PAB
Pesquisa Agropecuária Brasileira

ISSN 1678-3921

Journal homepage: www.embrapa.br/pab

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

Genetics/ Original Article

Adaptability and stability of black oat genotypes using the GGE biplot analysis

Luis Antônio Klein[1],
Volmir Sergio Marchioro[1 ✉],
Marcos Toebe[1],
Tiago Olivoto[2],
Daniela Meira[3],
João Vitor Alberti[1],
José Luiz Balansin Finatto[1],
Duana Cancian Garafini[1],
Bruna Scaravonatto[1],
Nitiele Silva de Azeredo[1],
Gaziela Ulbrik[1],
Carla Francine Osmari[1] and
Caroline Bandeira Foguesatto[1]

[1] Universidade Federal de Santa Maria, Campus Frederico Westphalen, Linha 7 de Setembro, s/nº, BR 386, Km 40, CEP 98400-000 Frederico Westphalen, RS, Brazil. E-mail: luis.antonio.klein@hotmail.com, volmir@marchioro.eng.br, m.toebe@gmail.com, joao.vitoralberti1702@gmail.com, josefinatto25@gmail.com, duana.garafini@acad.ufsm.br, brunascaravonatto1@gmail.com, nitisazeredo@hotmail.com, graziela.ulbrik@acad.ufsm.br, carlaosmari@gmail.com, caroline.foguesatto@acad.ufsm.br

[2] Universidade Federal de Santa Catarina, Centro de Ciências Agrárias, Rodovia Admar Gonzaga, nº 1346, Itacorubi, CEP 88034-000 Florianópolis, SC, Brazil. E-mail: tiagoolivoto@gmail.com

[3] Centro de Ensino Superior Riograndense, Rodovia Leonel de Moura Brizola, BR 386, Km 138, Beira Campo, CEP 99560-000 Sarandi, RS, Brazil. E-mail: dmdanielameira94@gmail.com

✉ Corresponding author

Received
August 15, 2023

Accepted
December 19, 2023

Abstract – The objective of this work was to identify the most adapted and stable genotypes for dry mass and seed yield using the genotype plus environment interaction (GGE) biplot technique. The experiment was conducted in the municipality of Frederico Westphalen, in the state of Rio Grande do Sul, Brazil, in 2018, 2019, 2020, and 2021, using five lines and two cultivars of black oat, in a randomized complete block experimental design, with three replicates. The adaptability and stability of the genotypes, as well as their behavior in the environments, were evaluated using the GGE biplot. The seed yield of black oat genotypes is highly influenced by the environmental conditions over the four studied cultivation years. The UFSMFW 2-07 genotype stands out, but shows instability. The UFSMFW 2-07 and 'UPFA 21-Moreninha' genotypes show adaptability in specific years. Mega environments are formed for the dry mass trait in 2018 and 2021 and seed yield in 2018, 2020, and 2021, whereas, 2019 is considered the year for genotype discrimination.

Index terms: *Avena strigosa*, environment-genotype interaction, genotype selection, seed yield.

Adaptabilidade e estabilidade de genótipos de aveia-preta com uso da análise GGE biplot

Resumo – O objetivo deste trabalho foi identificar os genótipos mais adaptados e estáveis para massa seca e produtividade de sementes, com uso da técnica genótipo + interação genótipo-ambinete (GGE) biplot. O experimento foi conduzido no município de Frederico Westphalen, no estado do Rio Grande do Sul, Brasil, em 2018, 2019, 2020 e 2021, tendo-se utilizado cinco linhagens e duas cultivares de aveia-preta, em delineamento experimental de blocos ao acaso, com três repetições. A adaptabilidade e a estabilidade dos genótipos, bem como seu comportamento nos ambientes, foram avaliados pelo GGE biplot. A produtividade de sementes de genótipos de aveia-preta é altamente influenciada pelas condições ambientais ao longo dos quatro anos de cultivo estudados. O genótipo UFSMFW 2-07 destaca-se, mas apresenta instabilidade. Já os genótipos UFSMFW 2-07 e 'UPFA 21-Moreninha' apresentam adaptabilidade para produção de massa seca em anos específicos. São formados mega-ambientes para o traço massa seca em 2008 e 2021 e para produtividade de sementes em 2018, 2020 e 2021, enquanto 2019 é considerado o ano para discriminação de genótipos.

Termos para indexação: *Avena strigosa*, interação genótipo-ambiente, seleção de genótipos, produtividade de sementes.

Pesq. agropec. bras., Brasília, v.59, e03483, 2024
DOI: 10.1590/S1678-3921.pab2024.v59.03483

How to cite
KLEIN, L.A.; MARCHIORO, V.S.; TOEBE, M.; OLIVOTO, T.; MEIRA, D.; ALBERTI, J.V.; FINATTO, J.L.B.; GARAFINI, D.C.; SCARAVONATTO, B.; AZEREDO, N.S. de; ULBRIK, G.; OSMARI, C.F.; FOGUESATTO, C.B. Adaptability and stability of black oat genotypes using the GGE biplot analysis. **Pesquisa Agropecuária Brasileira**, v.59, e03483, 2024. DOI: https://doi.org/10.1590/S1678-3921.pab2024.v59.03483.

Introduction

The Southern region of Brazil is characterized by being a great producer of cold season cereals, among which black oats (*Avena strigosa* Schreb.) have been preferred by producers in recent years, for the excellent soil cover generated by its high biomass production, which can be used for forage production (Leite et al., 2012), and for the greater hardiness found among winter species. The advantages of growing black oats are reinforced by the possibility of harvesting the seeds at the end of the cycle, to be used in animal feed.

Efficient cultivation of a species or a specific cultivar, in an agroclimatic region, depends on its adaptability and stability of grain yield (Fayeun et al., 2018), which should be evaluated due to the possibility of the presence of genotype-environment interaction. This interaction is responsible for variations in the performance of genotypes in different cultivation environments, representing a great challenge for selection and recommendation of cultivars (Branquinho et al., 2014).

Information about the genotype and its interaction with the environment is very important to estimate its performance when cultivated in different locations. Therefore, genotype testing in various environments will help to identify cultivars with broad and specific adaptation (Noerwijati et al., 2014), besides allowing the selection and recommendation of genotypes that exploit their maximum grain yield potential (Yan, 2016).

Different methods have been developed to study the effect of genotype-environment interaction on the selection of superior genotypes in multi-environment assays, among these, there is the genotype main effect plus genotype-environment interaction (GGE) biplot. This method has gained popularity in the evaluation of multi-environment assays by providing graphical images (Yan, 2015) and by using a biplot to show the two factors (G plus GE), important in the evaluation of cultivars.

Since the introduction of the GGE biplot, studies have been carried out applying this technique with several crops, including wheat (Silva et al., 2015), barley (Kendal, 2016), soybean (Bhartia et al., 2017; Souza et al., 2021) and sweet potato (Karuniawan et al., 2021). The objectives usually are the identification and selection of superior more adapted and stable genotypes, as well as the identification of mega-environments and more representative and discriminative environments.

The objective of this work was to identify the most adapted and stable genotypes for dry mass and seed yield using the GGE biplot technique.

Materials and Methods

The experiment was conducted in the years 2018, 2019, 2020, and 2021, at Universidade Federal de Santa Maria, Frederico Westphalen Campus, in the state of Rio Grande do Sul (27°23'26"S, 53°25'43"W, at 461.3 m of altitude). The climate, according to Köppen-Geiger, is classified as Cfa, that is, humid subtropical, with a mean annual precipitation of 2,100 mm (Alvares et al., 2013) and the soil is classified as Latossolo Vermelho distrófico típico, according to Brazilian soil classification system (Santos et al., 2018), i.e., typical dystrophic Oxisol.

To conduct the experiments, five homozygous black oat lines (UFSMFW 2-01, UFSMFW 2-02, UFSMFW 2-04, UFSMFW 2-05, and UFSMFW 2-07) and two commercial cultivars (UPFA 21-Moreninha and IPR Cabocla) were used applying experimental design of randomized blocks, with three replications.

Each experimental unit consisted of six rows of 5 m in length, spaced 0.17 m apart, with a sowing density of 300 suitable seeds per m². The sowing was carried out at the end of May during the four years of cultivation. Cultural treatments, following the technical indications for black oat cultivation, were carried out to control weeds, pests, and diseases whenever necessary, and the soil was analyzed to choose the appropriate fertilizer.

To measure the dry mass in kg ha^{-1}, 1 m^2 of the plants at full flowering, this is, when 50% of them emitted inflorescences, were cut and dried in an oven until reaching constant mass. After the physiological maturation, the harvest was carried out and the seed yield in kg ha^{-1} was evaluated through the amount of seeds from the plot.

To identify the interaction between the genotypes and years of cultivation for the traits studied, based on the experimental design used, a joint analysis of variance and the F test ($p<0.05$) were performed considering balanced data and using the following statistical model: $Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B/A_{jk} + \varepsilon_{ijk}$, where Y_{ijk} is the observation obtained in the plot with i-th genotype in the j-th block, μ is the general mean of the experiment, G_i is the effect of the i-th genotype considered fixed, A_j is the effect of the j-th environment considered fixed, GA_{ij} is the effect of the i-th genotype interaction with the j-th environment, B/A_{jk} is the effect of the k-th block within the j-th environment considered random, and ε_{ij} is the random error effect. After identifying a significant difference through the analysis of variance, the mean group was tested using Scott & Knott's test (1974).

Once interaction between genotypes and environments was verified, the GGE biplot analysis was carried out to identify the ideal most adapted and stable genotypes, as well as the performance of the genotypes in each environment to select the best one for each genotype. The GGE biplot analysis was carried out according to the following statistical model:

$$\phi_{ij} = \hat{Y}_{ij} - \mu - \beta_j = \sum_{k-1}^{p} \xi_{ik}^{*} \eta_{jk}^{*}$$

where ϕ_{ij} is the interaction effect between genotype i and environment j; $\hat{Y}_{ij}$ is the mean yield of genotype i in environment j; μ is the overall mean; β_j is the main effect of environment j;

$$\xi_{ik}^{*} = \lambda_k^{\alpha} \xi_{ik} ; \eta_{jk}^{*} = \lambda_k^{\alpha-1} \eta_{jk},$$

where, λ_k k-th is the eigenvalue of Singular Value Decomposition ($k = 1, ...p$), with $p \leq \min(e, g)$; α is a singular value split factor for principal component k (Yan, 2002), ξ_{ik}^{*} and η_{jk}^{*} are the principal component k scores for genotype i and environment j, respectively.

In the generated figures, the notation Transform = 0 indicates that the data have not been transformed. In Scaling = 1, values are divided by the standard deviation of each environment, giving each one similar importance. The notation Centering refers to the model used, in which Centering = 2 contains the effect of GGE biplot (genotype + interaction × genotype + environment). Singular Value Partitioning = 1, focusing on genotypic performance, was used for the analysis of ideal genotypes, and Singular Value Partitioning = 2, focusing on the environment, was used for the other inferences tested (Yan et al., 2000). Data manipulation, variance analysis and GGE biplot analysis were performed in the R software, version 4.0.2 (R Core Team, 2020), using metan package (Olivoto & Lúcio, 2020).

Results and Discussion

The data obtained from this study met the assumptions of normality and homogeneity requirement. The joint analysis of variance revealed significance for the effects of years, genotypes, and interaction between genotypes and environments (Table 1) for the traits

Table 1. Summary of the joint analysis of variance for the dry mass and seed yield of seven black oat (*Avena strigosa*) genotypes, conducted in the municipality of Frederico Westphalen, state of Rio Grande do Sul, Brazil, in the years 2018, 2019, 2020, and 2021.

Source of variation	DF(1)	Mean square		
		Dry mass		Seed yield
Block/environments	8	463,500.44		9,031.89
Genotypes (G)	6	2,860,729.81*		1,604,300.16*
Years (Y)	3	55,801,139.70*		8,425,655.81*
G x Y	18	752,977.32*		391,446.61*
Error	48	280,534.21		21,046.00
Total	83			
Mean (kg ha^{-1})		7,333.07		2,283.16
CV (%)		7.22		6.35
S (%)		49.05		66.59
C (%)		50.95		33.41
Year	CV (%)	Mean (kg ha^{-1})	CV (%)	Mean (kg ha^{-1})
2018	7.83	7,823.11	7.40	2,917.01
2019	7.38	9,368.02	4.70	2,739.34
2020	2.94	6,520.22	6.91	1,721.50
2021	8.56	5,621.00	4.70	1,755.12

(1)DF, degrees of freedom; S, simple interaction component; C, complex interaction component; CV, coefficient of variation. *Significant at 5% probability of error.

dry mass and seed yield. This result demonstrates that there was a variation in the response of the genotypes tested during the four years of cultivation studied. For Noerwijati et al. (2014), testing genotypes in various environments helps identify the best ones for broad and specific adaptation. The presence of genotype-environment interaction enabled the application of the GGE biplot analysis and suggests that it might exist mega-environments with different succeeded genotypes.

The success of a new cultivar in the market depends on its agronomic performance and on the interaction with the growing environment (Nörnberg et al., 2014). The occurrence of interaction between genotypes and environments makes it difficult to select and recommend cultivars (Silva et al., 2011) so, it is necessary to carry out more precise evaluations to identify more adapted genotypes (Silva et al., 2015).

In general, the UFSMFW genotypes showed good potential for dry mass yield compared with the control cultivars (Table 2). The UFSMFW 2-07 genotype stood out with the highest average dry mass in 2019 (10,466.67 kg ha^{-1}), being superior to 'IPR Cabocla' and equal to 'UPFA 21-Moreninha'. The UFSMFW 2-01, UFSMFW 2-02, and UFSMFW 2-05 genotypes stood out when cultivated in 2018, 2020, and 2021, in the latter being statistically superior to 'UPFA 21-Moreninha', which was developed to present high yield of dry mass.

The highest seed yields were obtained in 2018 and 2019, which were higher than the general mean of the test for this trait (Table 2). The same behavior of the dry mass trait was observed for seed yield, with 2020 and 2021 being the least favorable years for higher yields. The period of water scarcity in 2020 and 2021 impaired the reproductive period and physiological maturation, decreasing seed yield. In 2021, there was excessive rainfall close to the harvest period, reducing the mass of seeds and, consequently, causing losses in yield.

However, in 2018, 2019, and 2020, the potential of all UFSMFW genotypes for seed yield was evident, because they were higher than the control in most cases. In 2018, the means of the UFSMFW genotypes did not differ statistically from each other. The UFSMFW 2-07 genotype stood out for being one the most productive in the four years of cultivation and for

Table 2. Means of dry mass and seed yield traits for seven black oat (*Avena strigosa*) genotypes, cultivated during four years, in the municipality of Frederico Westphalen, in the state of Rio Grande do Sul, Brazil$^{(1)}$.

Genotype	2018	2019	2020	2021
		Dry mass (kg ha^{-1})		
UFSMFW 2-01	8,440.80 Aa	9,040.00 Ab	6,700.27 Ba	5,774.58 Ca
UFSMFW 2-02	8,094.67 Ba	8,933.33 Ab	6,530.53 Ca	5,830.97 Ca
UFSMFW 2-04	7,516.93 Bb	9,013.33 Ab	6,430.40 Ca	6,074.72 Ca
UFSMFW 2-05	7,962.27 Ba	9,440.00 Ab	6,544.00 Ca	5,585.55 Da
UFSMFW 2-07	7,622.93 Bb	10,466.67 Aa	7,082.93 Ba	5,968.47 Ca
'UPFA 21-Moreninha'	8,000.67 Ba	10,933.33 Aa	6,746.13 Ca	5,305.14 Db
'IPR Cabocla'	7,125.87 Ab	7,746.67 Ac	5,606.40 Bb	4,808.33 Bb
		Seed yield (kg ha^{-1})		
UFSMFW 2-01	3,483.13 Aa	2,748.27 Bc	1,949.03 Ca	1,810.00 Ca
UFSMFW 2-02	2,999.85 Aa	2,725.90 Ac	1,579.72 Bb	1,863.50 Ba
UFSMFW 2-04	2,883.70 Aa	1,939.23 Bd	1,850.97 Ba	1,970.33 Ba
UFSMFW 2-05	3,202.47 Aa	3,234.43 Ab	1,886.66 Ba	1,580.00 Ba
UFSMFW 2-07	3,243.13 Ba	4,152.10 Aa	2,074.72 Ca	1,923.67 Ca
'UPFA 21-Moreninha'	2,498.60 Ab	2,257.17 Ad	1,370.97 Bb	1,636.83 Ba
'IPR Cabocla'	2,108.77 Ab	2,114.70 Ad	1,337.50 Bb	1,503.33 Ba

$^{(1)}$Means followed by equal letters, uppercase in the lines and lowercase in the columns, do not differ according to the mean grouping test by Scott-Knott, considering a 5% error probability.

having the highest yield in 2019, with 4,152.10 kg ha^{-1}, in addition to being the only one to exceed the 2,000 kg ha^{-1} mark in 2020. The year 2021 was the least favorable for seed yield, with the lowest productive means, and there was no statistical difference between the evaluated genotypes.

The GGE biplot analysis revealed that the first two principal components 1 and 2 showed 92.74% of the total variation, with principal component 1 (78.63%) and 2 (14.11%) for dry mass (Figures 1 A and 1 C). For seed yield (Figures 1 B and 1 D), the total variation of the principal components was 96.51%, principal

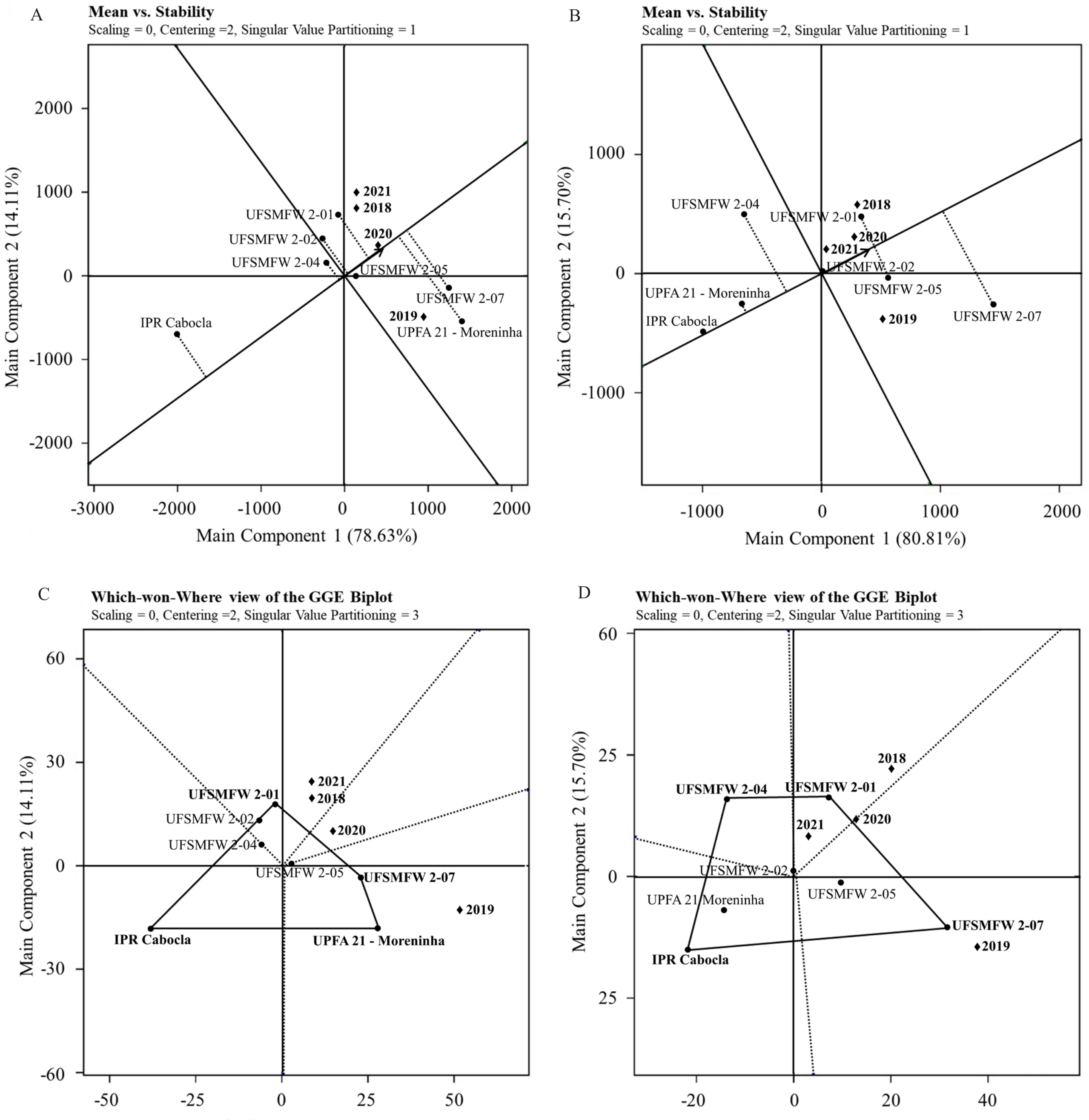

Figure 1. Genotype-environment interaction biplot in mean performance vs. stability (A, B) and who-won-where (C, D) for the dry mass (A, C) and seed yield (B, D), evaluated in seven black oat (*Avena strigosa*) genotypes, cultivated in the years of 2018, 2019, 2020, and 2021, in the municipality of Frederico Westphalen, in the state of Rio Grande do Sul, Brazil.

component 1 (80.81%) and 2 (15.70%). The first principal component 1 is represented on the X axis, and genotypes that have higher principal component 1 values are considered more productive, while the second principal component 2 is represented on the Y axis and describes the stability of the genotype (Yan et al., 2000).

When classifying genotypes based on their performance in an environment, a straight line drawn with an arrow at the end, passing through the origin of the biplot, is called the Average Environment Coordination (AEC) (Yan & Kang, 2003). Along this line, there is the classification of genotypes. The arrow shown on the AEC abscissa axis points in the direction of greater average performance of the genotypes and, consequently, ranks the genotypes in relation to average performance (Yan et al., 2007). The perpendicular line to the AEC axis represents the variability of performance in terms of stability, indicating that the greater the distance from the origin, the greater the instability of the genotype, in both directions (Yan, 2011).

The genotypes that stood out with above-average yields of dry matter were UFSMFW 2-07 and 'UPFA 21-Moreninha' (Figure 1 A). When analyzing the production stability, it is observed that they were unstable, which means they adapted to specific environmental conditions. The UFSMFW 2-05 and UFSMFW 2-04 genotypes proved to be the most stable genotypes to environmental variations in the four years of cultivation. When analyzing the mean performance for seed yield (Figure 1 B), it is observed that the UFSMFW 2-07 genotype was the most productive, followed by the UFSMFW 2-05 and UFSMFW 2-01 genotypes. However, for this trait, the genotype was again unstable to environmental variations between years. The most stable genotype was UFSMFW 2-02.

The pattern of being well succeeded in multi-environment analyzes is important to study the possible difference of mega-environments in a region. In this study, the presence of mega-environments may indicate the similarity between years of cultivation. A mega-environment is defined as a group of environments that consistently share one or more equal genotypes (Yan & Rajcan, 2002). The polygon view of a biplot is the best way to visualize patterns of interaction between genotypes and environments, Figure 1 C, for instance, shows the formation of four different sectors for dry mass.

The years 2018 and 2021 were grouped in the same sector, revealing themselves as a mega-environment and presenting the UFSMFW 2-01 genotype as the most productive. The genotypes of the vertices of the polygon for each sector are those with the highest grain yield in the environments that fit that sector (Farshadfar et al., 2013). The year 2019 was isolated in a sector and comprised two vertices, containing the genotypes UFSMFW 2-07 and 'UPFA 21-Moreninha', these being the most productive in this environment.

For the seed yield (Figure 1 D), four sectors and one mega-environment were formed containing the years 2018, 2020, and 2021, presenting the UFSMFW 2-01 genotype as the most productive. The year 2019 was allocated in isolation in a sector and contained the genotypes UFSMFW 2-07 (apex) and UFSMFW 2-05. The year 2019 was allocated separately from the others due to the higher productivity means for both traits evaluated in this environment, while in 2018, 2020, and 2021 the means were lower. Also, the similarity between the two environments, as observed by Silva et al. (2021) in wheat, happened because the tests were performed in the same location, with variation only between the evaluation years. The year effect is the most important factor in the multi-year analysis and a high performance over the years is a desirable trait (Yan, 2014).

In the lower left sector of the dry mass of GGE biplot and in the upper and lower left sectors of the GGE biplot for seed yield, in which no environment was included, there are the lines that did not have satisfactory productive performance in all environments by the method studied.

For a genotype to be considered ideal, it must present high productive performance associated with high stability (Silva et al., 2021). In the GGE biplot analysis, the ideal genotype is graphically defined by the longest vector in principal component 1, without projections in principal component 2, which means being closer to the smallest central concentric circle (Silva et al., 2015). Then, looking at concentric circles along the arrowhead, lines can classified according to inclusion in the circles and distance from the arrowhead.

The ranking of genotypes showed that there was no ideal genotype for both dry mass (Figure 2 A) or seed yield (Figure 2 B). Although this genotype is only symbolic, it serves as a reference to evaluate other genotypes (Oliveira et al., 2019). However, for dry mass, the genotype that came closest to the ideal was UFSMFW 2-07, which can be used as a reference when comparing genotypes. The general classification of the genotypes in the biplot was as follows: UFSMFW 2-07 > UFSMFW 2-01 > UFSMFW 2-05 > UFSMFW 2-02 > UFSMFW 2-04 > 'UPFA 21-Moreninha' > 'IPR Cabocla'. For the seed yield trait, the closest genotypes to the ideal were UFSMFW 2-01 and UFSMFW 2-05.

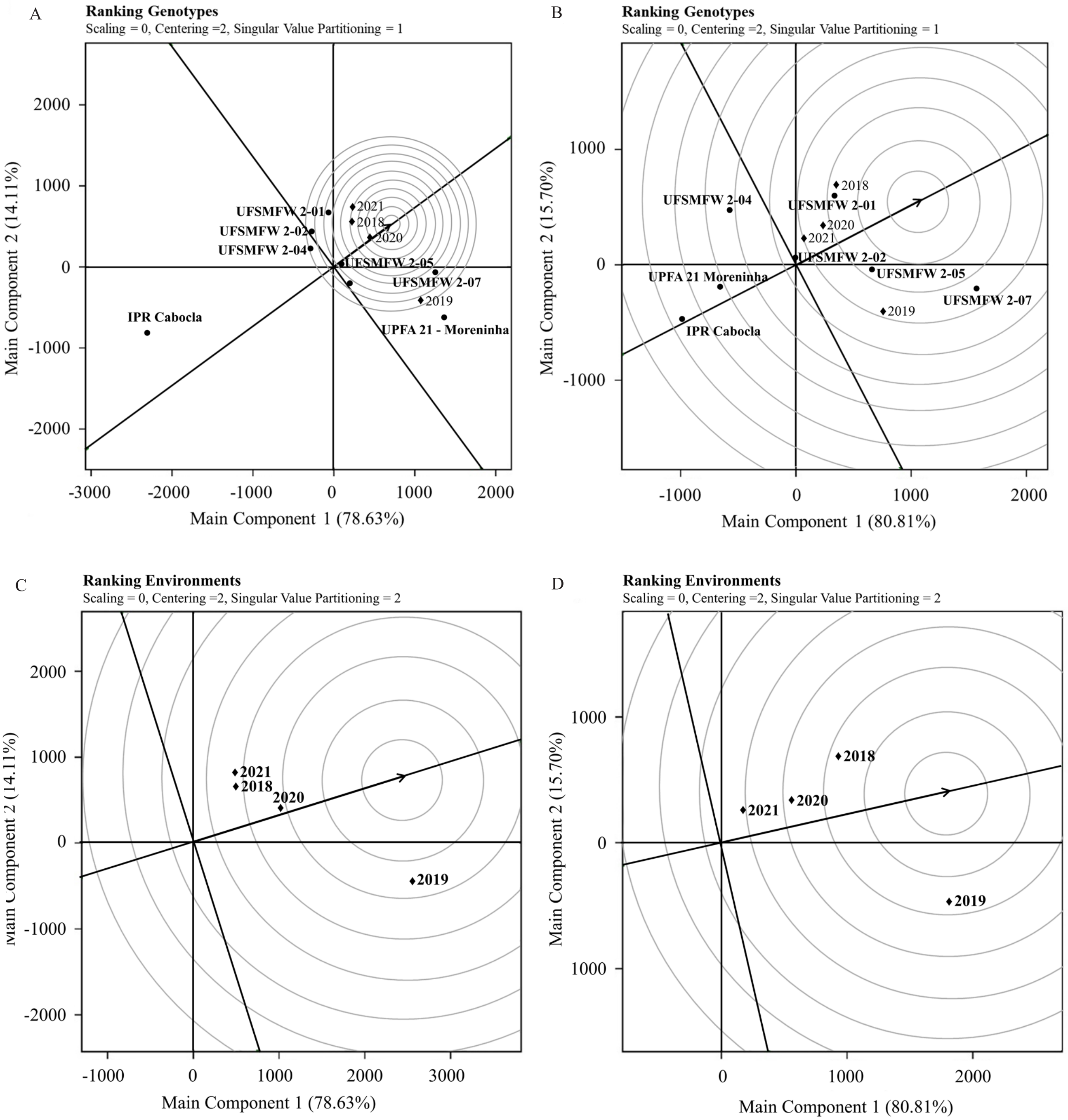

Figure 2. Genotype-environment interaction biplot representing the ideal genotypes (A, B) and environments (C, D) for the dry mass yield (A, C) and seed yield (B, D), evaluated in seven black oat (*Avena strigosa*) genotypes, cultivated in the years 2018, 2019, 2020, and 2021, in the municipality of Frederico Westphalen, in the state of Rio Grande do Sul, Brazil.

The overall classification was as follows: UFSMFW 2-01 > UFSMFW 2-05 > UFSMFW 2-07 > UFSMFW 2-02 > UFSMFW 2-04 > 'UPFA 21-Moreninha' > 'IPR Cabocla'.

The ranking of environments can be seen in Figures 2 C and 2 D. The ideal environment is represented by the circle at the head of the arrow. For dry mass, the environment closest to the ideal was the one in 2019. The years 2018 and 2021, which turned out to be a mega-environment, were the furthest from the ideal one. For the seed yield trait, the years 2018 and 2019 were the closest to the ideal, with 2021 as the furthest.

The biplot of the discriminant x representative pattern aimed at evaluating a test environment and identifying, in this case, the years of cultivation, ideal for selecting superior genotypes efficiently for a mega-environment. An ideal test environment should discriminate the genotypes and be representative of all test environments (Mushay et al., 2020).

The greater the vector length of a test site, the greater is its discriminative capacity, or genotype differentiation (Yan & Tinker, 2006). In this sense, for the dry mass (Figure 3 A), the year 2019 was the most discriminating, presenting the longest vector, superior to that of the genotypes, allowing to differentiate the behavior of the genotypes. For the seed yield trait, the years 2019 and 2018 were the most discriminating (Figure 3 B). Those years with short vectors are less discriminating, meaning that all genotypes show similar behavior, and, therefore, should not be used as a test year (Hongyu et al., 2015).

Another possible point to observe in this biplot pattern is the representativeness of the environments, that is, in this case, which years represent the others. In this analysis, the smaller the angle of the location vector in relation to the single arrow axis that represents the coordinate of the mean environment, the greater is the representativeness of this location in relation to the set of evaluated locations. Figure 3 shows that year 2020 was the most representative, representing the means of all years. The other years can be considered discriminating and not representative, serving to select genotypes with specific adaptation in mega-environments. Discriminating and representative

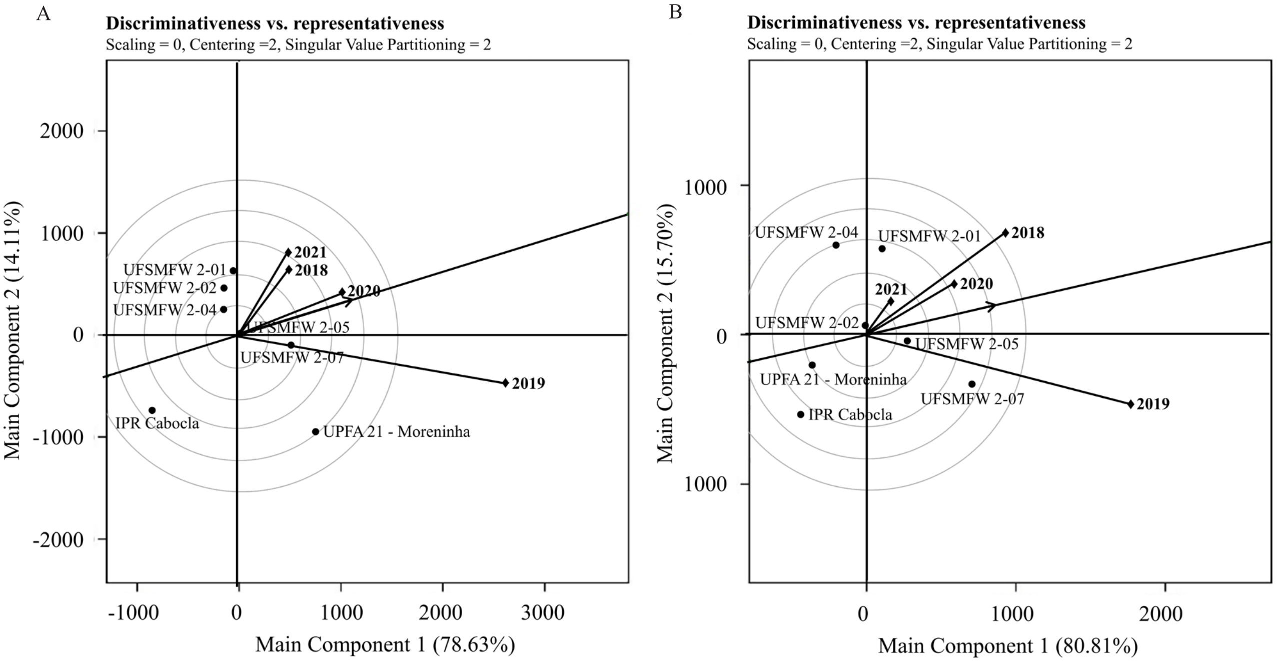

Figure 3. Genotype-environment interaction biplot representing discriminative and representative environments for the dry mass yield (A) and seed yield (B), evaluated in seven black oat (*Avena strigosa*) genotypes cultivated in the years 2018, 2019, 2020, and 2021, in the municipality of Frederico Westphalen, in the state of Rio Grande do Sul, Brazil.

environments are efficient for the selection of cultivars with wide adaptation, while discriminating but non-representative environments can be useful to discard unstable genotypes (Silva et al., 2015).

Conclusions

1. Seed yield of black oat (*Avena strigosa*) genotypes is highly influenced by the environmental conditions over the four years of cultivation studied. UFSMFW 2-07 genotype stands out, but it shows instability.
2. UFSMFW 2-07 and 'UPFA 21-Moreninha' show adaptability to specific studied years for dry mass production.
3. The years 2018 and 2021 form a mega-environment for the dry mass trait and the years 2018, 2020, and 2021, for seed yield, with 2019 being a year for genotype discrimination.

Acknowledgments

To Coordenação de Aperfeiçoamento de Pessoas de Nível Superior (CAPES), for financing, in part, this study (Finance Code 001); and to Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), for support.

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.

BRANQUINHO, R.G.; DUARTE, J.B.; SOUZA, P.I.M. de; SILVA NETO, S.P. da; PACHECO, R.M. Estratificação ambiental e otimização de rede de ensaios de genótipos de soja no Cerrado. **Pesquisa Agropecuária Brasileira**, v.49, p.783-795, 2014. DOI: https://doi.org/10.1590/S0100-204X2014001000005.

FARSHADFAR, E.; RASHIDI, M.; JOWKAR, M.M.; ZALI, H. GGE Biplot analysis of genotype × environment interaction in chickpea genotypes. **European Journal of Experimental Biology**, v.3, p.417-423, 2013.

FAYEUN, L.S.; ALAKE, G.C.; AKINLOLU, A.O. GGE biplot analysis of fluted pumpkin (*Telfairia occidentalis*) landraces evaluated for marketable leaf yield in Southwest Nigeria. **Journal of the Saudi Society of Agricultural Sciences**, v.17, p.416-423, 2018. DOI: https://doi.org/10.1016/j.jssas.2016.10.001.

HONGYU, K.; SILVA, F. de L.; OLIVEIRA, A.C.S. de; SARTI, D.A.; ARAÚJO, L.B. de; DIAS, C.T. dos S. Comparação entre os modelos AMMI e GGE biplot para os dados de ensaios multi-ambientais. **Revista Brasileira de Biomassa**, v.33, p.139-155, 2015.

KARUNIAWAN, A.; MAULANA, H.; USTARI, D.; DEWAYANI, S.; SOLIHIN, E.; SOLIHIN, M.A.; AMIEN, S.; ARIFIN, M. Yield stability analysis of orange - fleshed sweet potato in Indonesia using AMMI and GGE biplot. **Heliyon**, v.7, e06881, 2021. DOI: https://doi.org/10.1016/j.heliyon.2021.e06881.

KENDAL, E. GGE Biplot analysis of multi-environment yield trials in barley (*Hordeum vulgare* L.) cultivars. **Ekin Journal of Crop Breeding and Genetics**, v.2, p.90-99, 2016.

LEITE, J.G.D.B.; FEDERIZZI, L.C.; BERGAMASCHI, H. Mudanças climáticas e seus possíveis impactos aos sistemas agrícolas no Sul do Brasil. **Revista Brasileira de Ciências Agrárias**, v.7, p.337-343, 2012.

NOERWIJATI, K.; NASRULLAH; TARYONO; PRAJITNO, D. Fresh tuber yield stability analysis of fifteen cassava genotypes across five environments in East Java (Indonesia) using GGE biplot. **Energy Procedia**, v.47, p.156-165, 2014. DOI: https://doi.org/10.1016/j.egypro.2014.01.209.

NÖRNBERG, R.; RIBEIRO, G.; SILVEIRA, G. da; LUCHE, H. de S.; BARETTA, D.; TESSMANN, E.W.; WOYANN, L.G.; OLIVEIRA, A.C. de. Adaptabilidade e estabilidade de genótipos de aveia branca. **Revista Acadêmica: Ciências Agrárias e Ambientais**, v.12, p.181-190, 2014. DOI: https://doi.org/10.7213/academica.12.03.AO03.

OLIVEIRA, T.R.A. de; CARVALHO, H.W.L.C. de; OLIVEIRA, G.U.F.; COSTA, E.F.N.; GRAVINA, G. de A.; SANTOS, R.D. dos; CARVALHO FILHO, J.L.S. de. Hybrid maize selection through GGE biplot analysis. **Bragantia**, v.78, p.166-174, 2019. DOI: https://doi.org/10.1590/1678-4499.20170438.

OLIVOTO, T.; LÚCIO, A.D. 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.

R CORE TEAM. **R**: a language and environment for statistical computing. Vienna: R Foundation for Statistical Computing, 2020. Available at: <https://www.R-project.org>. Accessed on: Dec. 28 2021.

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; OLIVEIRA, J.B. de; CUNHA, T.J.F. **Sistema brasileiro de classificação de solos**. 5.ed. rev. e ampl. Brasília: Embrapa, 2018. 356p.

SCOTT, A.J.; KNOTT, M.A. A cluster analysis method for grouping means in the analysis of variance. **Biometrics**, v.30, p.507-512, 1974. DOI: https://doi.org/10.2307/2529204.

SILVA, C.L. da; BORNHOFEN, E.; TODESCHINI, M.H.; MILIOLI, A.S.; TREVISAN, D.M.; BENIN, G. Seleção de genótipos de trigo para rendimento de grãos e qualidade de panificação em ensaios multiambientes. **Revista Ceres**, v.62, p.360-371, 2015. DOI: https://doi.org/10.1590/0034-737X201562040005.

SILVA, C.M. e; MEZZOMO, H.C.; CASAGRANDE, C.R.; LIMA, G.W.; OLIVOTO, T.; NARDINO, M. Selection of tropical wheat lines based on classical and modern parameters of adaptability and stability. **Bulgarian Journal of Agricultural Science**, v.27, p.933-941, 2021.

SILVA, R.R.; BENIN, G.; SILVA, G.O. da; MARCHIORO, V.S.; ALMEIDA, J.L. de; MATEI, G. Adaptabilidade e estabilidade de cultivares de trigo em diferentes épocas de semeadura, no Paraná. **Pesquisa Agropecuária Brasileira**, v.46, p.1439-1447, 2011. DOI: https://doi.org/10.1590/S0100-204X2011001100004.

SOUZA, R.R. de; TOEBE, M.; MARCHIORO, V.S.; CARGNELUTTI FILHO, A.; MELLO, A.C.; MANFIO, G.L.; SOLDATELI, F.J.; SOARES, F. dos S.; MARTINS, V.; JUNGUES, D.L. Soybean grain yield in highland and lowland cultivation systems: a genotype by environment interaction approach. **Annals of Applied Biology**, v.179, p.302-318, 2021. DOI: https://doi.org/10.1111/aab.12709.

YAN, W. **Crop variety trials**: data management and analysis. Chichester: J. Wiley & Sons, 2014. 351p. DOI: https://doi.org/10.1002/9781118688571.

YAN, W. GGE biplot vs. AMMI graphs for genotype-by-environment data analysis. **Journal of the India Society of Agricultural Statistics**, v.65, p.181-193, 2011.

YAN, W. Mega-environment analysis and test location evaluation based on unbalanced multiyear data. **Crop Science**, v.55, p.113-122, 2015. DOI: https://doi.org/10.2135/cropsci2014.03.0203.

YAN, W. Singular-value partitioning in biplot analysis of multienvironment trial data. **Agronomy Journal**, v.94, p.990-996, 2002. DOI: https://doi.org/10.2134/agronj2002.9900.

YAN, W.; HUNT, L.A.; SHENG, Q.; SZLAVNICS, Z. Cultivar evaluation and mega-environment investigation based on GGE biplot. **Crop Science**, v.40, p.596-605, 2000. DOI: https://doi.org/10.2135/cropsci2000.403597x.

YAN, W.; KANG, M.S. **GGE biplot analysis**: a graphical tool for breeders, geneticists, and agronomists. Boca Raton: CRC Press, 2003. 288p. DOI: https://doi.org/10.1201/9781420040371.

YAN, W.; KANG, M.S.; MA, B.; WOODS, S.; CORNELIUS, P.L. GGE biplot vs. AMMI analysis of genotype-by-environment data. **Crop Science**, v.47, p.643-653, 2007. DOI: https://doi.org/10.2135/cropsci2006.06.0374.

YAN, W.; RAJCAN, I. Biplot analysis of test sites and trait relations of soybean in Ontario. **Crop Science**, v.42, p.11-20, 2002. DOI: https://doi.org/10.2135/cropsci2002.0011.

YAN, W.; TINKER, N.A. Biplot analysis of multi environment trial data: principles and applications. **Canadian Journal of Plant Science**, v.86, p.623-645, 2006. DOI: https://doi.org/10.4141/P05-169.