Classification and comparison of *Gliricidia* provenances using near infrared reflectance spectroscopy

S.J. Lister\(^a,\)*, M.S. Dhanoa\(^a\), J.L. Stewart\(^b\), M. Gill\(^c\)

\(^a\)Institute of Grassland and Environmental Research, Plas Gogerddan, Aberystwyth, Ceredigion SY23 3EB, UK
\(^b\)Oxford Forestry Institute, Department of Plant Sciences, University of Oxford, Oxford OX1 3RB, UK
\(^c\)Natural Resources International, Central Avenue, Chatham Maritime, Kent ME4 4TB, UK

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Abstract

There is an ever-increasing need to identify new feed resources in developing countries and the types of forages used tend to be more complex in terms of chemical composition. Near infrared reflectance spectroscopy (NIRS) has the potential to aid the evaluation of forages and in this study was employed to compare and classify *Gliricidia* spp. provenances. Multivariate statistical techniques, including biplot, principal component analysis (PCA), discrimination, hierarchical cluster and canonical variate analysis (CVA) were used to compare the dried foliage samples of 25 different provenances of *Gliricidia* spp. which were grown on one site in Honduras to avoid confounding provenance effects with environmental effects or interactions. Marked inter-provenance differences were observed in the 1560–1740, 2060–2170 and 2320–2360 nm spectral regions, particularly for provenance M23 (43/87). This provenance was found to be distinct in graphical plots from biplot, PCA and cluster analysis and is in fact a different species, i.e. *Gliricidia maculata*. In addition, inter-provenance distances between populations representing provenances G2, G5, H7, M10 and V17 when compared to their intra-provenance variation, were all found to be statistically significant, with the exception of that between G2 and H7. Discriminant analysis showed that of the remaining 20 individual provenances, samples were more similar to the composite (V17) and multiple introduction (H7) populations than the unique populations (G2 and G5). NIRS combined with multivariate techniques therefore shows potential to classify provenances on the basis of their spectral features, which are a comprehensive record of sample chemistry, and aid the selection of alternative forages. © 2000 Elsevier Science B.V. All rights reserved.

Keywords: *Gliricidia sepium*; *Gliricidia maculata*; Near infrared reflectance spectroscopy (NIRS); Classification; Multivariate; Multipurpose trees
1. Introduction

In developing countries, shortage of good-quality animal feed is a serious problem forcing livestock owners to incorporate leaves of shrubs and trees into the diets. Multipurpose browse tree legumes are potentially an important feed resource, yielding high protein forage during dry seasons when both the quality and quantity of other feed sources are in short supply. *Leucaena* spp. (*Leucaena*), has until recently, been a very important multipurpose tree, and relied upon heavily as a source of protein-rich forage (Sampet and Pattaro, 1987). However, devastation by the Leucaena psyllid has lead to a reduction in yield (Palmer et al., 1989; Bray and Woodroffe, 1991), and brought about the need to find alternative forage legumes. *Gliricidia* spp. (*Gliricidia*) is one such species which is being assessed as an alternative. *Gliricidia* is native to Central America and Mexico but has been introduced to many tropical areas (Hughes, 1987). The literature suggests that *Gliricidia* produces a range of useful products including fuelwood, green manure, live fences, shade for coffee and cocoa plants (Falvey, 1982; Hughes, 1987; Stewart, 1996). Characteristics such as fast height growth, good sprouting, easy propagation from cuttings, forage and improved soil conditions through nitrogen fixation, make the species extremely valuable (Chadhokar, 1982; Smith and van Houtert, 1987). It is only one of the few tree species capable of producing leaf yields similar to those of *Leucaena*, and it can be grown on a wide range of soils. The nutritive value of *Gliricidia* is comparable to alfalfa with high levels of crude protein (20–30%) and its digestibility is superior to most other tropical leguminous forages (Adejumo and Ademosun, 1985; Murugan et al., 1985), however, ambiguous results have been reported in the literature regarding the quality of the leaves as fodder for livestock (Mahadevan, 1956; Vearasilp, 1981; Chadhokar, 1982; Atta-Krah and Sumberg, 1987).

*Gliricidia* is currently used as a browse plant and source of fodder for ruminants in some tropical countries, but is little used in others where it is not considered to be suitable as fodder. The majority of work on browse has been essentially agronomic in nature, and comparatively little is known about its chemical composition and nutritive value as an animal feed. Assessment of nutritive value has demonstrated and standard methods of chemical analysis have indicated that some differences do exist between provenances of *Gliricidia*. However, the trials have generally been multisite, involving small numbers of different provenances and where the site effects have been dominant (Stewart et al., 1998; Wood et al., 1998). Dunsdon and Simons (1996) summarised details of international field trials carried out by the Oxford Forestry Institute to assess variation between and within populations of *Gliricidia sepium* in terms of growth, yield and fodder quality. Feeding trials to investigate the variation in fodder quality (Larbi et al., 1993; Stewart et al., 1998) found no evidence of a strong provenance effect in terms of nutritive value in *G. sepium*, however, it was clear that ruminants were able to distinguish between provenances, preferring the local land races to which they were accustomed to rather than particular provenances. The chemical basis for the selection between provenances is not fully understood. A review by Smith and van Houtert (1987) noted that the variability in chemical composition of *Gliricidia* could be accounted for by a number of factors, including age of plant, plant part, harvesting interval, season and location.
New systems to predict feed quality are required in developing countries to assess the available feed resources, and also in plant breeding programmes, where the nutritive value of the plant is likely to be an important factor in deciding the uptake of new varieties by farmers. A fast and reliable method to screen large numbers of samples is required and improved characterisation of available tree species relating to specific traits could allow farmers to plant the most appropriate varieties to suit their conditions and requirements.

The near infrared (NIR) reflectance spectrum of a forage can take into account further aspects of the chemistry as the spectrum represents an information-rich profile of chemical characteristics of a sample. For agricultural and food products, NIR has proved to be an accurate, precise and rapid for determining their composition (Osborne and Fearn, 1986; Williams and Norris, 1987). This approach requires calibration to correlate the spectral response from a set of samples with known chemical concentrations from laboratory analyses. However, NIR can also be used as a qualitative tool, where the aim is not to tell how much of any given component is present in an unknown compound or material but rather to classify it on the basis of its spectral features and attempt to detect the spectral features which differentiate material of one type or class from all other types or classes. NIR spectral data has been effectively combined with multivariate techniques such as principal component analysis (PCA), factor analysis and discriminant analysis for classification, discrimination and authentication purposes (see for example Downey, 1994; Sanderson et al., 1997).

The aim of the present study was to compare 25 different provenances of Gliricidia, grown on one site, to compare and classify the different provenances, based on the NIR spectral information alone, with a view to identifying provenances which exhibit marked differences.

2. Material and methods

2.1. Gliricidia samples

Dried and ground samples were supplied by the Oxford Forestry Institute. Trees of 25 provenances (Table 1) were grown on one site in Honduras (El Zamorano), in a randomized design (three plots for each provenance with approximately 21 trees in each plot). Samples of mature leaves were collected on 5 August 1990 from 10 trees (from one plot) and bulked before being oven dried at approximately 50°C for 48 h and then ground through a 1 mm screen.

On the basis of the provenance performance from the previous years, the following five provenances were selected as being the most different:

1. G2: top overall in performance and productivity but susceptible to very high aphid attack.
2. G5: good performance with very low aphid attack.
3. H7: lowest N content.
5. V17: highest digestibility.
For these five provenances, samples from 10 individual trees were supplied except for provenance H7, from which only eight trees were sampled, in addition to the bulk sample, resulting in a total of 73 samples.

2.2. NIR analysis

All 73 samples were scanned in duplicate using an NIRSystems 6250 scanning monochromator (FOSS UK Ltd., Didcot Oxon, UK). Data were collected at 2 nm intervals over the spectral range from 1100 to 2498 nm and stored as the logarithm of the reciprocal of the reflected ($R$) energy ($\log(1/R)$). Thus, a total of 700 data points were collected for each sample and the duplicate scans averaged. NSAS (NIRSystems Inc., Silver Spring, MD, USA) software was used to collect the spectra, which were then converted to ISI (Infrasoft International, Analytical Services, State College, PA 16801, USA) format.

The NIR spectrum of a dried and ground sample is comprised of diffuse and specular (mirror-like) reflected energy. The specular component carries information about the physical nature of the sample particle surfaces and is a result of random scatter of light at those surfaces. The diffuse component carries information regarding the chemical nature of the sample, and therefore, it is important to maximise the collection of the diffusely
reflected radiation. A mathematical approach is required to highlight the chemical differences between samples and reduce variation due to physical effects. This was achieved by the use of two spectral transformations, Standard Normal Variate (SNV) and De-Trend (DT) (Barnes et al., 1989). In this study, the transformations were applied in the reverse order, i.e. DT then SNV (Dhanoa et al., 1995), and will be referred to as DTS format. The program NIRTOOLS (Whitebytes, NIR software, Hurley, Berks. UK) was used to apply these transformations, resulting in individual spectra with a mean of 0 and variance equal to 1.

2.3. Chemical analyses

Dry matter (DM) was determined by oven-drying samples at 100°C overnight and ash measured by igniting the dried sample at 550°C for 16 h. Nitrogen (N) was determined by the micro-Kjeldahl technique as described by Sanderson et al. (1997). In vitro organic matter digestibility (IVOMD) was determined according to Tilley and Terry (1963).

2.4. Statistical analyses

For all statistical analysis, the transformed spectra (DTS) were reduced to 350 data points by averaging adjacent data points. The statistical package GENSTAT version 4.1 (GENSTAT, 1987) was used to perform the following analysis to investigate inter-provenance relationships.

Biplot (Gabriel, 1971) was used to obtain a graphical representation and overview of the relationships between the different provenances and \( \hat{r}_2 \) was used as a measure of rank 2 goodness of fit where \( \hat{r}_i \) are the eigenvalues from singular value decomposition.

PCA was used to reduce the dimensionality of the spectral data, the first 20 principal components were used in further analysis. Pair-wise plots of the various components were used to obtain a graphical representation and overview of inter-relationships between provenances. Hierarchical cluster analysis was used to investigate the relationships and study the natural groupings present among the 25 individual provenances. A similarity matrix was derived from the spectral data and utilised in cluster analysis using a furthest neighbour criterion, the results being summarised in the form of a dendrogram.

Samples from the individual trees for provenances G2, G5, H7, M10 and V17 were utilised in canonical variate analysis (CVA) to determine inter-provenance distances, i.e. Mahalanobis distances (Mahalanobis, 1936). CVA finds linear combinations of the original variables that maximise the ratio of between-group to within-group variation, thereby giving functions of the original variables that can be used to discriminate between the groups on the basis of the inter-group distances. A similarity matrix comprising similarity indices was formed from the matrix of inter-provenance distances (Gower and Ross, 1969). The maximum inter-group distance between any two provenances was taken as \( D_{\text{max}} \). The similarity index (SI) was calculated as follows:

\[
SI = 1 - \left( \frac{D^2}{D^2_{\text{max}}} \right)
\]
where $D$ is the inter-provenance Mahalanobis distance. By definition, the provenances exhibiting the maximum inter-group distance had a similarity of 0.0. The statistical significance of the distances between the five provenances was tested using a variance ratio test (Rao, 1952). Further, discriminant analysis was used to identify which of the five populations (G2, G5, H7, M10, V17) the remaining 20 provenances were most similar or most related to.

3. Results

Fig. 1 shows the log($1/R$) spectra of the 25 provenances which are typical of many forages. On this scale, NIR spectra are very difficult to interpret and chemical differences difficult to detect, largely due to particle size and pathlength effects which are seen as shifts on the $y$-axis. Application of DTS transformation (Dhanoa et al., 1995) to reduce these effects and enhance underlying chemical differences results in the transformed spectra shown in Fig. 2. De-trending corrects baseline curvature in the spectra, and SNV reduces the effects of particle size and scatter, so physical effects are reduced and spectral differences arise largely from differences in chemical composition. In these spectra, the main differences were observed in the following broad spectral regions: 1560–1740, 1800–2000, 2000–2400, and 2400–2500.

Fig. 1. Log($1/R$) spectra of the 25 different provenances of *Gliricidia* spp.
2060–2170, 2320–2360. Provenance M23 showed the largest variation in these spectral regions. This provenance was found to have the lowest IVOMD and nitrogen content compared with the other provenances in this study (Table 2). To further investigate the relationships between spectra, multivariate statistical techniques were employed.

Multivariate statistical techniques, namely biplot, PCA and cluster analysis, were used to examine the inter-provenance differences and to classify the 25 *Gliricidia* provenances. Graphical representation of biplot (Fig. 3) indicates the relationships between the 25 different provenances. The goodness of fit was assessed and in this case $\rho^2 = 0.9975$ which suggests that this biplot gave a good approximation of the matrix. Provenance M23 is clearly different from the majority of samples, sitting in the bottom right-hand corner of the diagram with the other provenances grouped towards the left-hand side. Of the latter group, provenances V17, M12 and C22 are set apart at the top right-hand side and CR20, G2, G5 and T24 set apart from the main group at the bottom right. Removal of provenance M23 from the set resulted in a biplot where provenances were more spread out but showed a similar pattern to Fig. 3 with $\rho^2 = 0.9978$.

PCA was used to simplify the data by reducing the number of variables into a smaller number of orthogonal variables which are linear combinations of the original wavelength variables and maximise the variation contained within them, thereby displaying most of the original variability in a smaller number of dimensions. Graphical presentation of the
pair-wise components allows the natural grouping of the samples to be observed, indicating the similarity between provenances and allowing different groups of provenances to be identified. In principal components derived from log(1/R) data, the first component accounts for a large amount of variation which is mainly due to physical effects, for example, particle size and path length (Cowe and McNicol, 1985; Barnes et al., 1989). The application of spectral transformations reduced these effects and the first principal component will no longer be associated with particle size effects (Barnes et al., 1989) but with chemical information. The first 20 principal components accounted for almost 100% variability in the sample population, with 53.15, 29.58, 6.61, 5.28, 2.37 and 1.12% of the variation associated with the first six components, respectively. The pair-wise plot of the first two components is presented in Fig. 4. No major groupings were observed, but some provenances were found to sit at the extremes: provenance M23, and provenances G2, T25, C22, V17 in the lower quadrats and provenances T24, G5, M14 and M12 show separation in the upper quadrats. In the third dimension, i.e. the third component, which is indicated as positive or negative, it is possible to get a clearer picture of which samples are closer to each other. Provenances originating from Mexico,
with the exception of M23, form a group in the top half of the plot, however in the third component, M10, M12 and M15 have positive scores, whereas M11, M13, M14 and M16 have negative scores. All other provenances originating from the same country do not appear to group together. Examination of the contribution of the principal component weights can give some indication of the variance relating to each component. Weights for the first two principal components are shown in Fig. 5 and the correlations between the weights for the first six principal components and DM, Ash, N and IVOMD are presented in Table 3. The first component was highly correlated with all constituents (Table 3) and was dominated by a trough in the 1900–2000 nm region, corresponding to two minima centred around 1920 and 1980 nm. The 1920 nm region is characteristic of the O–H combination band of water (Curcio and Petty, 1951), whereas the 1980 nm peak corresponds to the N–H stretch combination band (Goddu, 1960; Osborne and Fearn, 1986). Positive weightings were observed in the regions of 1500–1580, 1720–1730, 2070 and 2300 nm. The latter region is primarily associated with C–H stretch combination bands of waxes, oils, carbohydrate, lignin and protein (Barton and Himmelsbach, 1992). The broad peak between 1500 and 1600 nm showed maxima at 1530 nm, which is associated with an N–H stretch first overtone absorption band (Krikorian and Mahpour, 1973), and at 1580 nm which corresponds to O–H stretch first overtone generally associated with sugars (Osborne and Fearn, 1986). The 1720–1730 nm region represents

Fig. 3. Biplot representation showing the distribution of the *Gliricidia* spp. provenances.
C–H first overtone absorptions and has been associated with cell walls (Barnes, 1988), whereas the 2070 nm region represents either O–H or N–H combination bands associated with carbohydrate or protein, respectively. For the second principal component, the plot of weights versus wavelength showed one main positive peak with maxima in the region of 2157 nm which represents an amide combination band (Hecht and Wood, 1956) and

![Graph](image)

Fig. 4. Plot of the first and second principal components for the 25 different provenances of *Gliricidia* spp. (the sign of the third principal component is given).

Table 3
Correlation between dry matter (DM), ash, nitrogen (N), in vitro organic matter digestibility (IVOMD) (g/kg dry matter) and the weights for the first six principal components for the 25 provenances

<table>
<thead>
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<th>Principal component</th>
<th>Correlation with</th>
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<tr>
<td></td>
<td>DM</td>
</tr>
<tr>
<td>1</td>
<td>0.61</td>
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<tr>
<td>2</td>
<td>−0.21</td>
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</tr>
<tr>
<td>6</td>
<td>−0.25</td>
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2197 nm which indicates the presence of the C–H/C=O combination band (Goddu, 1960) indicative of carbohydrates. Negative peaks were observed in regions associated largely with C–H and N–H absorptions. The 1720 and 2301 nm regions were noted in the first component and appear in this component as small troughs. Other troughs were apparent in the 1345 and 1953 nm regions. It is the above spectral regions which account for the differences between provenances.

Hierarchical cluster analysis groups samples with multidimensional information into disjoint sets which may correspond to defining features of the samples. A furthest neighbour criterion was utilised, which joins two groups only if the most distant members of the combined groups are close enough together. Diagramatical output from cluster analysis for the 25 provenances is presented as a dendrogram which indicates the similarity at which the various groups are formed and join together (Fig. 6). At approximately 80% similarity, five main groups were evident as follows: (G1, T25, G4, M16, P21, H7), (G3, M15, N9, CR19, V17, H6, N8, H18, C22), (M10, M12), (G2, CR20, T24, G5, M11, M13, M14) and M23. The first two groups merged at 84.1% similarity, and the third group merged with these at 70.3% similarity. Provenance M23 merged with the fourth group at 68.4% similarity. This merged group clusters with the other grouping at 43.7% similarity. These two groups can also be seen on the plot of the first two principal components as samples with either positive or negative values for component 1
The only clustering based on country of origin was observed for some provenances from Mexico: (M10 and M12) and (M11, M13 and M14). Re-analysis after removal of M23 resulted in a dendrogram with the same main groupings as found previously, which fused together at 47.5% similarity. The smaller clusters were the same except that V17 now clusters with M10 and M12.

Further analyses were performed to test inter-provenance differences where samples from individual trees of provenances G2, G5, H7, M10 and V17 were utilised. Analysis of the spectral data using biplot, PCA and cluster analysis showed large amounts of overlap between some of the provenances, so the samples from 10 individual trees were used to represent the variation within a provenance with trees growing in competition with their neighbours, to allow CVA and discriminant analyses to be performed. From CVA, the first three canonical variates accounted for 43.93, 29.26 and 22.20% of the variation, respectively. The plot of the first two canonical variates is shown in Fig. 7a, with 95% tolerance regions constructed round each sample mean (Krzanowski, 1988). It is evident

Fig. 6. Dendrogram showing the emerging clusters from hierarchical cluster analysis using a furthest neighbour criterion for the 25 different provenances.
Fig. 7. (a) Plot of the first and second canonical variates showing the relationships between the five provenances G2, G5, H7, M10 and V17 where samples from replicate individual trees were available. (b) Plot of the second and third canonical variates for the five provenances G2, G5, H7, M10 and V17.
that some overlap exists between provenances G2 and H7 and between G5 and M10 and the first canonical variate separates G5 and M10 from G2, H7 and V17, whereas the second canonical variate separates V17 from the others. Fig. 7b shows the plot of the second and third canonical variates and indicates that the third canonical variate clearly separates G5 and M10. The canonical variates were derived using the first 20 principal components (which accounted for 99.96% of the variation). However, to test the level of significance of the inter-provenance distances, the number of principal components was reduced to 10 (which accounted for 99.71% of the variation) to increase the number of degrees of freedom available for the variance ratio test (Rao, 1952). The CVA plot calculated from 10 principal components did not show such a clear separation as that calculated from 20 components, possibly indicating that the later components may contain important information relating to the discrimination. The distance matrix for the five provenances is presented in Table 4, and these distances were tested using the variance ratio test. The maximum distance was found between provenances G5 and V17 and it can be seen that all distances were found to be significant with the exception of that between G2 and H7.

Discriminant analysis using the data from individual trees was used to identify which of these five provenances the remaining 20 bulk samples were most similar to. Seven provenances were found to be most similar to V17 (G1, N9, M13, C22, M23, T24, T25), six were similar to M10 (H6, M14, M15, H18, CR19, P21), five to H7 (G4, M11, M12, M16, CR20), one to G5 (N8), and one to G2 (G3). These results are not entirely surprising as V17 is a composite population and H7 is a multiple introduction population, whereas G5 and G2 are unique provenances.

4. Discussion

In many countries, multipurpose trees can provide a valuable feed source for livestock, particularly during the dry seasons. However, this potential is rarely utilised fully due to poor understanding of the nutritive value of such crops. In particular, there is a need to improve understanding of not only the management and agronomic features but also the compatibility of individual species of these shrubs and trees with livestock production.

<table>
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<tr>
<th>Table 4</th>
<th>Inter-group distances for provenances G2, G5, H7, M10 and V17</th>
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<tr>
<td>G5</td>
<td>5.156**</td>
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<tr>
<td>H7</td>
<td>3.996</td>
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<tr>
<td>M10</td>
<td>5.406**</td>
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<tr>
<td>V17</td>
<td>7.118**</td>
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<tr>
<td>G2</td>
<td>G5</td>
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* P<0.05.
** P<0.01.
*** P<0.001.
systems. To enable species to be selected for different environments and allow the production and use of feed to be more efficient, a rapid and simple technique to assess the quality of tree legume foliage is required. Further, large differences exist in the nutritive value of fodder tree species and individual chemical constituents alone are an inadequate indicator of nutritive value. Since the availability of nutrients from different forages is so complex and variable, there is a need to screen forages prior to feeding trials. This paper describes a preliminary study to compare and classify 24 provenances of *G. sepium* and one provenance of *Gliricidia maculata* grown on one site on the basis of their NIR spectra.

Biplot, PCA and hierarchical cluster analysis of the spectral data were used to obtain a general overview and provide graphical presentation of the population and to show the inter-relationships between provenances. The environment was identical for all samples, since they were grown on the same site (in Honduras) and were harvested on the same day, therefore, genotypic effects were not substantially confounded with environmental effects. By growing all trees on one site, the differences in chemical composition were independent of climate or location, although adaptation to this site may still be incomplete.

This study showed that differences between individual provenances do exist and some groupings were apparent. Provenance M23 exhibited marked differences from all other provenances. This provenance is in fact a different species, i.e. *G. maculata*, whereas the other provenances are all *G. sepium*. There has been some confusion at the species level, particularly over the distinction between *G. sepium* and *G. maculata*, both names being used indiscriminately in the literature. Hughes (1987) reinstated *G. maculata* as a separate species distinct from *G. sepium*, and this has been confirmed by other workers (Lavin et al., 1991; Chamberlain and Galwey, 1993). This study also supports this view. All of the other Mexican provenances were found to form a group in PCA and it is interesting to note that Larbi et al. (1993) found that Mexican ecotypes, including all of these provenances, were of low relative palatability compared to those from Costa Rica.

Results from provenance trials have shown that a large amount of genetic variation exists for *G. sepium* in seed and seedlings (Salazar, 1986; Ngulube, 1989). Salazar (1986) found that, in preliminary phases of provenance trials, a considerable amount of genetic variation existed, principally in seed traits, however, the diverse geographic and climatic distribution of the species may have given rise to major genetic variations within populations. The variations observed were largely within provenances and a family study was suggested to identify outstanding genotypes. Similarly, Ngulube (1989) found considerable genetic variation in nursery trials. Two studies have indicated possible genetic variation in leaf chemical composition as shown by the highly selective feeding behaviour of monkeys (Glander, 1977) and moths (Janzen, 1983) of certain Gliricidia trees in large populations. Significant differences between provenances have been noted for many traits including yield, quality, stem multiplicity, height, wood and leaf biomass (Simons, 1991; Bray et al., 1993; Dunsdon and Simons, 1996). In addition, evidence is supportive of the genetic variability in the content of anti-nutritive factors in the species (Pezo et al., 1990). To determine the level, structure and origin of genetic variation within and between populations, a number of molecular approaches (Dawson and Chamberlain, 1996) have been used. For example, random amplified polymorphic DNA (RAPD)
markers were used to investigate genetic variation between and within populations of *G. sepium* and *G. maculata* (Chalmers et al., 1992; Dawson et al., 1995). Extensive genetic variability was detected between species and the above technique allowed the genetic variation within single species to be partitioned and facilitated greater discrimination.

The damage caused to Leucaena by psyllid has emphasised the importance of diversification of the narrow genetic bases of tree legumes. Genetic improvement is dependent on the nature and extent of genetic variability available for manipulation and the partitioning of variation between and within populations will influence the breeding strategy employed. The extent and distribution of genetic diversity of *Gliricidia* needs to be investigated further. The evaluation and quantification of the variability is important as it offers the opportunity for further improvement of the species and will allow this species to be exploited as a multipurpose tree in tropical agriculture. Improved characterisation of available tree species according to their nutritive and anti-nutritive effects could help farmers to plant the most appropriate varieties to suit their conditions and requirements. An improved understanding of the factors influencing or causing the differences will assist in the development and identification of provenances with improved nutritive value, particularly the ones which may be utilised as forage feeds.

NIR has the potential to be used as an effective screening tool on the basis of spectral information, to classify samples and to identify provenances with specific traits which then can be related to agronomic information. The more traditional use of NIRS is to determine the concentration of chemical or quality components which requires the development of appropriate calibration models. This approach combined with qualitative analysis using multivariate techniques would provide a valuable, rapid and non-destructive characterisation of potential forages.

5. Conclusions

This study has shown that information regarding relationships within and between species can be derived from NIR spectral information alone using multivariate methods. The necessary agronomic data needs to be obtained and appraised together with results of applied nutrition trials on animal performance. Identification of provenances with a high feeding value, together with agronomic data, would enable the introduction of these provenances into areas where *Gliricidia* grows, but is not currently used for feeding purposes. NIR may be used for rapid assessment, and initial screening of multipurpose trees to assess the available feed resources, and thus, develop guidelines on optimal utilisation. This approach may also have a potential in plant breeding programmes, where the nutritive value of all or part of the plant is likely to be an important factor in deciding the uptake of new varieties by farmers.

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