UDESC

Genetic dissimilarity and agronomic performance of mutant and recombinant white oat progenies

Dissimilaridade genética e desempenho agronômico de progênies mutantes e recombinantes de aveia branca

João Pedro Dalla Roza [1(ORCID 0000-0001-7947-4900)], **Ivan Ricardo Carvalho** [*1(ORCID 0000-0001-7947-4900)], **Leonardo Cesar Pradebon** [2(ORCID 0000-0001-7827-6312)], **Murilo Vieira Loro** [2(ORCID 0000-0003-0241-4226)], **Jaqueline Piesanti Sangiovo** [1(ORCID 0000-0002-7599-9926)], **Gabriel Mathias Weimer Bruisma** [1(ORCID 0000-0001-8727-161X)], **José Antonio Gozalez da Silva** [1 (ORCID 0000-0002-9335-2421)]

[1]Universidade Regional do Noroeste do Rio Grande do Sul, Ijuí, RS, Brazil. *Corresponding author: carvalho.irc@gmail.com
[2]Universidade Federal de Santa Maria, Santa Maria, RS, Brazil.

ABSTRACT

White oat (*Avena sativa* L.) is the winter cereal with the highest nutritional quality, offering multifunctional characteristics due to its benefits to human health, animal nutrition and soil cover. In this way, this crop is highly valued in society. The aim of this study were to evaluate agronomic performance and verify whether there is genetic variability in recombinant and mutant segregating progenies of white oat. The study was conducted at Escola Fazenda UNIJUI (IRDeR), located in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil. The experimental design used followed an augmented block with interspersed controls. A total of 460 white oat progenies were sown and the intercrop control was represented by the cultivar URS Taura, arranged in three replications. The collected data were subjected to descriptive analysis to identify the number of informative progenies and the maximum, minimum, and average values for the measured variables. Frequency distribution graphs of characters with continuous distribution were generated, stratified by mutant and recombinant progenies. Based on the data obtained, a Bayesian approach was used with generalized mixed models through Monte Carlo and Markov Chains (MCMC). With this information, the genetic (VCV) and phenotypic variance components were estimated with significance based on the 5% probability by χ^2 (pMCMC). Afterwards, Euclidean distances were calculated and the distance dendrogram was carried out using the UPGMA clustering algorithm. Pearson's linear correlation coefficients were calculated between pairs of variables, with significance verified by the t test at 5% probability. The mutant progenies have greater tillering capacity, while the recombinant progenies have greater tolerance to diseases and lower natural grain threshing. There is a clear genetic variability between recombinant and mutant progenies for the evaluated characters.

KEYWORDS: *Avena sativa;* genetic variability; sustainable; segregating.

RESUMO

A aveia branca (*Avena sativa* L.) é o cereal de inverno de maior qualidade nutricional, com características multifuncionais devido aos seus benefícios à saúde humana, nutrição animal e cobertura do solo. Desta forma se dá a grande valorização da cultura na sociedade. Os objetivos deste trabalho foram avaliar o desempenho agronômico e verificar se existe variabilidade genética em progênies segregantes recombinantes e mutantes de aveia branca. O trabalho foi desenvolvido na Escola Fazenda UNIJUI (IRDeR), localizada no município de Augusto Pestana, no estado do Rio Grande do Sul, Brasil. O delineamento experimental utilizado foi o de blocos aumentados com controles intercalados. Foram semeadas 460 progênies de aveia branca e o consórcio controle foi representado pela cultivar URS Taura, disposta em três repetições. Os dados obtidos foram submetidos à análise descritiva, onde foram obtidos o número de progênies informativas, valores máximos, mínimos e médios para as variáveis mensuradas. Foram gerados gráficos de distribuição de frequência de caracteres com distribuição contínua, estratificados por progênies mutantes e recombinantes. Com base nos dados obtidos, foi utilizada uma abordagem Bayesiana com modelos mistos generalizados através de Monte Carlo e Cadeias de Markov (MCMC). Com essas informações, os componentes de variância genética (VCV) e fenotípica foram estimados com significância baseada na probabilidade de 5% pelo χ^2 (pMCMC). Posteriormente, foram calculadas as distâncias euclidianas e realizado o dendrograma de distâncias utilizando o algoritmo de agrupamento UPGMA. Foram calculados os coeficientes de correlação

linear de Pearson entre pares de variáveis, com significância verificada pelo teste t a 5% de probabilidade. As progênies mutantes apresentam maior capacidade de perfilhamento, enquanto as progênies recombinantes apresentam maior tolerância a doenças e menor debulha natural dos grãos. Existe variabilidade genética entre progênies recombinantes e mutantes para os caracteres avaliados.

PALAVRAS-CHAVE: *Avena sativa;* genetic variability; sustainable; segregating.

INTRODUCTION

White oats (*Avena sativa* L.) are winter cereals with the highest nutritional quality and multifunctional characteristics due to their benefits for human health, animal nutrition, and soil cover. The presence of beta-glucan in grains promotes the reduction of cholesterol levels. Therefore, due to its health benefits and agronomic multifunctionality, the crop is highly valued by society. This demand is demonstrated by the trends of increasing production areas in Brazil (CONAB 2023), followed by the development and adequate positioning of white oat genotypes (LORO et al. 2022, SCHIMIDT et al. 2023).

The continuous process of genetic improvement of white oats requires the creation of genetic variability. This phenomenon can be generated through crosses between contrasting parents or through natural or induced mutations (ALBOKARI 2014). From the generation of genetic variability, it is necessary to evaluate the magnitude of the population dissimilarity of the characters of interest. To this end, experiments were conducted to phenotypically evaluate progenies resulting from crosses or mutations. Therefore, heritability estimates (AZEVEDO et al. 2022, ROSA et al. 2021) and biometric models, such as Euclidean distance, are used to verify the existence of genetic variability in white oat progenies (ALBOKARI 2014, KEBEDE et al. 2023). Genetic variability in phenological and productive traits of oat mutant progenies was reported by KEBEDE et al. (2023). In oat genotypes resulting from recombination between parents, ALBOKARI (2014) described the formation of four distinct groups. The presence of genetic variability indicates the possibility of progeny selection within a population (CRUZ et al. 2012).

Thus, selection can be performed either directly or indirectly. In complex characters, selection can be based on secondary characters with higher heritability. Therefore, in addition to heritability, it is necessary to understand the relationship between characters. To achieve this, previous studies have used linear correlation analysis and regression tree analysis to determine the traits that determine the trait of interest. In white oats, studies carried out by TRETER et al. (2023), LORO et al. (2021), and BERLEZI et al. (2023) used correlation analysis to highlight relationships between characters. TRETER et al. (2023) identified that the greater tillering capacity of white oats is related to greater grain productivity. A positive correlation between grain yield and number of days to flowering was observed by LORO et al. (2021). BERLEZI et al. (2023) revealed that greater production of white oat grains is related to longer durations of the vegetative and reproductive stages. These studies can promote the indirect selection of plants with greater productive potential.

Therefore, verifying the existence of genetic variability and linear relationships between traits in the segregation of white oat populations is essential for the selection and development of superior genotypes. This approach allows the identification of genotypes with specific phenotypic characteristics that promote greater agronomic performance and sustainable development. In this context, the objectives of this work were to evaluate the agronomic performance of recombinant and mutant segregant progenies of white oats and to verify whether there is genetic variability.

MATERIALS AND METHODS

The study was conducted at Escola Fazenda UNIJUI (IRDeR), located in the municipality of Augusto Pestana (28º14'S, 52º22'W), in the state of Rio Grande do Sul, Brazil. The soil is deep red in color, well drained, and classified as typical dystroferric red Oxisol. The sowing of white oat progenies was carried out on March 15, 2022. The experimental design used was augmented blocks with interspersed controls. A total of 460 white oat progenies were sown, and the consortium was represented by the cultivar URS Taura, arranged in three replicates. The experimental unit consisted of three seeding lines spaced 0.18 m apart and 5 m long, totaling 2.70 m^2. The useful area was composed of the central row of each experimental unit. Phytosanitary management was carried out preventively to minimize biotic effects (pest insects and invasive plants) in the experiment.

The progenies used were from the Genetic Improvement Program of the Regional University of the Northwest of the State of Rio Grande do Sul (UNIJUÍ) Lineage: Grains and Covers, which were stratified by two origins: recombinants (F) and mutants (M). Thus, of the total of 460 progenies, 134 recombinant progenies of the F_3 generation (25% heterozygosity), 51 recombinant progenies of the F4 generation (12.50% heterozygosity), 84 M_4 mutant progenies (6.25% heterozygosity), and 191 M_5 mutant progenies (3.125%

heterozygosity).

In each experimental unit, the following variables were evaluated, expressed in categories: start-up at 5 days (S5D), start-up at 10 days (S10D), start-up at 15 days (S15D), start-up at 20 days (S20D), start-up at 25 days (S25D), and start-up at 30 days (S30D). For these variables, in each period, the initial start-up capacity was established using the following scores: score 0 (zero): absence of initial start-up; and score 1 (one) presence of initial start-up. Initial start-up was defined as the emergence and initial development capacity of seedlings in the plots.

The following morphological characteristics were evaluated: tillering capacity (TILL, 0: absence of tillering; 1: low tillering, 2: medium tillering and 3: high tillering); flag leaf size (FLS, 1: small, 2: medium and 3: large); flag leaf angle (FLA, 1: low, 2: medium, 3: high); panicle size (PANS 1: small, 2: medium and 3: large); presence of an arista (ARISTA, 0: absence of an arista and 1: presence of an arista); natural threshing (THRESHING, 0: absence of natural threshing and 1: presence of natural threshing); flowering uniformity of progenies in the plot (UNIFOR, 0: non-uniform plot and 1: uniform plot); peeling index (PEEL, 1: easy peeling, 2: medium peeling and 3: difficult peeling) and lodging (LOD, %).

The following traits related to the response of the progenies to diseases were evaluated: leaf rust (LR, 0: no rust, 1: low incidence of rust, 2: medium incidence of rust and 3: high incidence of rust); stem rust (SR, 0: no rust, 1: low incidence of rust, 2: medium incidence of rust and 3: high incidence of rust); bacteriosis (BAC, 0: absence of bacteriosis and 1: presence of bacteriosis); and leaf spot (LS, 0: no leaf spot, 1: low incidence of leaf spot, 2: medium incidence of leaf spot and 3: high incidence of leaf spot).

The progenies were phenologically characterized by means of the following variables: days from sowing to flowering (DF, days); days from sowing to physiological maturity (DMAT, days); days from sowing to physiological maturity (CYCLE, days); days from the beginning of maturity to the end of physiological maturity (DEM, days); and percentage of flowering plants in the plot (PFP, %), established by a diagrammatic scale (0 – 100%) based on the percentage of plants that emitted inflorescence and that presented their phenotype at complete anthesis. In the useful area of for each experimental unit, 10 plants were randomly collected to evaluate the following traits: plant height (PH, cm); grain weight per panicle (GWP, grams); and grain size (GSIZ, millimeters).

Data related to meteorological variables, maximum air temperature (Tmax, ºC), mean air temperature (Tmean, ºC) and minimum air temperature (Tmin, ºC) were obtained from the NASA Power platform (NASA POWER 2023). Using the duration of the phenological stages and the average air temperature data, the following variables were calculated: accumulation of degree days from sowing to flowering (DDF, ºC day); accumulation of degree days from the beginning of maturation to the end of maturation (DDM, ºC day); and accumulation of degree days for the total cycle (DDC, ºC day).

The data obtained were subjected to descriptive analysis, where the number of informative progenies, maximum, minimum, and average values were evaluated. for the measured variables. Frequency distribution graphs of traits with continuous distribution were generated and stratified by mutant and recombinant progenies.

Based on the obtained data, a Bayesian approach was used with generalized mixed models through Monte Carlo and Markov Chains (MCMC). For the estimates, standard a priori information was used for all approaches, 100,000 interactions, burning at 10,000, interval cut of 10. The probabilistic chains were evaluated using a posteriori probabilistic densities and the highest posterior densities (HPD), all within expectations, and the deviance information criterion (DIC). With this information, the genetic (VCV) and phenotypic variance components were estimated with significance based on the 5% probability by χ^2 (pMCMC).

The Euclidean distances were then calculated, and a distance dendrogram was created using the UPGMA clustering algorithm. Pearson's linear correlation coefficients were calculated between pairs of variables, with significance verified by the t-test at 5% probability. The parameters of the regression tree algorithm were estimated to predict grain weight per panicle (GWP, grams) as a function of the other variables evaluated. All analyses were performed in the R software using the *metan*, ggplot2, Vaqueiro, and MCMCglmm packages (R CORE TEAM 2023).

RESULTS AND DISCUSSION

Mutant progenies showed the highest S5D potential regardless of the level of heterozygosity, compared to recombinant progenies (Figure 1). There was no difference between the mutant and recombinant progenies with respect to heterozygosity for the S10D, S15D, S20D, and S30D variables. This indicates that from 5 days after emergence, there was homogeneity in the development of the recombinant and mutant progeny plants,

as well as between levels of heterozygosity. The mutant progenies showed the highest TILL capacity compared with the recombinants. According to TRETER et al. (2023), the greater tillering capacity of white oats is related to grain productivity. However, a higher incidence of LR and BAC was observed in mutant progenies, mainly at the heterozygosity level of 6.25%. The highest incidences of SR and LS were observed in mutants with 3.12% heterozygosity. These results indicate that the recombinant progenies showed the greatest potential for tolerance to these diseases.

The expression levels of FLS, FLA, and PANS were similar between mutant and recombinant progenies and at the segregation levels. However, ARISTA was greater at higher segregation levels in mutant and recombinant progenies. The greatest dissimilarity in phenotypic expression between progenies was observed at the THRESHING level. In this characteristic, the mutant progenies had the highest numbers, mainly in the progenies with greater heterozygosity. This indicates that recombinant progenies have a greater potential to reduce grain threshing in the panicle at physiological maturity. Recombinant progenies with 12.5% heterozygosity showed the highest UNIFOR and PEEL. The mutant progenies had a larger grain size.
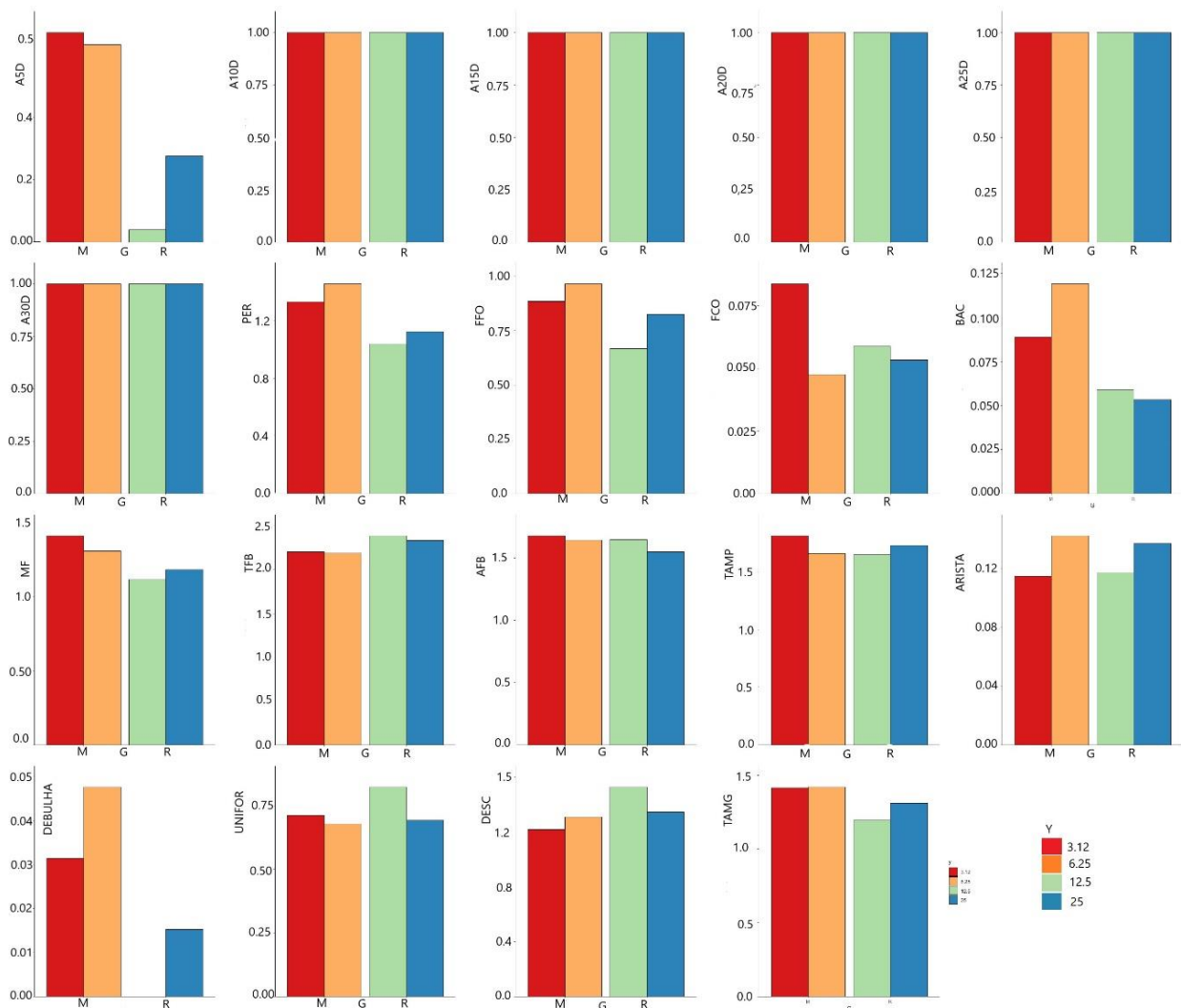

Figure 1. Descriptive analysis for the average effects of the traits: start-up at 5 days (S5D), start-up at 10 days (S10D), start-up at 15 days (S15D), start-up at 20 days (S20D), start-up at 25 days (S25D), start-up at 30 days (S30D), tillering capacity (TILL), leaf rust (LR), stem rust (SR), bacteriosis (BAC), leaf spot (LS), flag leaf size (FLS), flag leaf angle (FLA), panicle size (PANS), presence of arista (ARISTA), natural threshing (THR), flowering uniformity of progenies in the plot (UNIFOR), hulling index (PEEL), and grain size (GSIZ).

The frequency of mutant progenies with higher AP, LOD, DEM, and DDM values was higher than that of recombinant progenies (Figure 2). This indicates a greater probability of selection of plants with lower AP, LOD, DEM, and DDM in recombinant progenies. The recombinant progenies showed a higher frequency of plants with higher PFP, DMAT, CYCLE, DDF, and DDC values. Therefore, these results indicate that it is possible to identify which of the progeny groups (mutants and recombinants) is most likely to select progeny for the desired characteristics. ALBOKARI (2014) also identified promising mutant wheat progenies with

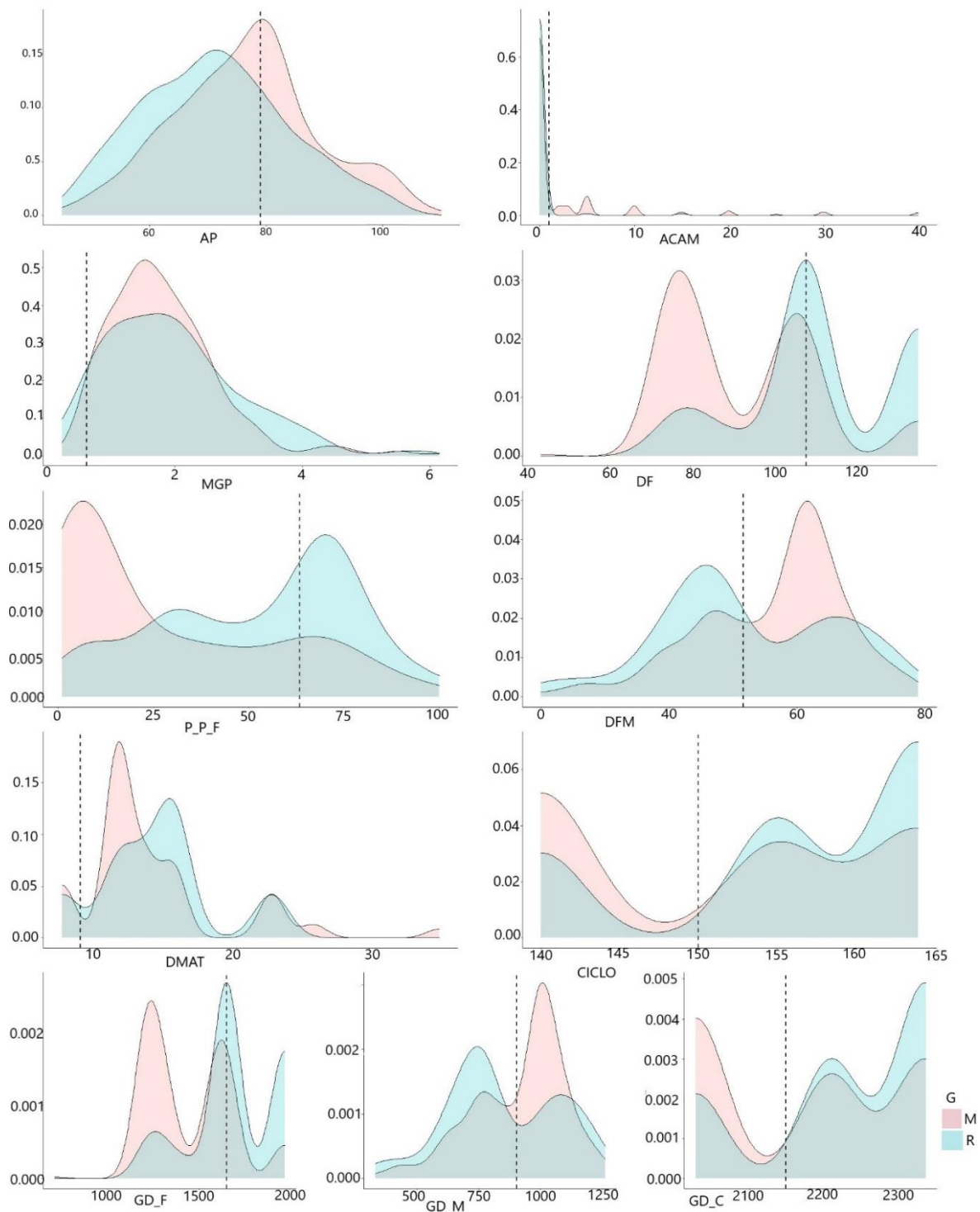promising phenological and productive characteristics.

Figure 2. Frequency distribution of the characters plant height (PH, cm), grain weight per panicle (GWP, g), percentage of flowering plants in the plot (PFP), days from sowing to physiological maturity (DMAT), accumulation of degree days from sowing to flowering (DDF), accumulation of degree days from the beginning of maturation to the end of maturation (DDM), lodging (LOD), days from sowing to flowering (DF), days from the beginning of maturation to the end of physiological maturity (DEM), days from sowing to physiological maturity (CYCLE), and accumulation of degree days for the total cycle (DDC). The vertical dashed line shows the average performance of the control cultivar.

To perform plant selection, it is necessary to highlight the extent to which genetic variation determines the expression of the characteristic of interest. This information also indicates the existence or not of genetic variability in a population (CRUZ et al. 2012). The heritability of the traits ranged from 0.43 to 0.67, 0.36 to 0.67, 0.46 to 0.67, and 0.43 to 0.77 for the progeny groups at 25%, 12.50%, 6.25%, and 3.125%, respectively (Table 1). Therefore, it can be inferred that the characters had heritability that was classified as moderate to

high (>0.25) (RESENDE & DUARTE 2007). Therefore, heritability estimates indicate the presence of genetic variability among white oat progenies, enabling the development of superior genotypes for the evaluated traits.

Table 1. Heritability estimates for the traits days from the beginning of maturation to the end of physiological maturity (DEM), percentage of flowering plants in the plot (PFP), days from sowing to flowering (DF), grain weight per panicle (GWP), days from sowing to physiological maturity (DMAT), degree-day accumulation for the total cycle (DDC), plant height (PH), days from flowering to physiological maturity (CYCLE), degree-day accumulation from sowing to flowering (DDF), and degree-day accumulation from the beginning of maturation to the end of maturation (DDM) for white oat crops.

LH	Characters									
	DEM	PFP	DF	GWP	DMAT	DDC	PH	CYCLE	DDF	DDM
25%	0.48	0.36	0.43	0.51	0.57	0.46	0.52	0.54	0.62	0.67
12.50%	0.50	0.36	0.53	0.51	0.50	0.46	0.60	0.59	0.62	0.67
6.25%	0.50	0.58	0.65	0.50	0.52	0.60	0.47	0.46	0.56	0.67
3.125%	0.43	0.58	0.39	0.50	0.50	0.60	0.72	0.77	0.56	0.67
H²	0.47	0.47	0.5	0.50	0.52	0.53	0.57	0.59	0.59	0.67
h²	0.11	0.11	0.2	0.12	0.13	0.13	0.14	0.14	0.14	0.16
Significance	***	***	***	***	***	***	***	***	***	***
PMCMC<5%	<1e-04	<1e-04	<1e-04	<1e-04	<1e-04	<1e-04	<1e-04	<1e-04	<1e-04	<1e-04

*LH: level of heterozygosity; H²: broad-sense heritability; H²: Narrow-sense heritability.

The DDM trait showed the highest heritability (0.67) in white oat progeny populations, with 25%, 12.50%, and 6.25% heterozygosity. In the 3.125% heterozygosity group, the CYCLE genotype had the highest heritability (0.77). Moderate to high heritability estimates were also obtained by AZEVEDO et al. (2022) for grain yield and days between emergence and flowering in white oats (0.58 and 0.53, respectively). ROSA et al. (2021) observed heritability greater than 0.90 for days to flowering and days to maturity in white oats. Moderate to high heritability suggests that it is feasible to select plants based on phenotypes because phenotypic expression is strongly influenced by genetics. Therefore, phenological characters have greater heritability than productive and morphological characters. Thus, initial selection in segregating populations should focus on phenological characteristics.

On average, narrow-sense heritability was 0.11–0.16. Heritability decreased in the following order: DDM, DDF, CYCLE, AP, DDC, DMAT, GWP, DF, PFP, and DEM (0.16 to 0.11). For example, for DDM, of the total phenotypic variance expressed, on average, 16% of the variation is heritable to the next generation. This indicates that in the first generations of segregation, selection should be based on phenological characters because they present greater heritability in the broad and restricted sense, thereby maximizing selection efficiency and thus genetic gains.

There were six, four, seven, and six large distinct groups of progeny with 25%, 12.50%, 6.25%, and 3.125% heterozygosity, respectively (Figures 3 and 4). This result reveals high genetic dissimilarity, which is manifested by the formation of distinct groups. The presence of genetic variability in white oat genotypes, expressed in the formation of four groups, was also observed by KEBEDE et al. (2023). The formation of these distinct groups suggests genetic complexity within the studied oat population. This dissimilarity may be essential for the adaptation of oats to different environments, resistance to pests or adverse conditions, and other specific genetic characteristics.

Considering the economic and agricultural importance of oats, these results have potential practical applications. Understanding genetic dissimilarity can guide the selection of desirable traits through indirect selection and the development of resistant and adaptable varieties. Furthermore, genetic conservation of these distinct groups can ensure food security and long-term sustainability.
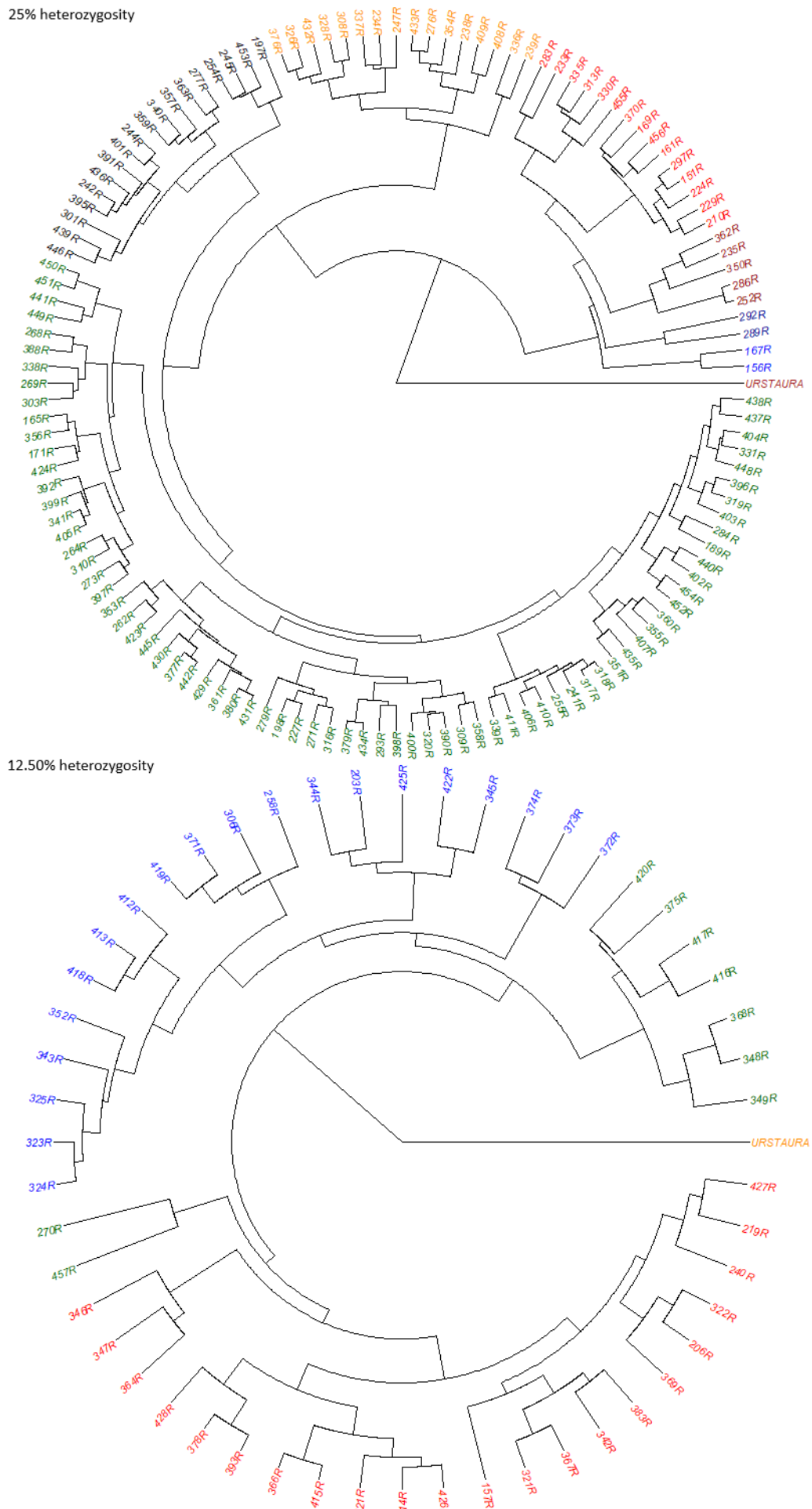
25% heterozygosity

12.50% heterozygosity

Figure 3. Genetic dissimilarity dendrogram of progeny groups with 25% and 12.50% heterozygosity.

Figure 4. Genetic dissimilarity dendrogram of progeny groups with heterozygosity of 6.25% and 3.125%.

There was a positive correlation between GWP and DF, DMAT, CYCLE, ARISTA, FLS, and PANS (r ≥ 0.20) (Figure 5). This indicates that the longer the duration of the developmental substages ARISTA, FLS, and PANS, the higher the GWP. Thus, it can be inferred that progenies with higher GWP can be selected indirectly through the traits DF, DMAT, CICLO, ARISTA, FLS, and PANS. Therefore, due to the ease of measurement, these traits may have a more efficient practical application for indirect selection. Berlezini et al. (2023) reported that the greater production of white oat grains is related to the longer duration of the vegetative and reproductive stages. A positive correlation between grain yield and number of days to flowering was also observed by LORO et al. (2021).

Figure 5. Pearson's linear correlation coefficient between pairs of white oat traits. Leaf rust (LR); stem rust (SR); lodging (LOD); days between onset of maturity and end of physiological maturity (DEM); leaf spot (LS); start-up in 5 days (S5D); plant height (PH); peeling index (PEEL); grain size (GSIZ); natural threshing (THR); flag lead angle (FLA); flowering uniformity of progenies in the plot (UNIFOR); days from sowing to flowering (DF); percentage of flowering plants in the plot (PFP); days from sowing to physiological maturity (DMAT); days from flowering to physiological maturity (CYCLE); tillering capacity (TILL); presence of an arista (ARISTA); flag leaf size (FLS); panicle size (PANS); grain weight per panicle (GWP); and bacteriosis (BAC).

Based on 460 segregating progenies, it was possible to predict eleven selection profiles for GWP, resulting in a range of 1,302–3,748 g (Figure 6). This indicates the complexity of the interaction of traits, highlighting the importance of a multifactorial approach in predicting GWP. The considerable variation in GWP values The genetic variability present in progenies, and an understanding of these selection profiles can be fundamental for effective genetic improvement strategies.
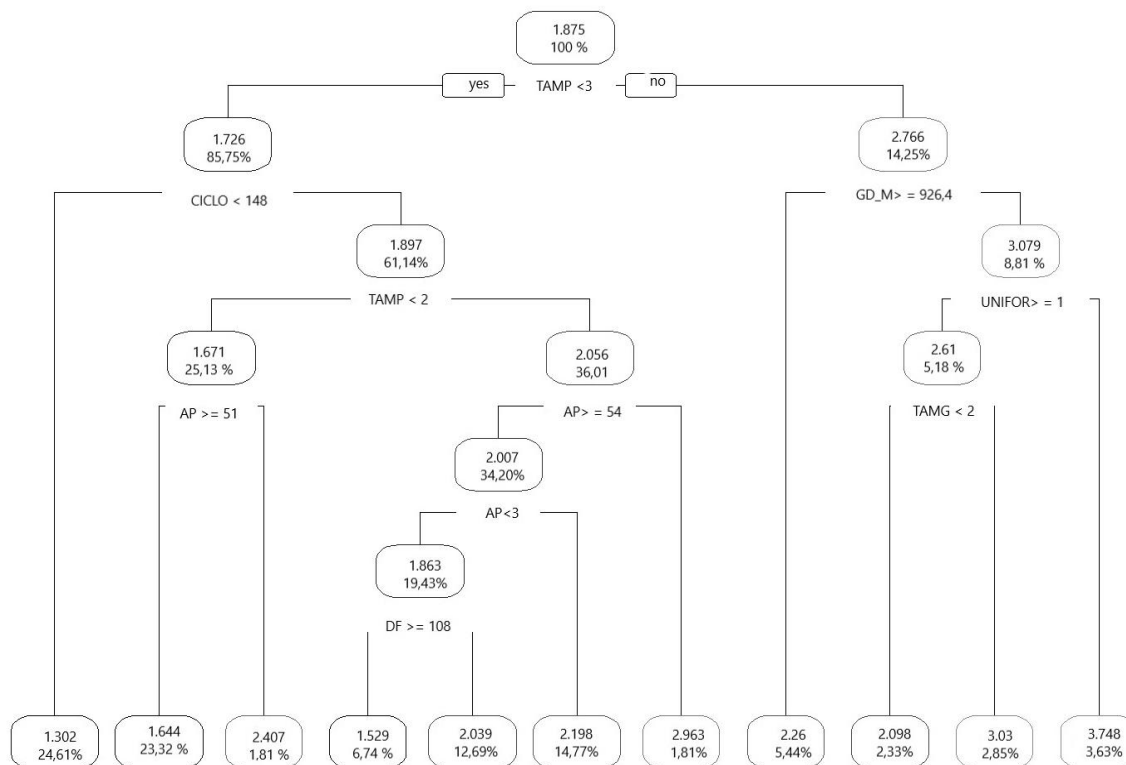

Figure 6. Regression tree for predicting grain weight per panicle (GWP, g) as a function of other traits.

PANS was the main character that determined the GWP. The highest GWP (3,748 grams) was observed in plants that presented the highest PANS, DDM lower than 926.40°D, and non-uniformity in the plot. However, GWP >3.00 g was also observed in plants with large PANS, DDM 926.40° days, and uniform plants with GSIZ >2 mm. The size of the white oat panicle is associated with a greater number of grains (FINNAN et al. 2019), which justifies its higher GWP.

Therefore, PANS and DDM, in that order, are the main traits that determine the GWP of white oat progenies and can be used for indirect selection. The high heritability of DDM (H² = 0.67 and h² = 0.17) indicates the possibility of genetic gains from indirect selection because GWP has a heritability lower than 0.67. The identification of DDM as a determining trait highlights the sensitivity of the crop to specific thermal conditions. This information also allows us to optimize agricultural practices by adapting them to the specific needs of different genetic profiles.

CONCLUSION

Mutant progenies have a greater tillering capacity, whereas recombinant progenies have greater disease tolerance and less natural grain threshing.

Genetic variability exists between recombinant and mutant progenies for the evaluated traits.

The traits of white oats related to phenology have broad and narrow heritability.

The highest GWP (3,748 grams) was observed in plants with larger panicles and a DDM lower than 926.40 °C.

REFERENCES

ALBOKARI M. 2014. Induction of mutants in durum wheat (*Triticum durum* desf cv. samra) using gamma irradiation. Pakistan Journal of Botany 46: 317-324.

AZEVEDO CF et al. 2022. Updated knowledge in the estimation of genetics parameters: a Bayesian approach in white oat (*Avena sativa* L.). Euphytica 218: 43.

BERLEZI JD et al. 2023. Selection of white oat genotypes for contrasting fungicide management conditions. Brazilian Agricultural Research 58: e03084.

CONAB. 2023. National Supply Company. Grains: 2022/23 harvest grains. 10th survey.

CRUZ CD et al. 2012. Biometric models applied to genetic improvement. 4.ed. Viçosa: UFV. 514 p.

FINNAN J et al. 2019. The plasticity of the oat panicle and associated changes in leaf area and grain weight. Field Crops Research 242: 107592.

KEBEDE G et al. 2023. Multivariate analysis for yield and yield-related traits of oat (*Avena sativa* L.) genotypes in Ethiopia. Ecological Genetics and Genomics: 100184.

LORO MV et al. 2021. Strategic positioning of white oat genotypes in the organic system. Scientia Agraria Paranaensis, p.336-345.

LORO MV et al. 2022. Decomposition of white oat phenotypic variability by environmental covariates. Brazilian Agriculture Journal 97: 279-302.

NASA. 2023. National Aeronautics and Space Administration. NASA Prediction Of Worldwide Energy Resources. Available on: https://power.larc.nasa.gov/. Access: May 20th 2023.

R CORE TEAM. 2023. R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna. Available on: <https://www.R-project.org> Access: May 2th 2023.

RESENDE MDV & DUARTE JB. 2007. Precision and quality control in cultivar evaluation experiments. Tropical Agricultural Research 37: 182-194.

ROSA TC et al. 2021. Genetic parameters and multi-trait selection of white oats for forage. Genetics and Molecular Research 20: gmr18451.

SCHIMIDT AL et al. 2023. Decomposition of phenotypic variation of white oats by meteorological and geographic covariables. Agronomy Journal 115: 2239-2259.

TRETER RJR et al. 2023. Agronomic performance of white oats in organic system in the northwest region of Rio Grande do Sul. Agronomy Science and Biotechnology 9: 1-11.