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Key descriptors for **fodder trees**



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THE INTERNATIONAL LIVESTOCK RESEARCH INSTITUTE and FOOD AND AGRICULTURE ORGANIZATION OF THE UNITED NATIONS on behalf of THE INTERNATIONAL TREATY ON PLANT GENETIC RESOURCES FOR FOOD AND AGRICULTURE

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The ILRI Forage Genebank was established in 1983 with the objective to conserve, make available and promote use of forage biodiversity, in compliance with international obligations, for current and future generations. It currently holds a diverse forage collection comprising 18,641 accessions of 1,350 species.

The objectives of the FAO International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) are the conservation and sustainable use of all plant genetic resources for food and agriculture (PGRFA) and the fair and equitable sharing of the benefits arising out of their use, in harmony with the Convention on Biological Diversity (CBD), for sustainable agriculture and food security.

The ITPGRFA text stresses the importance of *in situ* conservation and the need to collect and make publicly available related information. Particularly Article 5d which states that Contracting Parties shall *"Promote* in situ *conservation of wild crop relatives and wild plants for food production, including in protected areas, by supporting,* inter alia, *the efforts of indigenous and local communities"*.

Since 2015, the ITPGRFA has intensified its support to national institutions on the documentation and exchange of PGRFA data in the context of its Article 17 and the development of the Global Information System on PGRFA.

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Cover Photo: Calliandra calothyrsus flower

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CONTENTS

Preface	1
Introduction	2
Acknowledgements	3
Contributors	4
Fodder trees descriptors	6
Bibliography	12

PREFACE

The *Key descriptors for fodder trees* consist of an initial minimum set of characterization and evaluation descriptors for some species of the family Fabaceae (Leguminosae). This strategic set aims at facilitating access to and utilization of these species and it does not exclude the addition of other descriptors later.

This work has been done jointly with the International Livestock Research Institute (ILRI) and the FAO International Treaty on Plant Genetic Resources for Food and Agriculture. The list was based on a preliminary set of descriptors developed by ILRI. In addition, internet searches were carried out looking for the most updated information on relevant characteristics and traits. The original list was subsequently integrated with evaluation traits. Special attention was given to the inclusion of descriptors relevant to germplasm utilization and abiotic stresses of particular importance in the context of emerging adverse weather events, which are expected to intensify under current and future climate challenges.

The key set of access and utilization descriptors was defined through an online survey, in which 24 experts from 14 different organizations and universities from 13 countries participated. Survey results were subsequently validated in consultation with a Core Advisory Group (see "Contributors") led by Alice Muchugi and Jean Hanson from ILRI.

The strategic set of data standards is designed to facilitate access to and utilization of plant genetic resources for food and agriculture. Together with passport information (Alercia *et al.* 2015, 2018), descriptors are critical to the effective sharing of characterization and evaluation data and to the efficient use of plant genetic resources for food and agriculture.

INTRODUCTION

Fodder trees are an important feed resource for livestock, providing feed in the dry season when other forages may be in short supply. Their deep rooting nature and fast growth have made them a valuable feed resource to extend the use of sown forages over longer periods of the year in tropical and subtropical areas. Fodder trees come from a wide range of plant families, but these general fodder tree descriptors are intended to be used for characterization and evaluation of a group from the family Fabaceae (Leguminosae), *Calliandra calothyrsus, Cytisus proliferus, Gliricidia sepium, Sesbania sesban* and *Faidherbia albida*. These are all fast-growing species that are already being adopted by smallholder farmers worldwide.

Fodder trees have multipurpose functions. They may be coppiced to allow leaves and small branches to be easily harvested as cut fodder, fed fresh, wilted or dried, used for drying to make pellets, or grazed directly. These leguminous fodder trees provide an important source of protein for supplementation of lower quality crop residues and native pastures. They contribute to soil fertility through microbial nitrogen fixation and organic matter from leaf drop, while their deep-rooted nature supports soil stabilization and prevents soil erosion. The inedible woody parts are a valuable source of wood for construction and fuelwood in many rural households. However, while they have multiple benefits for smallholders, many fodder trees also contain secondary plant compounds, such as tannins, saponins, alkaloids and non-protein amino acids, that can limit their use as livestock feeds.

This descriptor list which follows the international standardized documentation system for the characterization and study of genetic resources (Alercia, 2011), is expected to support studies focusing on genetic and morphological diversity of fodder tree accessions, conservation of genetic resources, domestication and to increase production and use of its products. With such a wide range of species diversity under the fodder tree grouping, this descriptor list will only act as general guidelines for use where species specific descriptors may be lacking. These descriptors should also prove useful for describing other similar leguminous fodder trees, including other species of *Sesbania*, *Acacia*, *Albizia*, *Desmanthus*, *Leucaena*, and *Acaciella angustissima*, *Bauhinia variegata*, *Cratylia argentea* and *Medicago arborea*.

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Recognition goes to the Crop Leader, Alice Muchugi and to Jean Hanson for providing valuable scientific direction and to all the members of the Core Advisory Group and reviewers who participated in the survey for their advice. Their names are included in the "Contributors" list.

Special thanks are due to Ana Laura Cerutti for working at different stages of the production process including the preparation of the layout. Adriana Alercia, from the International Treaty on Plant Genetic Resources of FAO, coordinated and managed the entire production of this document and provided technical and scientific advice.

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FODDER TREES DESCRIPTORS

Descriptors are used for studying diversity in key characteristics of accessions within a species. They should be used when they are useful to users, either collection' curators for the management and maintenance of their germplasm material or to all other users of plant genetic resources for promoting their sustainable use. As far as possible, environmentally stable descriptors should be selected but some important plant traits show genotype x environment (GxE) interaction. Rather than avoid these important use traits, such as plant height, yield and nutritive value, it is suggested that comparisons between accessions should only be made using representative data generated with the same methodology from plantings on the same date in the same site and season. To this end, highly discriminating descriptors are listed below to facilitate selection of those best suited to user's needs and highlighted throughout the text along with their relevant definition.

MINIMUM SET OF CHARACTERIZATION AND EVALUATION DESCRIPTORS

This is an initial, key set of characterization and evaluation descriptors for a group from the family Fabaceae (Leguminosae), namely *Calliandra calothyrsus*, *Cytisus proliferus*, *Gliricidia sepium*, *Sesbania sesban* and *Faidherbia albida*. The strategic set aims at facilitating access to and utilization of these species and is useful in assisting researchers to describe and utilize accessions more easily. While these descriptors have been developed for the five species above, they should also prove useful for describing other similar leguminous fodder trees.

Descriptor number Descriptor name

- 1. Plant height (cm)
- 2. Leaf type
- 5. Adaxial leaflet surface
- 6. Pinnae number per leaf
- 7. Pinnule number per pinna
- 10. Flower colour
- 11. Number of flowers per raceme
- 12. Mature pod colour
- 13. Pod surface texture
- 14. Pod shape
- 18. Seed shape
- 21. 100-Seed weight (g)
- 22. Edible parts biomass yield (kg/tree)
- 23. Seed yield (kg/ha)
- 24. Protein content of leaves (%)
- 25. Condensed tannin content of leaves (%)

- 26. Saponin content of leaves (%)
- 27. Alkaloid content of leaves (%)
- 31. Reaction to waterlogging
- 32. Reaction to drought
- 33. Reaction to acidic soil

CHARACTERIZATION

Measure/count each descriptor on 10 randomly selected plants or plant parts and report as a mean, with standard deviation, if relevant, for the accession. For all colour descriptors the use of the Royal Horticultural Society (RHS) Colour Chart codes is recommended. If these are not available, colour charts that are tailored to a species and plant part can be made by colouring cells using the range of relevant custom colours available in the software being used, adding a code, and printing out a sheet for comparison.

1. Plant height (cm)

Measured from ground to the tip of the tallest branch at maturity.

2. Number of branches

Record the number of branches on the main stem.

3. Leaf type

Record the leaf type on a newly opened leaf from a mature tree. See Figure 1.

- 1 Imparipinnate (odd-pinnate)
- 2 Paripinnate (even-pinnate)
- 3 Bipinnate
- 4 Trifoliolate
- 99 Other (specify in the NOTES descriptor)

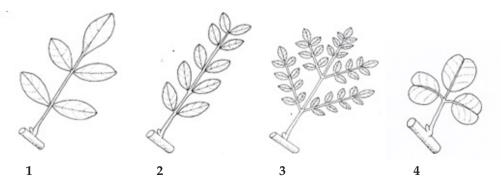


Figure 1. Leaf type (Hickey, M. & King, K. 2000)

4. Rachis length (cm)

Measure the length of the rachis from the branch to the base of the terminal leaflet of a newly opened leaf from a mature tree.

5. Adaxial leaflet surface

Record the surface texture of the upper side of a leaflet from a newly opened leaf from a mature tree.

- 1 Glabrous
- 2 Waxy
- 3 Pubescent
- 99 Other (specify in the NOTES descriptor)

6. Pinnae number per leaf

Record the number of pinnae making up one newly and fully opened leaf from a mature tree.

7. Pinnule number per pinna

Record the number of pinnules making up one pinna on a newly opened leaf from a mature tree.

8. Leaflet length (mm)

Measure the length of the lamina of a leaflet (pinnule) from a newly opened leaf from a mature tree.

9. Leaflet width (mm)

Measure the width of the lamina of a leaflet (pinnule) from a newly opened leaf from a mature tree.

10. Flower colour

Record the predominant flower colour on the upper side of a fully newly opened corolla/ petal.

- 1 White
- 2 Grey
- 3 Yellow
- 4 Pink
- 5 Green
- 6 Red
- 7 Purple
- 99 Other (specify in the NOTES descriptor)

11. Number of flowers per raceme

Record the number of flowers on one raceme, flower cluster, capitulum or inflorescence from a mature tree.

12. Mature pod colour

Record the predominant colour of mature pods.

- 1 Grey
- 2 Yellow
- 3 Orange
- 4 Green
- 5 Red
- 6 Brown
- 7 Black
- 99 Other (specify in the NOTES descriptor)

13. Pod surface texture

Record the predominant texture of the seed pod.

- 1 Glabrous
- 2 Fine hairs
- 3 Bristles
- 4 Waxy
- 5 Reticulate
- 99 Other (specify in the NOTES descriptor)

14. Pod shape

Record the predominant pod shape. See Figure 2.

- 1 Linear
- 2 Curved
- 3 Falcate
- 4 Spiral
- 5 Oblong
- 99 Other (specify in the NOTES descriptor)

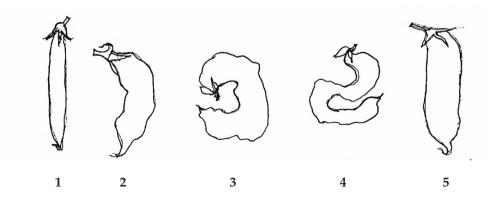


Figure 2. Pod shape

15. Pod length (cm)

Record the length of a mature pod at the longest point.

16. Pod width (cm)

Record the width of a mature pod at the widest point.

17. Number of seeds per pod

Record the number of seeds in a mature pod.

18. Seed shape

See Figure 3.

- 1 Ellipsoid
- 2 Oval
- 3 Rounded
- 4 Subcylindrical
- 99 Other (specify in the NOTES descriptor)

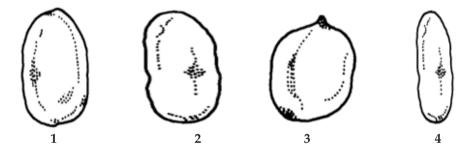


Figure 3. Seed shape

19. Seed length (mm)

Record the length of the longest axis of a mature seed.

20. Seed width (mm)

Record the width of a mature seed at the widest point.

21. 100-Seed weight (g)

Record the weight of 100 randomly selected mature seeds taking replicates to obtain a mean.

EVALUATION

All evaluation descriptors are environmentally influenced and therefore care needs to be taken when collecting evaluation data. To present reliable and reproducible information about characters that have significant GxE interaction, it is encouraged that measurements for these descriptors are taken from a carefully managed trial where the planting date, agronomic treatments, environmental conditions (soil characters and fertility, rainfall, temperature), season, age of plants and physiological stage at time of measurement and plant treatments after harvest are the same for all accessions and are fully described and documented.

All nutritional traits reported should be from comparable samples using analyses done according to standard accredited methods from the same laboratory. Data on drought tolerance must be collected from a drought stress trial. While data from different seasons and locations may be presented to better represent environmental adaptation of the accession, it is not advisable to use them for comparison among accessions. Data are reported as means with standard deviation for the accession.

22. Edible parts biomass yield (kg/tree)

Record the dry matter weight of all edible parts (leaf and <2mm stems) using representative samples that are dried and converted to kg dry matter per tree.

23. Seed yield (kg/ha)

Weight of pure seeds after threshing and cleaning recorded from representative samples taken from a tree and converted to kg/ha.

24. Protein content (%)

Percentage of total protein in a sample of all edible parts (leaf and <2mm stems) based on an analytical assessment determined on a dried ground sub-sample of leaves.

25. Condensed tannin content (%)

Percentage of total condensed tannins in a sample of all edible parts (leaf and <2mm stems) based on an analytical assessment determined on a dried ground sub-sample of leaves.

26. Saponin content (%)

Percentage of saponins in a sample of all edible parts (leaf and <2mm stems) based on an analytical assessment determined on a dried ground sub-sample of leaves.

27. Alkaloid content (%)

Percentage of alkaloids in all edible parts (leaf and <2mm stems) based on an analytical assessment determined on a dried ground sub-sample of leaves.

BIOTIC STRESS SUSCEPTIBILITY

Scored as percentage infection from a specific trial to induce disease or insect infestation, under conditions which are clearly specified. In each case, it is important to state the origin of the infestation or infection, i.e., natural, field inoculation, laboratory. Record such information in descriptor **35. NOTES**. These are coded on a susceptibility scale from 1 to 9:

- 3 Low
- 5 Intermediate

Causal organism

7 High

Common name

- 28.Fusarium oxysporum29.Meloidogyne spp.Root-knot
- 30. Callosobruchus chinensis

Wilt Root-knot nematode Bruchids

ABIOTIC STRESS SUSCEPTIBILITY

Scored as percentage survival from a specific trial to induce stress, under conditions which are clearly specified. Drought trials are often performed under greenhouse conditions or rain-out shelters.

31.	Reaction to waterlogging
32.	Reaction to drought
33.	Reaction to acidic soil

34. Reaction to cold

35. NOTES

Specify here any other additional information here. Add any additional traits that are important to describe the diversity among accessions within this species.

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