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Wheat grouping using infrared sensors and forage fractions in three samplings

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Abstract

Wheat is an important crop for human food and an extraordinary forage alternative for livestock. In Mexico, it is not cultivated specifically for that purpose, but work is being done on the generation of genotypes for forage purposes using emerging technology. Twenty-two wheat genotypes and three controls of another species were evaluated in four environments during the autumn-winter cycles 2017-2018 and 2018-2019 by means of a randomized complete block design with three repetitions, in order to group genotypes through three samplings (at 75, 90 and 105 days after sowing) and estimate the association between variables. With the means of the genotypes across the environments, principal component and cluster analyses were performed for each sampling. The results of the analysis of variance justified studying the samplings separately. Up to five groups were retained in each sampling, with groups of wheats with dry forage yields equal to or greater than that of oats. In early stages, there was a greater proportion of leaves, which decreased as the phenological stage progressed, while the fraction of spikes increased, with a slight decrease in the fraction of stems. There are groups of forage wheats that may represent an option to replace oats, with the wheats AN-229-09, AN-241-13, AN-268-99, AN-217-09 and AN-263-99 standing out. A positive association between NDVI, FSH and COB was detected, which lasted through the samplings, suggesting that the use of infrared sensors can be used in the estimation of dry leaf matter.

Keywords: dry forage, forage fractions, NDVI, samplings, wheat.

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Introduction

Wheat is one of the cereals that sustains human food, occupying about a third of the total area of cereals in the world, providing carbohydrates and protein in the diet. Indirectly, it could provide a greater amount of protein through milk or meat that can be produced when supplied as forage to livestock. The way of using the forage is variable, existing from direct grazing, which is the cheapest option, to options such as green fodder, haylage and silage. Similarly, the time in which it is used is as variable as the needs of the livestock and the type of exploitation, there are occasions that it is required to use winter forages fifty days after sowing (das) and sometimes its harvest is postponed up to more than 110 das.

In Mexico, wheat is not grown specifically for that purpose, but in some countries such as Argentina and Canada it has a significant presence as a source of forage (Gill *et al*., 2013). In Mexico, oats are the main annual crop under irrigation for forage production during the winter. In the agricultural year 2018, the national forage oats had a sown area of 31 056.98 ha, with a production of 822 825.9 t (SAGARPA, 2017; SIACON, 2018). There is an extraordinary potential for the use of winter cereals in the semi-arid zone of Mexico, since the least water losses due to evaporation occur at the time when they are grown and most cereals have desirable characteristics for forage production, tolerance to low temperatures and generally also have adequate nutritional value.

However, there are few varieties developed for use as a source of dry forage (aerial biomass) in many of the cereal species such as triticale, barley and wheat. The institutions that develop research make efforts to generate new forage options in the mentioned species; however, for the evaluation of new forage genotypes, destructive methodologies (forage cutting) are generally used to evaluate their productivity and if one wants to obtain information of production at various stages of development, it is necessary to carry out more samplings or cuttings, with the effort and cost they represent; recently the use of various tools has been implemented for the non-destructive evaluation of biomass production through the use of infrared sensors, such is the case of the normalized difference vegetation index (NDVI), which has been used to monitor the yields of biomass production, estimating the quantity and quality of food and vegetation growth, as well as the presence of diseases that reduce vegetation indices (Cabrera-Bosquet *et al*., 2011 and Pask *et al*., 2012).

The sensors have also been used to measure other variables such as temperature, with the use of the infrared thermometer that allows it to be recorded remotely without interfering with the crop, using the information obtained for the diagnosis of stress; likewise, it is possible to estimate with sensors a chlorophyll content index to relate it to the nutritional status of the crop (Reynolds *et al*., 2013).

Recently, it has been reported that there are wheat lines that present adequate production and quality of forage similar to oats (Zamora *et al*., 2016) and, in barley, studies where the yield of oats is equaled or exceeded have been carried out and they have even carried out groupings of forage genotypes with the intention of characterizing and selecting them (Colín *et al*., 2007; Torres *et al*., 2019). In wheat for grain, groupings based on genes of agronomic interest have been carried out (Suaste *et al*., 2015). The objective of this research was to evaluate the production of dry forage, its fractions, estimate the association with infrared sensors and other agronomic variables, to group genotypes of awnless wheat in three samplings.

Materials and methods

The study was conducted in three localities in northeastern Mexico: Zaragoza and San Pedro de las Colonias, Coahuila and Navidad, Nuevo León. Only in Zaragoza, Coahuila, the genotypes were evaluated in two production cycles, so the particular combination of the locality and cycle will be called as an environment: the Experimental field of the Antonio Narro Autonomous Agrarian University in the Municipality of Zaragoza, Coahuila, during the autumn-winter (AW) cycles 2017-2018 and 2018-2019 gave rise to environments 1 and 3, respectively, environment 4 was constituted by the experimental field Ing. Humberto Treviño Siller, owned by the Antonio Narro Autonomous Agrarian University, located in Navidad, NL, during the AW cycle 2018-2019 and the ejido San Ignacio, Municipality of San Pedro de las Colonias, Coahuila, during the AW 2018-2019 constituted environment 2.

Zaragoza, Coahuila, is located at 28° 33” north latitude and 100° 55” west longitude, at an altitude of 350 m, with dry, semi-warm, extreme climate, with cool winter, with an average annual temperature of 21.4 °C. The locality of San Ignacio is located at 25° 32” north latitude and 103° 15” west longitude, at an altitude of 1 100 m, with arid and semi-arid climate and an annual temperature of 19.1 °C. Navidad, N., is located at 25° 04” north latitude and 100° 37” west longitude; with an altitude of 1 895 masl, semi-arid, temperate climate and an average annual temperature of 14.6 °C (Arriaga *et al*., 2000).

Twenty-two lines of forage awnless wheat were evaluated, using as controls an oat (cv. Cuauhtémoc), a forage barley (*cv* GABYAN95) and a grain triticale (*cv* Eronga-83), whose identification and number appear in Table 1. These genotypes were established in a randomized complete block design with three repetitions, considering the experimental plot of 6.48 m^2 (6 furrow of 3 m in length, spaced at 0.36 m). The preparation of the land was in accordance with the traditional practices in the regions where wheat is grown, under irrigation conditions, carrying out the fallow, harrowing and leveling, sowing dry, manually and by steady flow at a density of 120 kg ha^{-1}.

Table 1. Genotypes evaluated in the four test environments.

Genotype	Identification	Genotype	Identification
G1	AN-249-99	G14	AN-228-09
G2	AN-268-99	G15	AN-229-09
G3	AN-263-99	G16	AN-264-09
G4	AN-267-99	G17	AN-326-09
G5	AN-244-99	G18	AN-7-09
G6	AN-236-99	G19	AN-241-13
G7	AN-209-09	G20	AN-409-13
G8	AN-216-09	G21	AN-246-13

Genotype	Identification	Genotype	Identification
G9	AN-217-09	G22	AN-310-13
G10	AN-218-09	G23	AVENA
G11	AN-220-09	G24	NARRO 95
G12	AN-221-09	G25	ERONGA
G13	AN-222-09		

At sowing, 60 units of nitrogen were applied using urea as a source and 80 units of phosphorus using monoammonium phosphate (MAP). In the first supplemental irrigation, another 60 units of nitrogen were applied. In all the localities, a sowing irrigation and three supplemental irrigations were carried out, providing an approximate total irrigation sheet of 40 cm during the crop cycle. The broadleaf weeds were controlled with 2,4-D amine at a dose of 1.5 L ha^{-1}, complemented with manual weeding, no fungicide or insecticide was applied given the low incidence of insects and fungal diseases.

Three forage samplings were carried out at 75, 90 and 105 days after sowing (das), cutting the forage with a sickle, at a height of approximately 5 cm above the soil surface, harvesting 50 cm from a row with full competence. Samples of green forage harvested in each sampling were placed in kraft paper bags and taken to a closed sundeck to dry the forage at room temperature, constantly moving them to prevent rotting.

It was monitored until they reached constant weight and the dry forage yield in grams was recorded, each sample was separated into the fractions: dry stem forage (FST), dry leaf forage (FSH), dry spike forage (FSE), subsequently transforming to tones per hectare, the total dry forage (FSTOT) was calculated with the sum of these fractions. At the time of forage cutting, in each of the three samplings, the following variables were recorded: plant height in centimeters (ALTURA), land cover in percentage (COB), canopy temperature in degrees Celsius (TEMP), chlorophyll concentration index (CLORO), normalized difference vegetation index (NDVI) and the phenological stage (ETAPA) according to the scale of Zadocks *et al*. (1974).

TEMP was measured with an IP-54 infrared thermometer, Fluke brand, with a laser sight, pointing towards the middle of each experimental plot to record the variable. To measure the chlorophyll content, a SPAD-502 chlorophyll meter, Konica Minolta brand, was used, making the reading in the middle part of 10 flag leaves. The NDVI, was measured through a portable sensor, Green Seeker^{TM} brand, evaluating in the central part of each plot. The information collected in the three samplings was analyzed by a subdivided plot model with random block arrangement, considering the environments as a large plot, the samplings as a medium plot and the genotypes as a small plot, the means were compared using the LSD test at 0.05% probability using the SAS program (1989).

With the means of the genotypes across the environments, multivariate analyses of principal components (PCA) and clusters (CA) were performed for each sampling, the PCA in order to reduce the dimensionality of the data, detect associations between variables and the partial characterization of the genotypes (Manly, 1986) and the CA to form groups of genotypes similar to each other and different from those of other groups, using the methodology of Ward (1963), these analyses were performed with the Statistica program (Statistica, 1994).

Results and discussion

The analysis of variance reported significance ($p \leq 0.01$) between environments, samplings, the samplings by environment interaction and between genotypes for all variables evaluated, the effect of samplings caused the largest mean squares in almost all variables, except in dry leaf forage (FSH), chlorophyll content (CLORO) and land cover (COB), in which the effect of localities promoted greater variation. The genotype by environment interaction was not significant for the canopy temperature variable and was only significant ($p \leq 0.05$) in the total dry forage, while in the rest of the variables, high significance was detected. The samplings by genotype interaction was highly significant for the variables dry spike forage (FSE), plant height (ALT), normalized difference vegetation index (NDVI), (CLORO) and (ETAPA), significant in FSH and not significant in COB, canopy temperature (TEMP), dry stem forage (FST) and total dry forage (FSTOT).

The triple interaction was significant for NDVI, highly significant in CLORO, ALT, ETAPA and FSE, while in FSTOT, FST, FSH, TEMP and COB it was not significant, reaffirming that the temperature of the canopy showed little interaction, while the chlorophyll content, plant height, phenological stage, dry spike forage and NDVI strongly interacted with the environments and samplings.

The comparison of means of the environments (LSD at 0.05 probability) reported that environment 2 (San Ignacio, Coahuila, AW 2018-2019) was the most productive environment, with the highest number of stems and leaves, highest values of NDVI and land cover, meanwhile, Navidad, NL, AW 2018-2019 (environment 4) showed the highest temperature of the canopy, the most advanced phenological stage and the highest number of spikes.

Environment 1 (Zaragoza, Coahuila, AW 2017-2018) registered the highest chlorophyll contents. Shao *et al*. (1995); Torres *et al*. (2019) have highlighted the importance of the effect of environments on forage production, coinciding with what was found in the present study, extending this asseveration to the other variables studied. Regarding the samplings, the third (carried out at 105 das) was the one that reached the highest values in almost all variables, except NDVI and CLORO, the NDVI registered the highest mean in the first sampling (75 das), while the chlorophyll content registered the highest mean in the second sampling (90 das).

This means that, in general, as time progresses the plant accumulates more biomass, increases its phenological stage and continues its growth; however, the NDVI being an index that measures the greenness of the plant showed its highest values in juvenile stages and decreased as the plant matured, this behavior did not occur with the chlorophyll content, which, in this study, reached its highest value in the medium tasseling stage, when the plant prepares for grain filling.

Among the genotypes, the mean test rated the forage barley GABYAN95 as the most productive, followed by the wheat genotypes AN-229-09, AN-241-13, AN-268-99, AN-217-09 and AN-263-99, all of them statistically exceeding oats cv. Cuauhtémoc, confirming previous reports of the existence of other cereals that productively exceed oats (Zamora *et al*., 2002; Colín *et al*., 2009; Zamora *et al*., 2016; Torres *et al*., 2019). Due to the significance detected between the samplings and the magnitude of the variance caused, as well as having information that allows the use of the forage produced in a short time, multivariate analyses were carried out for each sampling, to partially characterize the genotypes and establish similarities and differences between them.

Principal component analysis (PCA) for the first sampling (carried out at 75 das) explained 67.15% of the total variance with the first two principal components (PC). PC1 contained 44.65% of the variance, where FSTOT, FSE, FST, ALT and COB were positively associated with each other and with this PC1. PC2 had 22.5% of the total variance and explained the positive relationship between NDVI and FSH (although both were negatively related to component 2).

Figure 1 was constructed with the first two components, which shows the association between the variables FSE, ALT, FST, ETAPA, TEMP, CLORO, among others, highlighting the strong association of FST with ALT and FSE associated with FSTOT, which coincides with the relationship reported by Colín *et al*. (2009); Gill *et al*. (2013); Torres *et al*. (2019), regarding the association of higher forage production with high genotypes. The negative relationship between NDVI and CLORO is confirmed, which has been reported in forage barleys (Torres *et al*., 2019), as well as the negative relationship between the NDVI and ETAPA detected by them.

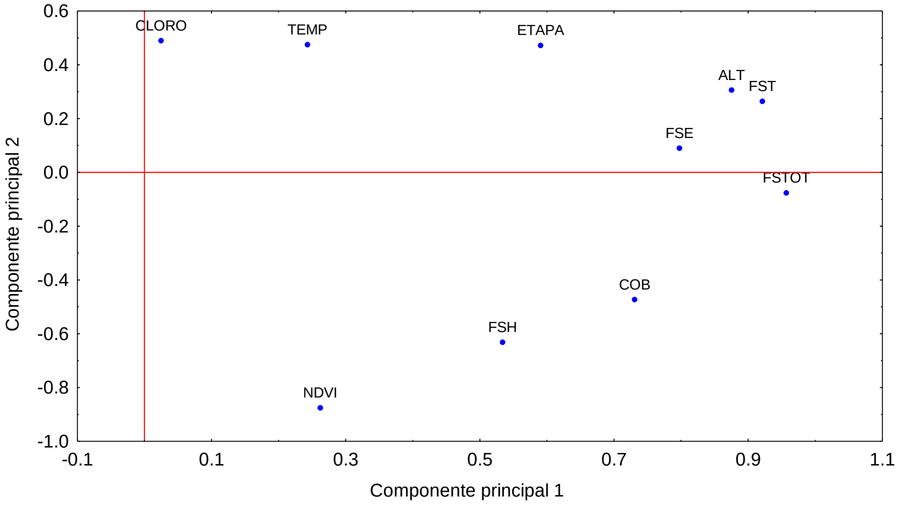

Figure 1. Relationships between the variables evaluated in the plane of the two principal components in a first sampling (75 days).

It has been reported in other studies that PCA is a useful tool in the partial characterization of genotypes and its complementarity with a cluster analysis (Colin *et al*., 2007; Suaste *et al*., 2015; Torres *et al*., 2019), due to which the cluster analysis was carried out using the methodology of Ward (1963), where five groups were retained, since Colín *et al*. (2007); Torres *et al*. (2019) have reported in barley the existence of at least five groups of genotypes different from each other and with interesting characteristics for forage production.

In this study, the first group detected at 75 das was made up of 14 genotypes (AN-249-99 (G1), AN-267-99 (G4), AN-220-09 (G11), AN-218-09 (G10), AN-236-99 (G6), AN-216-09 (G8), AN-221-09 (G12), AN-264-09 (G16), AN-244-99 (G5), AN-217-09 (G9), AN-209-09 (G7), AN-222-09 (G13) and AN-241-13 (G19)), which showed a behavior similar to that of the control oats *cv*

Cuauhtémoc (G23), which was part of this group and as a whole were characterized by not presenting the fraction corresponding to the spikes, because they were on average in the phenological stage of beginning of flag leaf production, they were the latest of Table 2, reinforcing the asseveration regarding the existence of forage wheats with characteristics similar to those of oats (Zamora *et al*., 2016).

Table 2. Number of members (n) means of the variables in the groups generated by the cluster analysis at a first sampling of 75 days.

Variables	Group 1	Group 2	Group 3	Group 4	Group 5
N	14	1	8	1	1
FSTOT	3.11	4.71	3.28	3.87	3.02
FST	1.25	2.31	1.56	1.93	1.28
FSE	0	0.12	0.02	0	0.05
FSH	1.86	2.29	1.71	1.94	1.69
TEMP	14.82	14.81	15.19	23.65	14.66
ALT	51.8	68.75	55.63	62.5	51.67
NDVI	0.75	0.78	0.72	0.7	0.72
CLORO	38.01	39.08	38.8	39.51	46.76
COB	71.63	87	69.71	69.58	72.25
ETAPA	36.07	38.83	37.81	37.5	38.5

FSTOT= total dry forage (yield); FST= dry stem forage; FSE= dry spike forage; FSH= dry leaf forage; TEMP= canopy temperature; ALT= plant height; NDVI= normalized difference vegetation index; COB= plant cover; ETAPA= phenological stage.

Another group of genotypes (Group 3) was made up of the wheats AN-268-99 (G2), AN-263-99 (G3), AN-228-09 (G14), AN-326-09 (G17), AN-409-13 (G20), AN-310-13 (G22), AN-7-09 (G18) and AN-246-13 (G21), which showed an average FSTOT yield of 3.28 t ha^{-1}, slightly higher than that of Group 1, with a higher proportion of stems, but less leaf and a small fraction due to the spike and are also characterized by their higher plant height and phenological stage. The most different genotype in its behavior during the first sampling was the barley GABYAN95 (G24), which showed the largest distance detected by the analysis and was placed as the only member of Group 2, with the highest forage yield, surpassing triticale *cv* Eronga 83 (only member of group 5) by more than 1.7 t ha^{-1}.

It is noteworthy in Table 1 that the genotype AN-229-09 (the only member of group 4) showed the second highest yield of dry forage, plant height, FSH and FST combined with the highest plant temperature and low NDVI, which distinguished it from other wheats and placed it intermediate between triticale (group 5) and barley (group 2). Torres *et al*. (2019) mention that the cluster analysis has been able to differentiate or separate into different groups the control species, in a similar way to what is reported here. At 75 das, they have reported higher forage yields (up to 11.9 t ha^{-1}), which are mainly due to the rapid development of barley compared to other cereals (Domínguez *et al*., 2016) and due to which it produces forage and grain in less time (Colin *et al*., 2009; Wilson *et al*., 2017).

In this sampling, the leaves were the most abundant fraction with 56.01% of contribution to the FSTOT, followed by the stems with 43.61%, while the spikes represented only 0.37%. The PCA for the second sampling, carried out 90 days after sowing, explained with the first two components 74.02% of the total variance. The first component contained 44.2% of the variance and detected the positive association between NDVI, FSH and COB.

The second component explained 29.81% of the variance, explaining the positive association with each other and the negative association with the component of the variables TEMP, CLORO and ETAPA. Figure 2 was constructed with the information of the first two components, which shows the association between NDVI, FSH and COB located in the first quadrant, and which indicates that the greatest land cover occurs when there is more forage due to the leaves, which has an impact on a higher greenness index.

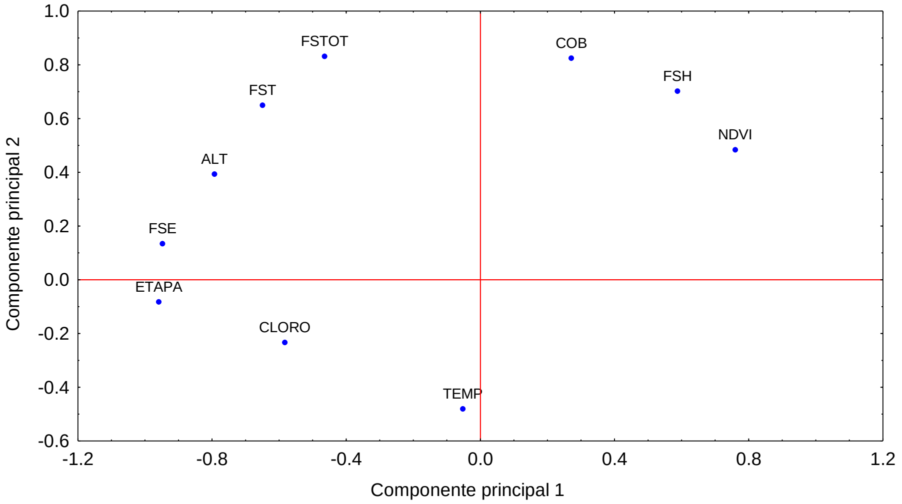

Figure 2. Distribution of genotypes in the plane of the two principal components in a second sampling (90 days).

Total dry forage was more related to higher forage of stems, spikes and higher plant height, also confirming in this sampling the relationship already reported between plant height and forage production (Colín *et al*., 2009; Gill *et al*., 2013; Torres *et al*., 2019). According to the cluster analysis (CA) performed at 90 das, up to 5 different groups were distinguished from each other. The first group made up of the wheat genotypes AN-249-99 (G1), AN-267-99 (G4), AN-216-09 (G8), AN-264-09 (G16), AN-244-99 (G5), AN-217-09 (G9), AN-209-09 (G7), AN-218-09 (G10), AN-221-09 (G12), AN-222-09 (G13) and oats *cv* Cuauhtémoc, which obtained an average yield of 5.72 t ha^{-1}, preserved the lowest phenological stage detected since the previous sampling and presented the least number of spikes, as shown in Table 3.

The second group included the genotypes AN-268-99 (G2), AN-263-99 (G3), AN-236-99 (G6), AN-326-09 (G17) and AN-220-09 (G11) with an average yield of 6.24 t ha^{-1} and intermediate characteristics for the rest of the variables compared to the other groups detected. Group 3 contained the genotypes: 15 (AN-229-09), 19 (AN-241-13) and the forage barley GABYAN95, which showed the highest forage production (7.48 t ha^{-1}) combined with the highest amount of FST, FSH, ALT, COB and NDVI. Confirming in this sampling the existence of wheats with characteristics similar to said barley.

Table 3. Number of members (n) means of the groups generated by the cluster analysis at a first sampling of 90 days.

Variables	Group 1	Group 2	Group 4	Group 5	Group 1
n	11	5	3	2	4
FSTOT	5.72	6.24	7.48	5.9	6.09
FST	2.8	3.19	3.94	3.12	3.29
FSE	0.28	0.58	0.69	0.63	0.77
FSH	2.64	2.47	2.86	2.15	2.03
TEMP	19.59	19.75	19.43	20.04	19.47
ALT	80.23	83.5	96.11	89.17	91.35
NDVI	0.72	0.68	0.71	0.66	0.67
CLORO	39.6	40.17	41.84	47.57	41.75
COB	75.41	73.38	79.11	72	72.02
ETAPA	50.39	54.23	55.39	56.75	58.96

FSTOT= total dry forage (yield); FST= dry stem forage; FSE= dry spike forage; FSH= dry leaf forage; TEMP= canopy temperature; ALT= plant height; NDVI= normalized difference vegetation index; COB= plant cover; ETAPA= phenological stage.

Triticale Eronga 83 (G25) was grouped with the wheat genotype 14 (AN-228-09) and formed Group 4, which according to Table 2, were distinguished by having the highest TEMP and CLORO combined with lower NDVI and COB of the retained groups. Finally, Group 5 was made up of the wheat genotypes: 18 (AN-7-09), 20 (AN-409-13), 22 (AN-310-13) and 21 (AN-246-13), which showed the highest phenological stage and FST combined with a yield of 6.09 t ha^{-1}. At similar sampling times (90 das), Torres *et al*. (2019) reported that oats and triticale Eronga 83 were grouped into the same group, which did not happen in this study probably due to environmental effects. In this second sampling, stems were the most abundant fraction (51.07%), followed by leaves (40.81%) and spikes contributed 8.12% to FSTOT.

In the last sampling, carried out at 105 das, the PCA continued to detect the positive association between NDVI, FSH and COB, which, apparently, is characteristic in the genotypes evaluated. Similarly, the relationship between plant height and dry forage produced continued positively, as can be seen in Figure 3 and allows confirming that this association, previously reported in forage barleys also exists in the wheats evaluated (Colín *et al*., 2009; Gill *et al*., 2013; Torres *et al*., 2019).

Of the five interest groups detected by the cluster analysis, the first of these included the wheat genotypes: 1 (AN-249-99), 6 (AN-236-99), 17 (AN-326-09), 4 (AN-267-99), 12 (AN-220-09), 5 (AN-244-99), 8 (AN-216-09), 11 (AN-220-09), 16 (AN-264-09), 7 (AN-209-09), 13 (AN-222-09), 10 (AN-218-09) and 9 (AN-217-09). In this sampling unlike the previous ones, oats *cv* Cuauhtémoc was the only member of Group 3, showing the lowest phenological stage of the retained groups and according to Table 4, the members of Group 1 exceeded the production of oats by an average of 1.4 t ha^{-1}, with lower FSH, NDVI, CLORO and COB than this, but with higher proportions of FST, ESF, possibly due to the higher ETAPA registered by Group 1.

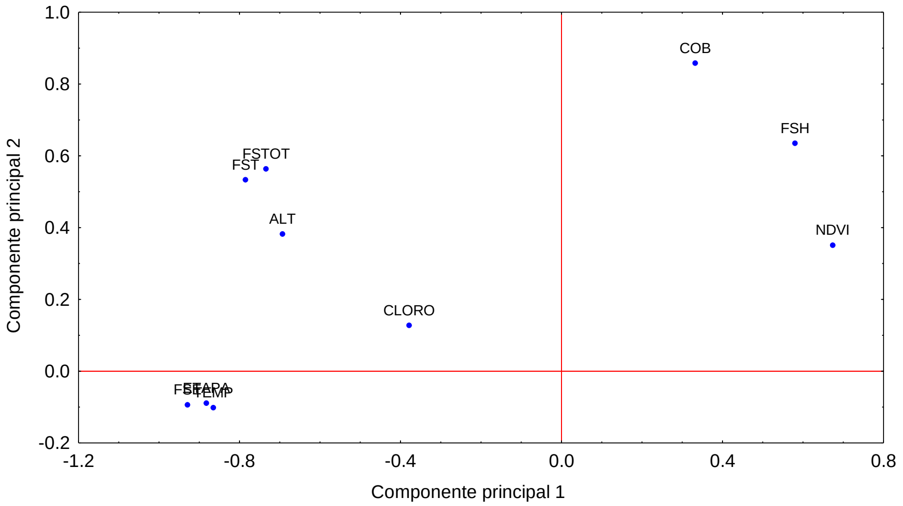

Figure 3. Distribution of genotypes in the plane of the two principal components in a third sampling (105 days).

Group 2 was formed with wheats 2 (AN-268-99), 3 (AN-263-99), 18 (AN-7-09), 22 (AN-310-13), 14 (AN-228-09), 15 (AN-229-09) and 20 (AN-409-13), which shared similar characteristics with triticale cv. Eronga 83, such as the second highest yield (10.01 t ha^{-1}), the highest TEMP, low NDVI and COB. For its part, the forage barley GABYAN95 was the only member of Group 4, showing the highest yield of dry forage, plant height, COB and ETAPA combined with high FST and FSH values. Group 5 with wheat genotypes 19 (AN-241-13) and 21 (AN-246-13) was characterized by a yield of 9.85 t ha^{-1} combined with high proportion of spikes and the highest plant height, as seen in Table 4.

Table 4. Number of members (n), mean of the groups generated by the cluster analysis at a first sampling of 105 days.

Variables	Group 1	Group 2	Group 3	Group 4	Group 5
n	13	8	1	1	2
FSTOT	9.02	10.01	7.63	11.56	9.85
FST	4.47	5.19	3.89	5.72	5.18
FSE	1.74	2.44	0.59	2.27	2.48
FSH	2.81	2.39	3.15	3.56	2.19
TEMP	24.46	25.28	24.28	25.07	24.63
ALT	100.26	112.08	111.67	113.75	119.17
NDVI	0.59	0.54	0.64	0.55	0.61
CLORO	38.74	42.64	46.63	39.48	42.21
COB	80.37	78.72	86.83	89.25	83
ETAPA	71.4	75.64	61.5	78	75.71

FSTOT= total dry forage (yield); FST= dry stem forage; FSE= dry spike forage; FSH= dry leaf forage; TEMP= canopy temperature; ALT= plant height; NDVI= normalized difference vegetation index; COB= plant cover; ETAPA = phenological stage.

At 105 das, stems continued to be the most abundant fraction (51.07%), followed by leaves (28.26%) and spikes (20.95%), coinciding in the order of contribution reported by Zamora *et al*. (2016) at 118 das in the wheats evaluated by them, but differing in their percentages, since they reported 50.98, 36.11 and 12.91% for stems, leaves and spikes, respectively.

In this study, it was possible to verify that, in early stages such as at 75 das, there is a greater proportion of leaves, which decrease as the phenological stage progresses, while the fraction of spikes increases, with a slight decrease in the fraction due to the stems. Colín *et al*. (2007, 2009); Zamora *et al*. (2016); Torres *et al*. (2019) have used the plane generated by the first two principal components to graph and partially characterize the genotypes and when subsequently performing the clusters, they have visualized the complementarity of both multivariate analyses and that they can effectively support the selection of genotypes according to their possible final use.

Thus, in this study, it was detected that at 75 das there are groups of wheats that provide equal or more production than oats, at 90 das this asseveration is maintained and wheats with behavior like that of barley or triticale evaluated were detected, while at 105 das there were groups of wheats that exceeded the production shown by oats *cv* Cuauhtémoc.

Conclusions

The time taken to carry out the samplings caused significant variation in the variables evaluated, higher than that caused by the study environments and probably related to the change in the proportions provided by fractions of forage studied. The forage barley GABYAN95 obtained the highest forage yields in this study. There are groups of forage wheats that may represent an option to replace oats *cv* Cuauhtémoc, offering higher yields of dry forage and could be included in productive schemes, individually the wheats AN-229-09, AN-241-13, AN-268-99, AN-217-09 and AN-263-99 stood out for their dry forage yield superior to that of oats through the test environments. In the genotypes evaluated, a positive association between NDVI, FSH and COB was detected, which lasted through the samplings carried out, which suggests that the use of infrared sensors can be employed in the estimation of dry matter of leaves.

Acknowledgements

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