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Phenotypic variance of black oat growing in crop seasons reveals genetic effects predominance

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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 crop season. Seventy-six black oat families and three controls (BRS Madrugada, BRS Centauro, BRS 139 Neblina) were evaluated in two crop seasons (2016 and 2017), using families with intercalary controls experimental design. The results reveled high potential of black oat families to compose a breeding program, due to families and controls variance were similar, variance components expressed greater genetic variance origin for crop season. Panicle weight and panicle grain weight presented high heritability and, these are correlated with panicle length. Thus, these traits can be used to select superior genotypes. Divergent meteorological conditions between crop seasons expressed few variations among phenotypic, genetic and environmental correlations, and it did not alter magnitude and sense of phenotypic and genetic correlations.

Key words: *Avena strigosa*, genetic correlation, genetic parameters, plant breeding.

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). This crop is directly influenced by photoperiod and air temperature, and it can be observed cycle (Castro et al. 2012, Leite et al. 2012) and yield variations according to meteorological conditions (Ferris et al. 1998).

The genotypes x environments (G × E) interaction may vary according to sowing season, local and crop season, favoring the complexity of this interaction, showing that direct selection for yield may be mistaken (Bennett et al. 2012, Rebetzke et

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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 searched oat genotypes with high potential for forage and grain yield. 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 genetic 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 crop seasons can lead to divergent phenotypic, genetic and environmental variances; (ii) selection made in only one crop season 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 crop seasons.

MATERIALS AND METHODS

The trials were carried out at Frederico Westphalen, Rio Grande do Sul, Brazil (27º39’S; 53º42’O, at 461.3 asl), from Jun to Oct in 2014 and 2015 crop season. 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 (Alvares et al. 2013), and the soil is classified as Hapludox.

Black oat families used in this work is originated from Black Oat Breeding Program of Federal University of Santa Maria, campus Frederico Westphalen. Seventy - six black oat families and three cultivars (BRS Madrugada, BRS Centauro, BRS 139 Neblina), considered as control, were growth in two crop seasons. Families with intercalary controls experimental design was used. The sowing was carried out on Jun 14th in 2016 crop season, and Jun 12th in 2017 crop season. 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 crop (Lângaro and Carvalho 2014).

Traits evaluated were: days from emergence to flowering (EF), considered when 50% of plants had panicle. And when families were in physiological maturity, eight plants per family were evaluated: 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).

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 (Jun 14th 2016 to Oct 31st 2016) and 2017 (Jun 12th 2017 to Oct 10th 2017). For that, instantaneous, maximum and minimum air 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 et al. 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:

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

$\mu\mu$: general controls average;

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

$\varepsilon_{ij}\varepsilon_{ij}$: random error involving controls.

And for families, considering non-regular treatments:

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

Where:

y_iy_i: value of trait for i-th family; $\mu_f\mu_f$: general families average; F_iF_i: i-th family effect;

$\varepsilon_i\varepsilon_i$: random error involving families.

For controls have:

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

$$N = \sum_{i=1}^{t} r_i \quad N = \sum_{i=1}^{t} r_i$$

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 et al. 2014). After data correction, variance components and genetic parameters were estimated for controls and families.

For 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).

RESULTS

According to variance analysis, for 2016 crop season, 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 crop seasons, 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.

Considering accumulated precipitation in crop period was observed 680.2 and 720.8 mm for 2016 and 2017, respectively. Difference between crop seasons in precipitation distribution was observed. 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 crop seasons, 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 (Tables I and II). This phenotypic difference is linked to meteorological conditions during oat cycle for two crop seasons (Figure 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

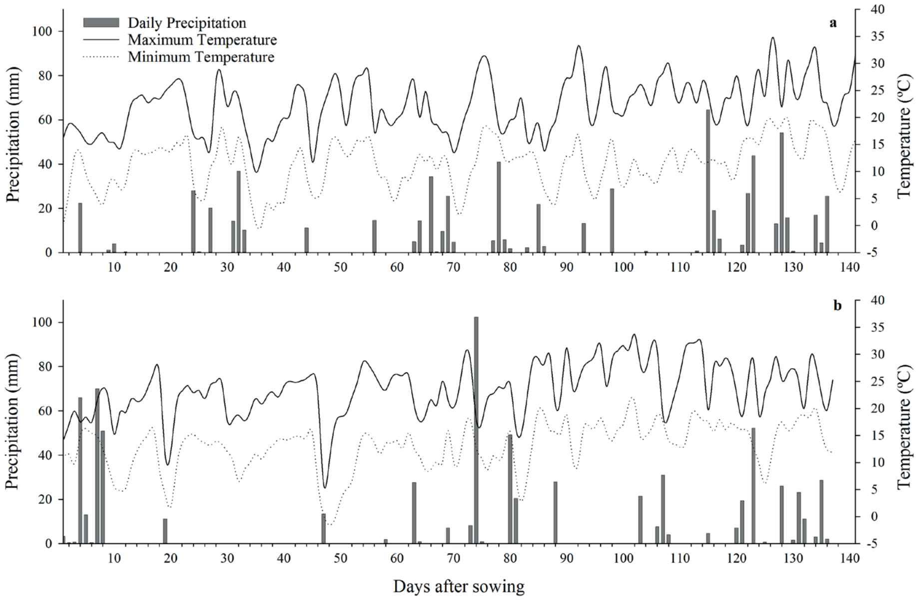

Figure 1 - Meteorological data of daily precipitation, maximum and minimum temperatures during black oat cultivation period in 2016 (**a**) and 2017 (**b**) agricultural years. Source: INMET, (Frederico Westphalen - A854) Frederico Westphalen – RS automatic weather station.

TABLE I
Variance components and genetic parameters estimated for families and controls for 2016 crop season.

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
Ratio 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[1]	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.

in 2016 and 2017 (Tables I and II). PH showed the highest variance values for families and controls in crop seasons, 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 crop seasons, with highest values of 5.315 and 7.204 for 2016 and 2017, respectively, which could lead to more effective selection gains (Tables I and II). NT presented higher heritability amplitude, CVg and ratio CVe CVe^{-1}, evidencing in 2016 (Table I), most favorable meteorological conditions promoted this greater differentiation in phenotypic response of families. Controls showed same tendency as families (Tables I and II). EF phenotypic variance was higher for 2017 (Table II).

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 III). PH revealed positive and moderate magnitude phenotypic association with PL, PW and PGW (Table III). The relationship among PL, PW and PGW revealed significant positive and moderate magnitude phenotypic association for crop seasons (Table III). RPG is directly linked to PW and PGW, showing positive-valued, moderate to high magnitude for genetic and phenotypic correlation.

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

DISCUSSION

Oat crop has a high plasticity to develop 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), in temperature and rainfall variation between 2016 and 2017 crop seasons.

Oat cycle duration varies from 118 to 120 days of emergence to physiological maturation (Carvalho et al. 2009, Oliveira et al. 2011). Winter cereals cycles 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, black oat cycle was reduced in 2017 when compared to 2016 crop season. 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 species has optimum, minimum and maximum air temperature to the best development. Simulation and experiments conducted in field by Mantai et al. (2017) corroborate with these results. The authors noting 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, can reduces 6% 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.

TABLE II
Variance components and genetic parameters estimated for families and controls for 2017 crop season.

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[1]**	**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.

It was highlighted that PGW can be used to select superior genotypes, and reach effective genetic 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 crop seasons (Table III). 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 photoassimilates production and accumulation, 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. Vasconcelos et al. (2016), emphasize that the relation of grain weight and bark weight are aspects relevant to oat breeding. Panicle weight may be

TABLE III
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) crop seasons.

Trait		EF[1]	PH	PL	NT	PW	PGW	RPG
EF[1]	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 weight.

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 crop season, especially in 2017 (Table III).

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 crop seasons, 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 crop seasons and locals are essential.

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 crop seasons. Panicle weight and panicle grain weight presented high heritability and, these are correlated with panicle length. Thus, these traits can be used to select superior genotypes. Divergent meteorological conditions between crop seasons 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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AUTHOR CONTRIBUTIONS

DM and CM performed data collection, wrote and organized the manuscript; TO and MN, performed data analysis, wrote and organized the manuscript; AR, LAK performed data collection; BOC, VSM, VQS were the advisors, critically revised the manuscript and approved the final version.

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