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Proximal sensing of Urochloa grasses increases selection accuracy

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Extensive areas in the Tropics are dedicated to livestock production. Grazing activities in these areas, however, are highly restricted by forage availability. By using sensors in place of conventional methods of forage evaluation, higher number of forages can be reliably evaluated, while incurring minimal additional cost. The use of digital cameras and hyperspectral sensors to evaluate forage characteristics and production were found effective and potentially useful for selecting outstanding hybrids.

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| 1 | Proximal sensing of Urochloa grasses increases selection accuracy |
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| 3 | Juan de la Cruz Jiménez ^{1*} , Luisa Leiva ² , Juan A. Cardoso ³ , Andrew N. French ⁴ and Kelly R. Thorp ⁴ |
| 4 | |
| 5 | ¹ UWA School of Agriculture and Environment, Faculty of Science, The University of Western Australia, |
| 6 | 35 Stirling Highway, Crawley, WA 6009, Australia. |
| 7 | ² Department of plant breeding, Swedish University of Agricultural Sciences, Alnarp, Sweden. |
| 8 | ³ Tropical Forage Program, International Center for Tropical Agriculture (CIAT), Km 17 Recta Cali – |
| 9 | Palmira, Colombia. |
| 10 | ⁴ USDA-ARS, U.S. Arid Land Agricultural Research Center, 21881 N Cardon Ln, Maricopa, AZ 85138, |
| 11 | United States. |
| 12 | |
| 13 | |
| 14 | |
| 15 | * Corresponding author: Juan de la Cruz Jiménez: juan.jimenezserna@research.uwa.edu.au |
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21 Abstract

In the American Tropics, livestock production is highly restricted by forage availability. In 22 23 addition, the breeding and development of new forage varieties with outstanding yield and high 24 nutritional quality is often limited by a lack of resources and poor technology. Non-destructive high throughput phenotyping offers a rapid and economical means to evaluate large numbers of 25 26 genotypes. In this study, visual assessments, digital color images, and spectral reflectance data were collected from 200 Urochloa hybrids in a field setting. Partial least squares regression 27 (PLSR) was applied to relate visual assessments, digital image analysis and spectral data with 28 29 shoot dry weight (DW), crude protein (CP) and chlorophyll content. Visual evaluations of biomass and greenness, digital color imaging, and hyperspectral canopy data were collected in 68, 40 and 30 80 minutes, respectively. Root mean squared errors of prediction for PLSR estimations of DW, 31 CP, and chlorophyll were lower for digital image analysis followed by hyperspectral analysis and 32 visual assessments. This study showed that digital color image and spectral analysis techniques 33 have the potential to improve precision and reduce time for tropical forage grass phenotyping. 34

35 Keywords: High throughput phenotyping, *Urochloa*, tropical forage grasses, plant breeding.

36

37 Introduction

Livestock productivity depends on forage availability and quality. Grasses from the *Urochloa* (syn. *Brachiaria*) genus have been widely planted in the tropics as forage for grazing ruminant livestock and are considered the most important forages in the American Tropics (Miles et al. 2004). The International Center for Tropical Agriculture (CIAT) in Colombia conducts a *Urochloa* breeding program aimed at developing hybrids with outstanding performance on infertile, acidic soils with

superior forage productivity and nutritional quality. The hybrid development process is difficult 43 and time consuming. In a regular, three-year breeding cycle, over 7000 hybrids are produced by 44 open pollination, but fewer than 2% of these are retained for full evaluation. Approximately half 45 of the population is discarded based on their reproductive mode (sexual genotypes are discarded 46 and apomictic hybrids are kept); another major proportion is discarded based on visual evaluations; 47 48 and only a limited number of hybrids (approximately 100) are finally evaluated for different biotic and abiotic stresses (Valheria Castiblanco, personal communication). The evaluation of genotypes 49 is restricted mainly by insufficient economic resources and technology for rapid screening. 50

Forage grasses exhibiting great biomass production and high nutritional quality are key 51 determinants of the productivity of grazing animals (Herrero et al., 2013). Therefore, evaluations 52 of shoot biomass production and quality parameters (i.e. crude protein) are among the most 53 important traits for improvement in any forage grasses breeding program. However, owing to the 54 destructive nature of these measurements and the insufficient economic resources, the evaluation 55 of these parameters is postponed to final stages of the breeding program characterized by a reduced 56 number of genotypes. Instead of analytical measurements of forage quality and destructive 57 biomass harvests, periodic visual evaluations of plant performance (i.e., plant biomass and 58 59 greenness) over time is traditionally used in *Urochloa* breeding programs to select superior plants at initial stages of the breeding scheme (Miles et al. 2004; Miles 2007). These visual evaluations 60 61 are laborious and may not be sufficiently accurate especially in breeding populations characterized by high genetic diversity and substantial genotype x environment interaction (Walter et al. 2012). 62

The use of new technologies for in-field non-destructive, high throughput phenotyping (HTP), including digital image analysis and proximal hyperspectral sensing, offers the possibility to precisely evaluate a larger number of genotypes than feasible in traditional ways, achieved at low

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cost, and implemented in a short period of time (Montes et al. 2007; White et al. 2012; Andrade-66 Sanchez et al. 2014). Proximal hyperspectral sensing provides continuous information along the 67 visual and near-infrared electromagnetic spectrum. This information often relates to plant traits 68 and has successfully been studied in grasses to estimate quality parameters (Skidmore et al. 2010; 69 Pullanagari et al. 2012; Thulin et al. 2012; Ferner et al. 2015; Safari et al. 2016), diversity (Lopatin 70 71 et al. 2017) and nutrient content (Fava et al. 2009; Knox et al. 2012; Ramoelo et al. 2013; Adjorlolo et al. 2015; Foster et al. 2017). Likewise, plant image analysis for phenotyping purposes is based 72 on image segmentation to separate the soil background and the plant for further quantification of 73 74 regions of interest (Tucker 1979; Woebbecke et al. 1995; Camargo 2004; Hunt et al. 2005). Digital image analysis has also been used for quantifying vegetation indices related to plant growth, 75 greenness and nutritional status (Meyer and Camargo 2008; Hunt et al. 2013). Very few reports of 76 hyperspectral (Numata et al. 2008) or image analysis of Urochloa grasses exist in literature 77 (Jimenez et al. 2017). 78

No studies combining hyperspectral information and image analyses and comparing them to 79 conventional phenotyping methods is available. Moreover, hyperspectral data have not been used 80 to evaluate target traits in *Urochloa* breeding programs. In this study, in-field visual evaluations, 81 82 proximal hyperspectral data, and digital imaging were collected over canopies of Urochloa hybrids. Partial least squares regression was used to relate hyperspectral information to field 83 measurements and machine learning (i.e. naive Bayes multiclass) was used to extract vegetation 84 indices from overhead canopy images. The objectives of this study were to: 1) develop PLSR 85 models for predicting CP, forage DW, and chlorophyll content; 2) extract plant traits from digital 86 image analysis to relate with CP, forage DW, and chlorophyll; and 3) demonstrate the superiority 87 of HTP techniques as compared to conventional visual evaluation of traits. Crude protein, forage 88

DW, and chlorophyll content were chosen as target traits in this study as they are key parameters determining both plant and cattle productivity. The development of HTP methodologies to evaluate tropical forages will increase the number of hybrids evaluated per selection cycle, thus permitting more intense selection and hence, genetic gain. The identification of new hybrids with outstanding performance (i.e. higher biomass, greener and high CP) will result in more productive pastures with concomitant increases in milk and meat production in livestock systems in tropical savannahs.

96 Materials and methods

97 *Field experiment*

98 Field data were obtained in August 2016 at the International Center for Tropical Agriculture (CIAT) in Cali, Colombia (Lat. 3° 29' N; Long. 76° 21' W; altitude 965 m). Four thousand 99 Urochloa hybrids generated from crosses between the CIAT's Urochloa breeding program 100 population SX12 and U. decumbens cv. Basilisk (CIAT 606) were initially planted in an andisol 101 soil in an augmented block design and spaced at 1.5x1.5 m. These plants were visually evaluated 102 four times (data not shown) for persistence, vigor and greenness after sequential cuttings every 103 three months for one year. After that period, 200 hybrids were randomly selected for further visual 104 and HTP analysis. These 200 hybrids, instead of the entire population, were selected for economic 105 and practical reasons. Visual evaluations of biomass and greenness, imaging and spectra collection 106 107 were performed after 3 months re-growth after cutting (see information below). Plant heights ranged from 20 to 50 cm and shoot architecture varied with both decumbent and erectus growth. 108 Visual evaluation 109

Plant biomass was assessed using a nine-point visual scale, where level '9' indicated high shootbiomass with many tillers and leaves while level '1' indicated stunted growth with fewer tillers

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and leaves. Plant greenness was visually evaluated using a five-point visual scale, where level '5'
represented intense dark green in all the leaves of the plant and level '1' indicated yellow-pale

114 color in all leaves of the plant. This visual evaluation was conducted in 68 minutes one week before

the HTP measurements (Table 1).

116 Imaging collection and analysis

117 Individual, digital color images for each of the 200 hybrids were taken at 1.2 m above the soil surface using a commercial digital 13-Megapixel camera (Coolpix P6000, Nikon, Japan) fixed to 118 a buggy tractor. Digital images were saved in 4224 x 3168 pixel JPG format. The canopy cover 119 120 (CC) and six vegetation indices including the normalized green red difference index (NGRDI), excess green index (ExG), excess red index (ExR), excess green minus excess red (ExGR), green 121 ratio (GR) and green leaf index (GLI) were created using the formulae as indicated in Table 2. The 122 canopy cover was extracted by dividing the total number of pixels representing the plant by the 123 total number of pixels in each image. The vegetation indices were extracted using naive Bayes 124 multiclass. Briefly, the distribution of colors in a set of digital color images (training set) was used 125 to estimate the probability density function for each of the different region of interest (i.e. plant 126 and background). Once the regions of interest were defined in the training set, the machine learning 127 process was applied to all images to accurately classify and separate regions of interest. Therefore, 128 every pixel in an image was classified into the previously defined plant and background classes. 129 Every pixel characterizing the plant (but not the background) was then decomposed into red (R), 130 131 green (G), and blue (B) channels. These channels were then normalized as follows:

132

133
$$r = \frac{R}{R+G+B}; g = \frac{G}{R+G+B}; b = \frac{B}{R+G+B}$$

Normalization makes the variations of light intensities uniform across the spectral distribution, 135 thus, the individual color components (i.e. r,g,b) are independent from the overall brightness of 136 the image (Cheng et al. 2011). Normalized channels were further used for the quantification of the 137 vegetation indices (Table 2). Image analysis code was written in Java and run in ImageJ software 138 (National Institutes of Health, Bethesda, Maryland, USA). Images were collected early in the 139 140 morning to avoid beam solar radiation interferences. Digital images contained the whole plant in addition to the 23-cm diameter field-of-view (as indicated below for hyperspectral measurements, 141 Supplementary Fig 1). The collection process took 40 minutes (Table 1). 142

143

144 Spectral collection and analysis

Hyperspectral field data collections were performed on clear days at full sun exposure around 11 145 am by positioning a hand-held field spectroradiometer (Fieldspec 2, Malvern Panalytical, Malvern, 146 UK) directly above the plant canopy. The instrument was used with no foreoptics, which provided 147 a 25-degree full conical angle field-of-view. To avoid soil background noise, the bare optical input 148 was positioned at 50 cm from the top of the plant canopy to yield a 23-cm diameter field of view. 149 The instrument collected information in 750 narrow wavebands from 325 to 1075 nm in 1 nm 150 151 intervals. One or ten spectral scans were collected per plant and 50 plants were evaluated daily in about 20 minutes. Differences in the collection protocols were tested to evaluate the most effective 152 153 way. Different spectra collection processes (1 or 10 scans) did not yield significant differences in 154 the root mean squared error of prediction for the different traits evaluated (Supplementary Table 1). Radiometric collections over a 99% Spectralon panel (Labsphere, Inc., North Sutton, New 155 156 Hampshire) were used to describe incoming solar irradiance throughout the data collection 157 process. The radiometric collections over the calibration panel were made before starting and after 158 every five canopy scans or when slight changes in solar irradiance due to cloud cover occurred.

The values of the Spectralon panel radiance were used to compute the canopy reflectance of the plants in each wavelength over the time of spectra collection. Subsequently, 401 bands from 500 to 900 nm were used for analysis. Based on visual inspection of reflectance spectra, these bands were typically less noisy, as compared to bands at the bounds of detector sensitivity. Spectral collection process was run in 80 minutes (Table 1).

164 *Laboratory sample collections*

Plants were immediately harvested after spectra collection. Aboveground tissue was removed by 165 cutting the area defined by a 23-cm diameter plastic circle co-located with the spectral data 166 collection area. Tissues were packed in plastic bags and stored on ice in a cooler in the field and 167 then transported to the laboratory. The extraction of chlorophyll was performed by adding 100 mg 168 of fresh tissue to 80% (v/v) cold methanol, and the mix was homogenized using a pestle in a mortar 169 until the plant residue was clear and the solution was uniform. This solution was then filtered and 170 absorbance was determined with a spectrophotometer (Synergy HT, Biotek, Winooski, USA). 171 Total chlorophyll concentration was calculated according to Lichtenthaler and Welburn (1983). 172 Dry weight (DW) was measured on an electronic balance (PB602S, Mettler Toledo, LLC, 173 Columbus, OH, USA) after oven-drying the samples for three days at 60 °C. Nitrogen 174 175 concentrations in the dry tissue were determined by using an automated nitrogen-carbon analyser (Sercon, Crewe, UK). Urochloa and common bean (Phaseolus vulgaris) leaves were used as 176 reference tissues for confirmation of the reliability of the analyses. The crude protein content was 177 calculated by multiplying nitrogen content with 6.25, as protein is assumed to contain 16% 178 nitrogen on average. 179

180

181 *Statistical analysis*

Visual evaluations, digital image analysis, spectral reflectance, and plant trait data were 182 incorporated into a partial least squares regression (PLSR) algorithm (Mevik and Wehrens 2007) 183 within the R Project for Statistical Computing (http://www.r-project.org). Models were developed 184 to predict each plant trait (i.e. CP, DW and chlorophyll) and to compare the precision for prediction 185 of each of the different methods of phenotyping. Partial least squares regression was used in 186 187 preference to conventional least squares analysis to reduce co-linearity effects. Thorp et al. (2011) provided the details on the PLSR methodology used in the present study. Briefly, if Y is an $n \times 1$ 188 vector of responses (i.e. CP, DW or chlorophyll content) and X is an *n*-observation by *p*-variable 189 matrix of predictors (a set of visual evaluations, digital image analysis, or spectral reflectance 190 data), PLSR aims to decompose X into a set of A orthogonal scores such that the covariance with 191 corresponding Y scores is maximized. The X-weight and Y-loading vectors that result from the 192 decomposition are used to estimate the vector of regression coefficients, β_{PLS} , such that 193

194 $\mathbf{Y} = \mathbf{X} \boldsymbol{\beta}_{PLS} + \boldsymbol{\epsilon}$

195 where ε is an $n \times 1$ vector of error terms.

Leave-one-out cross validation was used to test model predictions for independent data. Results were reported for PLSR models with the number of factors that minimized the root mean squared error of cross validation. Pearson's correlation coefficients were calculated for the different traits extracted from digital color images taken from *Urochloa* hybrids.

200 Results

In this study, visual evaluations of biomass and greenness, digital color imaging and hyperspectral
data were collected on 200 *Urochloa* hybrids in 68, 40 or 80 minutes, respectively (Table 1). High
variability for the different characteristics of DW, CP and chlorophyll content evaluated on 200 *Urochloa* hybrids was found (Table 3).

205 Visual assessments

Partial least squares regressions for measured traits of DW, CP and chlorophyll based on visual
evaluations of biomass and greenness performed with a root mean square error of prediction
(RMSEP) of 8.47 g plant⁻¹, 1.76% and 0.60 mg g FW respectively (Fig 1).

209 Spectral data and digital image phenotyping

210 The PLSR models developed from the digital image analysis estimated DW, CP and chlorophyll with a RMSEP of 7.81 g plant¹, 1.53% and 0.57 mg g FW, respectively (Fig 2). Differences on 211 the correlation coefficients among traits extracted from image analysis indicated that including 212 different indices into the model added independent information to build stronger PLSR models 213 (Supplementary Fig 2). The contribution of each trait extracted from digital image analysis to the 214 overall prediction of each destructively-measured trait is shown in Table 4. The GLI had the 215 stronger positive influence on the PLSR model for predicting DW. The ExGR had the stronger 216 positive influence on the PLSR model for predicting both CP and chlorophyll content. 217

218 The fitted PLSR models developed from 401 wavebands of canopy spectral reflectance estimated DW, CP and chlorophyll with a RMSEP of 7.90 g plant⁻¹, 1.63% and 0.55 mg g FW, respectively 219 (Fig 3). The contribution of each spectral waveband to the overall prediction of each destructively-220 measured trait is shown in the Fig 4. In the PLSR model for DW, local extrema in regression 221 coefficients were found at 701 and 674 nm, corresponding to red light near the inflection band and 222 red light, respectively (Fig 4a). Strong positive contribution to DW estimation were with NIR (700-223 750), and a strong negative contribution with red light (674-640). In the PLSR models for CP and 224 chlorophyll, regression coefficient plots exhibited strong positive contribution for traits estimation 225 226 in the visible green light (Fig 4b and c). The PLSR models for CP contrasted wavebands in the visible spectrum with positive contribution from wavebands around 503 nm and negative 227

contributions from wavebands at 678 nm. Similarly, regression coefficients for total chlorophyll
indicated strong positive contribution in the visible spectrum around 504 nm and negative
contribution throughout the visible wavebands, especially at 625 and 643 nm (Fig 4c). This is
sensible considering visible light absorption is increased with additional leaf chlorophyll.

232 Discussion

The results from this study demonstrate that the current visual assessment methodology at initial steps of the breeding cycle in the CIAT *Urochloa* breeding program can be improved using nondestructive HTP techniques. Color imaging, hyperspectral analysis, and PLSR models are more precise and faster than visual evaluations, thus increasing the number of plants evaluated in the tropical forage breeding program.

238 Visual evaluations of plant growth and greenness (characteristics associated with N content, and therefore CP and chlorophyll concentration in leaves) have traditionally been used to discard 239 *Urochloa* hybrids at initial stages of plant phenotyping. The visual evaluation of an entire breeding 240 population (i.e., 7,000 hybrids) is a slow, costly and tedious process, and is often biased by 241 subjectivity and human fatigue, especially when phenotypic variation of such traits is high (Table 242 3). In this study, the estimation of DW, CP, and chlorophyll content was more precisely and 243 consistently estimated by HTP techniques. Dry weight and CP predictions were more accurate 244 using digital image analysis, followed by spectral analysis and visual evaluations. Chlorophyll 245 246 content was better estimated by the analysis of 401 spectral wavebands, followed by color image analysis and finally visual evaluations (Fig 1, 2 and 3). The time required to run non-destructive 247 HTP evaluations was considerably shorter by 28 minutes per 200 plants for color image analysis 248 249 than visual evaluations, but longer by 12 minutes per 200 plants in hyperspectral than in visual evaluations (Table 1). 250

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The moderate trends in the relationship between Urochloa canopy imaging and reflectance and 251 measured DW, CP and chlorophyll may indicate that the method is not appropriate for very precise 252 estimations of these traits. However, for breeding purposes where a large percentage of hybrids 253 are discarded without detailed evaluation due to scarce resources, a difference in DW of 7.90 g 254 plant⁻¹ or a difference of 1.63% in the CP content of plants may be acceptable during initial stages 255 256 of plant breeding. This moderate trend between *Urochloa* canopy analysis and measured traits in this study can be explained by dissimilarities in the canopy architecture of the Urochloa genotypes 257 (Numata et al. 2008), as well as different growth patterns during recovery from cutting. The further 258 259 evaluation of breeding populations with contrasting canopy architecture will improve the accuracy of the PLSR model to predict the targeted traits. Nonetheless, by combining both digital image and 260 hyperspectral analysis techniques, higher precision accuracy for DW, CP and Chlorophyll content 261 can be achieved. 262

The vegetation indices (see Table 2) extracted from color images of 200 Urochloa hybrids were 263 originally developed to separate green plants from the background by extracting green and red 264 colors from digital images. These indices have been related to different plant characteristics 265 including biomass, chlorophyll content and nutritional status (Tucker 1979; Woebbecke et al. 266 267 1995; Camargo 2004; Hunt et al. 2005; Meyer and Camargo 2008; Hunt et al. 2013; Lee and Lee 2013; Wang et al. 2013). In this study, digital image analysis performed better than hyperspectral 268 scanning analysis to estimate DW and CP (Fig 2 and 3). Nonetheless, the use of spectral analysis 269 270 over grasses becomes more important when this technique is used to detect either nutritional or anti-nutritional compounds (i.e. metabolisable energy, digestibility, fiber) that are better estimated 271 with the near-infrared regions of the electromagnetic spectra (Curran 1989; Pullanagari et al. 2012; 272 Ferner et al. 2015). In this sense, the use of digital color image analysis and hyperspectral analysis 273

is complementary because by using both techniques a diverse set of plant traits can accurately be predicted and by adding extra factors to the prediction model, higher prediction accuracy can be achieved (cf. Numata et al. 2008). Future efforts will use data mining to fine-tune the spectral bands included in the PLSR model (Thorp et al. 2017), which can reduce model error and improve model fit statistics. Although testing multiple methods of analysis was not the intention of this study, future research could also test other techniques (e.g., artificial neural networks) for relating HTP measurements to plant traits.

The regression coefficients for the PLSR for DW and chlorophyll content obtained in this study 281 highlight that the key wavelengths for the prediction of these traits occur in the green, red, red-282 edge and NIR regions of the electromagnetic spectrum (Fig 4). Previous hyperspectral studies have 283 highlighted those regions as being highly representative for dry mass and chlorophyll content in 284 plants (Lichtenthaler et al. 1996; Thenkabail et al. 2000; Mutanga and Skidmore 2004; Fava et al. 285 2009; Thorp et al. 2011; Adjorlolo et al. 2015; Dou et al, 2018). Although some similarities were 286 287 found between wavebands among the different traits, the general regression coefficients differed among the traits, thus demonstrating that the reflectance data in a given waveband contributed 288 differently toward the estimation of a given trait. Given the logistical burden to collect and analyze 289 290 hyperspectral scans, the identification of informative key bands associated with each evaluated trait can improve the HTP process (Thorp et al. 2017). Results from this study will help guide 291 292 selection of optimal bands in the construction of multispectral sensors tailored to predict specific traits of interest in tropical forage breeding programs. 293

The PLSR models for predicting DW, CP and chlorophyll content can be now used to evaluate the
 next generation of hybrids from the same *Urochloa* gene pool (i.e. *U. ruziziensis – U. brizantha – U. decumbens*). The accuracy of this prediction models relies on collection protocols similar to the

explained in the Materials and Methods section and evaluations on plants with comparable growth 297 characteristics as the hybrids evaluated here (i.e. about three months after regrowth). The 298 prediction accuracy will likely be reduced on larger plants with higher biomass (Hill 2004) and a 299 greater proportion of senescent leaves (Asner 1998). The development of more precise PLSR 300 models to predict variables of interest in a breeding program requires an ongoing effort. The 301 302 collection of ground data every year while making improvements to standardize collection protocols and incorporate wider range of genotypes will result in more accurate and robust models. 303 Larger data sets will increase estimation precision. 304

305

306 Conclusions

307 In this study, 200 Urochloa hybrids were monitored in 40 and 80 minutes by digital imaging and spectral analysis, respectively (Table 1). At this pace, more than 1000 Urochloa hybrids could be 308 evaluated in a period of less than 7 hours. This means that forage biomass and quality in a high 309 number of genotypes would be reliably evaluated with minimal increased acquisition costs relative 310 to destructive harvest. This demonstrates the superiority of HTP techniques as compared to 311 conventional visual evaluation of traits. The PLSR models for predicting CP, forage DW, and 312 chlorophyll content developed in this study supports the evaluation of higher numbers of genotypes 313 at initial stages of the breeding program. The greater numbers of plants evaluated reliably every 314 315 year in the Urochloa breeding program, the greater the genetic gain will be. Therefore, the use of image analysis and hyperspectral monitoring over Urochloa hybrids canopies will benefit the on-316 going breeding program. The application of this HTP method could be of great help in rural remote 317 areas lacking facilities to perform destructive harvest and plant chemical analysis. Research is 318 underway to improve the utility of proximal sensing by considering a greater range of canopy 319

320 architectural configurations and evaluating the potential to assess nutritional quality, including

321 characteristics such as metabolisable energy, fiber, digestibility, lignin and cellulose fractions in

Urochloa grasses.

323

324 **Conflict of interest**

325 The authors have no conflicts of interest to declare.

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- **Table 1**. Phenotyping techniques used in the present study, the time of evaluation, its application,
- 483 advantages and disadvantages.

| Phenotyping technique | Time of evaluation* | Applications | Advantages | Disadvantages |
|---|------------------------|---|--|---|
| Visual evaluation | 68 min | Visual observations of different plant characteristics | Easy operation, low cost, evaluations can be performed under diverse conditions and environments | Evaluation of low number of genotypes, evaluation subjected to human bias and fatigue |
| Image analysis | 40 min | Quantification of canopy cover and vegetation indices in the visible electromagnetic spectrum | Easy operation, low cost, greater number of plants evaluated, determination of several vegetation and water indices | Changes in ambient light conditions limit calculation of vegetation indices, data analysis is moderately complex |
| Hyperspectral analysis | 80 min | Canopy reflectance information in the visible and near infra- red regions of the electromagnetic spectrum. Information can be used to predict biochemical composition of plants | Moderately easy operation, greater number of plants evaluated, determination of nutritional and biochemical composition of leaf/canopy | Low solar radiation or cloudy days limit analysis, sensor and white reference calibration is frequently needed, data analysis is complex |
| * The time of evaluation refers to 200 Urochloa plants evaluated under the conditions of the present study. | | | | |

Table 2. Canopy cover and vegetation indices calculated from digital images of 200 *Urochloa*hybrids. Vegetation indices were extracted using a naive Bayes multiclass machine learning
approach. Indices were then incorporated into a PLSR model to predict crude protein, dry weight
biomass and chlorophyll content.

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| Plant traits | Name | Formula* | Reference |
|---------------------|--|-------------------|------------------------|
| CC** | Canopy cover | Nc/Nt | - |
| NGRDI | Normalized green red difference index | (g-r)/(g+r) | Hunt et al., 2005 |
| ExG | Excess green index | 2g-r-b | Woebbecke et al., 1995 |
| ExR | Excess red index | 1.3r-g | Meyer et al., 1998 |
| ExGR | Excess green minus excess red | ExG-ExR | Camargo 2004 |
| GR | Green ratio | g/(r+g+b) | Tucker 1979 |
| GLI | Green leaf index | (2g-r-b)/(2g+r+b) | Louhaichi et al. 2001 |

*r, g and b denote the normalized pixel values of each channel on the RGB colour mode. ** No normalization was performed for the canopy cover quantification. Nc= total number of pixels representing the canopy, Nt= total number of pixels in the picture.

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504 **Table 3**. Plant traits measured in 200 *Urochloa* hybrids.

| _ | Trait | Min | Max | Mean | CV (%) |
|-----|-------------------------------------|------|-------|-------|--------|
| _ | Dry Weight (g plant ⁻¹) | 6.74 | 64.1 | 30.22 | 34.81 |
| | Crude Protein (%) | 6.76 | 21.58 | 11.23 | 19.68 |
| | Chlorophyll (mg g FW) | 0.87 | 6.41 | 2.88 | 24.31 |
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- 521 **Table 4**. Regression coefficients of the fitted partial least square regression models of seven traits
- 522 extracted from digital image analysis. Positive and negative coefficients indicate positive and
- 523 negative influence on the prediction model, respectively.

| | Traits* | Dry weigth (g.plant ⁻¹) | Crude protein (% DW) | Chlorophyll (mg.g ⁻¹) |
|---------------------------------|---|--|--|--|
| | CC | 3.760545 | -0.23114345 | -0.01673706 |
| | NGRDI | 9.948634 | 0.08600517 | -0.03532585 |
| | ExG | -14.3163 | 0.07760486 | 0.0730642 |
| | ExR | -32.126212 | -0.39106455 | -0.07758547 |
| | ExGR | 3.724492 | 0.26592971 | 0.10326555 |
| | GR | -34.770799 | -0.31158671 | -0.03624834 |
| | GLI | 80.87152 | -0.31108316 | -0.0357783 |
| 524 525 526 527 528 | * CC= cano ExR= exces leaf index. | py cover, NGRDI= normal s red index, ExGR= excess | lized green red difference ind s green minus excess red, GF | lex, ExG= excess green index, R= green ratio and GLI= green |
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- 540 Fig 1. Modeled versus measured dry weight, crude protein and chlorophyll content when fitting
- 541 partial least square regression models to relate each biophysical characteristic to visual evaluations
- of biomass and greenness of 200 *Urochloa* hybrids.
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Fig 2. Modeled versus measured dry weight, crude protein and chlorophyll content when fitting
partial least square regression models to relate each biophysical characteristic to digital image
analysis of 200 *Urochloa* hybrids.

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587 Fig 4. Regression coefficients of the fitted partial least squares regression models for dry weight,

588 crude protein and chlorophyll content. The regression coefficients represents the contribution of

each spectral waveband to the overall prediction of each destructively-measured trait.



Supplementary information

Supplementary Table 1. Different protocols of spectral data collection and their respective root

mean squared error of prediction (RMSEP) for crude protein, dry weight and chlorophyll content.

| 607 - | Collection | Trait | Factors¥ | RMSEP |
|-------|------------|-------------------------------------|----------|-------|
| _ | | Dry weight (g plant ⁻¹) | 4 | 9.23 |
| 608 | Day 1* | Crude protein (%) | 11 | 1.29 |
| | | Chlorophyll (mg g FW) | 4 | 0.49 |
| | | Dry weight (g plant ⁻¹) | 4 | 8.20 |
| 609 | Day 2* | Crude protein (%) | 10 | 1.26 |
| | | Chlorophyll (mg g FW) | 7 | 0.50 |
| 610 | | Dry weight (g plant ⁻¹) | 4 | 7.63 |
| | Day 3** | Crude protein (%) | 11 | 2.07 |
| | | Chlorophyll (mg g FW) | 5 | 0.54 |
| 611 | | Dry weight (g plant ⁻¹) | 6 | 8.14 |
| | Day 4** | Crude protein n (%) | 2 | 1.21 |
| 612 | | Chlorophyll (mg g FW) | 3 | 0.58 |
| 012 | | Dry weight (g plant $^{-1}$) | 6 | 7.90 |
| | All days | Crude protein (%) | 5 | 1.63 |
| 613 | | Chlorophyll (mg g FW) | 5 | 0.55 |

Fifty plants were evaluated daily * One scan collected per plant. ** Ten scans collected per plant. ¥ Number of factors for which the root mean squared error of prediction was minimized in the model prediction.

Supplementary Fig 1. Schematic representation of the observation geometry of hyperspectral analysis (a) and digital image analysis (b) techniques evaluated in 200 *Urochloa* hybrids. White circle positioned at the center of the plant canopy in figure (a) represents the 23-cm field of view of the spectroradiometer at a distance of 50mm from the plant canopy. For the digital image analysis (figure b), the whole plant, and not the 23-cm section, was used for segmentation and further analysis. Scale bar= 10 cm.



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Supplementary Fig 2. Binary relationships and Pearson's correlation coefficients between seven plant traits extracted from digital images of 200 *Urochloa* hybrids. CC= canopy cover, NGRDI= normalized green red difference index, ExG= excess green index, ExR= excess red index, ExGR= excess green minus excess red, GR= green ration and GLI= green leaf index. Pearson's correlation coefficients are indicated with their statistical significance as follows: $*P \le 0.1$, $**P \le 0.01$, $***P \le 0.001$.

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| 1 | Proximal sensing of Urochloa grasses increases selection accuracy |
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| 3 | Juan de la Cruz Jiménez ^{1*} , Luisa Leiva ² , Juan A. Cardoso ³ , Andrew N. French ⁴ and Kelly R. Thorp ⁴ |
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| 5 | ¹ UWA School of Agriculture and Environment, Faculty of Science, The University of Western Australia, |
| 6 | 35 Stirling Highway, Crawley, WA 6009, Australia. |
| 7 | ² Department of plant breeding, Swedish University of Agricultural Sciences, Alnarp, Sweden. |
| 8 | ³ Tropical Forage Program, International Center for Tropical Agriculture (CIAT), Km 17 Recta Cali – |
| 9 | Palmira, Colombia. |
| 10 | ⁴ USDA-ARS, U.S. Arid Land Agricultural Research Center, 21881 N Cardon Ln, Maricopa, AZ 85138, |
| 11 | United States. |
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| 15 | * Corresponding author: Juan de la Cruz Jiménez: juan.jimenezserna@research.uwa.edu.au |
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21 Abstract

22 In the American Tropics, livestock production is highly restricted by forage availability. In 23 addition, the breeding and development of new forage varieties with outstanding yield and high 24 nutritional quality is often limited by a lack of resources and poor technology. Non-destructive high throughput phenotyping offers a rapid and economical means to evaluate large numbers of 25 26 genotypes. In this study, visual assessments, digital color images, and spectral reflectance data were collected from 200 Urochloa hybrids in a field setting. Partial least squares regression 27 28 (PLSR) was applied to relate visual assessments, vegetation indices digital image analysis and 29 spectral data with shoot dry weight, nitrogen (N) content (DW), crude protein (CP) and chlorophyll content. Visual evaluations of biomass and greenness, digital color imaging, and hyperspectral 30 31 canopy data were collected in 68, 40 and 80 minutes, respectively. Root mean squared errors of prediction for PLSR estimations of dry weight, NDW, CP, and chlorophyll were lower for 32 vegetation indices digital image analysis followed by hyperspectral analysis and visual 33 34 assessments. This study showed that digital color image and spectral analysis techniques have the potential to improve precision and reduce time for tropical forage grass phenotyping. 35

36 Keywords: High throughput phenotyping, *Urochloa*, tropical forage grasses, plant breeding.

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38 Introduction

Livestock productivity depends on forage availability and quality. Grasses from the *Urochloa* (syn. *Brachiaria*) genus have been widely planted in the tropics as forage for grazing ruminant livestock
and are considered the most important forages in the American Tropics (Miles et al. 2004). The
International Center for Tropical Agriculture (CIAT) in Colombia conducts a *Urochloa* breeding

program aimed at developing hybrids with outstanding performance on infertile, acidic soils with 43 superior forage productivity and nutritional quality. The hybrid development process is difficult 44 and time consuming. In a regular, three-year breeding cycle (three years), over 7000 hybrids are 45 produced by open pollination, but fewer than 2% of these are retained for full evaluation. 46 Approximately half of the population is discarded based on their reproductive mode (sexual 47 48 orgenotypes are discarded and apomictic hybrids are kept); another major proportion is discarded based on visual evaluations; and only a limited number of hybrids (approximately 100) are finally 49 evaluated for different biotic and abiotic stresses (Valheria Castiblanco, personal communication). 50 51 The evaluation of genotypes is restricted mainly by insufficient economic resources and lacking technology for rapid screening. 52 PeriodicForage grasses exhibiting great biomass production and high nutritional quality are key 53 determinants of the productivity of grazing animals (Herrero et al., 2013). Therefore, evaluations 54 of shoot biomass production and quality parameters (i.e. crude protein) are among the most 55 important traits for improvement in any forage grasses breeding program. However, owing to the 56 destructive nature of these measurements and the insufficient economic resources, the evaluation 57 of these parameters is postponed to final stages of the breeding program characterized by a reduced 58 59 number of genotypes. Instead of analytical measurements of forage quality and destructive biomass harvests, periodic visual evaluations of plant performance (i.e., plant biomass and 60 greenness) over time has been is traditionally used in the CIAT's Urochloa breeding 61 programprograms to select superior plants at initial stages of the breeding scheme (Miles et al. 62 63 2004; Miles 2007). These visual evaluations are laborious and may not be sufficiently accurate especially in breeding populations characterized by high genetic diversity and substantial genotype 64 x environment interaction (Walter et al. 2012). In this sense, the 65

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The use of new technologies for in-field non-destructive, high throughput phenotyping (HTP), including digital image analysis and proximal hyperspectral sensing, representsoffers the possibility to precisely evaluate a larger number of genotypes than feasible in traditional ways, achieved at low cost, and implemented in a short period of time (Montes et al. 2007; White et al. 2012; Andrade-Sanchez et al. 2014).

71 Proximal hyperspectral sensing provides continuous information along the visual and near-infrared electromagnetic spectrum. This information often relates to plant traits and has successfully been 72 73 studied in grasses to estimate quality parameters (Skidmore et al. 2010; Pullanagari et al. 2012; Thulin et al. 2012; Ferner et al. 2015; Safari et al. 2016), diversity (Lopatin et al. 2017) and nutrient 74 content (Fava et al. 2009; Knox et al. 2012; Ramoelo et al. 2013; Adjorlolo et al. 2015; Foster et 75 al. 2017). Likewise, plant image analysis for phenotyping purposes is based on image 76 segmentation to separate the soil background (i.e., soil) and the plant for further quantification of 77 regions of interest (Tucker 1979; Woebbecke et al. 1995; Camargo 2004; Hunt et al. 2005). Digital 78 79 image analysis has also been used for quantifying vegetation indices related to plant growth, greenness and nutritional status (Meyer and Camargo 2008; Hunt et al. 2013). Very few reports of 80 hyperspectral (Numata et al. 2008) or image analysis of Urochloa grasses exist in literature 81 82 (Jimenez et al. 2017).

No studies combining hyperspectral information and image analyses and comparing them to
conventional phenotyping methods is available. Moreover, hyperspectral data have not been used
to evaluate target traits in *Urochloa* breeding programs. In this study, in-field visual evaluations,
proximal hyperspectral data, and digital imaging were collected over canopies of *Urochloa*hybrids. Partial least squares regression (PLSR)-was used to relate hyperspectral information to
field measurements and machine learning (i.e. naive Bayes multiclass) was used to extract

vegetation indices from overhead canopy images. The objectives of this study were to: 1) develop 89 PLSR models for predicting NCP, forage dry weightDW, and chlorophyll content; 2) compute 90 vegetation indices extract plant traits from digital image analysis to relate with NCP, forage dry 91 weightDW, and chlorophyll; and 3) demonstrate the superiority of HTP techniques as compared 92 to conventional visual evaluation of traits. Hyperspectral data or image analysis have not been 93 94 used to evaluate forage biomass, N or chlorophyll in Urochloa breeding programs. Moreover, no studies combining hyperspectral information and image analysis and comparing it to conventional 95 phenotyping methods is available. Nitrogen, forage dry weightCrude protein, forage DW, and 96 97 chlorophyll content were chosen as target traits in this study as they are key parameters determining both plant and cattle productivity. The development of HTP methodologies to 98 evaluate tropical forages will increase the number of hybrids evaluated per selection cycle, thus 99 100 permitting more intense selection and hence, genetic gain. The identification of new hybrids with 101 outstanding performance (i.e. higher biomass, greener and high N-contentCP) will result in more productive pastures with concomitant increases in milk and meat production in livestock systems 102 in tropical savannahs. 103

104 Materials and methods

105 *Field experiment*

Field data were obtained in August 2016 at the International Center for Tropical Agriculture (CIAT) in Cali, Colombia (Lat. 3° 29' N; Long. 76° 21' W; altitude 965 m). Four thousand *Urochloa* hybrids generated from crosses between the CIAT's *Urochloa* breeding program population SX12 and *U. decumbens* cv. Basilisk (CIAT 606) were initially planted in an andisol soil in an augmented block design and spaced at 1.5x1.5 m. These plants were visually evaluated four times (data not shown) for persistence, vigor and greenness after sequential cuttings every three months for one year. After that period, 200 hybrids were randomly selected for further visual
and HTP analysis. These 200 hybrids (and not, instead of the entire population), were selected for
economic and practical reasons. Visual evaluations of biomass and greenness, imaging and spectra
collection were performed after 3 months regrowthre-growth after cutting (see information below).
Plant heights ranged from 20 to 50 cm and shoot architecture varied from very prostrate to with
both decumbent and erectus growth.

118 Visual evaluation

Plant biomass was assessed using a nine-point visual scale, where level '9' indicated high shoot biomass with many tillers and leaves while level '1' indicated stunted growth with fewer tillers and leaves. Plant greenness was visually evaluated using a five-point visual scale, where level '5' represented intense dark green in all the leaves of the plant and level '1' indicated yellow-pale color in all leaves of the plant. This visual evaluation was conducted in 68 minutes <u>one week before</u> the HTP measurements (Table 1).

125 Imaging collection and analysis

Individual, digital color images for each of the 200 hybrids were taken at 1.2 m above the soil 126 surface using a commercial digital 13-Megapixel camera (Coolpix P6000, Nikon, Japan) fixed to 127 128 a buggy tractor. Digital images were saved in 4224 x 3168 pixel JPG format and vegetation indices were analyzed. The canopy cover (CC) and six vegetation indices including the normalized green 129 130 red difference index (NGRDI), excess green index (ExG), excess red index (ExR), excess green 131 minus excess red (ExGR), green ratio (GR) and green leaf index (GLI) were created using the formulae as indicated in Table 2. The canopy cover was extracted by dividing the total number of 132 133 pixels representing the plant by the total number of pixels in each image. The vegetation indices 134 were extracted using naive Bayes multiclass. Briefly, the distribution of colors in a set of digital 135 color images (training set) was used to estimate the probability density function for each of the

different region of interest (i.e. plant and background). Once the regions of interest were defined, in the training set, the machine learning process was applied to all images to accurately classify and separate regions of interest; therefore. Therefore, every new-pixel in an image was classified into the previously defined plant and background classes. Every pixel characterizing the plant (but not the background) was then decomposed into red₇ (R), green₇ (G), and blue (RGBB) channels for. These channels were then normalized as follows:

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$$\underline{r} \equiv \frac{\underline{R}}{\underline{R} \pm \underline{G} \pm \underline{B}}; \underline{g} \equiv \frac{\underline{G}}{\underline{R} \pm \underline{G} \pm \underline{B}}; \underline{b} \equiv -\frac{\underline{B}}{\underline{R} \pm \underline{G} \pm \underline{B}};$$

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Normalization makes the variations of light intensities uniform across the spectral distribution, 145 thus, the individual color components (i.e. r,g,b) are independent from the overall brightness of 146 the image (Cheng et al. 2011). Normalized channels were further used for the quantification of the 147 vegetation indices. Seven vegetation indices including canopy cover, normalized red green 148 difference index (Tucker 1979), excess green index (Woebbecke et al. 1995), excess red index 149 (Meyer et al. 1998), excess green minus excess red (Camargo 2004), green ratio, and green leaf 150 index (Louhaichi et al. 2001) were calculated. (Table 2). Image analysis code was written in Java 151 and run in ImageJ software (National Institutes of Health, Bethesda, Maryland, USA). Images 152 were collectingcollected early in the morning to avoid beam solar radiation interferences. Digital 153 154 images contained the whole plant in addition to the 23-cm diameter field-of-view (as indicated below for hyperspectral measurements, Supplementary Fig 1). The collection process took 40 155 minutes (Table 1). 156

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158 Spectral collection and analysis

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Hyperspectral field data collections were performed on clear days at full sun exposure around 11 159 am by positioning a hand-held field spectroradiometer (Fieldspec 2, Malvern Panalytical, Malvern, 160 UK) directly above the plant canopy. The instrument was used with no foreoptics, which provided 161 a 25-degree full conical angle field-of-view. To avoid soil background noise, the bare optical input 162 was positioned at 50 cm from the top of the plant canopy to yield a 23-cm diameter field of view. 163 164 The instrument collected information in 750 narrow wavebands from 325 to 1075 nm in 1 nm intervals. One or ten spectral scans were collected per plant and 50 plants were evaluated daily in 165 about 20 minutes. Differences in the collection protocols were deliberately done for comparison 166 167 purposes tested to evaluate the most effective way. Different spectra collection paradigmsprocesses (1 or 10 scans) did not yield significant differences in the root mean squared 168 error of prediction for the different traits evaluated (Supplementary FigTable 1). Radiometric 169 170 collections over a 99% Spectralon panel (Labsphere, Inc., North Sutton, New Hampshire) were used to describe incoming solar irradiance throughout the data collection process. The radiometric 171 collections over the calibration panel were made before starting and after every five canopy scans 172 173 or when slight changes in solar irradiance due to cloud cover occurred. The values of the Spectralon panel radiance were used to compute the canopy reflectance of the plants in each 174 wavelength over the time of spectra collection. Subsequently, 401 bands from 500 to 900 nm were 175 used for analysis. Based on visual inspection of reflectance spectra, these bands were typically less 176 177 noisy, as compared to bands at the bounds of detector sensitivity. Spectral collection process was 178 run in 80 minutes (Table 1).

179 *Laboratory sample collections*

Plants were immediately harvested after spectra collection. Aboveground tissue was removed bycutting the area defined by a 23-cm diameter plastic circle co-located with the spectral data

collection area. Tissues were packed in plastic bags and stored on ice in a cooler in the field and 182 then transported to the laboratory. The extraction of chlorophyll was performed by adding 100 mg 183 of fresh tissue to 80% (v/v) cold methanol, and the mix was homogenized using a pestle in a mortar 184 until the plant residue was clear and the solution was uniform. This solution was then filtered and 185 absorbance was determined with a spectrophotometer (Synergy HT, Biotek, Winooski, USA). 186 187 Total chlorophyll concentration was calculated according to Lichtenthaler and Welburn (1983). Dry weight (DW) was measured on an electronic balance (PB602S, Mettler Toledo, LLC, 188 Columbus, OH, USA) after oven-drying the samples for three days at 60 °C. Nitrogen 189 concentrations in the dry tissue were determined by using an automated nitrogen-carbon analyser 190 (Sercon, Crewe, UK). Urochloa and common bean (Phaseolus vulgaris) leaves were used as 191 reference tissues for confirmation of the reliability of the analyses. The crude protein content was 192 calculated by multiplying nitrogen content with 6.25, as protein is assumed to contain 16% 193 194 nitrogen on average.

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196 Statistical analysis

197 Visual evaluations, vegetation indicesdigital image analysis, spectral reflectance, and plant trait 198 data were incorporated into a partial least squares regression (PLSR) algorithm (Mevik and Wehrens 2007) within the R Project for Statistical Computing (http://www.r-project.org)). Models 199 200 were developed to estimate predict each plant trait (i.e. CP, DW and chlorophyll) and to compare 201 the precision for prediction of each of the different methods of phenotyping. Partial least squares regression was used in preference to conventional least squares analysis to reduce co-linearity 202 effects. Thorp et al. (2011) provided the details on the PLSR methodology used in the present 203 204 study. Briefly, if Y is an $n \times 1$ vector of responses (i.e. N, dry weight CP, DW or chlorophyll content) and **X** is an *n*-observation by *p*-variable matrix of predictors (a set of visual evaluations, vegetation indicesdigital image analysis, or spectral reflectance data), PLSR aims to decompose **X** into a set of *A* orthogonal scores such that the covariance with corresponding **Y** scores is maximized. The X-weight and Y-loading vectors that result from the decomposition are used to estimate the vector of regression coefficients, β_{PLS} , such that

210 $Y = X \beta_{PLS} + \epsilon$

211 where ε is an $n \times 1$ vector of error terms.

Leave-one-out cross validation was used to test model predictions for independent data. Results were reported for PLSR models with the number of factors that minimized the root mean squared error of cross validation. <u>Pearson's correlation coefficients were calculated for the different traits</u> extracted from digital color images taken from *Urochloa* hybrids.

216 **Results**

In this study, visual evaluations of biomass and greenness, digital color imaging and hyperspectral data were collected on 200 *Urochloa* hybrids in 68, 40 or 80 minutes, respectively (Table 1). High variability for the different characteristics of dry weight, nitrogenDW, CP and chlorophyll content evaluated on 200 *Urochloa* hybrids was found (Table 2<u>3</u>).

221 Visual assessments

222 Partial least squares regressions for measured traits of DW, NCP and chlorophyll and based on

- visual evaluations of biomass and greenness performed with a root mean square error of prediction
- (RMSEP) of 8.47 g plant⁻¹, 1.76% and 0.60 mg g FW respectively (Fig 1).
- 225 Spectral data and digital image phenotyping

226 The PLSR models developed from seven vegetation indices the digital image analysis estimated DW, NCP and chlorophyll with a RMSEP of 7.7981 g plant⁻¹, 1.53% and 0.57 mg g FW, 227 respectively (Fig 2). Differences on the correlation coefficients among traits extracted from image 228 analysis indicated that including different indices into the model added independent information 229 to build stronger PLSR models (Supplementary Fig 2). The contribution of each trait extracted 230 231 from digital image analysis to the overall prediction of each destructively-measured trait is shown in Table 4. The GLI had the stronger positive influence on the PLSR model for predicting DW. 232 The ExGR had the stronger positive influence on the PLSR model for predicting both CP and 233 234 chlorophyll content.

The fitted PLSR models developed from 401 wavebands of canopy spectral reflectance estimated
DW, NCP and chlorophyll with a RMSEP of 7.90 g plant⁻¹, 1.63% and 0.55 mg g FW, respectively
(Fig 3).

The contribution of each spectral waveband to the overall prediction of each destructively-238 239 measured trait is shown in the Fig. 4. In the PLSR model for DW, three bands characterized the dry weight of Urochloa. Locallocal extrema in regression coefficients were found at 543, 668701 240 241 and 744674 nm, corresponding to visible green light, red light near the inflection band and NIR radiationred light, respectively (Fig. 4a). Strong positive contribution to dry weightDW estimation 242 were with green light (543) and NIR (744700-750), and a strong negative contribution with red 243 244 light (668674-640). In the PLSR models for NCP and chlorophyll, regression coefficient plots exhibited a noisy pattern with less defined extrema strong positive contribution for traits estimation 245 in the visible green light (Fig 4b and c). The PLSR models for NCP contrasted wavebands in the 246 247 visible spectrum with positive contribution from wavebands around 513503 nm and negative contributions from wavebands at 676678 nm. Wavebands at 600 nm and in the NIR contributed 248

less to the model for N (Fig. 4b). RegressionSimilarly, regression coefficients for total chlorophyll
indicated strong positive contribution from NIR wavelengths and strong in the visible spectrum
around 504 nm and negative contribution throughout the visible wavebands, especially from 525
toat 625 nm, and at the red edge at 705643 nm (Fig. 4c). This is sensible considering visible light
absorption is increased with additional leaf chlorophyll. In the PLSR model for chlorophyll, local
extrema in regression coefficients were found at 567, 674, 705 and 763 nm, which correspond to
green light at the edge of yellow, red light, red light near the red inflection band and NIR radiation.

256 **Discussion**

The results from this study demonstrate that the current visual assessment methodology at initial steps of the breeding cycle in the CIAT *Urochloa* breeding <u>program</u> can be improved by the use of using non-destructive high throughput phenotyping<u>HTP</u> techniques. The use of color<u>Color</u> imaging, hyperspectral analysis, and PLSR models <u>isare</u> more precise and faster than visual evaluations, thus increasing the number of plants evaluated in the tropical forage breeding program.

Visual evaluations of plant growth and greenness (characteristics associated with N content, and 263 therefore CP and chlorophyll concentration in leaves) have traditionally been used to discard 264 Urochloa hybrids at initial stages of plant phenotyping. The visual evaluation of an entire breeding 265 266 population (i.e., 40007,000 hybrids) is a slow, costly and tedious process, and is often biased by 267 subjectivity and human fatigue, especially when phenotypic variation of such traits is high (Table 23). In this study, the estimation of DW, NCP, and chlorophyll content was more precisely and 268 consistently estimated by HTP techniques. Dry weight and NCP predictions were more accurate 269 270 using vegetation indicesdigital image analysis, followed by spectral analysis and visual evaluations. Chlorophyll content was better estimated by the analysis of 401 spectral wavebands, 271

followed by color image analysis and finally visual evaluations (Fig 1, 2 and 3). Likewise, the The
time required to run non-destructive HTP evaluations was considerably shorter by 28 minutes per
200 plants for color image analysis than visual evaluations, but longer by 12 minutes per 200 plants
in hyperspectral than in visual evaluations (Table 1).

The moderate trends in the relationship between Urochloa canopy imaging and reflectance and 276 277 measured DW, NCP and chlorophyll may indicate that the method is not appropriate for very precise estimations of these traits. However, for breeding purposes where a large percentage of 278 hybrids are discarded without detailed evaluation due to scarce resources, a difference in DW of 279 280 7.90 g plant⁻¹ or a difference of 1.63% in the NCP content of plants may be acceptable during initial stages of plant breeding. This moderate trend between Urochloa canopy analysis and 281 282 measured traits in this study can be explained by dissimilarities in the Urochloa genotypes canopy architecture of the Urochloa genotypes (Numata et al. 2008), as well as different growth patterns 283 during recovery from cutting. The further evaluation of breeding populations with contrasting 284 canopy architecture will improve the accuracy of the PLSR model to predict the targeted traits. 285 Nonetheless, by combining both digital image and hyperspectral analysis techniques, higher 286 precision accuracy for DW, CP and Chlorophyll content can be achieved. 287

The vegetation indices (see <u>materials and methodsTable 2</u>) extracted from color images of 200 *Urochloa* hybrids were <u>originally</u> developed to <u>extractseparate green plants from the background</u> by extracting green and red colors from the image data to estimatedigital images. These indices <u>have been related to</u> different plant characteristics including biomass, chlorophyll content and the nutritional status of plants-(Tucker 1979; Woebbecke et al. 1995; Camargo 2004; Hunt et al. 2005; Meyer and Camargo 2008; Hunt et al. 2013; Lee and Lee 2013; Wang et al. 2013). -In this study, vegetation indices digital image analysis performed better than hyperspectral scanning analysis to

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295 estimate DW and NCP (Fig 2 and 3). Nonetheless, the use of spectral analysis over grasses becomes more important when this technique is used to detect either nutritional or anti-nutritional 296 297 compounds (i.e. proteinmetabolisable energy, digestibility, fiber) that are better estimated with the near-infrared regions of the electromagnetic spectra (Curran 1989; Pullanagari et al. 2012; Ferner 298 et al. 2015). In this sense, the use of digital color image analysis and hyperspectral analysis is 299 300 complementary because by using both techniques a diverse set of plant traits can accurately be predicted- and by adding extra factors to the prediction model, higher prediction accuracy can be 301 achieved (cf. Numata et al. 2008). Future efforts will use data mining to fine-tune the spectral 302 303 bands included in the PLSR model (Thorp et al. 2017), which can reduce model error and improve model fit statistics. Although testing multiple methods of analysis was not the intention of this 304 study, future research could also test other techniques (e.g., artificial neural networks) for relating 305 HTP measurements to plant traits. 306

The regression coefficients for the PLSR for DW and chlorophyll content obtained in this study 307 highlight that the key wavelengths for the prediction of these traits were located occur in the green, 308 red, red--edge and NIR regions of the electromagnetic spectrum (Fig 4). Previous hyperspectral 309 studies have highlighted those regions as being highly representative for dry mass and chlorophyll 310 311 content in plants (Lichtenthaler et al. 1996; Thenkabail et al. 2000; Mutanga and Skidmore 2004; Fava et al. 2009; Thorp et al. 2011; Adjorlolo et al. 2015; Dou et al. 2018). Although some 312 313 similarities were found between wavebands among the different traits, the general regression coefficients differed among the traits, thus demonstrating that the reflectance data in a given 314 waveband contributed differently toward the estimation of a given trait. Given the logistical burden 315 to collect and analyze hyperspectral scans, the identification of informative key bands associated 316 with each evaluated trait can improve the HTP process (Thorp et al. 2017). Results from this study 317

- will help guide selection of optimal bands in the construction of multispectral sensors tailored topredict specific traits of interest in tropical forage breeding programs.
- 320 The PLSR models for predicting DW, CP and chlorophyll content can be now used to evaluate the
- 321 <u>next generation of hybrids from the same Urochloa gene pool (i.e. U. ruziziensis U. brizantha –</u>
- 322 *U. decumbens*). The accuracy of this prediction models relies on collection protocols similar to the
- 323 explained in the Materials and Methods section and evaluations on plants with comparable growth
- 324 characteristics as the hybrids evaluated here (i.e. about three months after regrowth). The
- prediction accuracy will likely be reduced on larger plants with higher biomass (Hill 2004) and a
- 326 greater proportion of senescent leaves (Asner 1998). The development of more precise PLSR
- 327 models to predict variables of interest in a breeding program requires an ongoing effort. The
- 328 collection of ground data every year while making improvements to standardize collection
- 329 protocols and incorporate wider range of genotypes will result in more accurate and robust models.
- 330 Larger data sets will increase estimation precision.
- 331

332 Conclusions

In this study, 200 *Urochloa* hybrids were successfully monitored in 40 and 80 minutes by digital imaging and spectral analysis, respectively (Table 1). At this pace, more than 1000 *Urochloa* hybrids cancould be evaluated in a period of less than 7 hours. This means more that forage biomass and quality in a high number of genotypes couldwould be reliably evaluated with minimal increased acquisition costs (compared relative to destructive harvest). This demonstrates the superiority of HTP techniques as compared to conventional visual evaluation of traits. The PLSR models for predicting CP, forage DW, and chlorophyll content developed in this study supports

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340 the evaluation of higher numbers of genotypes at initial stages of the breeding program. The greater numbernumbers of plants evaluated reliably every year in the Urochloa breeding program, the 341 greater the genetic gain will be. Therefore, the use of image analysis and hyperspectral monitoring 342 over Urochloa hybrids canopies will benefit the on-going breeding program. Likewise, the The 343 application of this methodologyHTP method could be of great help in rural remote areas without 344 345 appropriate lacking facilities to perform destructive harvest and plant chemical analysis. Additional studies on Urochloa plants with contrasting architectures need to be performed to optimize PLSR 346 models. Moreover, more careful field measurements over plants with similar regrowth capacity 347 348 are required Research is underway to improve the prediction models. Furthermore, utility of proximal sensing by considering a greater range of canopy architectural configurations and 349 evaluating the potential to assess nutritional quality traits, including protein characteristics such as 350 metabolisable energy, fiber, digestibility and non-digestible fractions of the forage (, lignin and 351 cellulose) must be evaluated through proximal hyperspectral sensing to improve phenotyping 352 fractions in Urochloa grasses. 353

354

355 **Conflict of interest**

356 The authors have no conflicts of interest to declare.

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| 526 | Table 1 . Phenotyping techniques used in the present study, the time of evaluation, its application, |

527 advantages and disadvantages.

| | Phenotyping technique | Time of evaluation* | Applications | Advantages | Disadvantages |
|------------|--------------------------------|---------------------|---|--|---|
| | Visual evaluation | 68 min | Visual observations of different plant characteristics | Easy operation, low cost, evaluations can be performed under diverse conditions and environments | Evaluation of low number of genotypes, evaluation subjected to human bias and fatigue |
| | Image analysis | 40 min | Quantification of canopy cover and vegetation indices in the visible electromagnetic spectrum | Easy operation, low cost, greater number of plants evaluated, determination of several vegetation and water indices | Changes in ambient light conditions limit calculation of vegetation indices, data analysis is moderately complex |
| | Hyperspectral analysis | 80 min | Canopy reflectance information in the visible and near infra-red regions of the electromagnetic spectrum. Information can be used to predict biochemical compositionscomposition of plants | Moderately easy operation, greater number of plants evaluated, determination of nutritional and biochemical composition of leaf/canopy | Low solar radiation or cloudy days limit analysis, sensor and white reference calibration is frequently needed, data analysis is complex |
| 529 530 | * The time of e present study. | valuation refe | ers to 200 Urochloa plant | s evaluated under the co | onditions of the |
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| - | Trait | Min | Max | Mean | CV (%) |
|-----|-------------------------------------|------|-------|-------|--------|
| - | Dry Weight (g plant ⁻¹) | 6.74 | 64.1 | 30.22 | 34.81 |
| | NitrogenCrude Protein (%) | 6.76 | 21.58 | 11.23 | 19.68 |
| | Chlorophyll (mg g FW) | 0.87 | 6.41 | 2.88 | 24.31 |
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- 565 **Table 4**. Regression coefficients of the fitted partial least square regression models of seven traits
- 566 <u>extracted from digital image analysis</u>. Positive and negative coefficients indicate positive and
- 567 <u>negative influence on the prediction model, respectively.</u>

| | <u>Traits*</u> | Dry weigth (g.plant ⁻¹) | <u>Crude protein (% DW)</u> | <u>Chlorophyll (mg.g⁻¹)</u> |
|------------|----------------|-------------------------------------|--------------------------------|--|
| | <u>CC</u> | 3.760545 | -0.23114345 | <u>-0.01673706</u> |
| | <u>NGRDI</u> | <u>9.948634</u> | 0.08600517 | -0.03532585 |
| | ExG | <u>-14.3163</u> | <u>0.07760486</u> | 0.0730642 |
| | <u>ExR</u> | -32.126212 | -0.39106455 | -0.07758547 |
| | ExGR | <u>3.724492</u> | 0.26592971 | 0.10326555 |
| | <u>GR</u> | -34.770799 | -0.31158671 | -0.03624834 |
| | <u>GLI</u> | 80.87152 | <u>-0.31108316</u> | <u>-0.0357783</u> |
| 568 | * CC= cano | py cover, NGRDI= normal | lized green red difference inc | lex, ExG= excess green index, |
| 569 | ExR = excess | s red index, ExGR= excess | s green minus excess red, GI | <u>R = green ratio and GLI= green</u> |
| 570 F71 | leaf index. | | | |
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Fig 1. Modeled versus measured dry weight, <u>nitrogencrude protein</u> and chlorophyll content when
fitting partial least square regression models to relate each biophysical characteristic to visual
evaluations of biomass and greenness of 200 *Urochloa* hybrids.

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Fig 2. Modeled versus measured dry weight, <u>nitrogencrude protein</u> and chlorophyll content when
 fitting partial least square regression models to relate each biophysical characteristic to <u>vegetation</u>
 indices<u>digital image analysis</u> of 200 *Urochloa* hybrids.

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Fig 3. Modeled versus measured dry weight, <u>nitrogencrude protein</u> and chlorophyll content when
fitting partial least square regression models to relate each biophysical characteristic to canopy
spectral reflectance of 200 *Urochloa* hybrids.

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649 Supplementary information

Supplementary Table 1. <u>Different protocols of spectral data collection and their respective root</u>
 mean squared error of prediction (RMSEP) for <u>nitrogencrude protein</u>, dry weight and chlorophyll

652 content.

| 653 — | Collection | Trait | Factors¥ | RMSEP |
|-------|------------|-------------------------------------|----------|-------|
| | | Dry weight (g plant ⁻¹) | 4 | 9.23 |
| 654 | Day 1* | NitrogenCrude protein (%) | 11 | 1.29 |
| | | Chlorophyll (mg g FW) | 4 | 0.49 |
| | | Dry weight (g plant ⁻¹) | 4 | 8.20 |
| 655 | Day 2* | NitrogenCrude protein (%) | 10 | 1.26 |
| | | Chlorophyll (mg g FW) | 7 | 0.50 |
| 656 | | Dry weight (g plant ⁻¹) | 4 | 7.63 |
| | Day 3** | NitrogenCrude protein (%) | 11 | 2.07 |
| | | Chlorophyll (mg g FW) | 5 | 0.54 |
| 657 | | Dry weight (g plant ⁻¹) | 6 | 8.14 |
| 658 | Day 4** | NitrogenCrude protein n (%) | 2 | 1.21 |
| 000 | | Chlorophyll (mg g FW) 🛛 < | 3 | 0.58 |
| | | Dry weight (g plant ⁻¹) | 6 | 7.90 |
| 659 | All days | NitrogenCrude protein (%) | 5 | 1.63 |
| | | Chlorophyll (mg g FW) | 5 | 0.55 |

Fifty plants were evaluated daily * One scan collected per plant. ** Ten scans collected per plant.
 ¥ Number of factors for which the root mean squared error of cross validationprediction was
 minimized in the model prediction.







