yield (y) | 839 | y = –617 + 173.9x; r = 0.23; *P* <0.0001 |
| Haulm in vitro ME (x) versus pod yield (y) | 860 | y = 734 + 365x; r = 0.13; *P* <0.0001 |
| Haulm in vitro ME (x) versus haulm yield (y) | 839 | y = –5816 + 1129x; r = 0.27; *P* <0.0001 |
| Haulm yield (x) versus pod yield (y) | 839 | y = 2671 + 0.31x; r = 0.46: *P* <0.0001 |
| Digestible haulm yield (x) versus pod yield (y) | 839 | y = 2708 + 0.52x; r = 0.45; *P* <0.0001 |

1. N = Nitrogen; OMD = Organic matter digestibility; ME = Metabolizable energy.

determination of in vitro OMD and metabolizable energy content assessed on the basis of inoculation of substrate with rumen microorganism. NIRS analysis is much quicker and cheaper than conventional analysis and is easy to integrate into routine crop improvement work, while conventional analysis is not. Establishment of accurate NIRS equations for predictions of groundnut haulms quality is, therefore, an important step towards implementing groundnut improvement for haulms fodder quality.

**Variations amongst genotypes for haulm fodder quality traits.** Highly significant differences amongst genotypes were found for nitrogen content, in vitro OMD and metabolizable energy content of the haulms (Table 2). Further, the range in these traits was large enough to have important relevance for livestock feeding. For example, low nitrogen content is often considered the most limiting factor in utilization of crop residues as fodder. Rumen microbes require a minimum of 1 to 1.2% nitrogen (or 6.25 to 7.5% protein, since protein is calculated as N × 6.25) in the fodder to effectively degrade it. Nitrogen content below this threshold results in low voluntary feed intakes and therefore low livestock productivity (Van Soest 1994). Nitrogen content of haulms among genotypes varied by almost 100% (Table 2), ranging from 1.2 to 2.3% (or 7.5 to 14.4% protein content) with a mean value of 1.7%. Thus, haulms even from genotypes relatively low in nitrogen will supply minimum microbial nitrogen requirement resulting in acceptable levels of intake and therefore livestock productivity (see also Blümmel et al. 2005). Similarly, a range of about 10 units in in vitro OMD (Table 2) will have important effects on livestock productivity. As shown recently (Blümmel et al. 2005), the differences amongst genotypes for haulm digestibility of 7.1% (in vivo) and 7.5% (in vitro) were associated with differences in live weight gain in sheep of about 100 g day$^{-1}$.

The range in metabolizable energy content amongst genotypes was proportionally slightly higher than the range in in vitro OMD, confirming the important differences amongst genotypes for haulm quality. Briefly, metabolizable energy content is potentially a more precise estimate of fodder quality than digestibility because losses in urinary and methane energy are taken into account, and metabolizable energy values can be directly used to predict milk yield and meat production.

Broad sense heritability for fodder traits estimated in 12 cultivars (that served as checks in the two consecutive growing seasons) grown in 2001/02 and 2002/03 postrainy seasons was 0.72 for nitrogen content, 0.72 for in vitro OMD and 0.67 for metabolizable energy content.

**Relationship between pod yields and haulm quantity and quality.** The relationships between haulm fodder quality traits and pod and haulm yield in 860 genotypes are reported in Table 3. It is encouraging to note that haulm fodder quality traits and pod and haulm yields were not inversely related. Even though highly significant, the relationships were generally weak (Table 3). The strongest relationship ($R^2 = 0.21$) was observed between pod and haulm yield, but even in this relationship most of the variation (79%) remained unaccounted for. The latter finding suggests that haulm yields should be recorded in its own right in groundnut improvement since a considerable degree of independence seems to exist between pod and haulm yields and high pod yield is not automatically associated with high haulm yield. To summarize, the relationships presented in Table 3 show that high pod yield and superior haulm quality and quantity are compatible traits.

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