

Genetic parameters and multi-trait selection of white oats for forage

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ABSTRACT. *Avena sativa* is the sixth most produced cereal in the world. It is widely used for human consumption. Due to the bromatological quality of its forage, it is used for direct grazing, hay and silage. Due to the large number of interesting characteristics of forage white oats, the selection of unique characteristics becomes difficult and expensive for breeders. In this sense, the use of analysis with multiple characteristics can facilitate the process. Therefore, the objective of this work was to estimate genetic parameters of morphological characteristics, productivity, and quality of forages, as well as to define multiple characteristics that assist in the selection of promising white oat genotypes with forage profile through factor analysis. Field trials were carried out during the agricultural year of 2013 in the municipality of Capão do Leão, RS. The experimental design was in randomized blocks, with treatments arranged in four replications. The treatments corresponded to the genotypes CHIARASUL (G1), FAEM006 (G2), BARBARASUL (G3), BRISASUL (G4) CGF03006 (G5), CGF07023-1 (G6), CGF07-74 027-1 (G7), CGF07033 (G8), CGF07033-1 (G9), CGF07041 (G10), CGF0705-7 (G11), CGF07060-2 (G12) and CGF07060-3 (G13). The

characteristics analyzed were: plant height, leaf area, weight of fresh plants, weight of dry plants, number of tillers and levels of nitrogen, crude protein, phosphorus, potassium, calcium, magnesium, copper, zinc, manganese and iron. The data were submitted to the normality test and to various components of variance. Statistical analyses were performed using Selegen®, SAS® and Genes® software. The white oat genotypes expressed high genetic variability and possibility of selection for leaf area, fresh forage mass, dry forage mass, number of tillers and calcium content. Simultaneously the magnesium content with multiple traits + zinc content, dry matter + fresh mass, nitrogen content + calcium content, crude protein + potassium content and number of tillers, showing potential to select genotypes of interest for genetic improvement.

Key words: *Avena sativa*; Generation mean analysis; Effects of genes; Factor analysis

INTRODUCTION

White oats (*Avena sativa* L.) is the sixth most produced cereal in the world (Suttie and Reynolds, 2004), can be used for human consumption (Nava et al., 2010), in management techniques for soil cover, crop rotation and nutrient cycling (Kim et al., 2014), direct pasture, hay and silage (Huuskonen, 2009). Thus, white oats have great potential for feeding meat and dairy herds, to be used in crop rotation, and crop-livestock integration systems, aiming to maximize the sustainability of agricultural systems (David et al., 2010).

Genetic breeding prioritizes the development of white oat genotypes with forage profile that present high forage yield and quality, digestibility and acceptability by the animals (Suttie and Reynolds, 2004). However, traits of importance for forage production are generally controlled by numerous genes with low heritability and strong influence of the growing environment. Considering it, the knowledge about the genetic nature of traits of interest is essential to define which are determinant for forage yield and quality, as well as to verify the influence of growing environments. This information guides breeders to select the best genotypes through one or more traits of interest (Roy et al., 2013). To achieve genetic gains through selection, breeders must understand the nature of the objective trait and quantify the fractions of total variation by estimating variance components and genetic parameters. These estimations will support the selection of genotypes based on predicted genetic value of the trait of interest (Lourenço et al., 2017). Therefore, mixed models enable to maximize genotypes selection through accurate and efficient estimates of variance components and genetic parameters (Resende, 2016). The restricted maximum likelihood (REML) allows to estimate genetic parameters to be used in the prediction of genetic value through the best linear unbiased predictor (BLUP) approach (Ticona-Benavent and Silva Filho, 2015). The combined use of these methodologies allows to rank and select promising genotypes for traits of interest (Borges et al., 2010).

Due to the large number of traits of interest for forage white oats, selecting single traits becomes difficult and expensive for breeders (Rocha et al., 2017). In order to identify which traits should compose a multi-trait, the analysis of factors, widely diffused for the

stratification of environments, adaptability and stability (Nuvunga et al., 2015; Carvalho et al., 2016), may be pioneeringly used to identify multi-traits aimed to select white oat genotypes with forage profile. It would allow to simultaneously select morphological aspects, components of forage yield and bromatological quality. Therefore, the objective of this work was to estimate genetic parameters of morphological traits, forage yield and quality, as well as to define multi-traits that aid the selection of promising white oat genotypes with forage profile through factor analysis.

MATERIAL AND METHODS

Field trials were conducted during 2013 agricultural year in the experimental area of the Plant Genomics and Breeding Center of the Federal University of Pelotas, located in the municipality of Capão do Leão - RS. The geographic coordinates correspond to latitude 31°47'58" S and longitude 52°31'02" W, with altitude of 13.24 m. According to Köppen, the climate is characterized as Cfa subtropical, and the soil as dystrophic yellow red Argisil.

The experimental design was randomized blocks, with treatments arranged in four replications. The treatments corresponded to the genotypes CHIARASUL (G₁), FAEM006 (G₂), BARBARASUL (G₃), BRISASUL (G₄), CGF03006 (G₅), CGF07023-1 (G₆), CGF07-027-1 (G₇), CGF07033 (G₈), CGF07033-1 (G₉), CGF07041 (G₁₀), CGF0705-7 (G₁₁), CGF07060-2 (G₁₂) and CGF07060-3 (G₁₃).

The experimental area was managed under no-tillage system, with base fertilization of 400 kg ha⁻¹ of NPK in the formulation 05-20-20, and 150 kg ha⁻¹ of nitrogen at full tillering stage (stage 21) of the scale of Zadoks et al. (1974). The population density used for all genotypes was 300 plants m⁻². The experimental units were composed by five rows, spaced 0.17 meters (m), with five meters (m) length, totaling 4.25 m² per parcel. The management of weeds and pest insects were carried out according to the crop's demand to minimize biotic effects. The traits were measured at the booting stage (stage 41) (Zadoks et al., 1974), being them: plant height (PH, cm); leaf area (LA, vol mL⁻¹); fresh mass of plant (FM, g plant⁻¹); dry mass of plant (DM, g plant⁻¹); NT: number of tillers (NT, units m⁻¹); nitrogen content (N, g kg⁻¹); crude protein (CP, %); phosphorous content (P, g kg⁻¹); potassium content (K, g kg⁻¹); calcium content (Ca, g kg⁻¹); magnesium content (Mg, g kg⁻¹); copper content (Cu, mg kg⁻¹); zinc content (Zn, mg kg⁻¹); manganese content (Mn, mg kg⁻¹) and iron content (Fe, mg kg⁻¹).

The data were submitted to normality test by Shapiro Wilk (1965), and Deviance analysis at 5% of probability by the chi-square test (X²). The components of variance and genetic parameters for white oat genotypes were estimated using the statistical model $y = Xr + Zg + e$, where: y is the data vector, r are the effects of replicates (fixed) added to the general average; g are the genetic effects (random); e are the effects of residue (random). The variance components were: genetic variance ($\hat{\sigma}^2g$), residual variance ($\hat{\sigma}^2e$), phenotypic variance ($\hat{\sigma}^2p$), broad sense heritability (H^2g), broad sense heritability of genotypes' average (H^2ml), accuracy of selection ($Aclinh$), coefficient of genetic variation ($CVgi$), coefficient of residual variation (CVe) and overall mean of the experiment (OM). After, the factor analysis was applied (Murakami and Cruz, 2004), following the statistical model $X_j = I_j1F1 + I_j2F2 + \dots + I_jmFm + \epsilon_j$, where X_j corresponds to the trait of interest ($j = 1, 2, \dots, v$), I_j represents the factorial load of the j^{th} variable associated to the k^{th} factor, where $k = 1, 2, \dots, m$ (number of common factors); F_k represents the j^{th} factor, and ϵ_j refers to the error associated to a

specific factor (Murakami and Cruz, 2004). Statistical analyzes were performed through the software Selegen[®] (Resende, 2016), SAS[®] (SAS Institute, 2018) and Genes[®] (Cruz, 2016).

RESULTS AND DISCUSSION

Components of variance and genetic parameters

Deviance analysis by the Likelihood Ratio Test (LRT) revealed significance at 5% of probability through the chi-square (χ^2) test for the traits plant height (PH), leaf area (LA), fresh mass of forage (FM), nitrogen content (N), crude protein (CP), phosphorus content (P), potassium content (K), calcium content (Ca), dry mass of forage (DM), number of tillers (Ca), magnesium content (Mg), zinc content (Zn) and manganese content (Mn). On the other hand, the traits copper content (Cu) and iron content (Fe) did not reveal significance (Table 1).

The estimates of genetic variance obtained were high for most of the measured and significant traits. In general, controlling phenotypic variation through the adjustment of experimental techniques allows to increase broad sense heritability and thereby to understand the total genetic variation present in a specific breeding situation. It will increase the probability of identifying genotypes that attend the agronomic ideotype. Plant height (PH) evidenced that 77.5% of the phenotypic manifestation was due to total genetic effects ($\hat{\sigma}_g^2$), which comes from a high broad sense heritability (H^2_g : 0,77) (Table 1). Researchers defined estimates of H^2_g : 0.67 for PH, similar with this study (Roy et al., 2013). The genetic breeding of white oats prioritizes genotypes with determined stature which would allow to minimize unnecessary assimilate expenses in the development of expendable structures (drains), to reduce lodging, and to direct assimilates for the maximum accumulation of biomass in leaves and stems. Intermediate magnitudes of PH, ranging between 48 and 108.5 cm, are prioritized for forage white oats (Gill et al., 2013; Irfan et al., 2016), which covers the general mean of the studied genotypes (OM: 66.51 cm).

Leaf area (LA) evidenced that 89.9% of the phenotypic variance was due to genetic causes, resulting in high broad sense heritability (Table 1). Although this trait is strongly dependent and influenced by intrinsic edaphoclimatic conditions of each growing environment. The high magnitude of genetic variance determines the possibility of obtaining gains with selection and thus incrementing the objective trait.

Fresh mass (FM) and dry mass of forage (DM) represent the forage yield per unit of area, considering that the evaluation of green mass is not accurate and might be influenced by the fraction of liquids present on plant tissues at the moment of evaluation (Table 1). Therefore, estimates and inferences are based on dry mass in order to obtain greater accuracy of selection (Joubert and Myburgh, 2014). The phenotypic variations observed for FM and DM were determined in 92.59 and 91.87%, respectively, by total genetic effects, which is reaffirmed by their respective estimates of broad sense heritability (0.92 and 0.91). These estimates are higher than those observed by Dubey et al. (2014) ($H^2_g = 0.68$) and Roy et al., (2013) ($H^2_g = 0.39$) for dry mass of forage. The number of tillers (NT) presented high genetic variance (94.10%), close to the value obtained by Bibi et al. (2012), who verified broad sense heritability of 0.99%. The increase on the number of tillers is associated to higher forage and grain yield (Deiss et al., 2014).

The evaluation of nitrogen content (N) indirectly allows to estimate the fraction of crude protein (CP) in the forage. CP gathers the true protein fraction and the non-protein nitrogen fraction, as both of which play determinant physiological role on animal organism (Kumar et al., 2017). These traits present 50% and 73% of total genetic effects determining their phenotypic variation, respectively. Roy et al. (2013) found 76.74% of broad sense heritability evaluating crude protein content in white oats forage, therefore, this high magnitude indicates the possibility of achieving genetically superior individuals through phenotypic selection.

The physiological and nutritional performance of forage plants depends on the availability of macro and micronutrients in their forage. The proportion of these elements found in plants varies according to intrinsic characteristics of genotype, phenological stage, growing environment and genotype by environment interaction, therefore, their evaluation is essential (Liu and Mahmood, 2015). The macro minerals phosphorus (P), potassium (K), calcium (Ca) and magnesium (Mg) play important structural and physiological role in the animal organism (Soetan et al., 2010). Thereby, forages with higher accumulation of these nutrients tend to meet animal's demands. The phenotypic variations observed for phosphorus (P) and magnesium (Mg) were determined by 67.5 and 68.0% of total genetic effects. In contrast, potassium (K) and calcium (Ca) revealed 0.74 and 0.81% of genetic contributions on their respective phenotypic variations. These macro minerals presented high estimates of broad sense heritability. Evaluating different varieties of forage white oats, Gill et al. (2013) verified overall means of macro minerals ($P = 0,4 \text{ g kg}^{-1}$; $K = 16,2 \text{ g kg}^{-1}$; $Ca = 2,8 \text{ g kg}^{-1}$; $Mg = 12,0 \text{ g kg}^{-1}$) inferior to those verified by this study, except for Mg ($P = 5,24 \text{ g kg}^{-1}$; $K = 41,95 \text{ g kg}^{-1}$; $Ca = 4,52 \text{ g kg}^{-1}$; $Mg = 2,87 \text{ g kg}^{-1}$) (Table 1).

The microminerals or trace elements analyzed present a diverse range of functions in both animal and plant organisms, however the proportion of microminerals required is lower than macrominerals (Yatoo et al., 2013). Among the microminerals analyzed, the highest percentage of genotypic variance was evidenced by manganese (Mn) content (0.73%), which presented high estimate of broad sense heritability. The content of zinc (Zn) verified in the forage presents 57% of genetic variance, and intermediate estimate of broad sense heritability Iron (Fe) and copper (Cu) presented the lowest percentages of genotypic variance (0.29% and 0.00%, respectively), evidencing low genetic control on these trait's manifestation and high influence of the environment, which hinders the achievement of superior individuals. The overall means observed for these microminerals ($Cu = 1,5 \text{ mg kg}^{-1}$; $Zn = 29,81 \text{ mg kg}^{-1}$; $Mn = 99,72 \text{ mg kg}^{-1}$; $Fe = 124,68 \text{ mg kg}^{-1}$) (Table 1), differed from the values observed by Gill et al. (2013) ($Cu = 5,35 \text{ mg kg}^{-1}$; $Zn = 19,5 \text{ mg kg}^{-1}$; $Mn = 66,9 \text{ mg kg}^{-1}$; $Fe = 288,8 \text{ mg kg}^{-1}$).

The reliability of results and precision of procedures used to estimate the genetic parameters may be verified through the selective accuracy (Aclinh). This parameter is associated with the precision of selection and refers to the ratio between predicted genetic value and the true genetic magnitude (Pimentel et al., 2014). Aclinh magnitudes vary from 0 to 1 and are classified as very high ($Aclinh \geq 0,90$), high ($0,70 \leq Aclinh < 0,90$), moderate ($0,50 \leq Aclinh < 0,70$) and low ($Aclinh < 0,50$) (Resende and Duarte, 2007). Aclinh estimates above 0.70 are sufficient to accurately infer the genetic value of genotypes (Resende, 2002). Considering the verified aclin values, only Cu content did not meet this requirement (Aclin: 0.10).

The coefficient of genetic variation (CV_{gi}) is a parameter commonly used to compare the genetic variability present in a trait of study (Resende, 2002). The CV_{gi} varied from low to high in the set of evaluated traits, being the lowest value presented by Cu (1.31%), which demonstrates its low genetic variability in relation to the average of genotypes studied. In contrast, high values of CV_{gi} were observed for the traits NT (CV_{gi} : 25.24), FM (CV_{gi} : 24.25), DM (CV_{gi} : 23.76) e LA (CV_{gi} : 22.01), which demonstrates their high genetic variability and enables the breeder to select superior individuals. The coefficients of residual variation (CV_e) were classified from low to medium for majority of the evaluated traits, with only Fe and Cu presenting intermediate to high CV_e (17.86 and 21.42, respectively) (Table 1). It demonstrates accuracy and expresses the reliability of the data. A relation between CV_{gi} and CV_e of 1 or more reflects favorable situation to achieve gains with selection (Vencovsky, 1978). This situation was verified for most of the studied traits, except Cu and Fe, which indicates the possibility of achieving gains with selection (Table 1).

Table 1. Estimates of variance components and genetic parameters for plant height (PH), leaf area (LA), dry mass of forage (DM), fresh mass of forage (FM), number of tillers (NT), nitrogen content (N), crude protein (CP), phosphorus content (P), potassium content (K), calcium content (Ca), magnesium content (Mg), copper content (Cu), zinc content (Zn), manganese content (Mn) and iron content (Fe) measured in white oat genotypes.

Components of variance ^a	PH ⁺⁺	LA	DM	FM	NT	N	CP	P
Deviance ⁺⁺	109.50	245.88	111.15	219.08	131.55	83.84	7.37	16.01
LRT	12.71**	29.98**	29.05**	31.34**	36.42**	8.36**	21.34**	16.85**
$\hat{\sigma}_g^2$	22.04	6066.79	47.13	2716.93	122.06	1.92	0.48	0.50
$\hat{\sigma}_e^2$	6.39	674.51	4.16	217.16	7.64	1.91	0.17	0.23
$\hat{\sigma}_p^2$	28.43	6741.30	51.30	2934.09	129.70	3.84	0.65	0.74
\hat{H}_g^2	0.77	0.89	0.91	0.92	0.94	0.50	0.73	0.67
H_{ml}^2	0.91	0.96	0.97	0.97	0.97	0.75	0.89	0.86
Ac_{linh}	0.95	0.98	0.98	0.98	0.98	0.86	0.94	0.92
CV _{gi} %	7.05	22.01	23.76	24.25	25.24	4.40	14.16	13.49
CV _e %	3.80	7.33	7.06	6.85	6.31	4.39	8.42	9.32
Overall mean	66.51 cm	353.85 vol mL ⁻¹	28.88 g plant ⁻¹	214.87 g plant ⁻¹	43.75 units m ⁻¹	31.54 g kg ⁻¹	4.92 %	5.24 g kg ⁻¹
Components of variance	K	Ca	Mg	Cu	Zn	Mn	Fe	
Deviance	78.2	24.44	47.7	37.91	118.89	241.11	269.46	
LRT	21.80**	20.29**	20.83**	0.00 ^{ns}	10.85**	18.08**	2.83 ^{ns}	
$\hat{\sigma}_g^2$	3.80	0.27	0.09	0.00	6.84	377.65	208.79	
$\hat{\sigma}_e^2$	1.26	0.06	0.04	0.10	5.13	136.57	496.29	
$\hat{\sigma}_p^2$	5.06	0.33	0.13	0.10	11.98	514.23	705.09	
H_g^2	0.74	0.81	0.68	0.00	0.57	0.73	0.29	
H_{ml}^2	0.89	0.92	0.86	0.01	0.79	0.89	0.55	
Ac_{linh}	0.94	0.96	0.93	0.10	0.89	0.94	0.74	
CV _{gi} %	4.64	11.49	10.59	1.31	8.77	19.48	11.58	
CV _e %	2.68	5.52	7.21	21.42	7.60	11.71	17.86	
Overall mean	41.95 g kg ⁻¹	4.52 g kg ⁻¹	2.87 g kg ⁻¹	1.50 mg kg ⁻¹	29.81 mg kg ⁻¹	99.72 mg kg ⁻¹	124.68 mg kg ⁻¹	

^a $\hat{\sigma}_g^2$: Genotypic variance; $\hat{\sigma}_e^2$: residual variance (environmental); $\hat{\sigma}_p^2$: phenotypic variance; \hat{H}_g^2 : Broad sense heritability of the genotype; \hat{H}_{ml}^2 : heritability of the lineage average; Ac_{linh} : Selective accuracy; CV_{gi} %: Coefficient of genetic variation; Ve %: Coefficient of residual variation; overall mean; ⁺⁺Deviance at 5% of probability by the chi-square test; LRT: Likelihood ratio test.

Best Linear Unbiased Predictor (BLUP)

The estimates of variance components and genetic parameters allowed to apply the BLUP methodology, and then estimate the percentage of gain with selection, the new mean and the predicted genetic value of each genotype (Resende, 2016). For the trait plant height

(PH) (Table 2), it is possible to obtain increment of 18% by selecting the genotype CGF03006. However, studies have defined that plant height is the main contributor to lodging, and consequently, yield reduction (Berry and Berry, 2015). Thus, genetic breeding of white oats for forage purposes preconizes the reduction of stem length and increment of leaves per plant (Tumino et al., 2017). In this context, the genotypes CGF07-027-1, BARBARASUL, CHIARASUL and CGF07023-1 presented the lowest predicted genetic values, and their selection does not result in plant height increment.

The selection of white oat genotypes with short stature due to a reduced length of internodes contributes to increase the leaf/stem ratio in the forage. The increment of leaf content in relation to stalk content is of great interest for forage breeders because of the higher nutritional quality and digestibility of foliar tissues (Tremblay et al., 2001). Also, the increase in leaf area results in larger photosynthetically active area, which elevates the plant's capacity to produce photoassimilates and consequently, dry matter of high quality per unit of area (Saleem et al., 2015). The highest gains with selection for leaf area (Table 2) were evidenced through the genotypes BRISASUL (14.30%), CGF07-027-1 (13.76%) and CGF0705-7 (11.20%). The selection of superior genotypes for this trait is fundamental to elevate leaf/stem ratio and forage yield. This situation is expressed by the genotypes BRISASUL and CGF07-027-1, which presented the highest predicted means (437.46 vol mL⁻¹ e 434,31 vol mL⁻¹, respectively). However, these same genotypes did not present similar estimates for fresh mass (FM) and dry mass (DM). These results limit their use for forage production, since the priority is to select genotypes with the greatest capacity for green and dry mass production. Considering it, the genotype CGF07033-1 evidenced the greatest predicted mean for FM (273.55 g plant⁻¹) and DM (41.19 g plant⁻¹), demonstrating potential for high forage yield.

The number of tillers (NT) (Table 2) presented dynamics similar to leaf area (LA). Thus, the highest predicted means were verified through the genotypes CGF07-027-1 and BRISASUL. However, the high number of tillers expected for their new means is followed by low estimate of green and dry mass production. This fact can be explained by the short stature of these genotypes, which result of a shorter stem length. The proportion of stem contributes largely to the mass produced per area, so a higher leaf/stem ratio may decrease the yield of fresh and dry mass. Therefore, the challenge of breeding programs of white oats with forage profile, from the morphological point of view, is to develop genotypes that present plant height, tillering and leaf area in balanced and efficient magnitudes, contributing to a higher bromatological quality, digestibility and forage yields. The white oat genotype that most approached this condition was CGF0705-7, which presented low predicted mean for PH (68.40 cm), and high estimates for NT (51.31 units m⁻¹), LA (419.31 vol mL⁻¹), FM (259.05 g plant⁻¹) and DM (38.14 g plant⁻¹).

Regarding crude protein content (CP), the genotypes with the highest gains (Table 3) were BARBARASUL (17.88%), BRISASUL (14.92%) and CGF07023-1 (13.80%). However, these genotypes were not ranked in the first positions for most of the macro and micronutrients measured. It results in a great difficulty to gather, in a same genotype, high protein contents and accumulation of essential nutrients. The genotype CGF0705-7 presented superiority of predicted genetic value for magnesium

(Mg), nitrogen (N) and calcium (Ca) content, thus, the selection of this genotype can simultaneously potentiate the accumulation of these nutrients in the forage. The genotype CGF07-027-1 showed superiority for accumulation of phosphorus (P) and potassium (K). The genotype FAEM006 presented superior accumulation of manganese (Mn), while the genotype CGF30006 for zinc content (Zn) (Table 3).

The results obtained through the BLUP revealed certain difficulty in selecting genotypes that simultaneously present suitable magnitudes of desirable morphological traits, high forage yield and bromatological quality. Therefore, it becomes necessary to apply a multivariate strategy to define which characters may be selected together, and also, to define which genotypes are intrinsic to these multi-traits.

Table 2. Ranking of white oats genotypes through best linear unbiased predictor (BLUP), gain with selection (%) and new predicted means for the traits plant height (PH); leaf area (LA); number of tillers (NT); fresh mass (FM); dry mass (DM) and crude protein (CP).

PH			LA			NT		
Lineage	Gain (%)	New mean (cm)	Lineage	Gain (%)	New mean (vol mL ³)	Lineage	Gain (%)	New mean (units m ³)
CGF03006	18.64	75.12	BRISA SUL	14.30	437.46	CGF07-027-1	13.08	54.93
CGF07041	14.78	73.34	CGF07-027-1	13.76	434.31	BRISA SUL	11.90	53.93
CGF07033-1	13.12	72.58	CGF0705-7	11.20	419.31	CGF07023-1	11.35	53.45
CGF07060-3	12.22	72.16	FAEM 006	9.75	410.86	CGF07033-1	10.51	52.73
CGF07033	10.26	71.25	CGF07060-3	8.80	405.29	CGF07041	9.62	51.98
FAEM 006	8.71	70.54	CGF03006	8.14	401.44	CGF0705-7	8.84	51.31
CGF07060-2	7.11	69.80	CGF07033-1	7.52	397.79	CGF07033	8.18	50.74
BRISA SUL	5.45	69.03	CGF07033	6.96	394.56	CGF07060-3	7.25	49.95
CGF0705-7	4.08	68.40	CGF07041	6.44	391.52	FAEM 006	6.44	49.26
CGF07-027-1	2.87	67.84	CGF07060-2	5.61	386.65	CGF07060-2	5.64	48.58
BARBARA SUL	1.84	67.37	CGF07023-1	4.91	382.58	CGF03006	4.79	47.85
CHIARA SUL	0.93	66.94	CHIARA SUL	2.60	369.08	BARBARA SUL	2.40	45.80
CGF07023-1	0	66.51	BARBARA SUL	0.00	353.86	CHIARA SUL	0.00	43.76
TOTAL	100.00		TOTAL	100.00		TOTAL	100.00	
FM			DM			CP		
Lineage	Gain (%)	New mean (g plant ⁻¹)	Lineage	Gain (%)	New mean (g plant ⁻¹)	Lineage	Gain (%)	New mean (%)
CGF07033-1	14.98	273.55	CGF07033-1	20.46	41.19	BARBARA SUL	17.88	6.16
CGF03006	13.25	266.79	CGF0705-7	15.39	38.14	BRISA SUL	14.92	5.96
CGF0705-7	11.28	259.05	CGF07041	11.51	35.81	CGF07023-1	13.80	5.88
CGF07023-1	9.95	253.87	CGF03006	9.44	34.57	CHIARA SUL	11.50	5.72
CGF07060-3	8.88	249.66	CGF07060-2	8.20	33.81	CGF0705-7	9.83	5.61
CGF07033	8.11	246.65	CGF07060-3	7.23	33.23	FAEM 006	8.50	5.51
CGF07060-2	7.42	243.96	CGF07033	6.49	32.79	CGF07033-1	6.88	5.40
CGF07041	6.82	241.59	BRISA SUL	5.81	32.38	CGF07041	5.66	5.32
BRISA SUL	6.22	239.25	CGF07023-1	5.19	32.01	CGF03006	4.57	5.24
CGF07-027-1	5.68	237.13	CGF07-027-1	4.58	31.64	CGF07033	3.36	5.16
FAEM 006	5.05	234.65	FAEM 006	3.91	31.24	CGF07060-3	2.12	5.07
CHIARA SUL	2.35	224.06	BARBARA SUL	1.80	29.97	CGF07-027-1	0.97	4.99
BARBARA SUL	0.00	214.88	CHIARA SUL	0.00	28.89	CGF07060-2	0	4.93
TOTAL	100.00		TOTAL	100.00		TOTAL	100.00	

Table 3. Ranking of white oats genotypes through best linear unbiased predictor (BLUP), gain with selection (%) and new predicted means for the traits phosphorus content (P); potassium content (K); calcium content (Ca); magnesium content (Mg); manganese content (Mn) and zinc content (Zn).

P			K			Ca		
Lineage	Gain (%)	New mean (g Kg ⁻¹)	Lineage	Gain (%)	New mean (g Kg ⁻¹)	Lineage	Gain (%)	New mean (g Kg ⁻¹)
CGF07-027-1	18.60	6.51	CGF07-027-1	13.22	44.07	CGF07060-3	16.90	5.39
CGF03006	14.73	6.25	CGF03006	12.77	44.00	CGF0705-7	15.60	5.33
CGF07041	12.55	6.10	CGF07041	12.41	43.94	CGF07060-2	13.41	5.21
CGF0705-7	10.77	5.98	CGF07023-1	11.28	43.76	CGF07041	11.91	5.14
CGF07023-1	9.62	5.90	CGF07060-2	10.10	43.57	CGF07033	10.02	5.04
CGF07033	8.47	5.82	CGF07060-3	9.03	43.40	CGF07033	8.09	4.94
BRISA SUL	7.26	5.74	CGF07033	7.95	43.22	BRISA SUL	6.63	4.87
CGF07060-2	5.94	5.65	CGF0705-7	6.71	43.03	FAEM 006	5.46	4.81
CGF07033-1	4.91	5.58	BRISA SUL	5.65	42.86	BARBARA SUL	4.49	4.76
CGF07060-3	3.59	5.49	CGF07033-1	4.73	42.71	CGF07-027-1	3.71	4.72
FAEM 006	2.42	5.41	FAEM 006	3.88	42.57	CGF03006	2.43	4.65
BARBARA SUL	1.16	5.32	BARBARA SUL	2.26	42.31	CGF07033-1	1.35	4.60
CHIARA SUL	0.00	5.25	CHIARA SUL	0.00	41.95	CGF07023-1	0.00	4.53
100.00			100.00					
Mg			Mn			Zn		
Lineage	Gain (%)	New mean (g Kg ⁻¹)	Lineage	Gain (%)	New mean (mg Kg ⁻¹)	Lineage	Gain (%)	New mean (mg Kg ⁻¹)
CGF0705-7	18.03	3.41	FAEM 006	18.03	134.13	CGF30006	15.37	33.39
CGF07041	15.94	3.35	CGF07023-1	16.19	130.60	BRISA SUL	14.07	33.08
CGF07033	12.96	3.26	CGF07-027-1	12.84	124.23	CGF07041	12.82	32.79
BRISA SUL	11.19	3.21	BARBARA SUL	11.17	121.04	CGF07033	11.81	32.56
CGF07-027-1	9.99	3.17	CGF07060-2	9.58	118.01	CGF07023-1	10.99	32.37
CGF03006	8.71	3.13	CHIARA SUL	8.44	115.82	CGF0705-7	9.37	31.99
CGF07060-2	7.01	3.08	CGF07041	7.39	113.82	CGF07-027-1	7.47	31.55
CGF07060-3	5.51	3.04	CGF07060-3	5.97	111.12	BARBARA SUL	5.98	31.20
FAEM 006	4.30	3.00	BRISA SUL	4.37	108.05	FAEM 006	4.81	30.93
CGF07023-1	3.19	2.97	CGF03006	3.05	105.54	CGF07060-3	3.68	30.67
BARBARA SUL	2.06	2.94	CGF07033-1	1.96	103.46	CGF07060-2	2.42	30.37
CGF07033-1	1.10	2.91	CGF07033	1.02	101.67	CGF07033-1	1.22	30.09
CHIARA SUL	0.00	2.88	CGF0705-7	0.00	99.73	CHIARA SUL	0.00	29.81
TOTAL 100.00			TOTAL 100.00					

Multi-trait selection through factor analysis

To attend this assumption, five final factors were considered (Table 4), which gathered an estimate of 85.42% of the total variation verified in the measured traits. Only traits that presented factorial loads equal to or greater than 0.7 were considered for definition of multi-traits due to the presence of correlation between them (Johnson and Wichern, 1992). Considering the factor I, factorial loads greater than 0.70 allowed to group the traits magnesium content (0.806) and Zinc (0.880), which formed the multi-trait I. Factor 2 reunited the traits dry mass (0.893) and fresh mass (0.835), forming the multi-trait II. Regarding the factor 3, it was possible to verify the affinity between nitrogen (0.832) and calcium (0.908) contents, which were considered as multi-trait III. Factor 4 enabled to group crude protein percentage (0.825) and potassium content (-0.792) which represented the multi-trait IV. In contrast, factor 5 did not allow associations between traits, so the number of tillers per linear meter (0.892) represented the multi-trait V. This condition was met by all analyzed traits (Table 4).

Table 4. Factor analysis for the morphological and bromatological traits of 13 white oat genotypes.

$\lambda^{(1)}$	Trait	Factorial loads after rotation					$\phi^{(2)}$
		Factor 1	Factor 2	Factor 3	Factor 4	Factor 5	
5.081	PH	0.157	0.679	0.058	-0.501	-0.242	0.801
2.787	NT	0.269	0.179	-0.465	0.932	0.892	0.911
1.621	DM	0.002	0.893	0.133	-0.036	0.264	0.886
1.399	FM	-0.250	0.835	-0.550	-0.266	0.381	0.917
1.070	LA	0.383	0.167	0.230	-0.047	0.648	0.651
0.721	CP	0.865	-0.213	-0.391	0.825	-0.091	0.895
0.515	N	-0.170	0.214	0.832	0.113	0.078	0.773
0.341	Ca	0.147	0.002	0.908	-0.096	0.170	0.885
0.231	Fe	0.177	-0.096	-0.292	-0.444	0.678	0.753
0.155	P	0.600	0.121	-0.181	-0.523	0.458	0.892
0.062	Mg	0.806	0.165	0.460	-0.126	0.230	0.959
0.006	Mn	-0.365	-0.744	-0.272	-0.120	0.170	0.804
-0.001	K	0.392	0.078	-0.107	-0.792	0.389	0.951
-0.000	Zn	0.880	0.063	-0.214	-0.050	0.217	0.873

⁽¹⁾Eigenvalues; ⁽²⁾commonalities. *Plant height (PH), number of tillers (NT), dry mass of forage (DM), fresh mass of forage (FM), leaf area (LA), crude protein (CP), nitrogen content (N), calcium content (Ca), iron content (Fe), phosphorus content (P), magnesium content (Mg), manganese content (Mn), potassium content (K) and zinc content (Zn).

In this way, five multi-traits were established for selection: multi-trait I (MG + Zn), multi-trait II (DM + FM), multi-trait III (N + Ca), multi-trait IV (CP + K) and multi-trait V (NT). The multi-traits were expressed graphically in order to select the genotypes, where quadrant I expresses the possibility of selecting genotypes for both multi-traits, the quadrants II and IV correspond to the selection for a specific multi-trait, while quadrant III reunites the genotypes that are not suitable for multi-trait selection.

Graph A (Figure 1) evidences that genotypes BRISASUL, CGF03006, CGF07033, CGF07033-1, CGF07041, CGF0705-7, CGF07060-2 and CGF07060-3 may be selected for the multi-traits FM + DM and MG + Zn, simultaneously. However, the genotypes CHIARASUL, FAEM006, BARBARASUL, CGF07023-1 and CGF07-027-1 may be selected exclusively through the multi-trait MG + Zn. In graph B (Figure 1), the genotypes BRISASUL, CGF03006, CGF07033, CGF07033-1, CGF07041, CGF0705-7, CGF07060-2 and CGF07060-3 may be considered for simultaneous selection through N + Ca and FM + DM. On the other hand, CHIARASUL, FAEM006, BARBARASUL, CGF07023-1 and CGF07-027-1 should be selected exclusively to increase the multi-trait N + Ca. Graph C (Figure 1) shows that all genotypes may be selected when the objective is to increase the multi-trait N+Ca. Graph D (Figure 1) evidenced that all genotypes have potential for increasing the NT multi-trait.

From the results verified in this study, the largest estimates of genetic variance were observed for number of tillers per linear meter, green and dry mass of forage, and leaf area, which demonstrates great influence of genetic effects on their phenotypic variation. Also, selection performed through the (BLUP) pointed the genotype CGF0705-7 as promising for morphological aspects, however it does not present the best magnitudes of traits regarding bromatological quality. The BLUP methodology demonstrated great efficiency in the selection of genotypes for specific and univariate traits, however, multivariate selection is expressed as a viable alternative in the identification of which genotypes should be selected. Furthermore, the analysis of factors allowed to define five multi-traits (MG+Zn, DM+FM, N+Ca, CP+K and NT) that could be used for multivariate selection. The highest efficiency of selection was obtained through the multi-trait N+Ca, which allowed to select the largest number of genotypes. The combined use of these methods allows to increase the efficiency

of univariate and multivariate selection, with potential to be used in the genetic breeding of white oats with forage purpose.

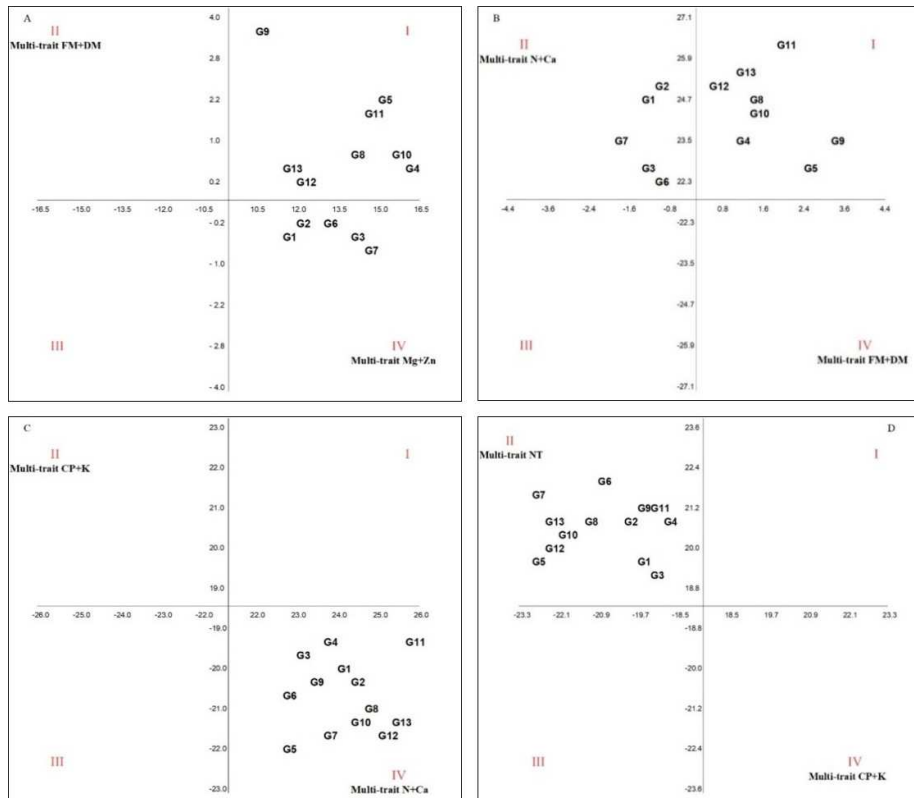


Figure 1. Graphic distribution of white oat genotypes (G1: CHIARASUL; G2: FAEM006; G3: BARBARASUL; G4: BRISASUL; G5: CGF03006; G6: CGF07023-1; G7: CGF07-027-1; G8: CGF07033; G9: CGF07033-1; G10: CGF07041; G11 CGF0705-7; G12: CGF07060-2; G13: CGF07060-3) according to the multi-trait scores defined through factor analysis.

CONCLUSIONS

The white oat genotypes expressed high genetic variability and possibility of selection for leaf area, fresh forage mass, dry forage mass, number of tillers and calcium content. Simultaneously the magnesium content with multiple traits + zinc content, dry matter + fresh mass, nitrogen content + calcium content, crude protein + potassium content and number of tillers showed potential for selection of genotypes for genetic improvement.

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

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