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CARACTERIZAÇÃO DE POPULAÇÕES DE AVEIA PRETA E ESTRATÉGIAS DE SELEÇÃO DE GENÓTIPOS SUPERIORES

Frederico Westphalen, RS
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Dissertação apresentada ao Curso de Pós-Graduação em Agronomia – Agricultura e Ambiente, da Universidade Federal de Santa Maria (UFSM, RS), como requisito parcial para obtenção do título de **Mestre em Agronomia**.

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Aprovado em 2 de março de 2018

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DEDICATÓRIA

À minha família, dedico este trabalho.

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RESUMO

CARACTERIZAÇÃO DE POPULAÇÕES DE AVEIA PRETA E ESTRATÉGIAS DE SELEÇÃO DE GENÓTIPOS SUPERIORES

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ORIENTADOR: Braulio Otomar Caron

O objetivo do estudo foi caracterizar populações de aveia preta por meio de modelos biométricos, a fim de obter informações para seleção de genótipos superiores. A pesquisa foi conduzida na área experimental do Laboratório de Melhoramento Genético e Produção de Plantas, da Universidade Federal de Santa Maria, Campus de Frederico Westphalen-RS. Para tanto foram utilizadas 14 populações de aveia preta, as quais foram coletas em municípios do Rio Grande do Sul. Avaliações iniciais foram procedidas com as populações coletadas: comprimento e largura de sementes (mm), massa de mil sementes (g), primeira contagem de germinação (%), germinação (%), comprimento de hipocótilo e raiz de plântulas (mm), matéria seca de plântula (g). Posteriormente, realizou-se experimento à campo conduzido em delineamento de blocos ao acaso, com 14 populações dispostos em três repetições, na safra agrícola de 2014. Em estádio de maturação fisiológica, foram mensurados: altura de planta (cm), número de afilhos, comprimento de panícula (cm), número de grãos por panícula, número de ramificações da panícula, relação de massa de grãos da panícula e massa de panícula, massa de mil grãos (g), rendimento de grãos (kg ha^{-1}). Famílias do programa de melhoramento de aveia preta foram utilizadas para demais estudos. Sendo 76 famílias de aveia preta e três testemunhas (BRS Madrugada, BRS Centauro, BRS 139 Neblina), as quais foram conduzidas em duas safras agrícolas (2016 e 2017), utilizando delineamento de famílias com testemunhas intercalares. E avaliados os seguintes caracteres: dias da emergência ao florescimento, altura de planta, comprimento da panícula (cm), número de afilhos férteis, massa da panícula (g) massa de grãos da panícula (g) e a relação entre a massa de panícula e a massa de grãos da panícula. A partir das informações obtidas, caracterizou-se as populações por meio de análise de correlação de Pearson, análise de trilha, componentes de variância e parâmetros genéticos, diversidade genética, além das correlações fenotípicas, genéticas e ambientais. Massa de mil sementes, percentagem de germinação, largura dos grãos, massa de grãos da panícula contribuem de forma expressiva para a diferenciação das populações de aveia preta, revelando que há variabilidade genética. Além disso, para maiores ganhos de seleção de genótipos superiores, deve-se priorizar comprimento de panícula, números de grãos, massa de panícula e massa de grãos de panícula. As associações entre largura de grãos e qualidade fisiológica, número de grãos por panícula com rendimento de grãos, e ainda altas herdabilidade reveladas pela massa de panícula e massa de grãos da panícula, devem ser destacadas para a eficiência de seleção. Apesar das condições divergentes safras agrícolas estudadas, a origem genética dos componentes de variância prevalece. A variância observada entre as populações e testemunhas, ressalta que a seleção de genótipos superiores, para compor programa de melhoramento genético de aveia preta é promissora.

Palavras-chave: *Avena strigosa*. Modelos biométricos. Correlação. Divergência genética.

ABSTRACT

CHARACTERIZATION OF BLACK OAT POPULATIONS AND SELECTION STRATEGIES OF SUPERIOR GENOTYPES

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ADVISOR: Braulio Otomar Caron

The aim of study was to characterize black oat populations through statistical and biometric models, in order to obtain information for selection of superior genotypes. Research was conducted in experimental area of Genetic Breeding and Plant Production Laboratory, Federal University of Santa Maria, Campus of Frederico Westphalen-RS. For this purpose, 14 black oat populations were used, which were collected in cities of Rio Grande do Sul. Initial evaluations were proceeded with populations collected: length and width seed (mm), weight of thousand seeds (g), first germination count (%), germination (%), aerial part and root length of seedlings (mm), dry matter of seedlings (g). Subsequently, a field experiment was carried out in a randomized block design, with 14 populations arranged in three replications, in agricultural year 2014. At physiological maturity stage, were measured: plant height (cm), number of tillers, panicle length (cm), number of grains per panicle, number of branches of panicle, ratio between panicle weight and panicle grain weight, weight of thousand grains, grain yield (kg ha^{-1}). Families of black oat breeding program were used to others studies, being 76 families of black oat and three controls (BRS Madrugada, BRS Centauro, BRS 139 Neblina), which were conducted in two agricultural crops (2016 and 2017), using families with intercalary controls experimental design. And following characters were evaluated: days of emergence to flowering, plant height (cm), panicle length (cm), number of fertile tiller, panicle weight (g), panicle grain weight (g) and ratio between panicle weight and panicle grain weight. Based on the information obtained, populations were characterized by Pearson correlation analysis, path analysis, variance components and genetic parameters, genetic diversity, as well as phenotypic, genetic and environmental correlations. Weight of thousand seeds, percentage of germination, grain width, panicle grain weight contribute significantly to differentiation of black oat populations, revealing that there is genetic variability. In addition, for greater selection gains of superior genotypes, it should be prioritized panicle length, number of grains per panicle, panicle weight and panicle grain weight. Associations between grain width and physiological quality, number of grains per panicle with grain yield, and still high heritability revealed by panicle weight and panicle grain weight, should be highlighted for selection efficiency. Despite divergent conditions between agricultural years studied, genetic origin of variance components prevails. The observed variance between populations and controls shows that the selection of superior genotypes to compose breeding program, is promising.

Key words: *Avena strigosa*. Biometric models. Correlation. Genetic divergence

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1 INTRODUÇÃO

Reconhecida entre os principais cerais de inverno, a aveia preta (*Avena strigosa* S.) é mundialmente cultivada, devido sua utilização para produção de grãos, forragem e principalmente como cobertura de solo (CAIERÃO et al., 2001). A aveia preta, segunda cultura de inverno de maior importância no Brasil, tem apresentado significativo aumento na área de cultivo, 13,7 % de 2016 para 2017. Sendo o Rio Grande do Sul responsável por mais de 70% da área cultivada, seguido pelo Paraná e Mato Grosso do Sul, totalizando área total no país de 340 mil ha^{-1} (COMPANHIA NACIONAL DE ABASTECIMENTO, 2017).

Desta forma, há crescente demanda por genótipos superiores de aveia preta com ciclo vegetativo e reprodutivo que venham a se ajustar as necessidades atuais do mercado consumidor, com maior potencial de produção de fitomassa. Recentemente, os programas de melhoramento genético de aveia têm buscado cultivares com alto potencial produtivo e qualidade. Para tanto, o sucesso do programa depende da capacidade e agilidade de identificar genótipos que atendam os caracteres desejados.

A genética quantitativa tornou-se de fundamental importância para o melhoramento genético. A identificação, acumulação e perpetuação dos genes favoráveis para caracteres quantitativos pode ser facilitada pela utilização de modelos biométricos. Por meio destes, é possível identificar a natureza da ação dos genes envolvidos, além de avaliar a eficiência de diferentes métodos e estratégias de seleção, seja oriundo de endogamia, cruzamentos ou apenas seleção (CRUZ et al., 2014). Inúmeras pesquisas tem relatado eficiência do uso destas estimativas em cereais de inverno, dentre as quais para a cultura da aveia (MEIRA et al., 2017; CARGNELUTTI FILHO et al., 2015; UARROTA et al., 2017), trigo (KAVALCO et al., 2014), e outras culturas produtoras de grãos, soja (TEODORO et al., 2015; FOLLMANN, et al., 2017), milho (SZARESKI et al., 2018), feijão (GUIDOTI et al., 2017), feijão caupi (RIBEIRO et al., 2016).

A interação genótipos x ambientes colabora na complexidade para seleção de genótipos (BENNET et al., 2012). A correlação fenotípica abrange as causas genéticas e de ambiente, por isso deve-se estratificar cada uma delas para melhor compreensão das correlações (VENCOVSKY & BARRIGA, 1992). O conhecimento das associações entre os caracteres possibilita desenvolver a melhor estratégia de seleção e a partir das covariâncias estimar os índices de seleção (CRUZ et al., 2014). Além disso, a magnitude e sinal das correlações revelam o grau de associação e o sentido entre os caracteres, indicando se há alteração do comportamento em função de outro caráter.

Assim, de posse destes dados, o programa de melhoramento pode avançar, em tempo, e aumentar as chances de sucesso na identificação de genótipos superiores, com potencial para compor linhas puras (RASMUSSON & PHILLIPS, 1997).

1.1 HIPÓTESES

Frente ao exposto, foram formuladas as seguintes hipóteses: (i) a partir das associações de causa e efeito, dos caracteres explicativos sobre um caráter principal, a escolha de caracteres agronômicos determinam a eficiência de seleção; (ii) a estrutura de populações de aveia pode ser caracterizada através de componentes de variância e parâmetros genéticos; (iii) ganho de seleção pode prever o comportamento de progênies selecionadas; (iv) cultivo em duas safras agrícolas, pode vir a expressar variâncias fenotípicas, genotípicas e ambientais divergentes; (v) seleção realizada em apenas uma safra agrícola é eficiente se ela fora baseada nos componentes de variância.

1.2 OBJETIVO GERAL

Diante das hipóteses traçadas, o presente trabalho objetivou caracterizar populações de aveia preta por meio de modelos e biométricos, a fim de obter informações para seleção de genótipos superiores.

1.3 OBJETIVOS ESPECÍFICOS

Estudar as associações de causa e efeito e variáveis canônicas a fim de apontar caracteres importantes para a seleção indireta e avaliar a variabilidade entre populações de aveia preta.

Caracterizar a estrutura da população em termos de componentes de variância e parâmetros genéticos entre e dentro de populações de aveia preta e distinguir as populações estudadas.

Determinar os componentes de variância e parâmetros genéticos, correlações fenotípicas, genéticas e de ambiente entre famílias de aveia preta cultivadas em diferentes ambientes.

2 ARTIGO I – DETERMINANTS TRAITS OF INDIRECT SELECTION FOR GRAIN YIELD IN BLACK OAT

Submetido para o periódico: Agronomia Colombiana

Situação: em avaliação

DETERMINANTS TRAITS OF INDIRECT SELECTION FOR GRAIN YIELD IN BLACK OAT

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2.1 ABSTRACT

This study aimed to identify important traits for indirect selection and to evaluate the variability among black oat populations through cause and effect relationships and canonical variables. Fourteen black oat populations were collected in the 2013 cropping season, which were evaluated in the laboratory and in the field, in the 2014 cropping season. Populations studied showed genetic dissimilarity. The population of Salvador das Missões presented agronomic traits distinct from the other populations. Weight of thousand seeds, first count of germination and seeds width had a greater contribution in differentiating black oat populations. seed width showed a strong and positive association with physiological quality of seeds. The number of grains had the greater direct effect on grain yield and may be used in indirect selection.

Key words: *Avena strigosa* S.; cause and effect; populations; breeding; variability

2.2 INTRODUCTION

Black oat (*Avena strigosa* S.) stand out among the most cultivated winter cereals worldwide. This cereal is widely used as soil coverage, as well as forage production during any gaps period in the Southern region of Brazil (Caierão et al., 2001). The growing demand for superior genotypes of black oat with vegetative and reproductive cycle more adequate to the current needs and greater potential for fresh and dry matter production, makes genetic breeding programs continually search for techniques that help in process of early genotypes selection. Another important factor considered by breeding programs is the association degree among traits of interest during selection process.

Among the most used techniques for identifying association among traits, stands out Pearson's linear correlation, which reveals the trends of sense and degree of linear association between two traits (Nogueira et al., 2012). However, quantification and interpretation of sense and magnitude correlation may result in misunderstandings in selection strategy, because a third or group of traits may be acting on the response of trait in evidence (Cruz and Carneiro, 2003).

Aiming at to mitigate possible bias caused by effect of other traits in correlation, path analysis is used. This allows understanding associations of cause and effect, that is, the direct and indirect effects of explanatory traits on main trait. The indirect selection by traits with easy measurement and high heritability, and which are associated with dependent trait, has made possible faster genetic gains in relation to use of direct selection (Cruz et al., 2004, Cruz, 2006; Falconer, 1989). Santos et al. (2014) highlight when character showed low to moderate possibility of gain from indirect selection, may be used multiple character and a genotype of better performance for success.

As breeding programs work with a high number of genotypes and/or populations, it is often necessary to determine dissimilarity degree among these individuals, in order to identify possible parents with higher recombination degree. Thus, cluster analysis brings together parents or populations in groups, which have similarity within the group and dissimilarity among groups.

The use of canonical variables allows simplifying the data set, reducing the number of traits into few components aiming at retaining most of variation and still present independence among them (Cruz, 2006). Classifications of these groups are obtained through genetic divergence, quantifying similarity or dissimilarity among them, by phenotypic traits. Groups distinction may contribute for choosing parents (Cruz et al., 2004).

It is crucial for breeders identify traits that most contribute to dissimilarity process, thus allowing planning the traits' selection (Kurek et al., 2002). Thus, one of the most used methodologies to determine relative traits contribution in the total variation is Singh's method (1981) (Marchioro et al., 2003; Kurek et al., 2002).

In front of few researches in this field on black oat, the aim of this work was to use cause and effect relationships and canonical variables to point out important traits for indirect selection and to evaluate variability among superior populations of black oat.

2.3 MATERIAL AND METHODS

The experiment was carried out in experimental area of Genetic Breeding and Plant Production Laboratory (GBPPL) of Federal University of Santa Maria, Campus Frederico Westphalen-RS, located at geographic coordinates of 27º23'26 "LS; 53º25'43 "LW, at 461 m. Region climate is classified as subtropical humid with average annual temperature of 19.1ºC and average annual precipitation of 1880 mm, and soil is classified as Red Dystrophic Latosol (Embrapa, 2006).

Initially, 3 kg samples of seeds of black oat populations from Rio Grande do Sul and Santa Catarina microenvironments were collected in the 2013 cropping season. A total of 14 populations were collected and named according to origin place: Taquaruçu do Sul – RS (1), Palmeira das Missões 1 – RS (2), Palmeira das Missões 2 – RS (3), Condor – RS (4), Alto Alegre – RS (5), Campos Borges – RS (6), Chapada – RS (7), Tenente Portela (8) Boa Vista das Missões – RS (9), Salvador das Missões – RS (10), Santa Rosa – RS (11), Espumoso – RS (12), Planalto – RS (13), Ajuricaba – RS (14).

In the GBPPL, some initial evaluations were performed from seed samples. The assessed traits were: seed length (SL) and seed width (SW) were obtained, for such, four replicates of ten seeds of each population were analyzed. Measurements were obtained with digital caliper, in millimeters (mm). The weight of thousand seeds of the population (WTS) was also obtained by counting eight replicates of 100 seeds of each black oat population, weighed in a precision balance, given in grams (g).

Physiological characters were evaluated in an experiment conducted in a germination chamber in a randomized block design with four replications. The test consisted of 400 seeds of each population, being four repetitions of 100 seeds for each experimental unit. Seeds were placed in germitest type paper, moistened with distilled water in a proportion of 2.5 times their dry weight. They were kept in a germination chamber type B.O.D, at a constant temperature of 20ºC (Brazil, 2009).

Traits evaluated in this experiment were first germination count (FGC), obtained by percentage of normal seedlings at five days after test installation; germination percentage (GP), evaluated at ten days, counting percentage of normal seedlings; aerial part length (AL) and root length of seedling (RL), obtained at end germination test, by measuring ten seedlings per replicate for all populations. Mean lengths were measured using a digital caliper, and results expressed in mm. Dry matter of seedlings (DMS) was also obtained from ten randomly selected seedlings per replicate, performed together at end germination test. Seedlings were conditioned in an oven with forced air circulation at 60ºC until reaching a constant mass. Afterwards, they were measured on a precision scale and results expressed in grams (g).

Field experiment was conducted with 14 treatments, in the 2014 cropping season in a randomized block design, arranged in three replications. Experimental units were composed of twelve 3-m long sowing rows, spaced between 0.17 m. Seeding was carried out on June 17th, 2014, with density of 300 suitable plants m^{-2}. Nutritional management was according to soil analysis.

Harvested were realized at physiological maturation stage, where 10 plants per experimental unit were randomly collected, being analyzed the following traits: plant height (PH), measured from base in the soil to plant apex, expressed in centimeters (cm); panicle length (PL), measured from insertion of first branch of panicle to panicle apex, given in cm; number of grains (NG), number of grains per main panicle, results in units; number branches of panicle (NB), from count of number branches present in each panicle, expressed in units; weight of panicle grains and weight of panicle ratio (GPR), obtained by ratio weight of grains of main panicle to weight of panicle.

By using harvest of plots, it was possible to assess thousand-grain weight (WTG), where with the grains harvested in the 2014 cropping season, were performed eight repetitions of 100 grains of each plot, measured with an analytical scale, expressed in g (Brazil, 2009); grains yield (GY), obtained by means of the total grain mass of ten plants collected per experimental unit, with subsequent moisture correction to 13%. Grain yield was adjusted by number of plants per experimental unit, obtaining yield expressed in kg ha^{-1}.

Data were submitted to ANOVA by F test, at $p \leq 0.05$, after observing the assumptions of variance homogeneity and residual normality, to obtain other parameters. The Pearson correlation analysis was obtained with all 15 traits obtained, and its magnitude classified according to Carvalho *et al*. (2004).

Variance analysis provided matrices of phenotypic covariance and residual variance for subsequent analyses. The multicollinearity of correlation matrix was diagnosed by condition number (CN), given by ratio between the largest and smallest eigenvalues of matrix, in order to verify dependence level among traits (Montgomery and Peck, 1981). In the case of severe multicollinearity CN> 1000, traces with highest weights associated to eigenvalues of smaller magnitude were excluded. Exclusion of traits that influenced multicollinearity followed up to multicollinearity reached acceptable values (CN <100) (Belsley *et al.*, 1980). Later, phenotypic path analysis considering GY as dependent trait was performed using as explanatory traits those that remained after multicollinearity adjustment. The relative contribution of each trait was estimated by method of Singh (1981). All statistical procedures were performed with Genes statistical software (Cruz, 2013).

2.4 RESULTS AND DISCUSSION

The SW, WTS, FGC, GP, DMS and AL showed positive and strong associations between them (Table 1). Seeds with higher SL tend to increase WTS; in addition, they may contain higher energy reserves, improving germination percentage and vigor. Ahmad *et al.* (2013) showed that selection for seeds length and width, associated to the number of leaves per plant, number of tillers, plant height, stem diameter, and weight of thousand seeds can facilitate plant breeding, aiming at a higher forage and seeds production with better quality.

NB presented negative and strong association with GP and RL; in this case it is verified increase in NB reduces seeds quality, due to reduction seed size. Alves and Kist (2011) verified the best rates of germination and vigor were obtained from seeds of higher weight, regardless evaluated oat genotype. It was also observed positive and strong association between traits NB and PL, revealing that larger panicle length results greater number of branches.

The NG, GPR showed strong and positive correlation, and WTG average correlation with GY, revealing that there is an increase in grain yield when the number of grains per plant and its weight are increased. In studies with white oats, Benin *et al.* (2003) observed that panicle weight, number of panicles per plant and average grain weight, might be used in the indirect selection for grain yield. The same was observed by Caierão *et al.* (2001) regarding traits, number of grains per panicle and grain weight. Kavalco *et al*. (2014), have indicated that for indirect selection in wheat, the number of tillers, grain weight and number of grains per spike, are traits that present prospects of success in the indirect selection aiming at higher grain yield.

Table 1. Pearson linear correlation of 14 black oat populations relative to 2014 cropping season.

	SL	SW	WTS	FGC	GP	DMS	AL	RL	PH	PL	NG	GPR	WTG	NB	GY
SL(1)	-	-0.17	-0.05	-0.26	-0.20	0.13	-0.09	-0.34	0.00	-0.03	-0.06	0.21	-0.07	0.22	0.01
SW		-	0.85**	0.82**	0.82**	0.82**	0.73**	0.30	-0.08	0.19	-0.10	-0.04	0.20	-0.24	0.00
WTS			-	0.78**	0.75**	0.91**	0.63*	0.44	-0.26	0.04	-0.03	0.07	-0.02	-0.32	0.02
FGC				-	0.97**	0.69**	0.65*	0.35	0.29	0.21	-0.17	0.05	0.14	-0.45	0.02
GP					-	0.71**	0.66*	0.35	0.31	0.03	-0.31	0.10	0.17	-0.56*	-0.06
DMS						-	0.69**	0.22	-0.20	-0.04	-0.06	0.26	0.17	-0.27	0.11
AL							-	0.46	-0.05	0.07	-0.07	0.39	0.52	-0.35	0.19
RL								-	-0.16	-0.27	-0.38	-0.13	-0.13	-0.55*	-0.38
PH									-	0.13	-0.22	0.09	0.03	-0.33	0.05
PL										-	0.35	-0.21	0.19	0.57*	0.30
NG											-	0.43	0.18	0.36	0.86**
GPR												-	0.62*	-0.28	0.75**
WTG													-	0.01	0.53*
NB														-	0.10
GY															-

**, * Pearson linear correlation coefficients (n=42) significant at 1 and 5% error probability, respectively. [1]SL: seed length; SW: seed width; WTS: weight of thousand seeds; FGC: first germination count; GP: germination percentage; DMS: dry matter of seedlings; AL: aerial part length of seedlings; RL: root length seedlings; PH: plant height; PL: panicle length; NG: number of grains; GPR: weight of panicle grains and weight of panicle ratio; WTG: weight of thousand grains; NB: number of branches of panicle; GY: grains yield.

The GPR showed strong and positive correlation with WTG (r=0.62), that is, increment WTG has positive effect on GPR, since heavier grains tend to increase the GY. The identification of genotypes that show association among NG, GPR, WTS with GY must be prioritized, but care must be taken because the increase in NG may lead to a reduction in grain weight due to a competition by photoassimilates. Valério *et al.* (2008), in wheat research concluded that increase in number of spikes results in lower grain filling, and when there is less tillering, a compensatory effect occurs, improving the efficiency use of photoassimilates.

In this sense, it is important the selection of plants with high capacity of photoassimilates production, with greater number of grains per panicle and maintenance of grain weight. Studies conducted by Valério *et al.* (2009), corroborate with results found, showing that there is an increase in grain yield when there is a greater number and grain weight per panicle.

When evaluating multicollinearity of phenotype correlation matrix, we observed severe multicollinearity effects caused by the traits SL, SW, WTG, FGC, AL, RL. Thus, these traits were removed from path analysis to circumvent multicollinearity effects, giving higher degree of accuracy (Olivoto *et al.*, 2017).

The phenotypic estimates of cause and effect, in path analysis, showed up trustworthy due to the high value of determination coefficient (0.99) and low residual effects (0.12). Thus, it is important to identify direct and indirect effects between explanatory traits and main trait in black oats populations (Table 2). Backes *et al*. (2003) and Gonçalves *et al.* (2003), working with soybean, show that use direct and indirect selection strategy aimed at increasing grain yield is efficient, since it is able to identify variables responsible for the gain.

GP expressed negative direct effect of weak magnitude on the dependent trait (GY). The indirect effects of GP revealed positive association and low magnitude with DMS, and moderate negative with NG. It is worth pointing out that populations' seeds were collected in small farmers, that is, they were saved seeds, and generation and quality of storage were not known.

DMS showed positive direct effect of low magnitude to GY, while to indirect effects, negative values of low magnitude are observed for GP, for other traits were verified null values.

Table 2. Phenotypic estimate of direct and indirect effects in eight traits on dependent trait, grain yield, of 14 black oat populations.

Effects	Explanatory traits							
	GP	DMS	PH	PL	NG	GPR	WTG	NB
Direct on GY$^{(1)}$	-0.20	0.21	0.23	0.10	0.75	0.19	0.25	-0.16
Indirect via GP	-	-0.14	-0.06	-0.01	0.06	-0.02	-0.03	0.11
Indirect via DMS	0.15	-	-0.04	-0.01	-0.01	0.05	0.04	-0.06
Indirect via PH	0.07	-0.05	-	0.03	-0.05	0.02	0.01	-0.08
Indirect via PL	0.00	0.00	0.01	-	0.04	-0.02	0.02	0.06
Indirect via NG	-0.24	-0.05	-0.17	0.27	-	0.33	0.14	0.27
Indirect via GPR	0.02	0.05	0.02	-0.04	0.08	-	0.12	-0.05
Indirect via WTG	0.04	0.04	0.01	0.05	0.05	0.16	-	0.00
Indirect via NB	0.09	0.04	0.05	-0.09	-0.06	0.05	0.00	-
Linear (r)	-0.06	0.11	0.05	0.30	0.86**	0.75**	0.53*	0.10
Determination coefficient								0.99
Variable residual effects								0.12
Condition number								47.38

**, * Pearson linear correlation coefficients (n=42) significant at 1 and 5% error probability, respectively. [1]GY: grains yield; GP: germination percentage; DMS: dry matter of seedlings; PH: plant height; PL: panicle length; NG: number of grains; GPR: weight of panicle grains and weight of panicle ratio; WTG: weight of thousand grains; NB: number of branches of panicle.

PH has positive and weak direct effect to GY. The NG have indirect effect on PH, and negative indirect effects with NG. In contrast, Hartwig *et al.* (2006) point out that, in white oat crosses, high plants tend to be more productive because they present physiological advantages over competitors, and also points out identification of genetic constitutions, which present associations of desirable quantitative traits with qualitative traits requires complex studies. Cargnelutti Filho *et al.* (2015), studying traits for dry and fresh matter production, showed plant height has a positive linear relation and can be used for indirect selection.

Direct effect of PL to GY was positive and low magnitude in relation, but it expressed a moderate indirect positive effect via NG, noting that increase of panicle may result in a higher number of grains, although, Pearson's correlation (r=0.30) expressed no significant coefficient. The NG has direct influence of positive sense and high magnitude in GY, and indirect effects are null in the other traits, with Pearson correlation significant to 1% probability of error, evidencing a high magnitude of positive relationship (r=0.86).

The GPR revealed direct positive effects of low magnitude to GY, and expressed positive and moderate indirect effect to NG and WTG. For Hartwig *et al.* (2006), studying generations of crosses, obtained high phenotypic correlations between number of grains per plant and grains weight per plant. On the other hand, Benin *et al.* (2003), point out that for success in selection of superior plants, highlight itself the traits with greatest direct and indirect effects, such as panicle weight, number of panicles per plant and average grain weight to grain yield main trait. Hartwig *et al.* (2006) evidenced that there is positive correlation between grain mass and grain yield per plant in generations of crosses.

The WTG expressed positive sense and weak magnitude, for direct effects to GY, and indirect effects via NG and GPR. Lorencetti *et al.* (2006), found that combination between panicle weight and weight of thousand grains traits; and, Benin *et al.* (2003) and Hartwig et al. (2006) that combination between number of panicles per plant and grain yield per plant, potentiate indirect selection, aiming grain yield. In wheat, Vesohoski *et al.* (2011) verified that indirect selection for grain yield from number of grains per spike, taking into account weight of thousand grains, is the best strategy.

NB showed negative and weak association for direct effect to GY, and indirect effects of positive sense of low and moderate magnitude for GP and NG. Thus, the higher NB indicates a greater amount of NG, but it cannot be claimed that an increase in GY occurs.

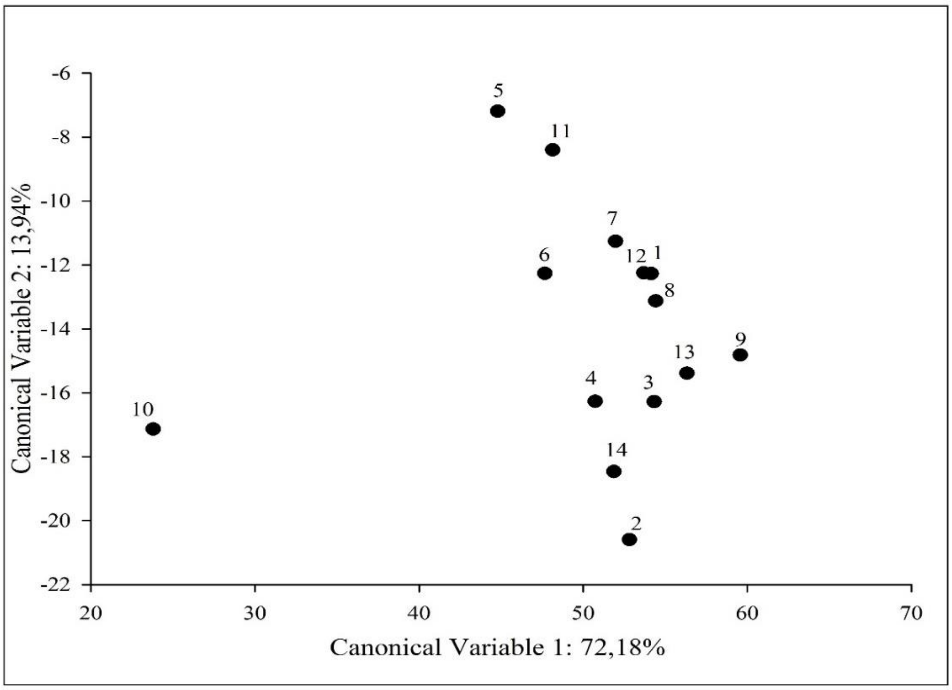

Figure 1. Graphical dispersion of scores obtained by canonical variables analysis of 14 black oat populations, being: Taquaruçu do Sul – RS (1), Palmeira das Missões 1 – RS (2), Palmeira das Missões 2 – RS (3), Condor – RS (4), Alto Alegre – RS (5), Campos Borges – RS (6), Chapada – RS (7), Tenente Portela (8) Boa Vista das Missões – RS (9), Salvador das Missões – RS (10), Santa Rosa – RS (11), Espumoso – RS (12), Planalto – RS (13), Ajuricaba – RS (14).

In the present study, it was verified that first two canonical variables (CV) explained 85.879% of total variation observed (CV1-71,969%, CV2-13,910%). Thus, accumulated variance in first two canonical variables may be considered efficient (Cruz and Carneiro, 2003), for two-dimensional graphic representation (Figure 1).

Table 3. Relative contribution of traits to divergence - Singh (1981) in 14 black oat populations.

Trait	**S.j**	**Value (%)**
SL(1)	1094.360	5.996
SW	1652.956	9.056
WTS	10011.203	54.850
FGC	549.092	3.008
GP	3153.909	17.280
DMS	234.528	1.285
AL	336.231	1.842
RL	390.136	2.138
PH	68.743	0.377
PL	115.751	0.634
NG	263.121	1.442
GPR	210.890	1.155
WTG	74.506	0.408
NB	13.519	0.074
GY	82.966	0.455

[1] SL: seed length; SW: seed width; WTS: weight of thousand seeds; FGC: first germination count; GP: germination percentage; DMS: dry matter of seedlings; AL: aerial part length of seedlings; RL: root length seedlings; PH: plant height; PL: panicle length; NG: number of

grains; GPR: weight of panicle grains and weight of panicle ratio; WTG: weight of thousand grains; NB: number of branches of panicle; GY: grains yield.

Graphic representation of canonical variables reveals the formation of two groups; group 1 being composed of the majority of populations (13), except population 10, from Salvador das Missões - RS, which composed group 2 (Figure 1). Priority should be given the cross between superior individuals contained in different groups, to maximize heterosis of progeny. Thus, crossover targeting of genotypes from population 10 (group 2) with genotypes from group 1 may be an effective strategy to obtain superior segregating genotypes.

Using the Singh method (1981) to determine relative contribution of agronomic traits that most influence on difference genotypes, it was verified that for 15 measured traits, the WTS, GP and SW contributed with 81.19% for differentiation of populations, and contribution of traits were 54.85%, 17.28% and 9.056%, respectively (Table 3). Scheffer-Basso *et al.* (2012) verified that in wild oats, base pilosity of grain and cycle are traits that contribute with greater percentage for dissimilarity. The GY, NB, WTG, PH and PL contributed with less than 2% for differentiation of oat populations studied. Thus, these traits can be disregarded in future studies of genetic divergence of black oats, reducing cost and time to measure these traits.

2.5 CONCLUSION

The populations studied present genetic dissimilarity, being that SW presents strong and positive association with physiological quality of oats seeds. The NG has a greater direct effect to GY of black oat, but it is worth noting that for selection success, we must take indirect effects of traits. Salvador das Missões – RS population presents agronomic traits distinct from the other populations. Traits WTS, GP and SW are main contributors to differentiation of black oat populations.

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3 CAPÍTULO II - ESTIMATES OF GENETIC PARAMETERS AMONG AND WITHIN BLACK OAT POPULATIONS

Submetido para o periódico: Bragantia
Situação: Aguardando revisão

ESTIMATES OF GENETIC PARAMETERS AMONG AND WITHIN BLACK OAT POPULATIONS

3.1 ABSTRACT

The aim of this study was to characterize black oat populations in terms of variance components and genetic parameters among and within population, as well as to distinguish studied populations. Experiment was carried out in randomized blocks design with three repetitions, with 14 black oat populations in 2014. Agronomic traits were carried out at physiological maturation stage. For variance analysis, randomized blocks with information within the plot were used, and from this information, variance components, genetic parameters, Mahalanobis generalized distance, relative contribution of traits, and canonical variables were estimated. 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 greater contribution to genetic divergence among studied populations. Formation of distinct groups indicated presence of genetic variability among populations. Crosses directed between individuals of these groups can generate segregant populations with great genetic variability.

Keywords: *Avena strigosa*, genetic divergence, genotypic variance.

3.2 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 to soil cover. Rio Grande do Sul 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 sought for cultivars with high productive potential and quality. To do so, program success depends on ability and agility to identify genotypes that meet desired traits. Hawerroth et al. (2014), emphasize 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 can be facilitated by estimating components of variance and genetic parameters. In this way, genetic parameters allow to identify action nature of genes involved, besides 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 know estimates genetic parameters from genotypic components. Parameters magnitude determines genetic properties of the population (Falconer, 1989). Thus, in possession of these data, breeder has more information for decision making, increasing selection efficiency.

For quantitative traits, the F = G + E model is used, where the phenotype (F) is the result of genotype (G) action under influence of environment (E) (Falconer, 1989; Cruz et al., 2014). Phenotypic variance ($\hat{\sigma}_F^2$) is composed by genotypic ($\hat{\sigma}_G^2$) and environmental variance ($\hat{\sigma}_E^2$) (Ramalho et al., 2012), the environmental variance being all non-genetic, which is not inheritable, which can be minimized with the use of appropriate experimental designs (Falconer, 1989; Ramalho et al., 2012), thus making it possible to show genetic variability of population. Therefore, genetic variance allows to understand genetic structure involved among the progenies, being determined by additive and non-additive effects (Baldissera et al., 2014).

In addition to these parameters, the estimating heritability importance is highlighted. Heritability in the broad sense expresses genetic variance proportion in relation to total variation, which has an important predictive function, which expresses phenotypic value confidence as a guide to genetic value. Although the phenotypic factor is directly measured, 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; Miranda, 2013).

In order to predict selected progenies behavior, selection gain is estimated (Souza and Sorrels, 1991). Thus, a breeding program can advance, in time, and increase the chances of success in identifying superior genotypes, with potential to compose pure lines that surpass parents (Rasmusson and Phillips, 1997). In literature cited, there are few studies about variance components and genetic parameters for black oat. Thus, the aim of this study was to characterize black oat populations in terms of components of variance and genetic parameters among and within population, as well as to distinguish studied populations.

3.3 MATERIAL AND METHODS

The study was conducted with black oat in Frederico Westphalen, state of Rio Grande do Sul, located at coordinates 27º39'S and 53º42'O, at an altitude of 461.3 meters. For this purpose, 14 black oat populations were carried out in agricultural year of 2014. Populations were obtained by collecting samples in several cities of Rio Grande do Sul (Figure 1), being Taquaruçu do Sul – RS (1), Palmeira das Missões 1 – RS (2), Palmeira das Missões 2 – RS (3), Condor – RS (4), Alto Alegre – RS (5), Campos Borges – RS (6), Chapada – RS (7), Tenente Portela (8) Boa Vista das Missões – RS (9), Salvador das Missões – RS (10), Santa Rosa – RS (11), Espumoso – RS (12), Planalto – RS (13), Ajuricaba – RS (14), grown by farmers for several generations. The experimental design was conducted in randomized block, with three repetitions. The experimental units were composed of 6 m², with a line spacing of 0.17m and density of 300 plants m^{-2}. Sowing was carried out on June 17th, 2014. Nutritional management was according to the soil analysis, and the phytosanitary management carried out preventively.

When populations reached physiological maturation stage, harvest of 10 plants per plot was performed and the following phenotypic traits were mensured: plant height (PH, in cm), number of tillering (NT), panicle length (PL, in cm), panicle weight (PW, in grams), panicle grain weight (PGW, in grams), number of grains per panicle (NGP).

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

$$Y_{ijk} = \mu + g_i + b_j + \varepsilon_{ij} + \delta_{ijk}$$

Where μ is experimental mean, g_i is population effect, b_j is block effect j, ε_{ij} is plot effect ij and δ_{ijk} is individual effect of k, of i-th population in j-th block.

Mean squares of variance analysis were deployed and mathematical expect were obtained, using randomized blocks with information within populations, with information obtained from 10 plants per plot (Cruz et al., 2014). From these information, variance components were estimated: phenotypic variance among ($\hat{\sigma}^2_{fe}$) and within ($\hat{\sigma}^2_{fd}$) of population, genotypic variance among ($\hat{\sigma}^2_{ge}$) and within ($\hat{\sigma}^2_{gd}$); and genetic parameter: heritability among (h^2_e) and within (h^2_d) of populations, and expected selection gain (Gs).

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

$$\hat{r}_{gg} = \left[\frac{1}{1 + (\frac{\hat{\sigma}^2_d}{\mathrm{r}})/\hat{\sigma}^2_e}\right]^{1/2}$$

In order to analyze populations behavior was used boxplot diagram, described by Tukey (1977), to evaluate empirical distribution of a series of quantitative data, showing indicative of mean estimation and deviations. For this, mean, lower quartile, upper quartile and lower and upper ends of data series were calculated. With quartiles values are drawn vertical lines, which form a rectangle. The diagrams were built using the Microsoft Office Excel® software.

For study genetic diversity of populations, Mahalanobis generalized distance matrix was estimated. From genetic distance matrix, clustering analysis 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 equation:

$$r = \bar{x} + (1.25.DP)$$

Where $\bar{x}$ represents mean of distances, and DP standard deviation of distances (Cruz, 2014). The adjustment was measured by means of the cophenetic correlation coefficient.

The analysis of relative contribution of each trait was estimated by Singh (1981). In view of the contribution of each trait, only traits with a relative contribution greater than 10% were used to analyze canonical variables, thus reducing dimensionality of data and obtaining a linear correlation of the same. All statistical analyses were performed using Genes (Cruz, 2016).

3.4 RESULTS AND DISCUSSION

Table 1 shows data variance analysis, where it is verified that there was no significant difference for the population. The data presented accuracy of low (CP), moderate (NG, MP, MGP) and high magnitude (AP, NAF).

In relation to variance components, the phenotypic variance, which includes both genetic and environmental variation, revealed higher values among populations than within populations for all studied traits (Table 2). This fact is due to the high contribution of environmental variation in the phenotypic variance composition. It can be further verified in

Table 2, where genetic variance among populations is smaller than genetic variance within populations.

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

For heritability estimation, values were observed among populations shorter than within populations for all analyzed traits (Table 2). From this information, it is assumed that selection within populations results in greater gains when compared to population selection. For this, PL is highlighted regarding heritability within population, followed by PW, NGP and PGW, because they have high heritability percentages, superior to 80%. The remaining NT and PH revealed values of 40 and 67%, respectively.

These results indicate that, due to the greater genetic variation proportion, it is possible to obtain selection effectiveness through secondary traits of higher heritability correlated with main interest trait (Fehr, 1987). As highlighted by Valério et al. (2013) when they observed for number of panicles per plant a heritability of 48.92%, and for grain yield per plant a heritability of only 29.64%.

The use of estimates of genetic parameters, mainly heritability, and components of genotypic and phenotypic variance, are additional information to mean and variance of 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. Herbability estimates are not specific to a particular trait, but rather to a number of factors intrinsic to the population, from genetic divergence of population to the environmental conditions that the plants are exposed to during selection process (Falconer, 1989; 1987).

PGW and NGP revealed the highest percentages of selection gain, followed by PW and PL. PH and NT showed to be traits with low estimates of selection gain, related to their low heritability. Therefore, selection for PGW, NGP, PW and PL according to Vencovsky (1987), may potentiate selection gains, since these traits responded more easily to selection as a function of the high heritability coefficients.

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

In studies with white oats, direct effect of positive direction and high magnitude of panicle mass on grain yield (0.84) were observed (Benin et al., 2003). In contrast, selection for increased productivity through indirect selection for panicle weight may result in plant higher (Hartwig et al., 2006). Zobel and Talbert (1984) emphasize the best selection strategy is to reduce variability within families and increase variability among families. That is, to combine selection among 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 means values observed for populations represented in boxplot graphs (Figure 2), PH reveals values between 89 cm (Population 8) and 169 cm (Population 13), with a mean of 125 cm. Highlight Population 12, that showed values with less amplitude. In white oats, Benin et al. (2005) observed height raged 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 effect on grain production (0.32).

NT presented a high discrepancy among and within populations. It was observed values of only one to 17 tiller per plant, with a general mean of 4.8 tiller per plant (Figure 2), this high amplitude observed is mainly due to environment effect observed in the composition of phenotypic variance in relation to genotypic variance (Table 2), highlighting the need to consider variance components in selection process for trait.

PL ranged from 14 cm to 32 cm, with mean of 24.15 cm. Populations 1, 4, 8, 9, 13 and 14 revealed greater values than 30 cm (Figure 2). For this characteristic a smaller amplitude was verified for the data, 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 oscillation was observed within populations (Figure 2), which can be proved by the high values of genotype variance within population ($\hat{\sigma}^2_{ge}$). It was observed mean of 46.45 grains per panicle, ranging from 8 to 112 grains. In addition to phenotypic variation observed, this trait has high heritability estimates, the association of these two components refers to a greater selection gain as seen in Table 3, of 45.245%.

PW presented raged from 0.135 g (Population 4) to 2,094 g (Population 5), and mean of 0.754 g per panicle. Regarding MGP, Population 4 showed lower value (0.071 g) and Population 5 had higher value (1,536 g). Populations 1, 5 and 8 expressed higher values for PW and PGW, with a ratio greater than 0.7 between traits, ie, higher PW actually results in higher PGW (Figure 2), that is, selected for one of these traits there are gains for the other.

Considering studied traits, it was observed for grouping analysis by UPGMA method, which uses distances among all pairs of populations, that formed three distinct groups (group 1: 4, 14, 1, 8, 3, 5, 2, 6, 11, group 2: 9, 12, 7, 13, group 3: 10). Clustering consistency is emphasized by the dendrogram's cophenetic correlation coefficient (r: 0.728), showing a good fit between graphic representation of distances and its original matrix (Figure 3).

According with propose by Rasmusson and Phillips (1997), success in breeding is maximized when elite genotypes are used to complement each other, so that when crossed, the progeny have genetic variability to overcome parents, forming superior pure lines. This fact leads us to the conclusion 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 at crosses, segregants may 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 traits contribution, through diversity of Singh (1981), PGW expressed the greatest contribution to genetic divergence among populations, representing 34% (Table 3). NT, PL and NGP contributed 17%, 12% and 18%, respectively. Studying white oats in two growing seasons, Santos et al. (2017) observed a relative contribution similar to present study for PL, ranging from 8 to 13%, and higher values for PH, with contribution between 11 and 13%.

Canonical variables, estimated by eigenvalues percentage in relation to their total, describe how much variation each canonical variable. For that, only traits with Singh's relative contribution higher than 10% were used, and PH and NGP were discarded. Observing Table 4, three canonical variables were required to explain more than 80% of genetic variation among populations. In this way, three-dimensional graphic representation was used to better visualize canonical variables (Figure 4). In graphic dispersion it is evident distancing of some populations in relation to the others, highlighting populations 5 and 10.

Based on graphical dispersion of populations shown in Figure 4, in a future definition of populations for cross-breeding program, in order to study a particular trait or to seek genetic recombination for interest traits, we must give preference to divergent parents for traits in question. In this case, hybridizations could be programmed, for example, between populations 5 and 10, 5 and 7, 5 and 11, 6 and 10, 11 and 10.

3.5 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 greater contribution to genetic divergence among studied populations.

The formation of distinct groups indicated presence of genetic variability among populations. Crosses directed between individuals of these groups can generate segregant populations with great genetic variability.

There is predominance of phenotypic variance among and genetic variance within populations, and this indicate potential to selection gain.

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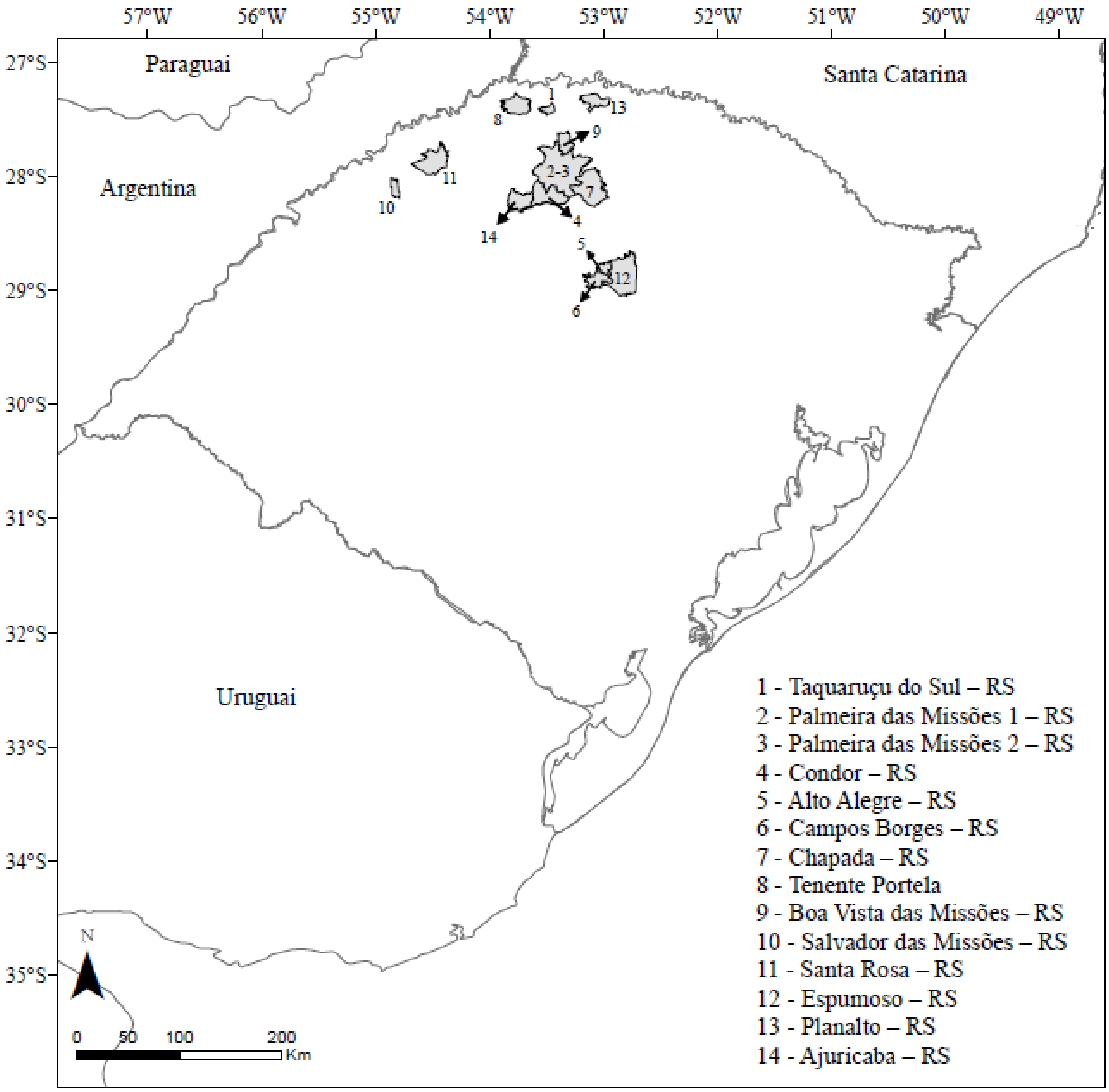

Figure 1. Collection sites map of the 14 populations of black oats in Rio Grande do Sul (RS).

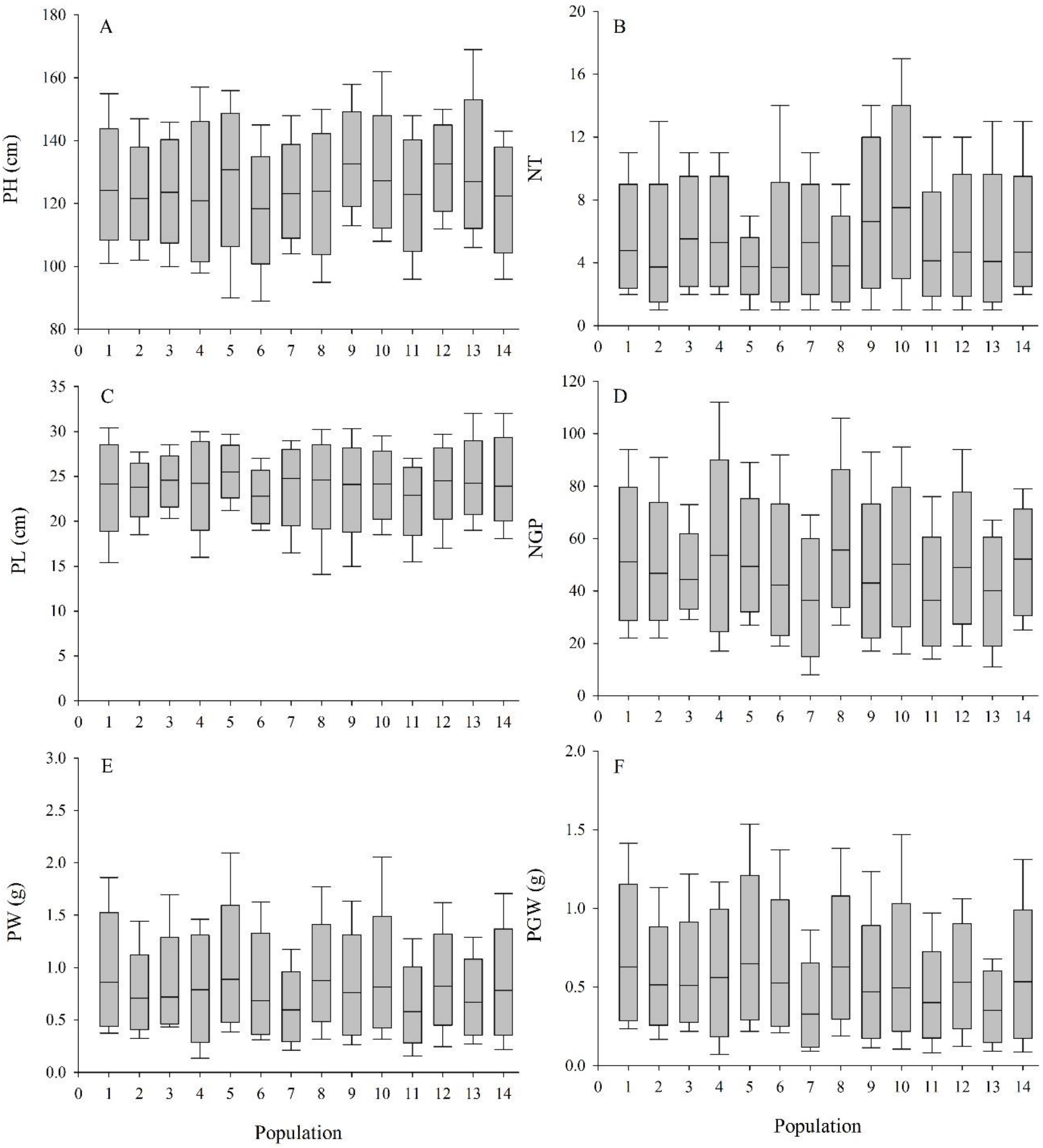

Figure 2. Boxplot of plant height (PH, A), number of tillering (NT, B), panicle length (PL, C), number of grains per panicle (NGP, D), panicle weight (PW, E), panicle grain weight (PGW, F) of 14 black oat populations.

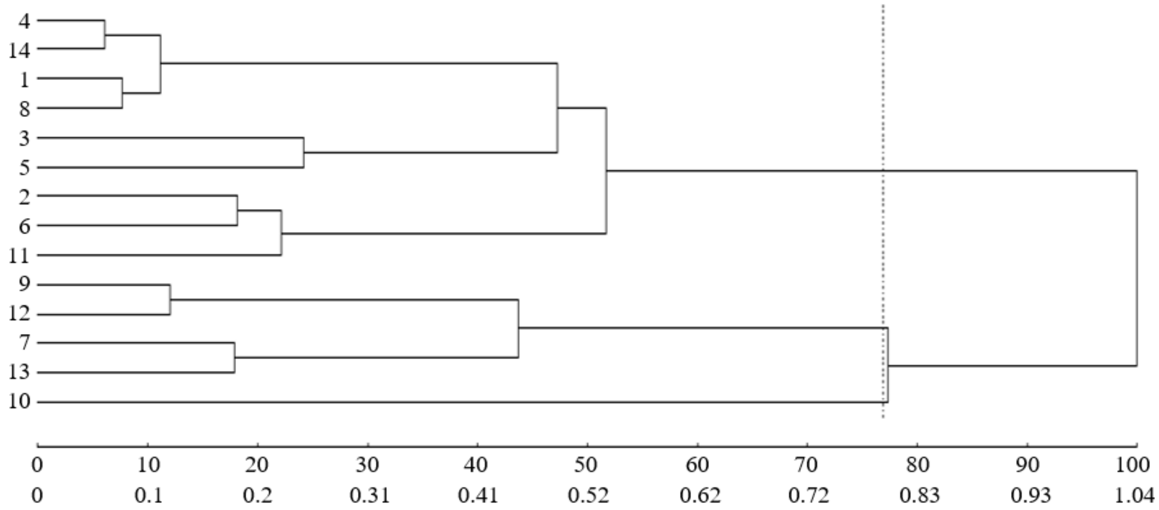

Figure 3. Dendrogram using unweighted pair group method with arithmetic mean (UPGMA) from Mahalanobis generalized distance matrix for 14 populations, obtained by means of phenotypic traits (six traits). Cophenetic correlation coefficient (r): 0.728.

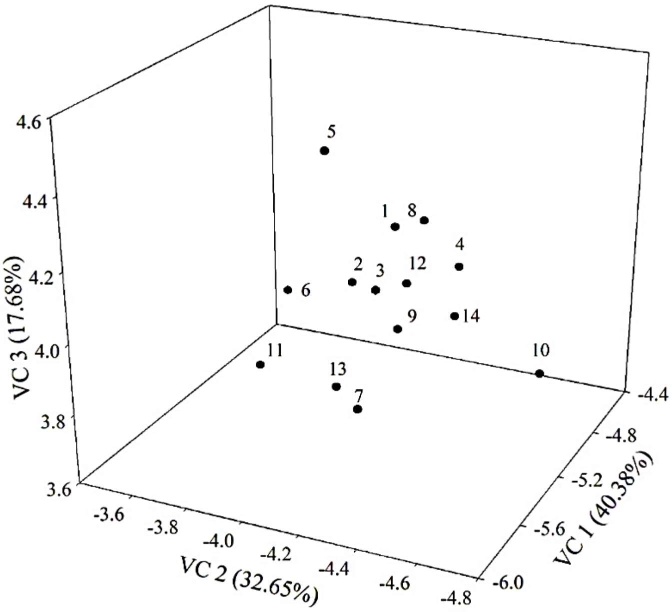

Figure 4. Graphic dispersion of first score (VC 1), second (VC 2) and third canonical variance (VC 3).

Table 1. Summary of variance analysis [degrees of freedom (DF) and mean square (MS) for source of variation], mean ($\bar{x}$) and accuracy ($\hat{r}_{gg}$) for 14 black oat populations.

		MS					
Source of variaion	DF	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}
Among 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						
$\bar{x}^1$		125.10	4.81	24.16	46.54	0.76	0.51
$\hat{r}_{gg}$		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 among ($\hat{\sigma}^2_{fe}$) and within ($\hat{\sigma}^2_{fd}$), genetic variance among ($\hat{\sigma}^2_{ge}$) and within ($\hat{\sigma}^2_{gd}$), heritability among (h^2_e) and within (h^2_d), genetic gain (Gs) for plant height (PH), number of tillering (NT), panicle length (PL), panicle weight (PW), panicle grain weight (PGW), number of grains per panicle (NGP) for 14 black oat populations.

Estimates	PH	NT	PL	NGP	PW	PGW
$\hat{\sigma}^2_{fe}$	180.24	8.95	8.71	340.55	0.12	0.08
$\hat{\sigma}^2_{fd}$	136.04	5.60	8.18	281.58	0.11	0.07
$\hat{\sigma}^2_{ge}$	0.07	0.01	0.04	12.74	0.01	0.01
$\hat{\sigma}^2_{gd}$	91.90	2.26	7.70	235.34	0.01	0.06
h^2_e (%)	0.04	0.14	0.47	3.74	1.20	3.91
h^2_d (%)	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

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), 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

Table 4. Variance (eigenvalues), percentage variance and acumulated variance of canonical variance, aiming to estimate the dissimilarity among 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

4 CAPÍTULO III - PHENOTYPIC VARIANCE IN BLACK OAT GROWING IN AGRICULTURAL YEARS REVEALS PREDOMINANCE OF GENETIC EFFECTS

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Situação: em avaliação

FRONT PAGE

Phenotypic variance in black oat growing in agricultural years reveals genetic effects predominance

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Keywords: *Avena strigosa*, genetic correlation, genetic parameters, plant breeding,

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4.1 ABSTRACT

This work aimed to determine variance components and genetic parameters, as well as phenotypic, genetic and environmental correlations among black oat (*Avena strigosa*) families grown in different agricultural year. Seventy-six families of black oat and three controls (BRS Madrugada, BRS Centauro, BRS 139 Neblina) were evaluated in two agricultural years (2016 and 2017), using families with intercalary controls experimental design. Variance observed between families and control, emphasize that studied families have potential to compose a plant breeding program. Variance components expressed greater genetic variance origin for agricultural years. Since panicle weight and panicle grain weight presented high heritability and, therefore, promising traits for selection. For this, the panicle length can be selected due to phenotypic and genetic correlation with high heritability traits. Divergent meteorological conditions between agricultural years expressed little variation among phenotypic, genetic and environmental correlations, but did not alter magnitude and sense of phenotypic and genetic correlations.

Keywords: *Avena strigosa*, genetic correlation, genetic parameters, plant breeding,

4.2 INTRODUCTION

Recognized among the major winter cereals, black oat (*Avena strigosa* S.) is cultivated worldwide. Its cultivation includes grain yield, forage and mainly soil cover. Despite developmental plasticity over a wide temperature range varying from 0 °C to 35 °C (Leite et al. 2012), crop suffers direct influence of photoperiod and air temperature, and may have variations in cycle (Pedro Júnior et al. 2004; Castro et al. 2012; Leite et al. 2012), and in grain yield (Ferris et al. 1998).

The genotypes x environments (G × E) interaction may vary according to sowing season, local and agricultural year, favoring the complexity of this interaction, showing that direct selection for yield may be mistaken (Bennett et al. 2012; Rebetzke et al. 2012). To quantify this environmental influence, Cruz et al. (2014) emphasize that it is necessary to consider that phenotypic expression of a given trait is a result of genetic plus environment effect, and if grown in more than one environment, G × E interaction effect is added.

Plant breeding programs have increasingly sought oat genotypes with high potential for forage and grain yield. To the present, satisfactory results have been achieved. On the other hand, artificial selection practice to obtain genotypes with high performance, can contributes to genetic variability reduction. Base population characterization of breeding program, in terms of genetic components, becomes relevant to maximize selection gains (Pereira and Amaral JR 2001). Obtaining estimates of variance components and genetic parameters can be achieved with phenotypic evaluations of interest traits (Cruz et al. 2014).

Phenotypic correlation include genetic and environmental effects, so may be stratify each one to better understand correlations. Associations knowledge between traits makes it possible to develop the best selection strategy and from covariances, to estimate selection indexes (Cruz et al. 2014). In addition, the magnitude and sense of correlations reveal association degree and sense between traits, indicating if there is a change in behavior in function of another trait.

Faced with hypotheses formulated: (i) two agricultural years can lead to divergent phenotypic, genetic and environmental variances; (ii) selection made in only one agricultural year is efficient if it was based on variance components; the study aimed to determine the variance components and genetic parameters, as well as phenotypic, genetic and environmental correlations among black oat families grown in different agricultural years.

4.3 MATERIAL AND METHODS

The experiment was carried out at Frederico Westphalen, Rio Grande do Sul, Brazil (27º39'S; 53º42'O, at 461.3 asl), from Jun to Oct 2014 and 2015. The climate is Cfa, described as subtropical with no defined dry season and annual average temperature is 19.6 °C, and annual rainfall is 1.398 mm, and dystrophic red latosol.

The black oat families used in this work is originated from Black Oat Breeding Program. Seventy - six families of black oat and three control (BRS Madrugada, BRS Centauro, BRS 139 Neblina) were used in two agricultural years, using families with intercalary controls experimental design. The sowing of families and controls was carried out on Jun 14 and 12, 2016 and 2017, respectively. Each family was composed of a line of 3 m in length and the controls were seeded intercalated in three replicates. Line spacing was 0.5 m and density of 60 seeds per linear meter. The cultural treatments were carried out according to technical indications for culture.

Traits evaluated were: days from emergence to flowering (EF), considered when 50% of plant of each line had panicle exposed. And when families reached physiological maturity, following traits were determined: plant height (PH, cm), panicle length (PL, cm), number of fertile tiller (NT), panicle weight (PW, g) panicle grain weight (PGW, g) and ratio between panicle weight and panicle grain weight (RPG), these traits were measured in 8 plants of each family.

The meteorological data were obtained from the Instituto Nacional de Meteorologia (INMET), referring to automatic weather station of Frederico Westphalen - RS (A854), located about 350 m from experiment, for cultivation period of 2016 (14 Jun 2016 to 31 Oct 2016) and 2017 (12 Jun 2017 to 10 Oct 2017). For that, instantaneous, maximum and minimum temperature recorded every hour was used, obtaining average for instantaneous, maximum and minimum temperature recorded for day. And for daily precipitation was carried out accumulation on a day.

The variance analysis was performed according to families with intermediate controls experimental design (Cruz 2014). Thus, families were evaluated using controls' variance components as an environmental effect.

The value of each observation for controls is given by the model of regular treatments:

$$Y_{ij} = \mu + T_i + \varepsilon_{ij}$$

Where:

Y_{ij}: value of trait for i-th control in the j-th repetition;

μ: general controls average;

T_i: i-th controls effect (i=1,2,...t);

ε_{ij}: random error involving controls.

And for families, considering non-regular treatments:

$$y_i = \mu_f + F_i + \varepsilon_i$$

Where:

y_i: value of trait for i-th family; μ_f: general families average; F_i: i-th family effect;

ε_i: random error involving families.

For controls have:

$$k = \frac{\mathrm{N}-(\frac{1}{\mathrm{N}}\sum_{\mathrm{i}=1}^{\mathrm{t}} \mathrm{ri}^2)}{\mathrm{t}-1} \text{ e } \mathrm{N} = \sum_{\mathrm{i}=1}^{\mathrm{t}} \mathrm{r_i}$$

Due to statistical model used, with families without repetitions, it is necessary to perform data correction. For this, it is admitted that there is a differential effect of environment between families, and thus, corrected from controls information (Cruz 2014). After data correction, variance components and genetic parameters were estimated for controls and families.

For the study of phenotypic, genetic and environmental correlations, covariance was estimated between two traits, and correlations were later estimated. To carry out all analyzes, was used statistical program Genes (Cruz 2016).

4.4 RESULTS

According to variance analysis, for agricultural year of 2016, PGW for families, and EF, PH, PL for controls revealed difference. In 2017, was observed difference for PH and PGW, for families and EF, PH and PGW for controls.

Temperatures observed during crop period was ideal to culture, with average of 16.2 °C and 17.5 °C for 2016 and 2017, respectively. Highlight temperature in flowering stage (76.8 and 70.6 days after emergence), which occurred in September, for both agricultural years, a minimum, average and maximum temperature of 4.1 °C, 16.3 °C and 33.2 °C in 2016 and 12.8 °C, 21.3 °C and 33.7 °C in 2017. Thus, showing that there was an increase of 5 °C in the average temperature in Sept 2017 compared to Sept 2016.

Figure 1.

Considering accumulated precipitation in crop period was observed 680.2 and 720.8 mm for 2016 and 2017, respectively. Difference between agricultural years in precipitation distribution was observed, and in 2016 rainfall was well distributed throughout crop period. While in 2017, after sowing there was sufficient precipitation for germination and emergence, then there were 27 days without precipitation, with July accumulated of 15.8 mm, lower than historical average for month (130 mm, data not shown).

In comparison to agricultural years, it should be noted that in 2017 there was a reduction of all traits studied (EF, PH, PL, NT, PW, PGW and RPG) in relation to 2016 for both families and controls (Table 1 and 2). This phenotypic difference is linked to meteorological conditions during oat cycle for two agricultural years (Figure 1).

Table 1.

As for phenotypic variance, it is verified that for both families and controls the highest variance is attributed to genetic factor (genetic variance) both in 2016 and 2017 (Table 1 and 2). PH showed the highest values of variance for families and for controls in agricultural years, being variable most influenced by the environmental variation.

The PGW revealed greater stability, when referring to ratio CVg CVe^{-1}, for this index compared to agricultural years, with highest values of 5.315 and 7.204 for 2016 and 2017, respectively, which could lead to more effective selection gains (Table 1 and 2). NT presented higher heritability amplitude, CVg and ratio CVg CVe^{-1}, evidencing in 2016 (Table 1), most favorable meteorological conditions promoted this greater differentiation in phenotypic response of families. Controls showed same tendency as families (Table 1 and 2). EF phenotypic variance was higher for 2017 (Table 2).

Table 2.

In relation to correlation, significant phenotypic correlations showed higher values of genetic correlation. EF showed significant positive phenotypic correlation with PL in 2016, and with RPG in 2017 (Table 3). PH revealed positive and moderate magnitude phenotypic association with PL, PW and PGW (Table 3). The relationship among PL, PW and PGW revealed significant positive and moderate magnitude phenotypic association for agricultural years (Table 3). RPG is directly linked to PW and PGW, showing positive-valued, moderate to high magnitude for genetic and phenotypic correlation.

Table 3.

Regarding environmental correlation between traits, it is observed that associations had variation between agricultural years (Table 3). The association between EF and PH revealed a greater environmental correlation in 2016. Whereas in 2017, association between EF and RPG was observed, evidencing that with EF reduction, consequently RPG also resulted in lower indexes.

4.5 DISCUSSION

The oat crop, has a high plasticity, develops over a wide temperature range, which can vary from 0 °C to 35 °C (Leite et al. 2012). This fact can be confirmed by analyzing meteorological data (Figure 1), for two agricultural years, where it is observed that there was variation of temperature and rainfall between 2016 and 2017.

Average duration of oat cycle is between 118-120 days of emergence to physiological maturation (Carvalho et al. 2009; Oliveira et al. 2011). The cycle of winter cereals grown in southern Brazil is directly influenced by photoperiod and air temperature, and the last predicts the crop cycle (Castro et al. 2012; Leite et al. 2012), and development cycle is accelerated by high temperatures.

In present work, in 2017 black oat cycle was reduced when compared to 2016. This reduction can be allied to long period without precipitation (about from 20 to 45 days after sowing, Figure 1) in the initial development stage and elevated temperature observed during oat development cycle.

It is known that each species has optimum, minimum and maximum temperature of development. Simulation and experiments conducted in field by Mantai et al. (2017) corroborate with these results, noting that for white oat minimum, optimum and maximum cardinal temperatures of 15, 25 and 35 °C, respectively, resulted in a reduction of nine days in cycle when compared to cardinal temperatures of 4, 22 and 30 °C. For wheat, temperature increase is detrimental to grain yield (Deryng et al. 2014), and Asseng et al. (2015) emphasize that every 1 °C increase in temperature, above 31 °C, occurs 6% reduction in grain yield.

Despite requirement of higher temperature and low humidity in maturation stage (Castro et al. 2012), high temperatures (> 31 °C) over four consecutive days at anthesis can result in reducing number of grains, grain weight and, therefore, reducing grain yield (Ferris et al. 1998). Thus, it can be highlighted that 2016 provided better meteorological conditions for oat growth and development.

It was highlight that PGW is a trait to be choice to have more effective gains. Kurek et al. (2002), in research with white oat, due to high coefficients observed suggests that panicle weight is used as a selection criterion, due to practicality of obtaining this trait.

In present study, higher phenotypic variance in 2017, to EF, can be justified by meteorological conditions, in the face of water availability and higher average temperature (Figure 1). Controls showed a shorter time between emergence and flowering, but this reduction was smaller. The lower influence on EF in controls, showing cultivars presented greater stability than the families studied.

Differences observed in genetic parameters, phenotypic and genetic correlations between traits showed similar values for two agricultural years (Table 3). Moreover, significant phenotypic correlations showed higher values of genetic correlation.

Phenotypic correlation showed between EF and PL in 2016, and EF and RPG in 2017, can be explained to vegetative period and longer cycle provide greater potential for production and accumulation of photoassimilates and, therefore, potentiating biomass accumulation (Lehmen et al. 2014) and grain yield (Ferris et al. 1998).

Noting the association among PL, PW and PGW, are important factor for a black oat breeding program, because PL is easy to measure. Vasconcellos et al. (2016), emphasize that the relation of grain weight and bark weight are aspects relevant to oat breeding. Panicle weight may be more efficient in eliminating low yield genotypes in selecting superior genotypes by eliminating lighter panicles (Chapko and Brinkman 1991).

As already pointed out, due to meteorological conditions in 2017 most of associations revealed greater environmental influence. Environmental correlation confirms above statements, that there was an environmental influence in agricultural year, especially in 2017 (Table 3).

Genetic correlations, inheritable fraction, can be caused by pleiotropic effects and/or gene link, and may still have changes due to environmental correlations, varying from year to year or by crop management (Falconer and Mackay 1996). In addition, to environmental variation between agricultural years, there is variation due to the application of fungicide, which influences agronomic traits in white oat (Benin et al. 2005). In this way, due to the environmental influence on traits, selection in more agricultural years and sites is essential.

4.6 CONCLUSION

Variance observed between families and controls, emphasize that families studied have potential to compose a breeding program. Variance components expressed greater genetic variance for agricultural years. Since PW and PGW presented high heritability and, therefore, promising selection traits. For this, PL, an easily measured trait, can be selected due to phenotypic and genetic correlation with high heritability traits.

Divergent meteorological conditions between agricultural years expressed little variation between phenotypic, genetic and environmental correlations, but did not alter magnitude and sense of phenotypic and genetic correlations.

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Table 1. Variance components and genetic parameters estimated for families and controls for agricultural year 2016.

Families							
Parameters	EF[1]	PH	PL	NT	PW	PGW	RPG
Fenotypic variance	9.672	34.431	5.931	8.955	0.150	0.104	0.004
Environmental variance	2.000	7.494	0.888	3.796	0.012	0.004	0.001
Genotypic variance	7.672	26.936	5.043	5.159	0.138	0.101	0.002
Heritability	79.322	78.234	85.024	57.612	92.053	96.581	68.598
CVg	3.628	3.663	9.625	20.882	29.351	34.790	6.949
Razão CVg CVe^{-1}	1.959	1.896	2.383	1.166	3.404	5.315	1.478
Families average	76.36	141.68	23.33	10.88	1.27	0.91	0.71
CV (%) Families	1.85	1.93	4.04	17.91	8.62	6.55	4.70
Controls							
Parameters	EF	PH	PL	NT	PW	PGW	RPG
Fenotypic variance	28.037	86.434	10.198	13.658	0.020	0.017	0.001
Environmental variance	0.667	2.498	0.296	1.265	0.004	0.001	0.000
Genotypic variance	27.370	83.936	9.902	12.392	0.016	0.015	0.000
CVgt	6.495	6.359	12.820	26.008	9.049	12.610	2.787
Ratio CVgt CVe^{-1}	3.699	3.347	3.339	1.807	1.146	2.081	0.555
Controls average	80.56	144.08	24.55	13.54	1.38	0.99	0.67
CV (%) Controls	1.76	1.90	3.84	14.39	7.90	6.06	5.02

[1] EF: days of emergence to flowering; PH: plant height; PL: panicle length; NT: number of fertile tiller; PW: panicle weight; PGW: panicle grain weight; RPG: ratio between panicle weight and panicle grain weight; CVg: coeficiente of genetic variation; CVe: coefficient of experimental variation; CVgt: coefficient of controls genetic variation; CV: coefficient of variation.

Table 2. Variance components and genetic parameters estimated for families and controls for agricultural year 2017.

Families							
Parameters	EF[1]	PH	PL	NT	PW	PGW	RPG
Fenotypic variance	9.171	38.173	3.730	2.070	0.091	0.065	0.007
Environmental variance	1.013	1.905	0.859	0.253	0.005	0.001	0.003
Genotypic variance	8.159	36.268	2.871	1.817	0.086	0.064	0.004
Heritability	88.959	95.009	76.975	87.775	94.121	98.110	62.679
CVg	4.101	4.979	7.744	34.803	25.955	35.060	10.245
Ratio CVg CVe^{-1}	2.839	4.363	1.828	2.680	4.001	7.204	1.296
Families average	69.66	120.96	21.88	3.87	1.13	0.72	0.64
CV (%) Families	1.44	1.14	4.24	12.99	6.49	4.87	7.90
Controls							
Parameters	EF	PH	PL	NT	PW	PGW	RPG
Fenotypic variance	38.399	65.026	0.551	0.256	0.024	0.034	0.010
Environmental variance	0.338	0.635	0.286	0.084	0.002	0.000	0.001
Genotypic variance	38.061	64.391	0.265	0.172	0.023	0.033	0.010
CVgt	7.824	6.372	2.311	13.505	15.580	33.681	17.485
Ratio CVgt CVe^{-1}	6.131	5.814	0.555	0.824	2.051	5.205	1.937
Controls average	78.85	125.94	22.27	3.07	0.96	0.54	0.56
CV (%) Controls	1.28	1.10	4.16	16.39	7.60	6.47	9.03

[1]EF: days of emergence to flowering; PH: plant height; PL: panicle length; NT: number of fertile tiller; PW: panicle weight; PGW: panicle grain weight; RPG: ratio between panicle weight and panicle grain weight; CVg: coeficiente of genetic variation; CVe: coefficient of experimental variation; CVgt: coefficient of controls genetic variation; CV: coefficient of variation.

Table 3. Estimatives of phenotypic (r_P), genetic (r_G) and environmental (r_E) correlations between seven morphological traits in black oat families evaluated in 2016 (upper diagonal) and 2017 (inferior diagonal) agricultural years.

Trait		EF[1]	PH	PL	NT	PW	PGW	RPG
EF	r_P	-	-0.08	0.30**	-0.08	0.21	0.18	-0.01
	r_G	-	-0.32	0.29	0.05	0.30	0.21	-0.05
	r_E	-	0.83	0.36	-0.39	-0.35	-0.07	0.12
PH	r_P	0.00	-	0.48**	0.19	0.40**	0.36**	0.02
	r_G	-0.06	-	0.41	0.36	0.46	0.44	-0.15
	r_E	0.67	-	0.79	-0.18	0.06	-0.22	0.51
PL	r_P	0.15	0.52**	-	-0.17	0.62**	0.54**	0.03
	r_G	0.19	0.60	-	-0.27	0.66	0.61	-0.20
	r_E	-0.03	0.06	-	0.05	0.38	-0.17	0.83
NT	r_P	-0.09	-0.37**	-0.17	-	-0.07	-0.08	-0.14
	r_G	-0.07	-0.40	-0.18	-	-0.29	-0.21	-0.32
	r_E	-0.27	0.01	-0.11	-	0.76	0.63	0.16
PW	r_P	0.18	0.33**	0.50**	-0.02	-	0.98**	0.49**
	r_G	0.15	0.32	0.55	-0.05	-	1.03	0.51
	r_E	0.51	0.46	0.27	0.34	-	0.21	0.57
PGW	r_P	0.21	0.18	0.43**	0.03	0.95**	-	0.65**
	r_G	0.19	0.17	0.49	0.06	0.98	-	0.78
	r_E	0.65	0.42	0.03	-0.54	0.27	-	0.10
RPG	r_P	0.26*	-0.07	0.21	0.06	0.47**	0.67**	-
	r_G	0.10	-0.21	0.18	0.14	0.49	0.83	-
	r_E	0.89	0.62	0.30	-0.20	0.62	0.38	-

**, *Significative to *t* test (p<0.01 and p<0.05). [1]EF: days of emergence to flowering; PH: plant height; PL: panicle length; NT: number of fertile tiller; PW: panicle weight; PGW: panicle grain weight; RPG: ratio between panicle weight and panicle grain weigh

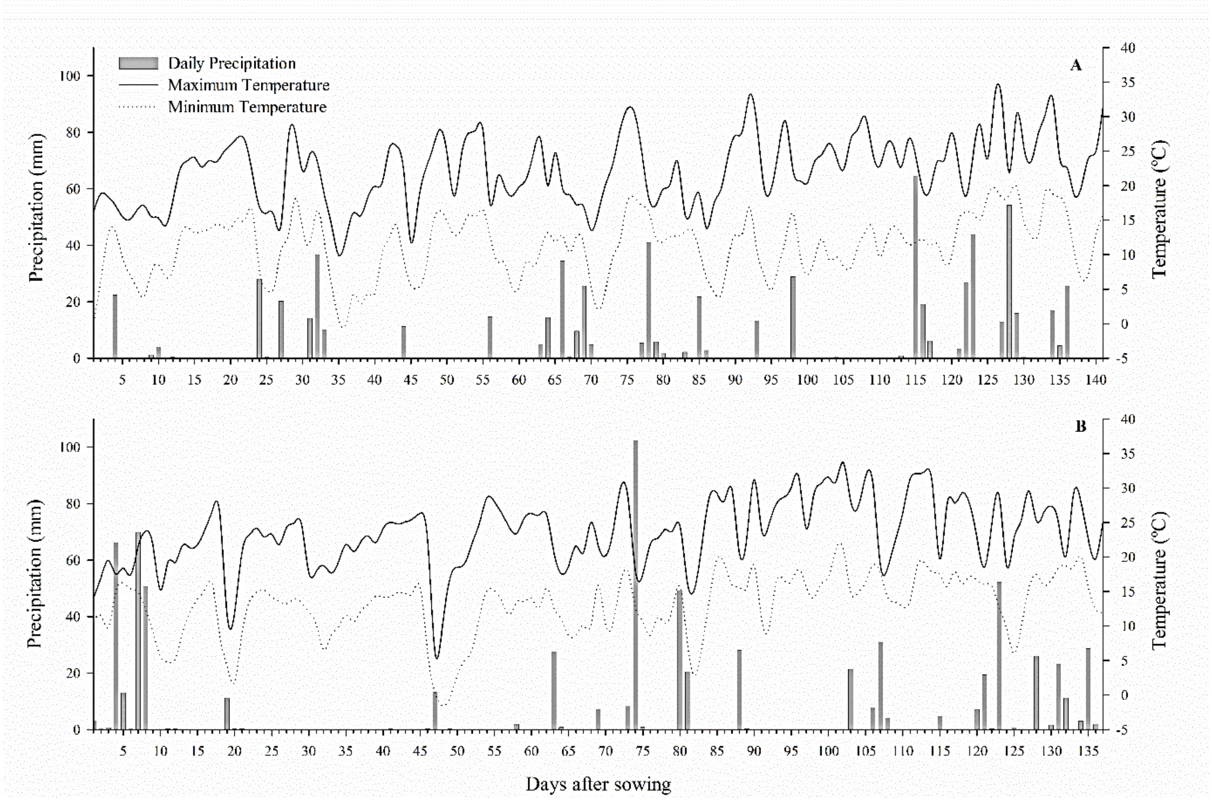

Figure 1. Meteorological data of daily precipitation, maximum and minimum temperatures during black oat cultivation period in 2016 (A) and 2017 (B) agricultural years. Source: INMET, (Frederico Westphalen - A854) Frederico Westphalen automatic weather station – RS.

5 CONSIDERAÇÕES FINAIS

As populações de aveia revelaram presença de variabilidade genética devido à formação de grupos distintos. Sendo assim, cruzamentos direcionados entre indivíduos destes grupos pode gerar populações segregantes com grande variabilidade genética. Essa variabilidade pode vir a contribuir com a diminuição do estreitamento da base genética de aveia preta e ser fonte de germoplasma para buscar características, além de fonte de resistência genética, principalmente a doenças.

Os caracteres massa de mil sementes, percentagem de germinação, largura dos grãos, massa de grãos da panícula contribuem de forma expressiva para a diferenciação de populações de aveia preta. Além disso, para maiores ganhos de seleção de genótipos superiores, pode-se utilizar os caracteres comprimento de panícula, números de grãos, massa de panícula e massa de grãos de panícula. As associações entre largura de grãos e qualidade fisiológica, número de grãos por panícula com rendimento de grãos, e ainda altas herdabilidade reveladas pela massa de panícula e massa de grãos da panícula, devem ser destacadas para a eficiência de seleção.

Apesar das condições divergentes entre as safras agrícolas, a origem genética dos componentes de variância prevalece, além das correlações fenotípicas, genotípicas e de ambiente permanecerem em magnitude e sentido. A variância observada entre as populações e testemunhas, ressalta que pode-se realizar seleção de genótipos superiores, os quais têm potencial para compor um programa de melhoramento.

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