

Estimates of genetic parameters between and within black oat populations

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ABSTRACT: The aims of this study were to characterize black oat populations by estimating between- and within-populations variance components and genetic parameters, as well as to distinguish the populations using multivariable statistics. The experiment was carried out in randomized blocks design with three repetitions, with 14 black oat populations collected in several municipalities of Rio Grande do Sul state. Agronomic important traits were assessed at physiological maturation stage. Variance components and genetic parameters were estimated considering within-block information. In addition, Mahalanobis distance, relative contribution of traits, and canonical variables were used to distinguish the populations. Selection based on panicle length, number of grains per panicle, panicle weight and panicle grain weight may result in higher selection gains. Panicle grain weight

presents a greater contribution to genetic divergence between studied populations. The formation of distinct groups indicated the presence of genetic variability among black oat populations in the northwestern of the Rio Grande do Sul state. Directed crosses between individual plants of populations from (i) Alto Alegre and Salvador das Missões, Chapada, or Santa Rosa or (ii) between plants of populations from Salvador das Missões and Campos Borges or Santa Rosa can generate segregating populations with great genetic variability. The predominance of between-phenotypic variance and a within-genetic variance indicate prospects for success in selection gain and possible selection of a new cultivar with fewer efforts compared to a cross-based method. This is supported by the high values of within-population heritability.

Key words: *Avena strigosa*, genetic divergence, genotypic variance.

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INTRODUCTION

Oat, the second most important winter crop in Brazil, has shown a significant increase in cultivation area, 14% from 2016 to 2017, and a large part of area is destined for soil cover. The Rio Grande do Sul state is responsible for more than 70% of oats' cultivation area in Brazil, followed by Paraná and Mato Grosso do Sul, totaling 340.9 thousand ha^{-1} (CONAB 2017).

Recently, oat breeding programs have aimed for cultivars with high productive potential and quality of grains; program success depends on the breeder's ability and agility to identify genotypes that meet the desired traits. Hawerth et al. (2014) emphasize that for traits such as grain yield, selection is difficult due a quantitative inheritance, controlled by several genes with low heritability.

Quantitative genetics is important for genetic breeding. Identification, accumulation and perpetuation of favorable genes for quantitative traits may be facilitated if the selection is based on variance components and genetic parameters. In this way, genetic parameters allow to identify the action nature of involved genes, as well as evaluating the efficiency of different selection methods and strategies, whether from endogamy, cross-breeding or selection (Cruz et al. 2014).

Phenotypic traits study makes it possible to estimate genetic parameters from genotypic components, while the magnitude of parameter estimates define the genetic properties of the population (Falconer 1989). Thus, in possession of these data, the breeder has more information for decision-making, increasing selection efficiency.

For quantitative traits, the following well-known model is used: $F = G + E$, where the phenotype (F) is the result of genotype (G) effect under influence of the environment (E) (Falconer 1989; Cruz et al. 2014). Phenotypic variance (σ_F^2) is composed by genotypic (σ_G^2) and environmental variance (σ_E^2) (Ramalho et al. 2012), the environmental variance being all non-genetic. In other words, it is not inheritable, thus, the use of appropriate experimental design is imperative (Falconer 1989; Ramalho et al. 2012). Therefore, genetic variance allows understanding of the genetic structure involved in the progenies, determined by additive and non-additive effects (Baldissera et al. 2014).

Estimating heritability is also important. Heritability in the broad sense expresses genetic variance as a proportion of genetic variance in relation to total variation (phenotypic

variation). This expresses phenotypic value confidence as a guide to genetic value. Although the phenotypic factor is directly measured, the genetic value determines its influence in subsequent generations (Falconer 1989). Heritability can be influenced by several factors, such as trait type (qualitative or quantitative), estimation method, population variability, endogamy level of population, sample size, number and type of environments considered, and experimental precision (Borém and Miranda 2013).

In order to predict selected progenies' behavior, selection gain is estimated (Souza and Sorrels 1991). Thus, a breeding program may advance in time, and increase the chances of success in identifying superior genotypes with potential to compose pure lines better than the parents (Rasmusson and Phillips 1997). In the cited literature, there are few studies about variance components and genetic parameters for black oat. Thus, the aims of this study were to characterize black oat populations by estimating between- and within-populations variance components and genetic parameters, as well as to distinguish the populations using multivariable statistics.

MATERIAL AND METHODS

The study was carried out in Frederico Westphalen, state of Rio Grande do Sul, Brazil, located at coordinates 27°39' S and 53°42' W, 461.3 m above sea level. Fourteen black oat populations were grown in the agricultural year of 2014. Populations were obtained by collecting samples of black oat grown in farms of several cities of Rio Grande do Sul state (Fig. 1) for many years. The experiment was conducted in a randomized complete block design with three repetitions. The experimental units were composed of a 6 m^2 plot, with row spacing of 0.17 m and with a plant density of 300 plants $\cdot \text{m}^{-2}$. Sowing was carried out on June 17, 2014. Nutritional management was according to the soil analysis, and the phytosanitary management carried out preventively.

When populations reached physiological maturity, 10 plants per plot were harvested and the following phenotypic traits were measured: plant height (PH, in cm), number of tillers (NT), panicle length (PL, in cm), panicle weight (PW, in grams), panicle grain weight (PGW, in grams), number of grains per panicle (NGP).

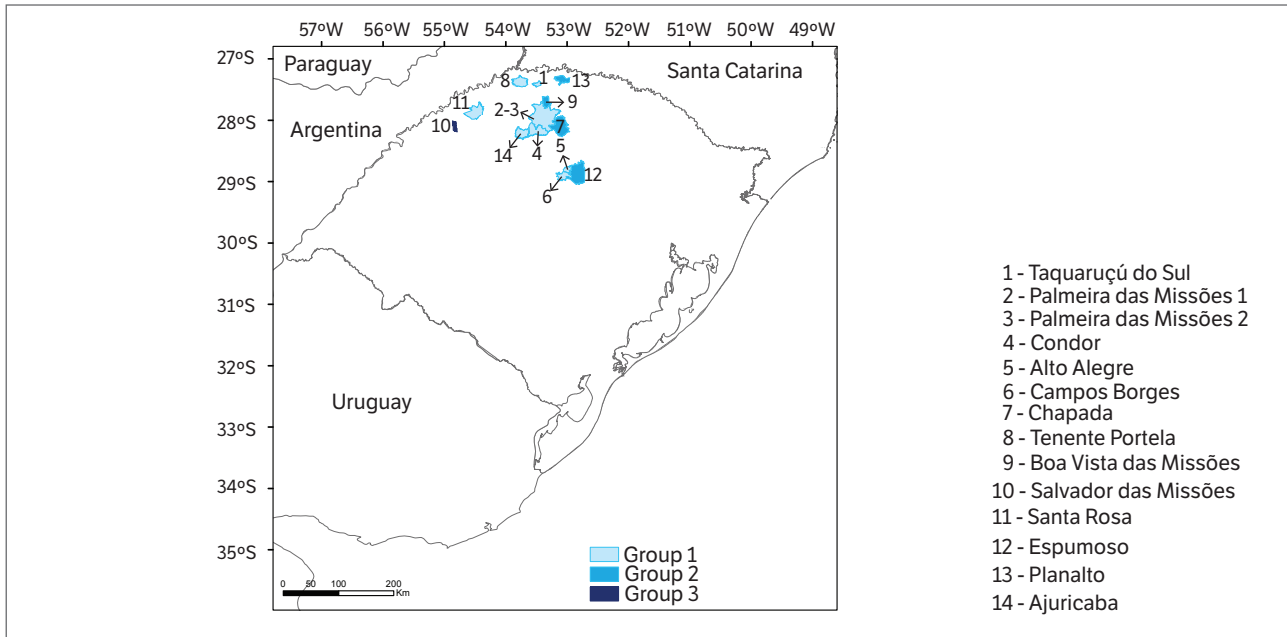


Figure 1. Collection sites map of the 14 black oats populations in Rio Grande do Sul state.

From the experimental design used, analysis of variance carried out at 5% significance level of F test were performed, using the statistical model below, considering balanced data (Eq. 1).

$$Y_{ijk} = \mu + g_i + b_j + \varepsilon_{ij} + \delta_{ijk} \quad (1)$$

where: Y_{ijk} is the observation of the k th plant of the i th population in the j th block; μ is the grand mean; g_i is the effect of the i th population; b_j is the effect of the j th block, ε_{ij} is the plot effect; and δ_{ijk} is individual effect of k th plant, of the i th population in the j th block. Except for the grand mean, all the effects were treated as random.

Mean squares of variance analysis were deployed and mathematical expect were obtained using within-plot information (Cruz et al. 2014). The following variance components were estimated: phenotypic variance between (σ_{fe}^2) and within (σ_{fd}^2) populations, genotypic variance between (σ_{ge}^2) and within (σ_{gd}^2) populations. In addition, the estimated genetic parameters were: heritability between (h_p^2) and within (h_d^2) population, and expected selection gain (Gs).

Assuming treatments effects as random, the accuracy was estimated. This parameter refers to correlation between true genotypic value and estimated or predicted value (Resende 2002), given by (Eq. 2):

$$\hat{r}_{gg} = \left[\frac{1}{1 + (\frac{\sigma_d^2}{\sigma_e^2}) / \sigma_e^2} \right]^{1/2} \quad (2)$$

In order to show the values of assessed traits we used boxplot diagram. Five statistics were shown in these plots. The solid line within hinges corresponds to the median. The lower and upper hinges correspond to the first and third quartiles (the 25th and 75th percentiles). The upper whisker extends from the hinge to the largest value no further than $1.5 \times \text{IQR}$ from the hinge (where IQR is the inter-quartile range). The lower whisker extends from the hinge to the smallest value at most $1.5 \times \text{IQR}$ of the hinge. The diagrams were built using the ggplot2 package in R 3.4.2 software (Wickham 2016).

To study genetic diversity of populations, Mahalanobis' generalized distance matrix was estimated. From genetic distance matrix, clustering analysis was done using the UPGMA (Unweighted Pair Group Method with Arithmetic Averages), and it was represented on a dendrogram. The cut level in the dendrogram, which separates populations into distinct groups, was determined by the Mojena's method (1977) (Eq. 3):

$$r = \bar{x} + kSD \quad (1)$$

where: \bar{x} is the mean of distances; SD is the standard deviation of distances; and k is a constant, considered here as $k = 1.25$ (Milligan and Cooper 1985). The adjustment was measured by means of the cophenetic correlation coefficient.

The analysis of relative contribution of each trait was estimated according to Singh (1981). In view of the contribution

of each trait, only traits with a relative contribution greater than 10% were used to perform canonical variables analysis, thus reducing dimensionality of data and obtaining a linear correlation of the same. All statistical analyses were performed using Genes (Cruz 2016).

RESULTS AND DISCUSSION

The variance analysis (Table 1) showed there was no significant difference for the population. The data presented accuracy of low (PL), moderate (NGP, PW, PGW) and high magnitudes (PH, NT).

In relation to variance components, the phenotypic variance (which includes both genetic and environmental variation) had higher values between populations than within populations for all studied traits (Table 2). This was due to the high contribution of environmental variation to the phenotypic variance. This can be seen in Table 2, where genetic variance between populations is smaller than genetic variance within populations.

Genotypic variances within populations were higher than estimated variance between populations for all studied traits. The great variation observed within populations can be explained by the absence of artificial selection, during several years the collected samples had been cultivated by farmers, suffering exclusively natural selection. The genetic variance observed within populations can serve as a source for superior population selection (Table 2).

Regarding the heritability estimates, we observed that between-population estimates were smaller than within-populations estimates for all analyzed traits (Table 2). Thus, it is assumed that selection within population results in greater gains when compared to the selection of population. PL had the highest value regarding heritability within population, followed by PW, NGP and PGW, all over 80%. NT and PH had values of 40% and 67%, respectively.

These results indicate that due to the greater genetic variation proportion, it is possible to obtain success with indirect selection through high-heritability secondary traits correlated with the main interest trait (Fehr 1987).

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Table 1. Summary of variance analysis – degrees of freedom (DF) and mean square (MS) for source of variation –, mean (\bar{x}) and accuracy (f_{gg}) for 14 black oat populations.

Source of variation	DF	MS					
		PH	NT	PL	NGP	PW	PGW
Block	2	199.44	59.77	15.15	1270.90	0.27	0.23
Population	13	578.62 ^{ns}	39.07 ^{ns}	14.08 ^{ns}	1096.60 ^{ns}	0.28 ^{ns}	0.27 ^{ns}
Between populations	26	576.27	38.62	12.87	726.92	0.23	0.18
Within populations	378	136.04	5.60	8.18	281.58	0.11	0.07
Total	419						
\bar{x}		125.10	4.81	24.16	46.54	0.76	0.51
\hat{f}_{gg}		0.70	0.80	0.39	0.57	0.52	0.57

PH = plant height (cm), NT = number of tillering, PL = panicle length (cm), NGP = number of grains per panicle, PW = panicle weight (grams), PGW = panicle grain weight (grams). ns Non significant values by F test ($p < 0.05$).

Table 2. Estimates of phenotypic variance between ($\hat{\sigma}_{pe}^2$) and within ($\hat{\sigma}_{pd}^2$), genetic variance between ($\hat{\sigma}_{ge}^2$) and within ($\hat{\sigma}_{gd}^2$), heritability between (h_e^2) and within (h_d^2), genetic gain (Gs) for plant height (PH), number of tillering (NT), panicle length (PL), panicle weight (PW), panicle grain weight (PGW), and number of grains per panicle (NGP) for 14 black oat populations.

Estimates	PH	NT	PL	NGP	PW	PGW
$\hat{\sigma}_{pe}^2$	180.24	8.95	8.71	340.55	0.12	0.08
$\hat{\sigma}_{pd}^2$	136.04	5.60	8.18	281.58	0.11	0.07
$\hat{\sigma}_{ge}^2$	0.07	0.01	0.04	12.74	0.01	0.01
$\hat{\sigma}_{gd}^2$	91.90	2.26	7.70	235.34	0.01	0.06
h_e^2 (%)	0.04	0.14	0.47	3.74	1.20	3.91
h_d^2 (%)	67.56	40.43	94.08	83.58	87.94	83.56
Gs (%)	0.51	1.09	20.36	45.24	25.28	46.34

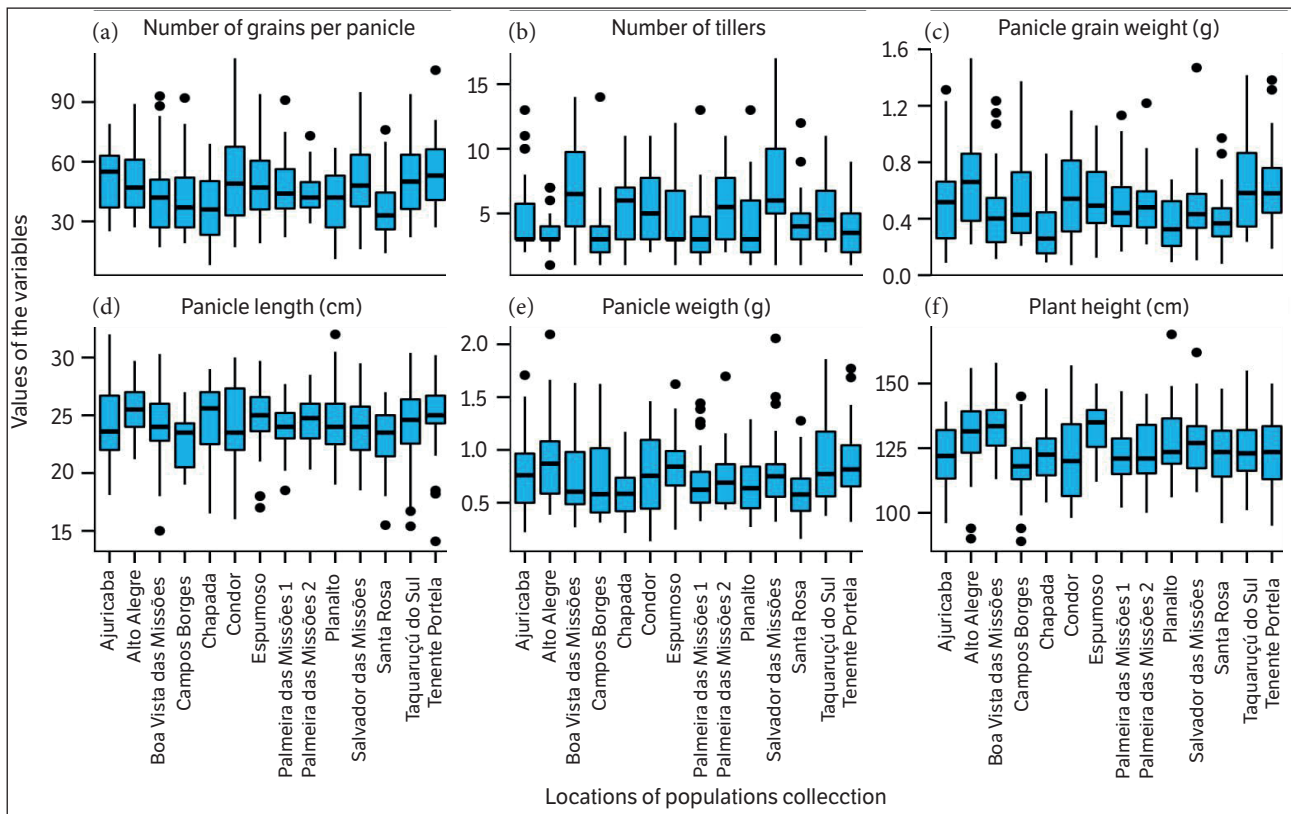


Figure 2. Boxplot of (a) number of grains per panicle, (b) number of tillering, (c) panicle grain weight, (d) panicle length, (e) panicle weight, and (f) plant height of 14 black oat populations.

As highlighted by Valério et al. (2013) who observed heritability of 49% for number of panicles per plant, but only 30% for grain yield per plant.

The use of estimates of genetic parameters and components of genotypic and phenotypic variance, are additional information to the mean and variance of the traits, often used in data analysis. This information contributes to better accuracy in populations selection with high genetic potential within a breeding program, thus maximizing selection efficiency (Vencovsky 1969). Heritability estimates are not specific to a particular trait, but can also be influenced by other factor, from genetic divergence of population to the environmental conditions that the plants are exposed to during selection process (Falconer 1989).

PGW and NGP had the highest percentages of selection gain, followed by PW and PL. PH and NT had low estimates of selection gain, related to their low heritability. Therefore, selection for PGW, NGP, PW and PL, according to Vencovsky (1989), may potentiate selection gains, since these traits responded more easily to selection as a function of the high heritability coefficients.

In white oats, the number of panicles per plant, number of grains per panicle and panicle weight are traits with less complexity in gene effects (Valério et al. 2013; 2009). In this way, these traits have greater potential of effective selection gain. Marchioro et al. (2004) pointed out that indirect selection through panicle weight can be used efficiently for grain yield in oat populations.

In studies with white oats it was observed positive- and high-magnitude direct effects (0.84) of panicle mass on grain yield (Benin et al. 2003). In contrast, selection for increased productivity through indirect selection for panicle weight may result in higher plants (Hartwig et al. 2006). Zobel and Talbert (1984) emphasized the best selection strategy is to reduce variability within families and increase variability between families. That is, to combine selection between- and within- populations to achieve high efficiency in the selection gain.

The descriptive analysis aims to describe variability direction and magnitude of traits within a population (Mather and Jinks 1984). Regarding minimum, maximum and values observed for populations (Fig. 2), the PH had values between 89 cm (Tenente Portela) and 169 cm

(Planalto), with a mean of 125 cm. We highlight Population 12, which showed values with less amplitude. In white oats, Benin et al. (2005) observed height ranged from 86 cm to 122 cm for cultivars UFRGS 15 and UPF 18, respectively. For Benin et al. (2003), plant height in white oats has a moderate direct effect (0.32) on grain yield.

NT presented a high variability between and within populations, with values of only 1 to 17 tillers per plant, with a general mean of 4.8 tillers per plant (Fig. 2). This variability is mainly due to environmental effect observed (Table 2), highlighting the need to consider variance components in selection process.

PL ranged from 14 cm to 32 cm, with mean of 24.15 cm. Populations 1, 4, 8, 9, 13 and 14 revealed values greater than 30 cm (Fig. 2). For this characteristic smaller amplitude was observed, which could generate difficulty in the selection, but due to high heritability observed (Table 2), selection efficiency can be maximized for this trait.

For NGP, a greater variation was observed within populations (Fig. 2), which was reflected by the high values of genotype variance within population (σ_{ge}^2). It was observed mean of 46.45 grains per panicle, ranging from 8 to 112 grains. In addition to phenotypic variation observed, this trait had high heritability estimates, the association of these two components refers to a greater selection gain as seen in Table 3, of 45%.

Table 3. Relative contribution of traits to divergence to Singh method for plant height (PH), number of tillering (NT), panicle length (PL), number of grains per panicle (NGP), panicle weight (PW), and panicle grain weight (PGW) of 14 black oat populations.

Trait	S _j	Value (%)
PH	6.015	8.94
NT	11.500	17.09
PL	8.278	12.30
NGP	12.587	18.71
PW	5.679	8.44
PGW	23.218	34.51

PW presented range from 0.135 g (Population from Condor) to 2.094 g (Population from Alto Alegre), and mean of 0.754 g per panicle. PGW followed a similar pattern (Population from Condor 0.071 g, and Population from Alto Alegre 1.536 g). Populations from Taquaruçu do Sul, Alto Alegre and Tenente Portela expressed higher values for PW and PGW, with a ratio greater than 0.7 between traits, i.e.,

higher PW actually results in higher PGW (Fig. 2); that is, selected for one of these traits there are gains for the other.

The cluster analysis by UPGMA method formed three distinct groups. The group 1 was composed by black oat populations from Condor, Ajuricaba, Taquaruçu do Sul, Tenente Portela, Palmeira das Missões 2, Alto Alegre, Palmeira das Missões 1, Campos Borges and Santa Rosa; group 2 by populations from Boa Vista das Missões, Espumoso, Chapada and Planalto; and population from Salvador das Missões composed a single group. The cophenetic correlation coefficient was $r = 0.728$, $p < 0.05$, showing a good fit between cophenetic and original matrix distances (Fig. 3). Although the black oat populations were collected in a relatively restricted area of the state, with relatively similar climate conditions we found variability between populations. The groups highlighted in the map are useful and show the pattern of variability between black oat populations in the northwestern of the Rio Grande do Sul State (Fig. 1). The population that formed a single group comes from Salvador das Missões; this municipality is located in the most extreme west region among the studied municipalities. Thus, our findings can provide important information for breeders that will be starting a black oat breeding program.

According to Rasmusson and Phillips (1997), the success in breeding is maximized when elite genotypes are used to complement each other, so that when crossed, the progeny have greater genetic variability than the parents, resulting in superior pure lines. This suggests that crosses between populations of different groups will form new populations with greater variability for studied traits, allowing greater selection gains.

Lorencetti et al. (2006) concluded for white oats that using genotypes with high grain yield as crosses, segregating might not be positive. Therefore, the rescue and study of black oat populations for hybridization purposes may enable greater variability within a breeding program.

Regarding relative contribution of the traits (Singh 1981), PGW expressed the greatest contribution (34%) to genetic divergence between populations (Table 3). NT, PL and NGP contributed with 17%, 12% and 18%, respectively. Studying white oats in two growing seasons, Santos et al. (2017) observed a relative contribution similar those we found in this study for PL, ranging from 8% to 13%, and higher values for PH, with contribution between 11% and 13%.

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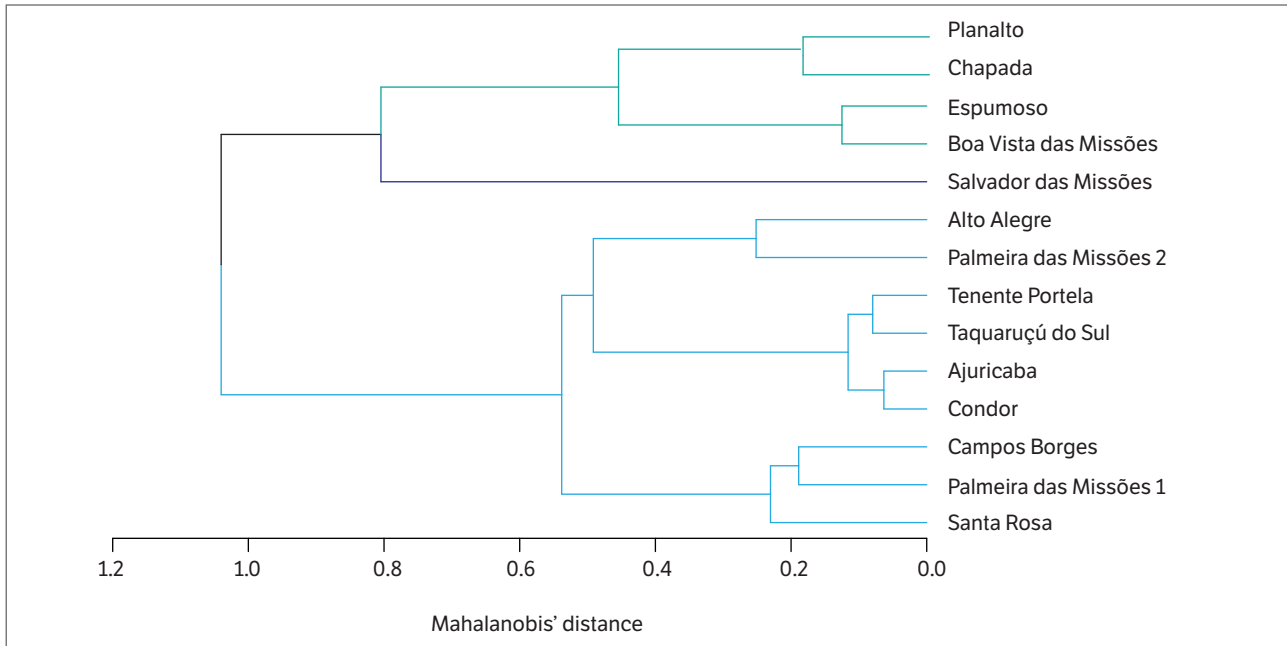


Figure 3. Dendrogram using unweighted pair group method with arithmetic mean (UPGMA) from Mahalanobis generalized distance matrix for 14 black oat populations, obtained by means of phenotypic traits (six traits). Cophenetic correlation coefficient (r): 0.728.

For canonical variables, only traits with Singh's relative contribution higher than 10% were used; PH and NGP were discarded. Observing Table 4, two canonical variables were required to explain more than 70% of genetic variation between populations. In this way, a bi-dimensional graphic was used to better visualize the canonical variables (Fig. 4). It is evident the distance of some populations in relation to the others, highlighting populations Salvador das Missões, Santa Rosa and Chapada.

Based on graphical dispersion of populations shown in Fig. 4, we must give preference to divergent parents for the desired traits in order to achieve higher genetic recombination. In this case, hybridizations could be programmed, for example, between populations from Alto Alegre and Salvador das Missões, Alto Alegre and Chapada, Alto Alegre and Santa Rosa, Campos Borges and Salvador das Missões, Santa Rosa and Salvador das Missões.

Table 4. Variance (eigenvalues), percentage variance and accumulated variance of canonical variance, aiming to estimate the dissimilarity between 14 black oat populations.

Trait	Variance (eigenvalues)	Percentage variance	Accumulated variances (%)
1	0.081	40.383	40.382
2	0.065	32.650	73.032
3	0.354	17.682	90.714
4	0.019	9.286	100.000

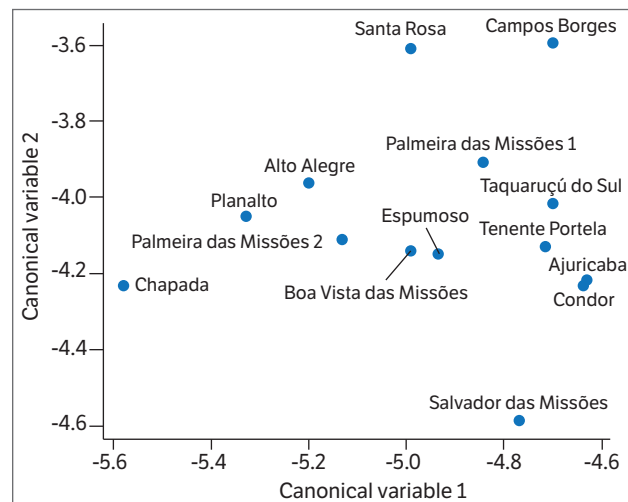


Figure 4. Graphic dispersion of first score (canonical variable 1) and second score (canonical variable 2) for black oat populations.

CONCLUSION

Selection based on panicle length, number of grains per panicle, panicle weight and panicle grain weight may result in higher selection gains. Panicle grain weight presents a greater contribution to genetic divergence between studied populations. The formation of distinct groups indicated the presence of genetic variability between black oat populations in the northwestern of the Rio Grande do Sul state. Directed crosses between

individuals plants of populations from (i) Alto Alegre and Salvador das Missões, Chapada, or Santa Rosa, or (ii) between plants of populations from Salvador das Missões and Campos Borges or Santa Rosa can generate segregating populations with great genetic variability. The predominance of between-phenotypic variance and a within-genetic variance indicates prospects for success in selection gain and possible selection of a superior cultivar with fewer efforts compared to a cross-based method. This is supported by the high values of within-population heritability.

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