



Genetic parameters and genetic dissimilarity of Gower in black oat

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ABSTRACT: This research evaluated the agronomic performance through mixed models, and determined the genetic divergence between black oat genotypes. The experiment was carried out at Federal University of Santa Maria, Frederico Westphalen/RS. Fourteen black oat genotypes were evaluated, being 11 lines developed by Breeding Program of University, and three commercial cultivars (IAPAR 61, UPFA 21 - Morezinha and, IPR Cabocla). We evaluated quantitative traits associated to plant height, cycle, dry mass yield and seeds yield; and 19 qualitative traits, being these morphological descriptors. The results showed that lines UFSMFW 2-05 and UFSMFW 2-07 stand out with characteristics such as early cycle, higher dry mass and grain yield. Divergence analysis revealed the formation of three distinct groups, indicating the presence of variability. These results suggested the potential for the development of new cultivars of black oat, presenting early cycle and good grain yield.

Key words: *Avena Strigosa* S., mixed models, genetic divergence.

Parâmetros genéticos e dissimilaridade genética de Gower em aveia preta

RESUMO: O objetivo deste trabalho foi avaliar o desempenho agrônômico por meio de modelos mistos e determinar a divergência genética entre genótipos de aveia preta. O experimento foi conduzido na Universidade Federal de Santa Maria, campus de Frederico Westphalen/RS. Catorze genótipos de aveia preta foram avaliados, sendo 11 linhagens desenvolvidas pelo Programa de Melhoramento da Universidade e três cultivares comerciais (IAPAR 61, UPFA 21 - Morezinha e IPR Cabocla). Foram avaliadas características agrônômicas quantitativas relacionadas ao porte, ciclo e produtividade de massa seca e de sementes; e 19 características qualitativas, sendo estes descritores morfológicos. Os resultados mostraram que as linhagens UFSMFW 2-05 e UFSMFW 2-07 se destacam com características como ciclo precoce, elevada produtividade de massa seca e de sementes. A análise de divergência revelou a formação de três grupos distintos, indicando presença de variabilidade. Os resultados demonstram o potencial de desenvolvimento de novas cultivares de aveia preta, apresentando precocidade e boa produtividade de sementes.

Palavras-chave: *Avena Strigosa* S., modelo misto, divergência genética.

INTRODUCTION

Black oat (*Avena strigosa* S.) is a winter cereal most cultivated in Rio Grande do Sul state (DEBIASI et al., 2007). Black oat cultivation has been increased due to high grain yield, forage quality and soil cover potential (SILVEIRA et al., 2014). There is an estimation that Rio Grande do Sul State is responsible for more than 70% of oat cultivation area in the country (CONAB, 2021).

The black oat cultivars available at market is still limited, this fact open new opportunities to breeding programs. Currently, the focus has been on the development of cultivars adapted to specific

environments, with uniformity, short cycle, reduced plant height and with potential for dry mass and grain yield (KLEIN et al., 2019).

Genetic variability is important to obtain continuous genetic gains in development of new cultivars (SILVEIRA et al., 2014). However, the environment effects on phenotype makes the selection not so easy for breeders (BERTOLDO et al., 2009). In this sense, the identification, accumulation and, perpetuation of desirable genes for quantitative traits may be facilitated by variance components and genetic parameters information (MEIRA et al., 2019).

Use of mixed models improve the selection efficiency of autogamous plants selection because those

with genotypic merit are identified (RAMALHO & ARAÚJO, 2011). Predict genetic values using Best Linear Unbiased Prediction (BLUP), with variance components estimated by Restricted Maximum Likelihood (REML) have shown successful results (RESENDE, 2007), and have been used in several crops.

In breeding programs innumerable traits are observed in a genotype. This characterization provides useful information to understand and use the genetic diversity (CERQUEIRA-SILVA et al., 2014), such as cultivars recommendation and choose potential combinations to be used in crosses. For this, the agglomerative methods are used in genetic divergence studies. Among them, there is the GOWER (1971) method, that allows to analyze the genetic divergence matching quantitative and qualitative traits. This statistical method has been successfully used in several crops, such as soybean (FOLLMANN et al., 2019; SILVA et al., 2022), coffee (FERRÃO et al., 2021), elephant grass (VIDAL et al., 2021), wheat (VIKRAM et al., 2019; MEIER et al., 2021) and oat (FOGARTY et al., 2019; PODYMA et al., 2019).

Thus, this study evaluated agronomic performance of black oat line and cultivars using mixed models, and analyzed genetic divergence through Gower algorithm based on quantitative and qualitative traits.

MATERIALS AND METHODS

The experiment was carried out in 2018, at Federal University of Santa Maria, Frederico Westphalen Campus (27° 23'26" S, 53°25'43" W and altitude of 461.3 m). Climate is classified as Cfa, humid subtropical without hot summer with annual precipitation mean of 2,100 mm, according to the Köppen climate classification (ALVARES et al., 2013). The soil is classified as Latossolo Vermelho Distrófico (SANTOS et al., 2018).

In this study, 11 homozygous black oat lines developed on Breeding Program of University were evaluated named as UFSMF 2-01, UFSMF 2-02, UFSMF 2-03, UFSMF 2-04, UFSMF 2-05, UFSMF 2-06, UFSMF 2-07, UFSMF 2-08, UFSMF 2-09, UFSMF 2-10 and UFSMF 2-11. Furthermore, three commercial cultivars were used as checks - UPFA 21 - Moreninha, IPR Cabocla and IAPAR 61, totalizing 14 genotypes.

Experimental trials were carried out in a randomized block design, with three replicates. The plots consisted of six 5-m-long rows spaced 0.17 m apart. On May 29th 2018, seeds were sown in plots at a density of 300 seeds m⁻². Base fertilization was

applied according to soil analysis, and disease, pests and weed control were performed following technical recommendation to black oat (COMISSÃO BRASILEIRA DE PESQUISA DE AVEIA, 2014).

Quantitative traits analyzed were days from emergence to flowering (DEF, days), total fresh mass (TFM, kg ha⁻¹), total dry mass (TDM, kg ha⁻¹), collected in flowering stage – when 50% of plants had panicle. After maturity stage, were performed the harvest and measured 10 plants per plot to plant height (PLH, cm), number of fertile tillers per plant (NTP), panicle weight (PNW, g), panicle grain weight (PGW, g), and grain yield (GY, kg ha⁻¹).

In order to better represent the genetic divergence, 19 qualitative traits were evaluated: growth habit, hairiness of leaf sheath, hairiness of leaf margin, frequency of plants with recurved flag leaf, flag leaf position, upper node hairiness, intensity of upper node hairiness, shape of panicle, angle of panicle branches to the main axis, spikelet position, glume length, floral axis length, glume shape, hairiness at basal part of primary grain, grain base fur length, rachilla length, waxiness of lemma, lemma color, and scurs type.

Components of variance were obtained by Restricted Maximum Likelihood (REML), using expectation-maximization algorithm (DEMPSTER et al., 1977). After deviance analyses, were performed the difference between deviances with and without effect models, resulting in getting the likelihood ratio (LR) (DEMPSTER et al., 1977).

A likelihood ratio test (LTR) was performed to evaluate random effects meaningful, and probability obtained by two-tailed chi-square with one degree of freedom (DEMPSTER et al., 1977). Genetic values were predicting by BLUP (Best Linear Unbiased Prediction) considering mixed model: $y = Xb + Zi + \varepsilon$, where y is vector of response variable; X is the matrix of known fixed effects; b is fixed effect vector of the unknown block and no observable; Z is the matrix incidence of random effects (known); i is vector of unknown random effects; ε is the residual random vector; considering n is the number of observations, p is the number of parameters and q is the number of random effects.

The confidence intervals for BLUPs were estimated according to the equation:

$$CI = Gv \pm t[(1 - r^2\hat{\alpha}) \sigma_g^2]^{0.5}$$

where CI is the confidence interval; Gv is the genotypic value; t is the value of Student's t distribution associated to a given significance level two-tailed test (considering $\alpha = 0.05$); $r^2\hat{\alpha}$ is the selective accuracy; and σ_g^2 is the genotypic variance.

Genetic divergence was studied using quantitative and qualitative variables, and using Gower algorithm (GOWER, 1971). In this sense, S_{ij} is the distance between the genotypes i and j , considering k variables, the distance is estimated by:

$$S_{ij} = \frac{\sum_{k=1}^p W_{ijk} \times S_{ijk}}{\sum_{k=1}^p W_{ijk}}$$

where k is the number of variables ($k = 1, 2, \dots, p$ = total number of evaluated traits); i and j , of any two individual; W_{ijk} is the weight for the comparison ijk , being value 1 for valid comparisons and 0 for invalid comparisons (when values are omitted for one or both genotypes); S_{ijk} is the contribution of the variable k in the divergence between the genotypes i and j , assuming values between 0 and 1. For a nominal variable, if the value of the variable k is the same for both genotypes, i and j , then $S_{ij} = 1$, otherwise, $S_{ij} = 0$. Considering a continuous variable, $S_{ijk} = 1 - |x_{ik} - x_{jk}| / R_k$ in which x_{ik} and x_{jk} are the values of the variable k for the individuals i and j , respectively, and R_k is the amplitude of the variable k in the dataset. The division by R_k remove the differences between variables scale, generating values between 0 and 1 and equal weights. The distance matrix was estimated using “gower.dist” function of StatMatch package (D’ORAZIO, 2017) in R software version 4.0.2 (R CORE TEAM, 2020).

Hierarchical clustering was obtained by the Unweighted Pair-Group Method Using an Arithmetic Average (UPGMA) method, using the Gower’s distances matrix. The number of groups was estimated

using the “pvclust” function of the pvclust package (SUZUKI & SHIMODAIRA, 2006) in R software version 4.0.2 (R CORE TEAM, 2020). This function assesses the uncertainty in hierarchical cluster analysis using multi-scale bootstrap resampling, based on 10,000 resampling, groups with approximately unbiased p-value < 0.05 were considered significant. The association between the graphical and original distance matrices was determined by the cophenetic correlation coefficient (CCC) (SOKAL & ROHLF, 1962). The CCC significance was determined by Mantel test with 1,000 permutations.

RESULTS AND DISCUSSION

Analyzing the variance components (Table 1), high values of genetic variance were obtained for all evaluated traits, indicating that a large part of the variation is due to genetic cause. Highest genetic variance was observed to days from emergence to flowering (DEF), reaching 98.76% of variation. Lowest value was found to NTP (72.09%), denoting that among the studied traits, NTP have more environmental effect.

The values observed in this study is superior than reported by COIMBRA et al. (2005), studying genetic parameter to white oat, and reached by MEIRA et al. (2019) in black oat. These studies highlight that phenotypic variance explained to low values of genetic variance are regular in quantitative traits, due to these traits are linked to the expression of many genes with little effect on the phenotype.

Table 1 - Likelihood ratio test, variance components and genetic parameter of 14 black oat genotypes for days from emergence to flowering (DEF), plant height (PLH), number of fertile tillers per plant (NTP), panicle weight (PNW), panicle grain weight (PGW), total fresh mass (TFM), total dry mass (TDM), grain yield (GY).

Parameters	DEF (dias)	PLH (cm)	NTP (n°)	PNW (g)	PGW (g)	TFM (kg ha ⁻¹)	TDM (kg ha ⁻¹)	GY (kg ha ⁻¹)
Vg	118.47 (98.76%)	63.74 (76.22%)	0.15 (72.09%)	0.02 (82.98%)	0.04 (93.35%)	71,623,703.92 (92.42%)	1,950,747.00 (90.88%)	481,638.51 (94.43%)
Ve	1.48 (1.24%)	19.88 (23.78%)	0.05 (27.91%)	0.004 (17.02%)	0.003 (6.65%)	5,870,571.32 (7.58%)	195,658.98 (9.12%)	28,411.19 (5.57%)
Vp	119.50	83.62	0.20	0.02	0.04	77,494,275.25	2,146,405.99	510,049.71
h2	0.98	0.76	0.72	0.83	0.93	0.90	0.91	0.94
h2mg	0.99	0.91	0.88	0.93	0.97	0.97	0.96	0.98
Selective accuracy	0.99	0.95	0.94	0.96	0.98	0.90	0.93	0.99
General mean	91.41	143.62	3.29	1.42	1.17	42,000.96	6,923.35	2,815.13
CVg (%)	11.90	5.56	11.60	9.84	17.36	20.14	20.17	24.65
Ratio CVg Cve	8.91	1.79	1.60	2.21	3.75	3.49	3.16	4.12
LRT	100.01	25.31	21.56	33.32	56.81	53.47	4.81	61.29
p-value	1.52E-23	4.89E-07	3.42E-06	7.78E-09	4.78E-14	2.61E-13	2.82E-12	4.92E-15

Vg: genetic variance; Ve: environmental variance; Vf: phenotypic variance; h2: broad heritability; h2mg: heritability based on mean; CVg: coefficient of genetic variation; Cve: coefficient of environmental variance.

Despite the divergence of genetic variance values found in this study and in the literature, this can be explained by the estimates of genetic parameters that are valid for a specific population and given environmental conditions (ALLARD, 1971).

For all traits were observed high heritability values, showing good perspectives of genetic gain. These values guarantee high selection precision, related to selective accuracy between 90% to 99%, classified as high magnitude according to RESENDE & DUARTE (2007). Selective accuracy mediates selection precision and to correlation between real genetic value and predictive one (PIMENTEL et al., 2014). The values found for the coefficients of genetic variation indicated the presence of genetic variability, which is desired when looking for superior genotypes.

The likelihood test revealed statistical significance for the estimated random effects of genotypes for all evaluated traits (Table 1). BLUP values to DEF (Figure 1) showed positive effects for cultivars IAPAR 61 and UPFA 21 - Moreninha, and black oat lines UFSMFW 2-08, UFSMFW 2-09 and, UFSMFW 2-11. For the lines UFSMFW 2-07, UFSMFW 2-05, UFSMFW 2-10, UFSMFW 2-01, UFSMFW 2-02, UFSMFW 2-04, UFSMFW 2-03 and, UFSMFW 2-06, and cultivar IPR Cabocla, the genetic effects were negatives. It is worth mentioning that the genotypic effect is represented in figures by the difference between the dot and the dashed line, which represents the general mean of the trait.

Reducing emergence to flowering period brings advantages, such as an earlier cycle, allowing for the anticipation of the subsequent crop and, therefore, is a desired trait in breeding programs. The line UFSMFW 2-07 showed earlier cycle, with DEF (83.03 days), followed by UFSMFW 2-05, UFSMFW 2-10, UFSMFW 2-01, UFSMFW 2-02 and, UFSMFW 2-04 (Figure 1). These black oat lines have potential to be a new cultivar with earlier cycle, a great advantage compared to IAPAR 61 with 123.86 days to DEF, statistically different from lines and cultivars. The cultivar IAPAR 61 is considered to have a long cycle, and in the state of Paraná its cycle is around 134 days (IAPAR, 2006).

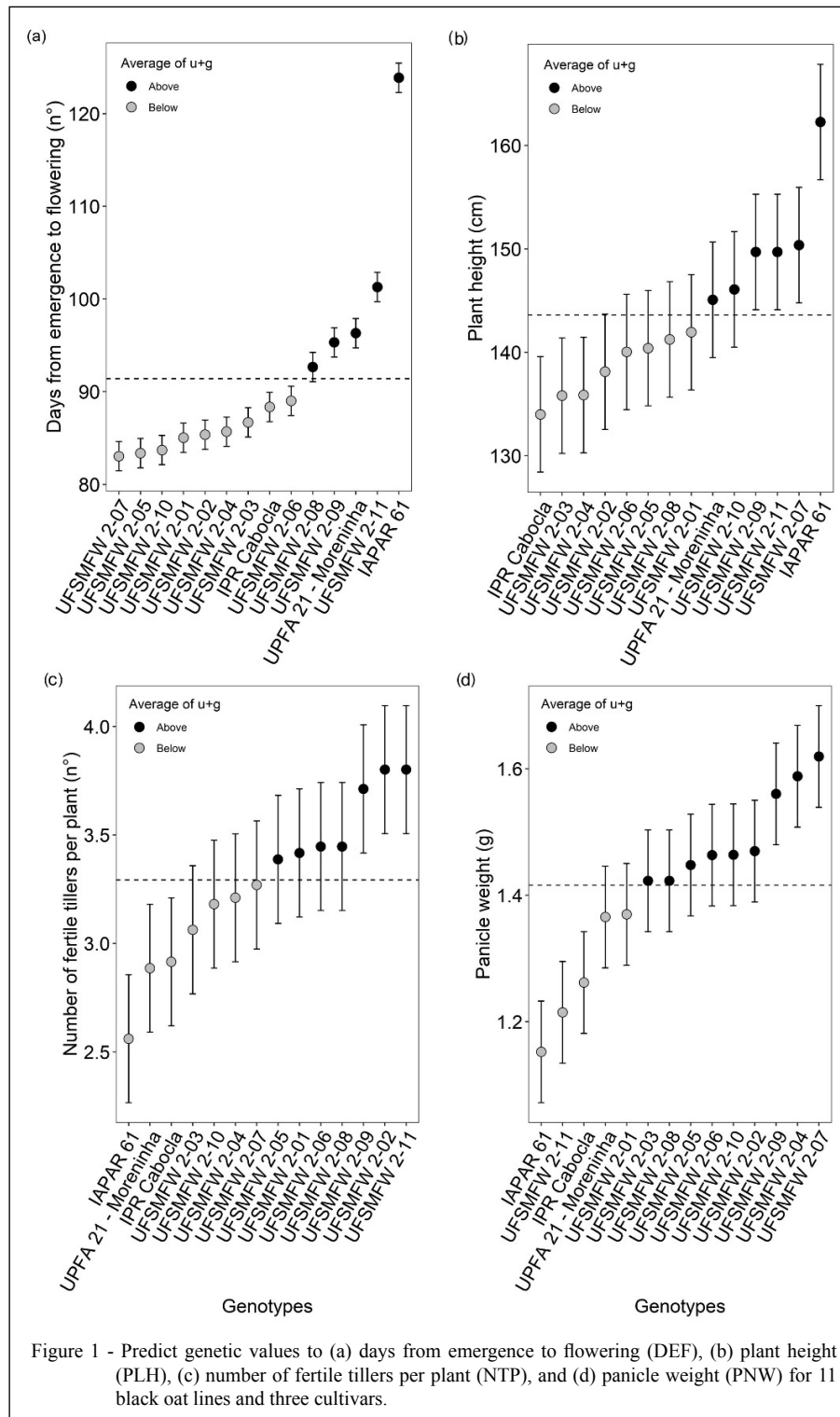
Higher predict mean for PLH, statistically different from others black oat cultivars and lines was IAPAR 61 (Figure 1). Negative genotypic effect to PLH was observed to IPR Cabocla and to UFSMFW 2-03, UFSMFW 2-04, UFSMFW 2-02, UFSMFW 2-06, UFSMFW 2-05, UFSMFW 2-08 and, UFSMFW 2-01. These lines show desirable genetic effects, because of the less plant height is an important trait to reduce plant lodging.

The number of fertile tillers per plant is a relevant trait to winter crops. Each tiller will present in its constitution stem and leaves, contributing to a greater dry mass production. Furthermore, the fertile tillers show panicles to improve grain yield. Thus, line UFSMFW 2-05, UFSMFW 2-01, UFSMFW 2-06, UFSMFW 2-08, UFSMFW 2-09, UFSMFW 2-02 and, UFSMFW 2-11 showed positive genetic effects for NTP (Figure). The tillering capacity is an important characteristic for black oat, as it confers plasticity in supporting plant density variations. However, it also depends on the edaphoclimatic conditions, as seen earlier, in this study this trait was greatest effected by environment. MUNDSTOCK (1999) highlighted high temperatures and low soil fertility as factors that reduce tillering potential.

The BLUP for PNW showed positive genotypic effect to lines UFSMFW 2-03, UFSMFW 2-08, UFSMFW 2-05, UFSMFW 2-06, UFSMFW 2-10, UFSMFW 2-02, UFSMFW 2-04 and, UFSMFW 2-07 (Figure). The line UFSMFW 2-07 presented higher predict mean for PNW (1.61 g). BENIN et al. (2003) observed direct effects and high magnitude of PNW on grain yield in white oat. Direct selection by PNW can be used efficiently to increase grain yield in oat (MARCHIORO et al., 2004). For PGW (Figure 2), except for UFSMFW 2-11, all lines and cultivars showed desirable genotypic effects, i.e., over than the general mean and, the lines UFSMFW 2-06 and UFSMFW 2-04 were superior statistically, showing great potential to grain yield. The BLUP value of PGW was to IAPAR 61, with 0.59 g.

In regarding to biomass, the TFM and TDM showed positive genotypic effects for cultivars UPFA 21- Moreninha and IAPAR 61 (Figure 2). The higher TDM was observed to IAPAR 61 with 9,314.87 kg ha⁻¹ and the line UFSMFW 2-01 (Figure 2). The high dry mass productivity for these cultivars was expected, due to their development for forage production. DEMÉTRIO et al. (2012) found superior dry mass production of 12,171 kg ha⁻¹ to IAPAR 61. On the other hand, NASCIMENTO JÚNIOR et al. (2015) evaluating 12 field trails including UPFA 21 - Moreninha, showed mean of 5,837 kg ha⁻¹ for dry mass production. The long cycle of cultivars allows greater mass accumulation due to period from emergence to reach flowering.

The lines UFSMFW 2-04, UFSMFW 2-07, UFSMFW 2-05, UFSMFW 2-02 and, UFSMFW 2-01 also presented positive genotypic effects to TDM, that did not differ from the cultivar check UPFA 21 - Moreninha (Figure 2). These black oat lines



- UFSMFW - showed good potential of dry mass production and a great advantage to get it in a short time, due to short cycle. Several benefits have been attributed to black oat straw, bringing great impact

of this culture to the no-tillage system. According to SANTOS et al. (2015), keeping straw on the soil surface protects against the impact of raindrops, consequently reducing soil erosion. FERREIRA et

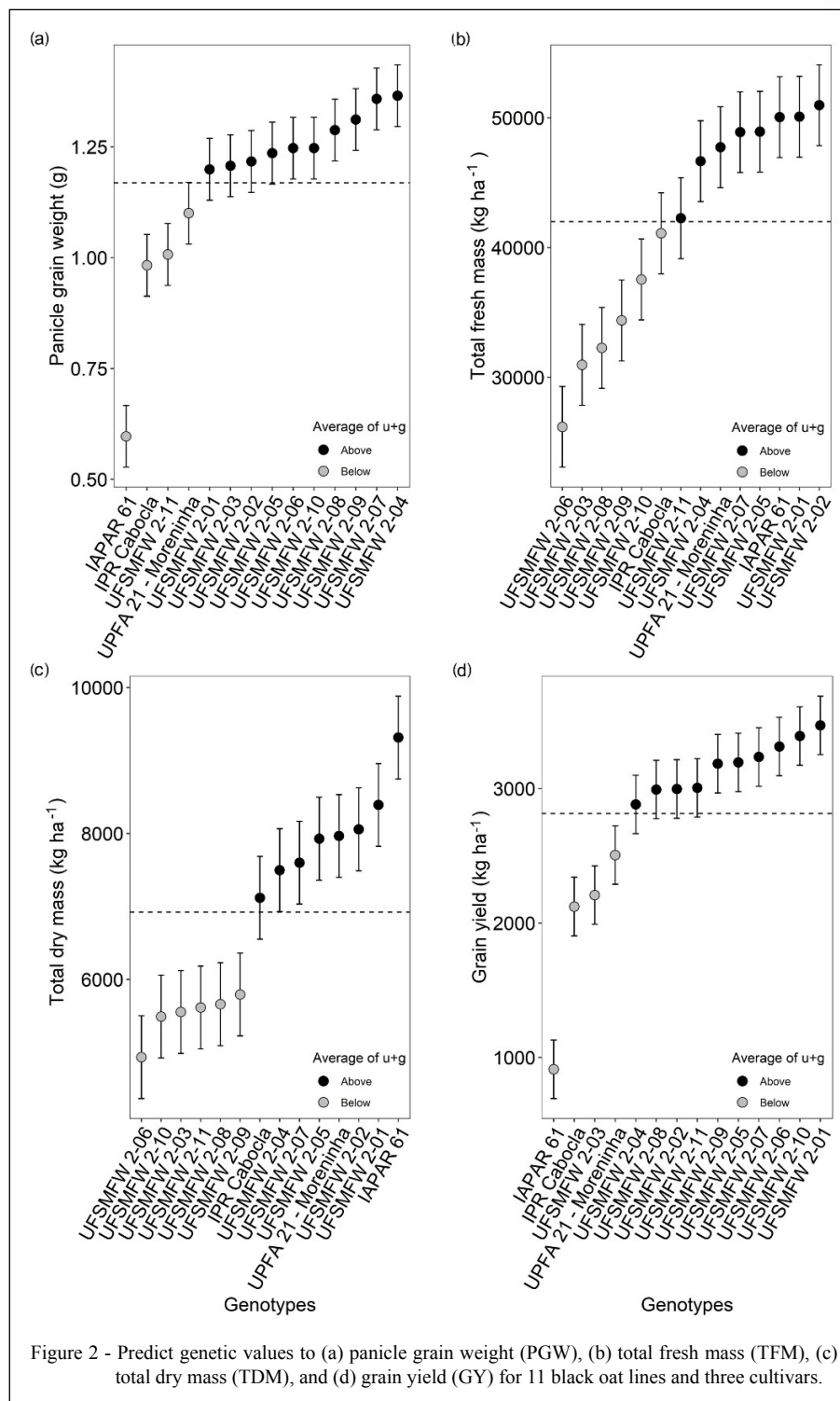


Figure 2 - Predict genetic values to (a) panicle grain weight (PGW), (b) total fresh mass (TFM), (c) total dry mass (TDM), and (d) grain yield (GY) for 11 black oat lines and three cultivars.

al. (2009) emphasized that straw reduces the effects of drought by protecting the soil from evaporation. SÁ et al. (2010) reported higher root development and higher grain yield in corn hybrid, due to black oat dry

mass as predecessor crop. According to ZANELLA et al. (2020), using black oat-soybean crop is a viable practice in system fertilization. These authors highlighted that fertilization management in the cover

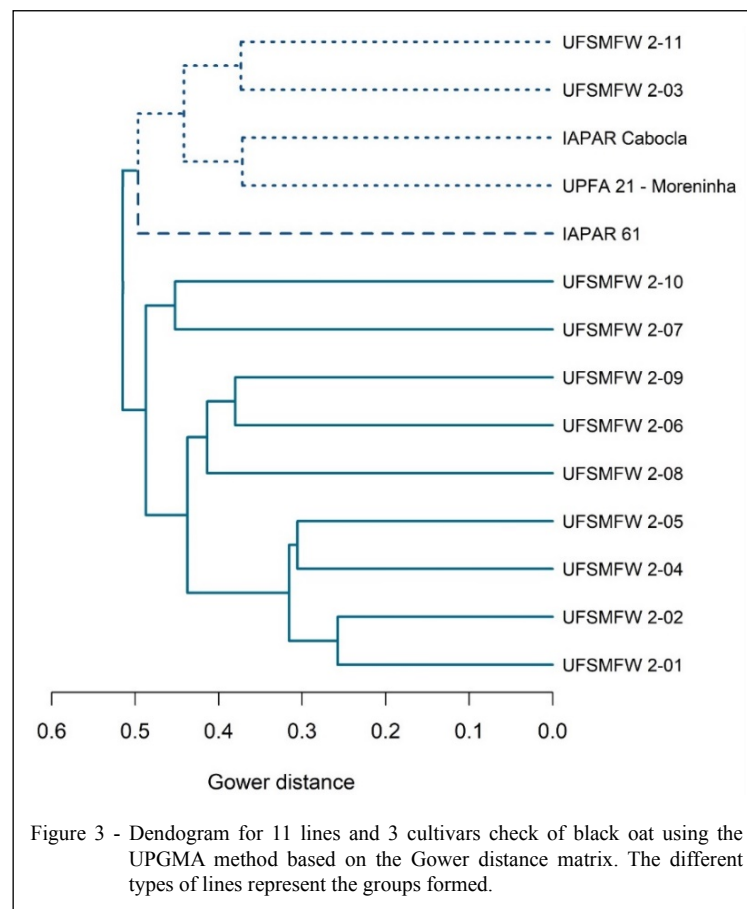
crop taking advantage of more attractive fertilizer prices, it favors higher dry mass production in cover crops, better nutrient utilization by row spacing of these crops, without losses in soybean yield.

Regarding to grain yield, the lines were superior than check cultivars (Figure 2). The best black oat lines were UFSMFW 2-01, UFSMFW 2-10, UFSMFW 2-06, UFSMFW 2-07, UFSMFW 2-05 and, UFSMFW 2-09, reaching grain yield over than 3,000 kg ha⁻¹. The cultivars UPFA 21 - Moreninha, IPR Cabocla and IAPAR 61 showed negative effects to predict grain yield of 2,504.71 kg ha⁻¹, 2,122.38 kg ha⁻¹ and 911.58 kg ha⁻¹, respectively. The increase in black oat grain yield is an aimed trait in breeding programs, due to current low grain yield. Grain yield potential of these lines may be important for the maintenance of black oat in cropping systems, where cultivation for dry mass and soil cover is predominant today.

Cluster analysis using UPGMA method based on Gower's distance matrix, presented three different groups, considering 5% of error probability (Figure 3). Groups are represented by different types

of lines. Group 1 (dotted line) was composed by the genotypes: UFSMFW 2-11, UFSMFW 2-03, IPR Cabocla and, UPFA 21 - Moreninha. Group 2 (dashed line) composed by only the genotype IAPAR 61. Group 3 was represented by UFSMFW 2-10, UFSMFW 2-07, UFSMFW 2-09, UFSMFW 2-06, UFSMFW 2-08, UFSMFW 2-05, UFSMFW 2-04, UFSMFW 2-02 and UFSMFW 2-01. The cophenetic correlation coefficient was 0.70, which indicated a good graphic representation of the original distance matrix (SOKAL & ROHLF, 1962).

The positioning of the UFSMFW black oat lines in different groups from the check cultivars, with the exception of UFSMFW 2-11 and UFSMFW 2-03, demonstrated the potential for developing new cultivars with quantitative and qualitative traits that differ from cultivars available at the market. Cultivars with different agronomic traits, such as plant type, cycle, plant height, dry mass, and grain yield, are desired by producers and important for the versatility of this culture, in the face of competition with other species cultivated in the Brazilian winter.



CONCLUSION

Black oat lines UFSMF2W 2-01, UFSMF2W 2-05, UFSMF2W 2-07 and, UFSMF2W 2-01 showed desirable predict genetic values for cultivar development with early cycle and superior grain and dry mass yield potential. The positioning of most UFSMF2W black oat lines in different groups from the check cultivars, proved the potential of these lines to become new commercial black oat cultivars.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest. The founding sponsors had no role in the design of the study; in the collection, analyses, or interpretation of data; in the writing of the manuscript, and in the decision to publish the results.

AUTHORS' CONTRIBUTIONS

All authors contributed equally for the conception and writing of the manuscript.

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