Information related to this report

CRP: Livestock

Cluster: 3.1.1 - On-farm, large-scale and global feed assessments and prioritization approaches

Activity: Report on the construction of portable NIRS equation to estimate forage quality in *Brachiaria decumbens-ruzisiensis-brizantha* species complex

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Summary:

The nutritive value of Brachiaria *Hybrids* is one of the most important parameters in the forages breeding program at the International Center for Tropical Agriculture (CIAT). It supports the selection and identification of promising genotypes. Using Near infrared reflectance spectroscopy (NIRS) we have been able to estimate protein contents (CP), neutral detergent fiber (NDF), and acid detergent fiber (ADF) with satisfactory results in the benchtop NIRS of the sample dried and ground. During 2021, the portable NIRS has been explored for the prediction of nutritional quality parameters without the destructive preprocessing of plants. This allows a rapid assessment of nutritive values. The objectives of this study were to evaluate the potential use of portable NIRS technology into the breeding program to predict the nutritional quality of *interspecific Brachiaria Hybrids* and extend the data set of calibration for building models for measure dry matter (DM), NDF, ADF and CP. The methodology applied used wavelengths of full range (350-2500nm) and NIR (1000-2500nm). Prediction accuracy of the obtained equations were in general better than previous models, but unfortunately still not robust enough to be applied. Further enrichment of the calibration set is required.

MATERIALS AND METHODS

Plant Materials

The samples used correspond to plants collected in assays of field in stations of Agrosavia (*Nataima, Tolima, Colombia*) and International Center for Tropical Agriculture (CIAT) (*Palmira, Valle del Cauca, Colombia*). The population BR12 (110 genotypes) was established with an experimental design *Alpha lattice* (10X 11) in plots measuring 1 X 1 m, and two repetitions. During the periods 2019 and 2020 were sampling during four seasons. The spectral data collection was acquired using a ASD LabSpec 4 Standard-Res (Analytical Spectral Devices, Inc., Boulder, CO) spectrometer over the 350 to 2500 nm wavelength range and 1 nm spectral resolution. The

reflectance data were collected between 1000 and 1500 h on clear days. The spectral reflectance values were measured from the five adjacent points in each plot at each sampling date were averaged.

Data Calibration and Validation Set

Through of function SELECT in WinISI II chemometric software version 4.9 (*Infrasoft International LLC*) were identified of population global a number 222 samples Brachiaria *Hybrids* spectra. The samples were processing in laboratory for chemical analysis and after were combined with their respective spectra to create the dataset calibration and Validation Set. Both datasets were selected random with other function in the WinISI II software and obtained 182 samples of calibration set and 20% remained for Validation set (40 samples).

Laboratory Analysis

Total samples both calibration and validation set (222 Samples) were used for measure in laboratory like reference method parameters dry matter at 60˚C, NDF, ADF and CP. All chemical analysis conducted at Animal nutrition and Forages Quality laboratory – CIAT. The chemical Analysis ADF and NDF were made in the, in accordance with the methods suggested by Van Soest et al. using an ANKOM 2000 fiber analyzer (ANKOM Technology Corporation, NY, USA). Crude protein was determined using a FOSS Kjeltec ™ 8100 complying with the guideline standards of AOAC 984.13: 1990. The samples were dry in oven dried MEMMERT UF750 model at temperature 60˚C for 72 h and after ground through a 1mm screen.

RESULTS

Equation Development and Validation

The spectral collective of 222 samples include wavelengths of full range (350-2500nm) (Figure 1). The spectra acquisition with samples were in fresh and measuring directly in plants before harvest and without any preprocessing (drying, milling).

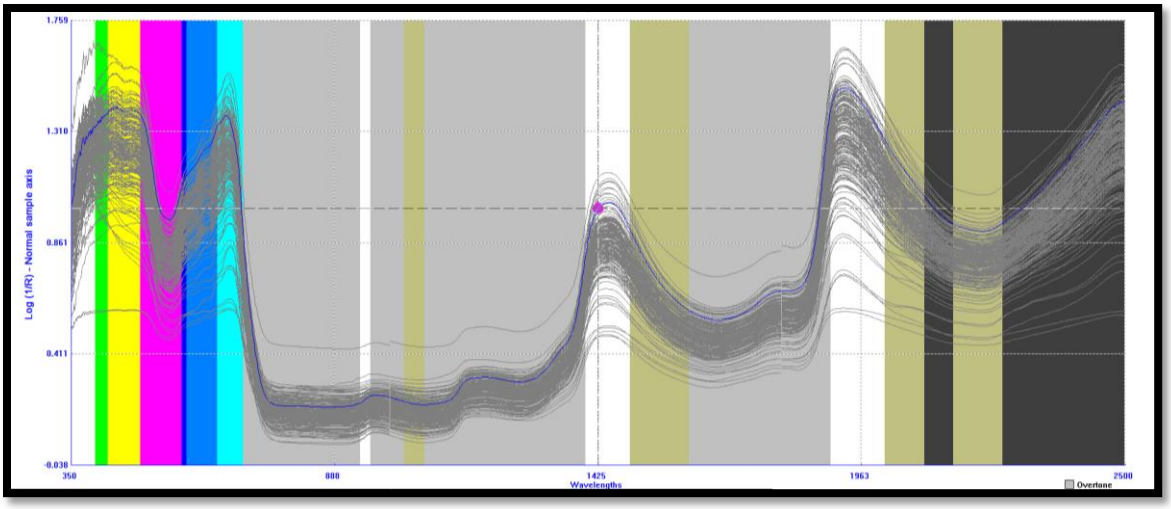

Figure1. Spectral of samples Brachiaria *Hybrids in* wavelengths of full range (350-2500nm).

The method used for developing the calibration models were regression Partial Least Squared Modificated (MPLS). Additionally, the spectra were processing with scatter correction Standard normal variate and Detrend (SNVD). For building calibrations equations were used the following four mathematical treatments: i) 1,4,4,1; ii) 2,4,4,1; iii) 1,20,4,1; iv) 2,20,4,1 and two range wavelengths: Full range with three segments (Seg 1: 350-1000nm; Seg 2; 1001-1800nm; Seg 3; 1801-2500nm) and NIR Range (Seg 2: 1000-1800nm, Seg 3: 18001-2500nm).

The equations models were building using WinISI II chemometric software version 4.9 (Infrasoft International LLC). In the next Tables (1,2,3,4) can observe results of statistical parameters NIRS equations for each nutrient evaluated:

Table 1. Statistical parameters NIRS equations Dry Matter

		CALIBRATION									***VALIDATION***				
Constituent	N	Mean	SD	Est. Min	Est. Max	SEC	RSQ	SECV	1-VR		***R^2***	***Slope***	***Intercept***	***SEP***	***RPD***
DM1	169	23.73	6.05	5.58	41.89	1.71	0.92	2.24	0.86		0.86	1.062	-0.74	3.14	2.61
DM2	163	23.67	5.99	5.69	41.65	1.97	0.89	2.26	0.87		0.86	0.970	1.22	3.64	2.25
DM3	169	23.75	6.07	5.54	41.95	1.72	0.92	2.16	0.87		0.86	0.99	0.62	3.08	2.66
DM4	165	23.98	6.48	4.54	43.41	1.80	0.92	2.15	0.89		0.85	0.93	2.05	3.17	2.59
DM5	163	23.39	5.68	6.36	40.43	1.56	0.92	2.09	0.86		0.82	0.94	2.18	3.52	2.33
DM6	162	23.77	6.12	5.41	42.13	1.88	0.91	2.34	0.85		0.71	0.94	2.46	4.47	1.83
DM7	167	23.44	5.86	5.87	41.01	1.93	0.89	2.19	0.86		0.84	1.01	0.28	3.26	2.51
DM8	163	23.71	6.25	4.96	42.45	1.71	0.93	2.09	0.89		0.83	0.92	2.31	3.40	2.41

The first four equations (For example: DM1, DM2, DM3, DM4) in each table correspond to models development with full range and next four (DM5, DM6, DM7,DM8) correspond to NIRS Range with two segments Seg 2: 1000-1800nm, Seg 3: 18001-2500nm).

In Predicted models for determined Dry matter at 60˚C (Table 1) found eight predicted models. DM8 were better model that show correlation coefficients of calibration neast 1.0 and low value in Standard error cross validation (SECV).

Table 2. Statistical parameters NIRS equations Neutral Detergent Fiber.

		CALIBRATION									***VALIDATION***				
Constituent	N	Mean	SD	Est. Min	Est. Max	SEC	RSQ	SECV	1-VR		***R^2***	***Slope***	***Intercept***	***SEP***	***RPD***
NDF1	164	13.27	3.10	3.99	22.56	1.03	0.89	1.41	0.80		0.78	1.13	-1.49	2.15	2.10
NDF2	169	13.28	3.20	3.66	22.89	1.53	0.77	1.67	0.73		0.74	1.09	-0.69	2.36	1.91
NDF3	167	13.17	3.07	3.95	22.39	1.10	0.87	1.33	0.81		0.79	1.07	-0.71	2.08	2.17
NDF4	171	13.40	3.44	3.09	23.71	1.37	0.84	1.52	0.80		0.81	1.00	0.10	1.93	2.35
NDF5	166	13.10	2.96	4.23	21.97	1.05	0.87	1.36	0.80		0.78	1.18	-1.88	2.27	1.99
NDF6	165	13.29	3.14	3.86	22.71	1.19	0.86	1.49	0.77		0.63	1.03	0.08	2.76	1.64
NDF7	167	13.16	3.04	4.05	22.26	1.17	0.85	1.36	0.81		0.79	1.16	-1.82	2.14	2.12
NDF8	163	13.05	2.93	4.25	21.85	1.12	0.85	1.28	0.81		0.79	1.06	-0.54	2.08	2.18

NDF models and ADF building show good correlation coefficients in both calibrations set, and validation set. In general, NDF4 and NDF8 for this parameter would be moderately useful, because ratio performance deviation (RPD) was 2.35-2.18.

Table 3. Statistical parameters NIRS equations Acid Detergent Fiber.

		CALIBRATION									***VALIDATION***				
Constituent	N	Mean	SD	Est. Min	Est. Max	SEC	RSQ	SECV	1-VR		***R^2***	***Slope***	***Intercept***	***SEP***	***RPD***
ADF1	162	5.96	1.17	2.44	9.47	0.57	0.76	0.69	0.66		0.75	1.17	-0.99	1.10	1.95
ADF2	169	6.09	1.39	1.93	10.26	0.71	0.74	0.75	0.71		0.72	1.24	-1.28	1.19	1.80
ADF3	169	6.11	1.36	2.04	10.18	0.61	0.80	0.71	0.73		0.76	1.23	-1.45	1.10	1.96
ADF4	165	5.97	1.22	2.31	9.63	0.55	0.80	0.65	0.73		0.77	1.25	-1.38	1.09	1.96
ADF5	165	6.08	1.40	1.88	10.28	0.65	0.79	0.73	0.73		0.67	1.03	-0.12	1.22	1.76
ADF6	167	6.07	1.31	2.13	10.01	0.59	0.80	0.74	0.68		0.65	1.23	-1.28	1.32	1.63
ADF7	166	5.98	1.22	2.32	9.64	0.64	0.72	0.72	0.68		0.71	1.30	-1.74	1.23	1.75
ADF8	165	5.95	1.20	2.36	9.55	0.59	0.76	0.67	0.71		0.77	1.40	-2.34	1.17	1.84

Table 4. Statistical parameters NIRS equations Crude Protein

		CALIBRATION									***VALIDATION***				
Constituent	N	Mean	SD	Est. Min	Est. Max	SEC	RSQ	SECV	1-VR		***R^2***	***Slope***	***Intercept***	***SEP***	***RPD***
CP1	169	2.53	0.68	0.50	4.56	0.24	0.87	0.32	0.77		0.66	0.77	0.66	0.45	1.58
CP2	164	2.49	0.59	0.72	4.26	0.28	0.78	0.34	0.69		0.48	0.68	0.87	0.56	1.28
CP3	168	2.54	0.68	0.50	4.58	0.30	0.80	0.34	0.75		0.60	0.70	0.78	0.50	1.42
CP4	166	2.51	0.65	0.56	4.47	0.23	0.88	0.30	0.81		0.62	0.75	0.68	0.48	1.50
CP5	168	2.53	0.68	0.50	4.56	0.28	0.83	0.34	0.75		0.61	0.71	0.77	0.50	1.44
CP6	172	2.54	0.68	0.51	4.57	0.25	0.86	0.36	0.71		0.51	0.64	0.99	0.57	1.25
CP7	168	2.51	0.63	0.63	4.40	0.27	0.82	0.33	0.72		0.70	0.91	0.30	0.40	1.80
CP8	168	2.52	0.67	0.52	4.52	0.23	0.88	0.30	0.80		0.66	0.76	0.67	0.45	1.58

In case, ADF and CP models correlation coefficients of calibration set explain into 70-88% of the variation in measured in these parameters. However, validation set evidence low correlations between Lab data versus spectral data (0.48-0.66). The ratio performance deviation (RPD) for ADF models were 1.63 -1.96 and 1.28- 1.80 respectively, indicated the models are less reliable and could not be used for quantification and only be useful for qualitative purposes for now.

CONCLUSIONS

Results obtained by NIRS portable for models explained from 80 to 93% of the variation total in NDF and DM parameters. These models would be moderately successful for predict nutritional value *in situ* of population brachiaria hybrids BR12. The extend data set of calibration for building models NDF, ADF and CP were better with respect last equation reported in 2020. ADF and CP models must be continued this study with objective eliminate wavelengths within atmospheric water vapor absorption regions and find better Statistical parameters in equations.

Acknowledgements

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LITERATURE CITED

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