PAB Pesquisa Agropecuária Brasileira 60 years

Genetics/ Original Article

ISSN 1678-3921

Journal homepage: www.embrapa.br/pab

For manuscript submission and journal contents, access: www.scielo.br/pab

Selection of superior white oat progenies based on agronomic ideotype via generalized additive model

Pedro Henrique Ruwer
Universidade Federal de Santa Maria, Centro de Ciência Rurais, Departamento de Fitotecnia, Santa Maria, RS, Brazil.
E-mail: pedro_ruwer@hotmail.com

Alessandro Dal'Col Lúcio
Universidade Federal de Santa Maria, Centro de Ciência Rurais, Departamento de Fitotecnia, Santa Maria, RS, Brazil.
E-mail: adlucio@ufsm.br

Ivan Ricardo Carvalho✉
Universidade Regional do Noroeste do Rio Grande do Sul, Departamento de Estudos Agrários, Ijuí, RS, Brazil.
E-mail: carvalhoirc@gmail.com

Willyan Júnior Adorian Bandeira
Universidade Federal de Santa Maria, Centro de Ciência Rurais, Departamento de Fitotecnia, Santa Maria, RS, Brazil.
E-mail: bandeira.wjab@gmail.com

Adriano Dietterle Schulz
Universidade Regional do Noroeste do Rio Grande do Sul, Departamento de Estudos Agrários, Ijuí, RS, Brazil.
E-mail: adriano.schulz@sou.unijui.edu.br

Gabriel Mathias Weimer Bruinsma
Universidade Regional do Noroeste do Rio Grande do Sul, Departamento de Estudos Agrários, Ijuí, RS, Brazil.
E-mail: gmwbruinsma@hotmail.com

José Antonio Gonzalez da Silva
Universidade Regional do Noroeste do Rio Grande do Sul, Departamento de Estudos Agrários, Ijuí, RS, Brazil.
E-mail: josé.gonzalez@unijui.edu.br

✉ Corresponding author

Received
November 07, 2025

Accepted
July 14, 2026

How to cite
RUWER, P.H.; LÚCIO, A.D.; CARVALHO, I.R.; BANDEIRA, W.J.A.; SCHULZ, A.D.; BRUINSMA, G.M.W.; SILVA, J.A.G. da. Selection of superior white oat progenies based on agronomic ideotype via generalized additive model. **Pesquisa Agropecuária Brasileira**, v.61, e04305, 2026. DOI: https://doi.org/10.1590/S1678-3921.pab2026.v61.04305.

Abstract – The objective of this work was to select superior white oat lines based on agronomic ideotype, using a generalized additive model (GAM) and multitrait selection. The experiment was carried out in an augmented Federer block design with intercropping controls. The regular treatments totaled 398 F_5 white oat recombinant lines, and the control consisted of three commercial cultivars. Eleven agronomic traits were evaluated, including lodging, plant height, disease incidence, panicle density, establishment, flowering and line uniformity, tillering, and flag-leaf size. The GAM was applied to estimate phenotypic values, isolate row and column effects, and reduce spatial dependence. The predicted values were used to determine ideotype through the multitrait genotype-ideotype distance index. The agronomic ideotype was designed to show a greater panicle density, flowering and line uniformity, and initial height, in addition to good establishment and reduced tillering, lodging, leaf size, and disease incidence. For most traits, the GAM effectively corrected spatial effects. Only 4.02% of the genotypes met the agronomic ideotype, with significant selection gains for panicle density and flowering and line uniformity. The L111 progeny ('URNRS22' × 'URS Taura') stands out as the closest to the ideal ideotype.

Index terms: *Avena sativa*, multivariate analysis, plant breeding.

Seleção de progênies superiores de aveia-branca com base em ideótipo agronômico via modelo aditivo generalizado

Resumo – O objetivo deste trabalho foi selecionar linhagens superiores de aveia-branca, com base no ideótipo agronômico, por meio de modelo aditivo generalizado (MAG) e seleção multicaracterística. O experimento foi realizado em delineamento de blocos aumentados de Federer, com testemunhas intercalares. Os tratamentos regulares totalizaram 398 linhagens recombinantes F_5 de aveia-branca, e as testemunhas foram três cultivares comerciais. Foram avaliadas 11 características agronômicas, incluindo acamamento, altura de planta, incidência de doenças, densidade de panículas, estabelecimento, uniformidade de florescimento e de linhagem, perfilhamento e tamanho da folha-bandeira. O MAG foi aplicado para estimar valores fenotípicos, isolar efeitos de linhas e colunas e reduzir a dependência espacial. Os valores preditos foram utilizados para determinar o ideótipo, por meio do índice de distância multicaracterística genótipo-ideótipo. O ideótipo agronômico foi concebido para apresentar maior densidade de panículas, uniformidade de florescimento e de linhagem e altura inicial, além de bom estabelecimento e menores perfilhamento, acamamento,

This is an open-access article distributed under the Creative Commons Attribution 4.0 International License

tamanho de folha e incidência de doenças. Para a maioria das características, o MAG corrigiu adequadamente os efeitos espaciais. Apenas 4,02% dos genótipos atenderam ao ideótipo agronômico, com ganhos significativos para densidade de panículas e uniformidade de florescimento e linhagem. A progênie L111 ('URNRS22' × 'URS Taura') se destaca como a mais próxima do ideótipo ideal.

Termos para indexação: *Avena sativa*, análise multivariada, melhoramento de plantas.

Introduction

Cereal yield losses caused by disease and lodging have been widely reported (Jevtić et al., 2017; Laidig et al., 2022; Chen et al., 2025). Although genetic improvement has promoted advances for the tolerance of white oat genotypes to the main pathogens affecting cereals, stalk stability and lodging tolerance have not kept pace with this progress (Laidig et al., 2021). These factors impose additional burdens on genetic improvement, requiring strategies to increase cultivar robustness. Maintaining or improving the genetic base and focusing on the most relevant agronomic traits are essential for the developing of resilient cultivars to diverse environmental conditions (Swarup et al., 2021). In this context, damage caused by fungi and plant breakage or toppling highlights the importance of genetic improvement focused on tolerance, showing the rising demands for producers of more stable and adapted plant varieties (Laidig et al., 2022).

Breeding programs aim to develop genotypes that meet grain yield, industrial quality, and stability, while consistently expressing the maximum number of desired agronomic traits (Berlezi et al., 2023). The combination of these attributes defines the agronomic ideotype, a theoretical model that guides breeders in plant selection by increasing efficiency and accuracy in the identification of superior genotypes (Van Oijen & Höglind, 2016). Dal Molin Savicki et al. (2023) described the ideal white oat genotype as having a short cycle, erect growth, a lodging-tolerant stem, and compact, vertically arranged leaves. Pradebon et al. (2024) also identified desirable traits, such as compact panicle, easy grain dehulling, grains larger than two millimeters, high stability, and high harvest index. To enable the selection of genotypes combining multiple attributes, different indexes have been applied, especially the multitrait genotype-ideotype distance index (MGIDI), which measures the distance between each genotype performance and a predefined ideotype, allowing more efficient and balanced selection (Olivoto & Nardino, 2021).

Creating an ideotype is a complex process that requires a precise definition of the target environment, including the identification of potential stresses, their probability, and impact on phenotypic expression (Trethowan, 2014). Modern white oat cultivars have a narrow gene pool, which makes it difficult to find genotypes that fit the desired ideotype (Cieplak et al., 2021). These challenges demand evaluating many progenies in modified experimental designs, such as Federer augmented block design. However, such experiments are commonly affected by spatial variability in locations where environmental interactions and random effects, such as fertility gradients, cause plot differences (Rodríguez-Álvarez et al., 2016). Thus, applying statistical models capable of isolating these effects is essential to obtain accurate estimates with lower-spatial error. Among these procedures, generalized additive models (GAMs) stand out for their flexibility in modeling nonlinear relationships between predictors and responses, using smooth functions to capture spatial patterns in agricultural data (Rodríguez-Álvarez et al., 2016; Wellington et al., 2023).

The combined application of generalized additive models and the MGIDI index allows of the selection of white oat lines closest to the agronomic ideotype, even under conditions of spatial variability.

The objective of this work was to select superior white oat lines based on agronomic ideotype, using a generalized additive model and multitrait selection.

Materials and Methods

The dataset used in the present study was extracted from an experiment conducted at Escola Fazenda, in Unijuí (28º26'20.31"S, 54º00'22.12"W, at 301 m altitude), located in the municipality of Augusto Pestana, in the state of Rio Grande do Sul, Brazil. The climate in the region is characterized as Cfa, humid subtropical (Alvares et al., 2013), and the soil is a Latossolo Vermelho distrófico típico (Santos et al., 2025), equivalent to a Typic Hapludox (Soil Survey Staff, 1999).

The experimental design was an augmented Federer block design with intercropping controls. The regular treatments corresponded to 398 recombinant inbred white oat lines (RILs) of the F_5 generation, obtained from 22 biparental crosses (C1 to C22 in Table 1), and the control treatments were the commercial cultivars IPR Afrodite, URS Taura, and URNRS22.

The experimental units consisted of five rows spaced at 0.18 cm apart and 5.0 m long, totaling 4.5 m^2. Sowing was carried out in the second half of April 2023, using a seeder-fertilizer spreader, at a density of 350 plants per square meter density. Fertilization was carried out in the seeding line, with the application of 150 kg ha^{-1} NPK 10-20-20 fertilizer. A topdressing of 100 kg ha^{-1} N fertilizer was applied at stage 21 according to the Zadoks et al. (1974) scale.

The phytosanitary management consisted of the preventive application of insecticides, to mitigate possible interference of biotic agents in the experimental results. Fungicide applications were not performed, to avoid interfering with disease evaluation.

The following variables were evaluated: lodging (%); initial plant height (cm); incidence of leaf spot (%), caused by the fungus *Drechslera avenae* (Eidam) Scharif; panicle density (%); initial establishment (%); flowering homogeneity (%); tillering (%); flag leaf size (cm); incidence of leaf rust (%), caused by the fungus *Puccinia coronata* f. sp. *avenae*; incidence of stem rust (%), caused by the fungus *Puccinia graminis* f. sp. *avenae*; and line homogeneity (%). Plant height was measured with a graduated ruler. The remaining variables were determined qualitatively, on a scale from 0 to 10, as described by Azevedo et al. (2024). Except for initial plant height and establishment, all evaluations were performed at stage 59 of plant growth, when inflorescence emergence is completed, according to Zadoks et al. (1974). Meteorological data for mean, maximum, and, minimum air temperature (°C), and precipitation (mm) were obtained from the NASA

Table 1. Identification of the crosses, description of the genealogy (cultivars used as parents), and number of white oat (*Avena sativa*) genotypes evaluated per cross.

Cross identification	Maternal parent	Paternal parent	Number of genotypes evaluated
C1	URNRS22	URS Taura	313
C2	URS Taura	URS Corona	10
C3	FAEM Brisasul	FAEM Barbarasul	9
C4	FAEM Carlasul	URS Altiva	9
C5	FAEM Brisasul	IPR Afrodite	6
C6	URS Altiva	IPR Afrodite	6
C7	UPFA Farroupilha	FAEM Carlasul	6
C8	URS Taura	FAEM Brisasul	5
C9	URS Altiva	URS Fapa Slava	5
C10	IPR Afrodite	FAEM Brisasul	4
C11	URS Fapa Slava	URS Corona	3
C12	FAEM Brisasul	URS Taura	3
C13	FAEM Carlasul	UPFA Farroupilha	3
C14	IPR Afrodite	FAEM Carlasul	3
C15	URS Monarca	UPFA Fuerza	2
C16	URS Corona	URS Fapa Slava	2
C17	URS Altiva	URS Taura	2
C18	IPR Afrodite	URS Fapa Slava	2
C19	FAEM Carlasul	FAEM Brisasul	2
C20	UPFA Gaudéria	FAEM Barbarasul	1
C21	URS Taura	URS Fapa Slava	1
C22	URS Fapa Slava	FAEM Carlasul	1

Power platform (Nasa Power, 2025), as shown in Figure 1.

The generalized additive model (GAM) was used to estimate phenotypic values, as well as to isolate row and column effects, and to reduce spatial dependence in augmented designs. The used additive model penalized smooth functions (P-splines), under the assumption of continuous, gradual spatial trends across rows and columns, according to the following equation:

$$y_{ijklm} = \mu + f1(L_i) + f2(C_j) + uL_k + uC_l + uTrat_m + \varepsilon_{ijklm},$$

where y_{ijklm} is the variable observed in the ith row, j^{th} column, k^{th} row range, and l^{th} column range and subjected to the mth treatment; μ is the global intercept that represents the expected mean value of the response variable, when all other effects of the model equal zero; $f1(L_i)$ and $f2(C_j)$ are smooth penalized functions that model the spatial trends, in association with the coordinates of the rows and columns of the experimental unit; $uL_kN(0, \sigma^2_L)$ and $uC_lN(0, \sigma^2_C)$ are random effects associated with the row and column ranges, respectively; $uTrat_mN(0,\sigma^2_{Trat})$ is the random effect associated with the mth treatment; and ε_{ijklm} is the random residual error.

The purpose of modeling all treatments, considering them as random, was not to infer a common genetic population, but to enable a unified spatial correction

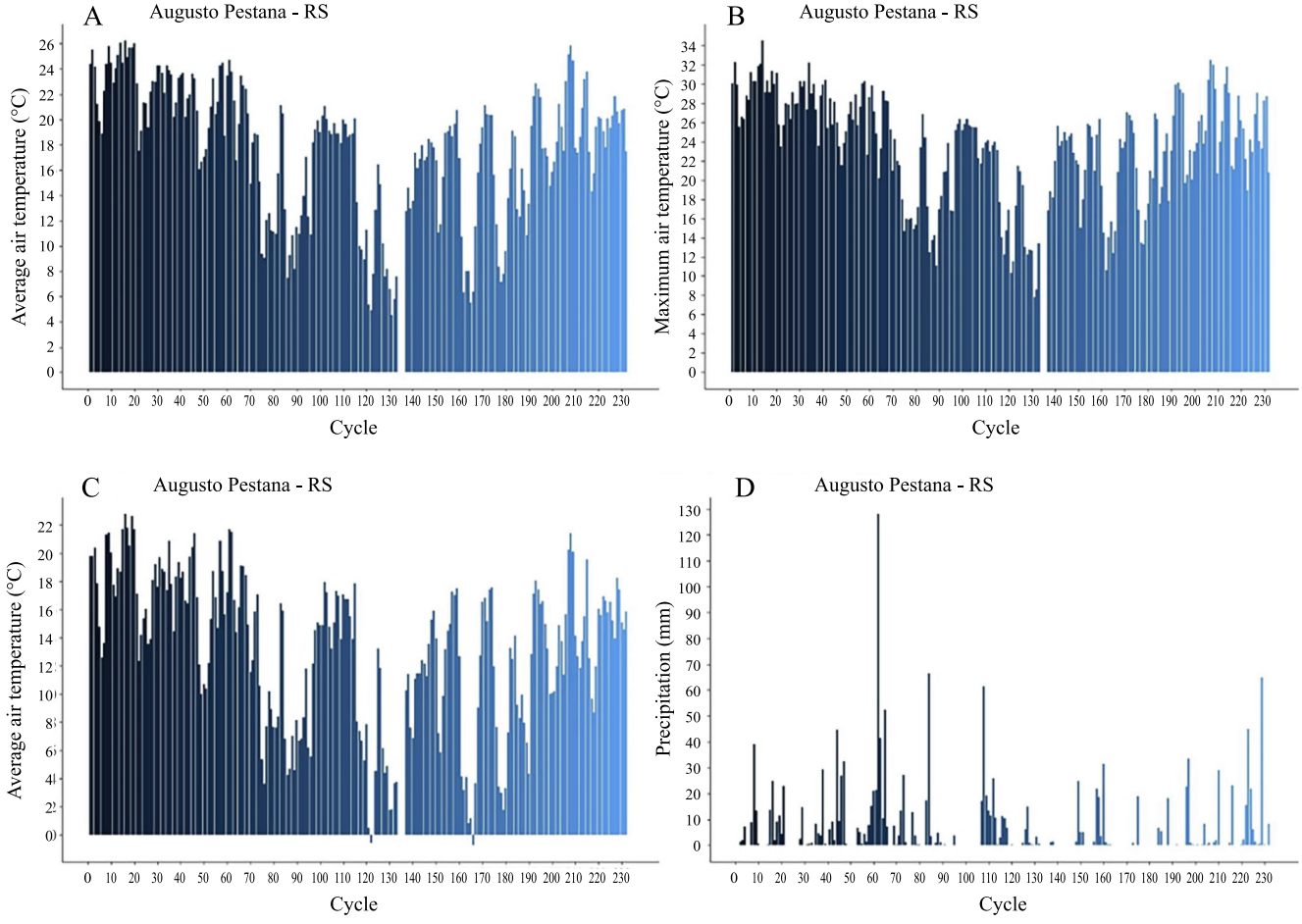

Figure 1. Meteorological data on mean, maximum, and minimum air temperature, and precipitation for the evaluation cycle of white oat (*Avena sativa*), in the municipality of Augusto Pestana, in the state of Rio Grande do Sul (RS), Brazil.

across all treatments in the experimental area. The models were adjusted with the functions of the 'mgcv' package, version 1.9-3, using the theoretical bases described by Wood (2017). Predicted values from the GAM were used to compute the ideotype via the multitrait genotype-ideotype distance index (MGIDI) method (Olivoto & Nardino, 2021). The number of factors was chosen based on the Kaiser criterion, derived from a principal component analysis. The agronomic ideotype targeted a higher-panicle density, flowering and line uniformity, initial height, and good establishment, plus lower tillering, lodging, flag-leaf size, and foliar/stem disease incidence. Treatments with the lowest MGIDI are closest to the ideotype; low contributions from a factor indicate its traits are near the ideal. This procedure was performed with the 'metan' package version 1.19 (Olivoto & Lúcio, 2020). The R software was used for statistical analyses (R Core Team, 2025).

Results and Discussion

The mean air temperature ranged from 4.56 to 26.26°C, averaging 17.74°C (Figure 1). Maximum and minimum temperatures ranged from 7.81 to 34.51°C, and from -0.77 to 22.79°C, with means of 23.40 and 13.11°C, respectively. Daily precipitation averaged 6.70 mm, reaching 128.11 mm in a single day, but was well distributed throughout the cycle and did not limit genotype development. According to Mantai et al., the respective minimum, optimum, and maximum temperatures for oat development are 4, 22, and 30°C from emergence to anthesis, and 15, 25, and 35°C from anthesis to maturity. Although some temperatures fell below the ideal minimum, average conditions remained within or close to the optimal range most of the cycle, indicating that temperature was not a restrictive factor for genotype development.

The estimated degrees of freedom indicate the complexity of the model in explaining the behavior of the response variable (Table 2). The generalized additive models (GAM) fitted to the studied variables showed between 8.48 and 401.01 estimated degrees of freedom, with higher values indicating a greater model complexity. More complex models were associated with the variables stem rust, initial establishment, and panicle density. The model fit metrics showed poor fit for lodging and leaf size, with good fits for the other variables, due to the higher penalized restricted maximum likelihood (fREML) values, evidenced by the high GAM deviance values.

The GAM models showed the ability to capture spatial variability for most evaluated traits, as indicated by the satisfactory fit metrics and the highly estimated degrees of freedom observed for variables such as stem rust, initial establishment, and panicle density (Table 2). Similar results have been reported in cereal studies, where GAMs efficiently described spatial and environmental variation, improving the interpretation of agronomic responses and genotype performance (Chen et al., 2019; Wellington et al., 2023).

Based on the predicted values for each variable, the ten superior genotypes were identified and ranked according to the desired agronomic ideotype (Table 3). Lodging varied between 21.2 and 57.4%, and genotype 'URNRS22' showed the best performance for this trait. Genotypes L194, L187, L207, L195, L129, L125, and L295 (C1 – 'URNRS22' × 'URS Taura'), as well as L319 (C9 – 'URS Altiva' × 'URS Fapa Slava') and L367 (C19 – 'FAEM Carlasul' × 'FAEM Brisasul') stood out for their reduced lodging. Predicted values for initial

Table 2. Adjustment parameters of the generalized additive model (GAM) for the variables measured in white oat (*Avena sativa*) genotypes.

Variable[1]	Estimated degrees of freedom	fREML[2]	GAM deviance
LOD (%)	150.75	1891.97	111675.10
IPH (cm)	289.24	1270.36	1018.88
FLH (%)	278.67	782.37	108.02
LH (%)	275.90	776.69	109.98
PD (%)	320.21	-7.17^{82}	3.26^{-25}
EST (%)	353.38	649.32	9.42
TIL (%)	255.88	478.85	33.74
FLS (%)	8.48	717.04	786.99
LS (%)	111.48	325.77	61.39
LR (%)	127.31	507.90	134.04
SR (%)	401.01	-165.92	6.40^{-26}

[1]LOD, lodging; IPH, initial plant height; FLH, flowering homogeneity; LH, line homogeneity; PD, panicle density; EST, initial establishment; TIL, tillering; FLS, flag leaf size; LS, leaf spot incidence; LR, leaf rust incidence; and SR, stem rust incidence. [2]fREML, restricted maximum likelihood penalized.

Table 3. Values predicted by the generalized additive model for agronomic traits measured in 398 white oat (*Avena sativa*) lines and three controls, indicating 5% of the superior and inferior genotypes based on the agronomic ideotype for lodging, initial plant height, flowering homogeneity, and line homogeneity. The values in parentheses indicate the cross-identification code, shown in Table 1.

Lodging (%)				Initial plant height (cm)			
Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value	Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value
URNRS22	21.16	L342(C7)	54.40	L346(C4)	48.81	L218(C1)	27.30
L194(C1)	22.60	L51(C1)	54.53	L212(C1)	48.40	L360(C12)	27.68
L207(C1)	23.49	L394(C9)	54.60	L286(C1)	47.57	L370(C5)	28.39
L187(C1)	23.49	L196(C1)	54.77	'URNRS22'	47.40	L174(C1)	29.34
L319(C9)	23.57	L393(C17)	54.91	L293(C1)	47.33	L380(C3)	29.46
L367(C19)	23.70	L164(C1)	55.00	L362(C9)	47.15	L271(C1)	29.71
L195(C1)	24.11	L154(C1)	55.00	L171(C1)	47.04	L394(C9)	29.94
L129(C1)	24.31	L120(C1)	55.68	L357(C4)	46.38	L260(C1)	30.00
L125(C1)	24.44	L359(C4)	55.86	L282(C1)	46.15	L367(C19)	30.05
L295(C1)	24.81	L202(C1)	56.01	L122(C1)	46.13	L292(C1)	30.06
L188(C1)	25.00	L192(C1)	56.01	'IPR Afrodite'	45.94	L314(C11)	30.65
L218(C1)	25.04	L251(C1)	56.36	L358(C4)	45.45	L179(C1)	30.98
L182(C1)	25.04	L357(C4)	56.48	L368(C6)	45.45	L321(C3)	31.55
L395(C1)	25.14	L347(C3)	56.48	L110(C1)	45.12	L144(C1)	31.59
L156(C1)	25.24	L346(C4)	56.80	L81(C1)	45.11	L304(C1)	31.60
L20(C1)	25.25	L96(C1)	56.92	L129(C1)	45.06	L21(C1)	31.74
L287(C1)	25.49	L65(C1)	56.93	L162(C1)	44.89	L147(C1)	31.81
L135(C1)	25.55	L45(C1)	56.93	L3(C1)	44.86	L329(C16)	31.82
L111(C1)	25.68	L230(C1)	57.21	L12(C1)	44.86	L97(C1)	31.86
L286(C1)	25.80	L344(C17)	57.42	L265(C1)	44.72	L223(C1)	32.07
Flowering homogeneity (%)				Line homogeneity (%)			
Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value	Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value
L3(C1)	9.89	290(C1)	5.72	L8(C1)	10.59	L227(C1)	5.90
L41(C1)	9.86	21(C1)	5.72	L11(C1)	10.50	L370(C5)	5.85
L11(C1)	9.86	370(C5)	5.69	L5(C1)	9.86	L290(C1)	5.85
L89(C1)	9.66	380(C3)	5.67	L3(C1)	9.84	L223(C1)	5.85
L86(C1)	9.62	378(C1)	5.66	L41(C1)	9.81	L380(C3)	5.83
L115(C1)	9.61	367(C19)	5.65	L89(C1)	9.77	L378(C1)	5.83
L103(C1)	9.58	329(C16)	5.64	L86(C1)	9.73	L329(C16)	5.82
L84(C1)	9.58	253(C1)	5.63	L115(C1)	9.72	L367(C19)	5.82
L83(C1)	9.56	363(C5)	5.60	L103(C1)	9.69	L363(C5)	5.77
L111(C1)	9.55	394(C9)	5.59	L111(C1)	9.67	L253(C1)	5.76
L121(C1)	9.55	304(C1)	5.58	L121(C1)	9.67	L394(C9)	5.75
'URS Taura'	9.42	50(C1)	5.52	L84(C1)	9.64	L304(C1)	5.75
L160(C1)	9.41	139(C1)	5.25	L83(C1)	9.62	L4(C1)	5.75
L149(C1)	9.39	165(C1)	5.20	L82(C1)	9.61	L21(C1)	5.71
L159(C1)	9.39	239(C1)	5.17	L51(C1)	9.60	L50(C1)	5.61
L167(C1)	9.37	143(C1)	5.17	L81(C1)	9.60	L139(C1)	5.38
L198(C1)	9.36	292(C1)	4.92	'URS Taura'	9.55	L143(C1)	5.31
L166(C1)	9.35	217(C1)	4.46	L160(C1)	9.50	L239(C1)	5.24
L156(C1)	9.35	287(C1)	4.30	L159(C1)	9.48	L292(C1)	5.07
L197(C1)	9.34	214(C1)	3.73	L149(C1)	9.48	L287(C1)	4.45

plant height started at 27.30 cm, for which the five best genotypes were L346, L212, L286, 'URNRS22', and L293, with values from 48.8 to 47.3 cm. Plant height is just one of many factors associated with lodging, and a moderate correlation was only observed when evaluating a large number of genotypes (Tumino et al., 2017). Furthermore, selecting taller and more productive progenies is not a hindrance, as management practices, such as the use of growth regulators, can reduce the susceptibility to lodging and maintain high productivity levels.

Flowering homogeneity (Table 3) showed that genotypes L11, L41, and L3 had the best performance (9.9%), followed by L89. The best genotypes considering line homogeneity were L8, L11, L5, L89, and L41, with 10.6, 10.5, 9.9, 9.8, and 9.8%, respectively. All genotypes that excelled for homogeneity traits were obtained from the C1 cross. In genetic breeding, line homogeneity is important to identify potential traits that represent variation, even in advanced breeding generations. These variations are mostly attributed to the environment; however, the genetic effect of segregation may still be present in some difficult-to-define traits (Fasoula et al., 2020).

Panicle density values ranged from 1.15 to 10.29%, with the ten superior genotypes − L124, L121, L118, L167, L151, L142, L202, L198, L197, and L230 − originating exclusively from the C1 cross (Table 4). The selection of white oat genotypes with compact panicles favors net photosynthesis by requiring fewer photoassimilates for differentiation (Rahman et al., 2025). The highest-predicted values for initial establishment occurred in genotypes with rapid and uniform emergence, notably L310 (C5 – 'FAEM Brisasul' × 'IPR Afrodite'), 'URNRS22', L309 (C10 – 'IPR Afrodite' × 'FAEM Brisasul'), L270, L200, L190, L187, L250, L189 (C1 cross), and L366 (C14 – 'IPR Afrodite' x 'FAEM Carlasul'), with values from 9.0 to 9.2%.

Values predicted for tillering ranged from 2.3 to 5.3 tillers per plant; genotypes L190 (C1) and L295 (C1) stood out (Table 4), with 2.3 and 2.4 tillers per plant on average. Tillering is important in winter cereals because it acts as a compensatory effect when adverse environmental conditions hinder initial establishment (Bauer & von Wirén, 2020). Selection targeting this trait should also consider genotype fitness. A greater tillering capacity is desirable in genotypes intended for forage production. Nevertheless, in grain production, this trait tends to have a smaller contribution, since the number of panicles per square meter can be more efficiently controlled by adjusting the seeding density (Laidig et al., 2022).

Flag-leaf size was uniform across genotypes (Table 4), explaining the lack of model fit (Table 2) and the negligible genotype effect; no stem rust incidence was observed (Table 5). Leaf spot incidence ranged from 6.3 to 7.3%, for which L152 (C1) showed the lowest value of 6.3%, and L345 (C14), L360 (C12), and L244 (C1) showed the highest values of 7.28, 7.23, and 7.18%, respectively (Table 5). Leaf rust incidence was high in all genotypes (7.1–8.4%), with the lowest values for L314 (C1), L361 (C2), and L380 (C3). One of the main challenges in white oat breeding is selecting genotypes with multiple resistance to foliar diseases, since a greater selection pressure may reduce gains for other traits. Similar difficulties have been reported in previous studies, which highlighted the complexity of combining multiple and durable resistance sources in oat breeding, due to the high variability and rapid evolution of pathogen populations (Park et al., 2022).

The MGIDI ideotype, as previously defined in the methodology, favored the simultaneous selection of desirable traits (Table 6). The first four principal components had eigenvalues higher than 1 and explained 64.2% of the total variability. Traits were grouped into four factors: FA1, panicle density and homogeneity; FA2, initial plant height, establishment, and tillering; FA3, lodging, flag-leaf size, and leaf rust; and FA4, leaf spots and stem rust. Communality ranged from 0.47 for leaf rust to 0.86 for flowering and line homogeneity. Significant selection differentials were observed for panicle density (1.68), flowering homogeneity (1.19), line homogeneity (1.21), and reduced lodging (-8.22); however, such selection differentials were not verified for tillering, flag-leaf size, or rust incidence. Among the selected genotypes, 16 originated from cross C1, one from C4, one from C18, one from C13, and one from C3. The significant gains obtained for lodging and plant uniformity

Table 4. Values predicted by the generalized additive model for agronomic traits measured in 398 white oat (*Avena sativa*) lines and three controls, indicating 5% of the superior and inferior genotypes based on the agronomic ideotype for panicle density, initial establishment, tillering, and flag-leaf size. The values in parentheses indicate the cross-identification code, shown in Table 1.

Panicle density (%)				Initial establishment (%)			
Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value	Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value
L118(C1)	10.29	L203(C1)	4.04	'URNRS22'	9.24	L180(C1)	5.59
L121(C1)	10.29	L205(C1)	4.04	L310(C5)	9.15	L209(C1)	5.51
L124(C1)	10.29	L223(C1)	3.94	L190(C1)	9.10	L179(C1)	5.51
L142(C1)	10.15	L227(C1)	3.94	L200(C1)	9.10	L177(C1)	5.47
L151(C1)	10.15	L243(C1)	3.94	L270(C1)	9.08	L315(C4)	5.47
L167(C1)	10.15	L238(C1)	3.94	L309(C10)	9.08	L175(C1)	5.42
L197(C1)	10.04	L240(C1)	3.94	L366(C14)	9.05	L321(C3)	5.32
L198(C1)	10.04	L270(C1)	3.84	L189(C1)	9.03	L203(C1)	5.30
L202(C1)	10.04	L267(C1)	3.84	L250(C1)	8.99	L292(C1)	5.28
L230(C1)	9.94	L275(C1)	3.84	L187(C1)	8.99	L181(C1)	5.27
L247(C1)	9.94	L287(C1)	3.84	L296(C1)	8.98	L271(C1)	5.25
L249(C1)	9.94	L312(C1)	3.74	L353(C13)	8.94	L221(C1)	5.16
L260(C1)	9.84	L333(C13)	3.74	L343(C4)	8.94	L143(C1)	5.10
L268(C1)	9.84	L308(C1)	3.74	L185(C1)	8.93	L66(C1)	5.07
L256(C1)	9.84	L332(C1)	3.74	L196(C1)	8.93	L210(C1)	4.71
L315(C4)	9.74	L244(C1)	2.94	L362(C9)	8.93	L394(C9)	4.64
L320(C2)	9.74	L239(C1)	2.94	L229(C1)	8.91	L174(C1)	4.48
L324(C18)	9.74	L253(C1)	2.84	L249(C1)	8.91	L290(C1)	2.06
L335(C2)	9.74	L33(C1)	2.62	L286(C1)	8.91	L295(C1)	1.96
L303(C15)	9.74	L135(C1)	1.15	L160(C1)	8.90	L218(C1)	1.86
Tillering (%)				Flag-leaf size (%)			
Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value	Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value
L290(C1)	2.31	L278(C1)	4.76	L112(C1)	3.16	L57(C1)	3.16
L295(C1)	2.37	L292(C1)	4.78	L4(C1)	3.16	L77(C1)	3.16
L142(C1)	2.63	L3(C1)	4.81	L217(C1)	3.16	L307(C1)	3.16
L139(C1)	2.66	L313(C4)	4.81	L358(C4)	3.16	L18(C1)	3.16
L175(C1)	2.73	L392(C5)	4.81	L64(C1)	3.16	L78(C1)	3.16
L174(C1)	2.74	L291(C1)	4.82	L66(C1)	3.16	L39(C1)	3.16
L66(C1)	2.77	L343(C4)	4.82	L40(C1)	3.16	L49(C1)	3.16
L50(C1)	2.78	L280(C1)	4.82	'URS Taura'	3.16	L309(C9)	3.16
L33(C1)	2.92	L8(C1)	4.83	L214(C1)	3.16	L30(C1)	3.16
L271(C1)	2.93	L348(C2)	4.84	L174(C1)	3.16	L80(C1)	3.16
L338(C19)	2.95	L7(C1)	4.85	L194(C1)	3.16	L300(C1)	3.16
L394(C9)	2.97	L352(C8)	4.86	L131(C1)	3.16	L320(C2)	3.16
L35(C1)	2.99	L362(C9)	4.86	L394(C9)	3.16	L284(C1)	3.16
L34(C1)	3.00	L309(C10)	4.88	L238(C1)	3.16	L118(C1)	3.16
L36(C1)	3.00	L41(C1)	4.88	L143(C1)	3.16	L44(C1)	3.16
L339(C5)	3.00	L26(C1)	4.89	L239(C1)	3.16	L15(C1)	3.16
L321(C3)	3.00	L103(C1)	5.10	L396(C8)	3.16	L28(C1)	3.16
L20(C1)	3.00	L153(C1)	5.11	L165(C1)	3.16	L48(C1)	3.16
L314(C11)	3.00	L45(C1)	5.28	L200(C1)	3.16	L70(C1)	3.16
L334(C3)	3.00	L51(C1)	5.28	L147(C1)	3.16	L14(C1)	3.16

Table 5. Values predicted by the generalized additive model for agronomic traits measured in 398 white oat (*Avena sativa*) lines and three controls, indicating 5% of the superior and inferior genotypes based on the agronomic ideotype for leaf spot incidence, leaf rust incidence, and stem rust incidence. The values in parentheses indicate the cross-identification code, shown in Table 1.

Incidence of leaf spot (%)			
Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value
L152(C1)	6.34	L187(C1)	7.03
L31(C1)	6.47	L193(C1)	7.03
L68(C1)	6.48	L140(C1)	7.03
L212(C1)	6.49	L128(C1)	7.03
L30(C1)	6.51	L168(C1)	7.03
L191(C1)	6.51	L284(C1)	7.04
L144(C1)	6.51	L122(C1)	7.06
L266(C1)	6.52	L121(C1)	7.06
L299(C15)	6.53	L33(C1)	7.08
L116(C1)	6.54	L81(C1)	7.09
L96(C1)	6.54	L239(C1)	7.09
L112(C1)	6.54	L228(C1)	7.09
L111(C1)	6.54	'URS Taura'	7.12
L64(C1)	6.56	L177(C1)	7.12
L63(C1)	6.56	L184(C1)	7.12
L370(C5)	6.58	L165(C1)	7.12
L349(C13)	6.58	'IPR Afrodite'	7.15
L367(C19)	6.58	L244(C1)	7.18
L385(C1)	6.59	L360(C12)	7.23
L384(C9)	6.59	L345(C14)	7.28

Leaf rust (%)			
Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value
L380(C3)	7.08	L78(C1)	8.11
L361(C2)	7.10	L269(C1)	8.11
L314(C11)	7.13	L358(C4)	8.12
L339(C5)	7.21	L277(C1)	8.12
L378(C1)	7.22	L84(C1)	8.13
L230(C1)	7.22	L133(C1)	8.13
L146(C1)	7.22	L83(C1)	8.14
L367(C19)	7.22	L243(C1)	8.15
L177(C1)	7.24	L241(C1)	8.16
L363(C5)	7.24	L35(C1)	8.17
L215(C1)	7.24	L323(C2)	8.19
L174(C1)	7.25	L125(C1)	8.22
L310(C5)	7.25	L123(C1)	8.23
L384(C9)	7.25	'URS Taura'	8.24
L291(C1)	7.26	L80(C1)	8.25
L299(C15)	7.26	L79(C1)	8.26
L181(C1)	7.27	'IPR Afrodite'	8.28
L98(C1)	7.31	L81(C1)	8.30
L103(C1)	7.33	L1(C1)	8.34
L111(C1)	7.34	L360(C11)	8.41

Stem rust (%)			
Superior genotypes (5%)	Predicted value	Inferior genotypes (5%)	Predicted value
L31(C1)	0	L387(C2)	0.03
L21(C1)	0	L397(C11)	0.03
L41(C1)	0	L388(C1)	0.03
L11(C1)	0	L398(C12)	0.03
L22(C1)	0	L379(C8)	0.03
L12(C1)	0	L389(C13)	0.03
L32(C1)	0	L380(C3)	0.03
L2(C1)	0	L390(C1)	0.03
L42(C1)	0	L360(C12)	0.03
L13(C1)	0	L39(C1)	0.97
L23(C1)	0	L55(C1)	0.98
L3(C1)	0	L49(C1)	0.98
L33(C1)	0	L112(C1)	0.99
L34(C1)	0	L110(C1)	0.99
L14(C1)	0	L145(C1)	0.99
L24(C1)	0	L203(C1)	1.00
L4(C1)	0	L222(C1)	1.00
L25(C1)	0	L279(C1)	1.01
L15(C1)	0	L351(C6)	1.02
L35(C1)	0	L1(C1)	1.97

Table 6. Selection of white oat (*Avena sativa*) genotypes based on agronomic ideotype, using the multitrait genotype-ideotype distance index (MGIDI) and considering multiple phenotypic traits.

Principal component analysis[1]							
PC	Eigenvalue	Variance (%)	Cum. variance (%)	PC	Eigenvalue	Variance (%)	Cum. variance (%)
PC1	3.13	28.4	28.4	PC7	0.68	6.18	85.6
PC2	1.67	15.2	43.6	PC8	0.59	5.34	91
PC3	1.2	10.9	54.6	PC9	0.54	4.89	95.9
PC4	1.06	9.64	64.2	PC10	0.4	3.67	99.6
PC5	0.97	8.79	73	PC11	0.05	0.44	100
PC6	0.71	6.48	79.5				
Variable[2]		Factor analysis[3]					
		FA1	FA2	FA3	FA4	Comm	Uniq
LOD (%)		0.17	0.22	0.75	0.18	0.67	0.33
IPH (cm)		-0.17	-0.76	0.1	-0.02	0.61	0.39
FLH (%)		-0.88	-0.29	0.08	-0.03	0.86	0.14
LH (%)		-0.88	-0.30	0.05	0	0.86	0.14
PD (%)		-0.69	0.08	-0.11	0.05	0.49	0.51
EST (%)		-0.17	-0.78	0.05	-0.08	0.65	0.35
TIL (%)		0.05	0.73	0.09	-0.11	0.56	0.44
FLS (%)		-0.44	-0.17	0.63	-0.1	0.63	0.37
LS (%)		-0.30	0.25	-0.05	0.7	0.65	0.35
LR (%)		-0.06	0.39	-0.5	0.26	0.47	0.53
SR (%)		-0.23	0.25	-0.04	-0.7	0.61	0.39
Variable	Factor	Selection differential[4]					
		Xo	Xs	SD	SDp	Sense	Goal
PD (%)	FA1	6.58	8.27	1.68	25.5	Increase	100
FLH (%)	FA1	7.78	8.97	1.19	15.3	Increase	100
LH (%)	FA1	7.92	9.13	1.21	15.3	Increase	100
IPH (cm)	FA2	38.8	39.5	0.65	1.67	Increase	100
EST (%)	FA2	7.52	7.68	0.16	2.13	Increase	100
TIL (%)	FA2	4.01	3.99	-0.03	-0.69	Decrease	100
LOD (%)	FA3	38.4	30.2	-8.22	-21.4	Decrease	100
FLS (%)	FA3	3.16	3.16	-0.00	-0.00	Decrease	100
LR (%)	FA3	7.7	7.7	-0.01	-0.08	Decrease	100
LS (%)	FA4	6.81	6.66	-0.15	-2.22	Decrease	100
SR (%)	FA4	0.037	0.01	-0.03	-84.7	Decrease	100

[1]Cum. variance, cumulative variance. [2]LOD, lodging; IPH, initial plant height; FLH, flowering homogeneity; LH, line homogeneity; PD, panicle density; EST, initial establishment; TIL, tillering; FLS, flag-leaf size; LS, leaf spot incidence; LR, leaf rust incidence; and SR, stem rust incidence. [3]Comm, commonality; and Uniq, singularity. [4]Xo, observed mean; Xs, mean of the selected genotypes; SD, selection differential; and SDp, percentage of selection differential.

traits indicate the effectiveness of the MGIDI index in simultaneous multivariate selection, allowing a balanced selection among correlated traits (Olivoto & Nardino, 2021). The combination of approaches used in the present study is novel for white oats, as it refines the multitrait selection, showing potential for use in studies with different numbers of parents and biparental crosses.

Conclusions

1. The use of generalized additive models and multitrait selection methods is effective in identifying superior white oat (*Avena sativa*) lines aligned with the agronomic ideotype.

2. Generalized additive models are effective in isolating the spatial effects of row and column for most traits evaluated in white oat.

3. From the evaluated genotypes, 4.02% meet the agronomic ideotype, meaning that significant selection gains can be obtained to increase panicle density, flowering homogeneity, and line homogeneity, as well as to reduce lodging.

References

ALVARES, C.A.; STAPE, J.L.; SENTELHAS, P.C.; GONÇALVES, J.L. de M.; SPAROVEK, G. Köppen's climate classification map for Brazil. **Meteorologische Zeitschrift**, v.22, p.711-728, 2013. DOI: https://doi.org/10.1127/0941-2948/2013/0507.

AZEVEDO, C.F.; FERRÃO, L.F.V.; BENEVENUTO, J.; RESENDE, M.D.V. de; NASCIMENTO, M.; NASCIMENTO, A.C.C.; MUNOZ, P.R. Using visual scores for genomic prediction of complex traits in breeding programs. **Theoretical and Applied Genetics**, v.137, art.9, 2024. DOI: https://doi.org/10.1007/s00122-023-04512-w.

BAUER, B.; von WIRÉN, N. Modulating tiller formation in cereal crops by the signalling function of fertilizer nitrogen forms. **Scientific Reports**, v.10, art.20504, 2020. DOI: https://doi.org/10.1038/s41598-020-77467-3.

BERLEZI, J.D.; CARVALHO, I.R.; SILVA, J.A.G. da; LORO, M.V.; SFALCIN, I.C.; PRADEBON, L.C.; PORT, E.D.; OURIQUE, R.S.; ROZA, J.P.D. Selection of white oat genotypes for contrasting fungicide management conditions. **Pesquisa Agropecuária Brasileira**, v.58, e03084, 2023. DOI: https://doi.org/10.1590/s1678-3921.pab2023.v58.03084.

CHEN, K.; O'LEARY, R.A.; EVANS, F.H. A simple and parsimonious generalised additive model for predicting wheat yield in a decision support tool. **Agricultural Systems**, v.173, p.140-150, 2019. DOI: https://doi.org/10.1016/j.agsy.2019.02.009.

CIEPLAK, M.; OKOŃ, S.; WERWIŃSKA, K. Genetic similarity of *Avena sativa* L. Varieties as an example of a narrow genetic pool of contemporary cereal species. **Plants**, v.10, art.1424, 2021. DOI: https://doi.org/10.3390/plants10071424.

DAL MOLIN SAVICKI, A.; CARVALHO, I.R.; LORO, M.V.; PRADEBON, L.C.; SCHMIDT, A.L.; SFALCIN, I.C.; SCHULZ, A.D.; MACHADO, P.P.N.; de CARLI ALCHIERI, A.; SILVA, J.A.G. da; ALBAN, A.A.; CHALLIOL, M.A. Positioning of white oat cultivars in different environments for high grain productivity in organic system. **Tropical and Subtropical Agroecosystems**, v.26, art.034, 2023. DOI: https://doi.org/10.56369/tsaes.4405.

FASOULA, D.A.; IOANNIDES, I.M.; OMIROU, M. Phenotyping and plant breeding: overcoming the barriers. **Frontiers in Plant Science**, v.10, art.1713, 2020. DOI: https://doi.org/10.3389/fpls.2019.01713.

JEVTIĆ, R.; ŽUPUNSKI, V.; LALOŠEVIĆ, M.; ŽUPUNSKI, L. Predicting potential winter wheat yield losses caused by multiple disease systems and climatic conditions. **Crop Protection**, v.99, p.17-25, 2017. DOI: https://doi.org/10.1016/j.cropro.2017.05.005.

LAIDIG, F.; FEIKE, T.; KLOCKE, B.; MACHOLDT, J.; MIEDANER, T.; RENTEL, D.; PIEPHO, H.P. Long-term breeding progress of yield, yield-related, and disease resistance traits in five cereal crops of German variety trials. **Theoretical and Applied Genetics**, v.134, p.3805-3827, 2021. DOI: https://doi.org/10.1007/s00122-021-03929-5.

LAIDIG, F.; FEIKE, T.; KLOCKE, B.; MACHOLDT, J.; MIEDANER, T.; RENTEL, D.; PIEPHO, H.P. Yield reduction due to diseases and lodging and impact of input intensity on yield in variety trials in five cereal crops. **Euphytica**, v.218, art.150, 2022. DOI: https://doi.org/10.1007/s10681-022-03094-w.

MANTAI, R.D.; SILVA, J.A.G. da; MAROLLI, A.; MAMANN, Â.T.W. de; SAWICKI, S.; KRÜGER, C.A.M.B. Simulation of oat development cycle by photoperiod and temperature. **Revista Brasileira de Engenharia Agrícola e Ambiental**, v.21, p.3-8, 2017. DOI: https://doi.org/10.1590/1807-1929/agriambi.v21n1p3-8.

NASA POWER. **NASA Prediction of Worldwide Energy Resources**. 2025. Available at: <https://power.larc.nasa.gov/>. Accessed on: Aug. 24 2026.

OLIVOTO, T.; LÚCIO, A.D.C. metan: an R package for multi-environment trial analysis. **Methods in Ecology and Evolution**, v.11, p.783-789, 2020. DOI: https://doi.org/10.1111/2041-210X.13384.

OLIVOTO, T.; NARDINO, M. MGIDI: toward an effective multivariate selection in biological experiments. **Bioinformatics**, v.37, p.1383-1389, 2021. DOI: https://doi.org/10.1093/bioinformatics/btaa981.

PARK, R.F.; BOSHOFF, W.H.P.; CABRAL, A.L.; CHONG, J.; MARTINELLI, J.A.; MCMULLEN, M.S.; MITCHELL FETCH, J.W.; PACZOS-GRZEDA, E.; PRATS, E.; ROAKE, J.; SOWA, S.; ZIEMS, L.; SINGH, D. Breeding oat for resistance to the crown rust pathogen *Puccinia coronata* f. sp. *avenae*: achievements and prospects. **Theoretical and Applied Genetics**, v.135, p.3709-3734, 2022. DOI: https://doi.org/10.1007/s00122-022-04121-z.

PRADEBON, L.C.; CARVALHO, I.R.; SILVA, J.A.G. da; ROZA, J.A.D.; LORO, M.V.; FERREIRA, L.L.; SANGIOVO, J.P. Development and selection of white oat genotypes for sustainable environments. **Brazilian Journal of Agriculture**, v.98, p.142-158, 2024. DOI: https://doi.org/10.37856/bja.v98i3.4338.

R CORE TEAM. **R**: a language and environment for statistical computing. Vienna: R Core Team, 2025. Available at: <https://www.R-project.org/>. Accessed on: Aug. 24 2026.

RAHMAN, A.; SAPKOTA, S.; AJAYI-MOSES, O.; NANDETY, R.S.; FIEDLER, J.D.; NARAGHI, S.M.; MCMULLEN, M.S.; BOCKELMAN, H.E.; KLOS, K.E.; CARLSON, C.H. A global assembly of landrace oat (*Avena sativa* L.) accessions is a discovery resource for adaptive variation, association mapping, and trait deployment. **G3: Genes, Genomes, Genetics**, v.15, jkaf093, 2025. DOI: https://doi.org/10.1093/g3journal/jkaf093.

RODRÍGUEZ-ÁLVAREZ, M.X.; BOER, M.P.; EEUWIJK, F.A. van; EILERS, P.H.C. Spatial models for field trials. **arXiv**, p.1-39, 2016. DOI: https://doi.org/10.48550/arXiv.1607.08255.

SANTOS, H.G. dos; JACOMINE, P.K.T.; ANJOS, L.H.C. dos; OLIVEIRA, V.Á. de; LUMBRERAS, J.F.; COELHO, M.R.; ALMEIDA, J.A. de; ARAÚJO FILHO, J.C. de; LIMA, H.N.; MARQUES, F.A.; OLIVEIRA, J.B. de; CUNHA, T.J.F. **Sistema**

brasileiro de classificação de solos. 6.ed. rev. e ampl. Brasília: Embrapa, 2025. 393p.

SOIL SURVEY STAFF. **Soil taxonomy**: a basic system of soil classification for making and interpreting soil surveys. 2nd ed. Washington: USDA-Natural Resources Conservation Service, 1999. 869p. (USDA Handbook, 436).

SWARUP, S.; CARGILL, E.J.; CROSBY, K.; FLAGEL, L.; KNISKERN, J.; GLENN, K.C. Genetic diversity is indispensable for plant breeding to improve crops. **Crop Science**, v.61, p.839-852, 2021. DOI: https://doi.org/10.1002/csc2.20377.

TRETHOWAN, R.M. Defining a genetic ideotype for crop improvement. In: FLEURY, D.; WHITFORD, R. (Ed.). **Crop Breeding**. New York: Springer, 2014. p.1-20. (Methods in molecular biology, v.1145). DOI: https://doi.org/10.1007/978-1-4939-0446-4_1.

TUMINO, G.; VOORRIPS, R.E.; MORCIA, C.; GHIZZONI, R.; GERMEIER, C.U.; PAULO, M.J.; TERZI, V.; SMULDERS, M.J.M. Genome-wide association analysis for lodging tolerance and plant height in a diverse European hexaploid oat collection. **Euphytica**, v.213, art.163, 2017. DOI: https://doi.org/10.1007/s10681-017-1939-8.

VAN OIJEN, M.; HÖGLIND, M. Toward a Bayesian procedure for using process-based models in plant breeding, with application to ideotype design. **Euphytica**, v.207, p.627-643, 2016. DOI: https://doi.org/10.1007/s10681-015-1562-5.

WELLINGTON, M.J.; LAWES, R.; KUHNERT, P. A framework for modelling spatio-temporal trends in crop production using generalised additive models. **Computers and Electronics in Agriculture**, v.212, art.108111, 2023. DOI: https://doi.org/10.1016/j.compag.2023.108111.

WOOD, S.N. **Generalized additive models**: an introduction with R. 2nd ed. Boca Raton: Chapman and Hall/CRC, 2017. DOI: https://doi.org/10.1201/9781315370279.

ZADOKS, J.C.; CHANG, T.T.; KONZAK, C.F. A decimal code for the growth stages of cereals. **Weed Research**, v.14, p.415-421, 1974. DOI: https://doi.org/10.1111/j.1365-3180.1974.tb01084.x.

Author contributions

Pedro Henrique Ruwer: conceptualization (equal), data curation (equal), investigation (lead), formal analysis (supporting), writing – original draft (lead); **Alessandro Dal'Col Lúcio:** methodology (equal), validation (lead), formal analysis (supporting), supervision (supporting), writing – review and editing (equal); **Ivan Ricardo Carvalho:** conceptualization (supporting), methodology (equal), project administration (lead), supervision (lead), resources (supporting), funding acquisition (supporting), writing – review and editing (equal); **Willyan Júnior Adorian Bandeira:** formal analysis (lead), software (lead), visualization (lead), methodology (supporting), validation (supporting), writing – review and editing (equal); **Adriano Dietterle Schulz:** conceptualization (equal), data curation (equal), investigation (supporting), writing – original draft (supporting); **Gabriel Mathias Weimer Bruinsma:** investigation (supporting), data curation (supporting), visualization (supporting), writing – original draft (supporting); **José Antônio Gonzalez da Silva:** funding acquisition (lead), resources (lead), project administration (supporting), supervision (supporting), writing – review and editing (supporting).

Chief editor: Edemar Corazza
Edited by: Mírian Baptista

Data availability statement

Data available upon request: research data are only available upon reasonable request to the corresponding author.

Declaration of use of AI technologies

No generative artificial intelligence (AI) was used in this study.

Conflict of interest statement

The authors declare no conflicts of interest.

Acknowledgments

To Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), for financial support.

Disclaimer/Publisher's note

The statements, opinions, and data contained in all texts published in Pesquisa Agropecuária Brasileira (PAB) are solely those of the individual author(s) and not of the journal's publisher, editor, and editorial team, who disclaim responsibility for any injury to people or property resulting from any referred ideas, methods, instructions, or products.

The mention of specific chemical products, machines, and commercial equipment in the texts published in this journal does not imply their recommendation by the publisher.