Clustering of environments in response to the cultivation of black oat genotypes

Agrupación de ambientes en respuesta al cultivo de genotipos de avena negra

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ABSTRACT

The aim of this research was to study the genotype-environment interaction with a focus on decomposing the simple and complex parts of the interaction of black oat genotypes and clustering similar environments. The experiment was conducted at the Federal University of Santa Maria, Campus de Frederico Westphalen/RS (Brazil), in 2018, 2019, 2020, and 2021, using five lines and two cultivars of black oat in a randomized block experimental design. The traits evaluated were total dry mass and seed productivity. After verifying the presence of interaction between genotypes and environments, the interaction was decomposed into simple and complex parts. The UFSMFW 2-07 line stood out in terms of total dry mass and seed productivity. The total dry mass and seed productivity of black oat genotypes were highly influenced by environmental conditions over the four years of cultivation, highlighting the complexity of studying the genotype-environment interaction for more than one trait of interest at the same time.

Key words: *Avena strigosa,* cultivation environment, phenotype, correlation.

RESUMEN

El objetivo de este trabajo fue estudiar la interacción del genotipo y el ambiente con atención en la descomposición de la parte simple y compleja de la interacción de los genotipos de avena negra y la agrupación de ambientes similares. El experimento fue realizado en la Universidade Federal de Santa Maria, Campus de Frederico Westphalen/RS (Brasil), en los años 2018, 2019, 2020 y 2021, con 5 líneas y 2 cultivares de avena negra, en un diseño experimental de bloques al azar. Las características evaluadas fueron masa seca total y producción de semillas. Una vez verificada la presencia de interacción entre genotipos y ambientes, la interacción se descompuso en partes simples y complejas. La línea UFSMFW 2-07 se destacó por masa seca total y producción de semillas. La masa seca total y la producción de las semillas de los genotipos de avena negra estuvieron altamente influenciadas por las condiciones ambientales durante los cuatro años de cultivo, lo que muestra la complejidad de estudiar la interacción del genotipo y el medio ambiente para más de un rasgo de interés al mismo tiempo.

Palabras clave: *Avena strigosa*, ambiente de cultivo, fenotipo, correlación**.**

Introduction

Black oat (*Avena strigosa* Schreb.) is one of the most cultivated winter cereals in Rio Grande do Sul (Brazil) due to its important agronomic characteristics such as fast growth, rusticity, high forage productivity, and ease of seed production, making it a versatile crop (Debiasi *et al.*, 2007). Black oat is an excellent option for soil cover due to its high potential for biomass production; it can also be used in forage production (Leite *et al.*, 2012) and has become an important crop in production systems.

With the growing importance of black oats in the market, developing new cultivars has gained significance. The selection and recommendation of more productive genotypes are basic objectives of genetic breeding programs for cultivated species (Cargnin *et al.*, 2006). To this end, experiments are carried out where different genotypes of black oat are evaluated in a series of environments, which may be locations or years of cultivation (Olivoto *et al.*, 2019).

The phenotype in plants is determined by the genotype and the environment. However, these two effects are not always additive, indicating the presence of the genotype-environment interaction. Genotype-environment interaction refers to the variation in performance of a genotype in different environments (Sharifi *et al.*, 2017). The existence of this interaction, depending on its nature (simple or

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complex), directly impacts the process of selecting superior genotypes, as well as the recommendation of cultivars (Cruz *et al.*, 2014).

There are several available methods for quantifying the interaction between genotypes and environments, including those based on analysis of variance (Plaisted & Peterson, 1959), simple linear regression (Eberhart & Russell, 1966; Finlay & Wilkinson, 1963) and multiple linear regression (Cruz *et al.*, 1989; Verma *et al.*, 1978). More recent methods include the Additive Main effect and Multiplicative Interaction method (AMMI), the Genotype plus Genotype and Environment interaction method (GGE), and the Best Linear Unbiased Prediction method (BLUP) via restricted maximum likelihood (REML) or analysis of variance (Souza *et al.*, 2021).

The genotype-environment interaction occurs due to changes in the performance of the genotypes from differences in environment. Estimating the magnitude of the interaction and its decomposition into simple and complex parts using the method proposed by Cruz and Castoldi (1991) is a strategy to consider. The decomposition of simple and complex interactions between genotypes and environments was used by Cargnin *et al.* (2006) with wheat, Nunes *et al.* (2006) with corn, Nunes *et al.* (2011) with melon, Pinto *et al.* (2012) with coffee, and Cardoso *et al.* (2019) with cotton.

The interaction of the genotype with the environment occurs when the phenotype undergoes changes because of the environment. The interaction changes due to changes in the proportion of genetic and environmental variation in the expression of the phenotype (Allard, 1999). In this sense, it is possible to decompose the interaction between genotypes and environments and, based on the decomposition, to group similar environments. The aim of this research was to study the genotype-environment interaction with a focus on decomposing the simple and complex parts of the interaction of black oat genotypes and clustering similar environments.

Materials and methods

The experiment was conducted in 2018, 2019, 2020, and 2021 at the Federal University of Santa Maria, Campus of Frederico Westphalen/RS, Brazil (27°23'26" S, 53°25'43" W, 461.3 m a.s.l.). The climate, according to Köppen, is classified as Cfa, humid subtropical, with an average annual precipitation of 2,100 mm (Alvares *et al.*, 2013).

Five homozygous lines of black oat (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 tested. A randomized block experimental design was used, with three replicates. Each experimental unit was composed of six rows of 5 m in length, spaced 0.17 m apart, with a sowing density of 300 seeds per m². Sowing in the four years of cultivation was carried out at the end of May. Fertilization was based on soil analysis and the cultural treatments were applied as needed to control weeds, pests, and diseases whenever necessary, following the technical indications for black oat cultivation.

The traits analyzed were a) total dry aerial mass (kg ha^{-1}) measured after cutting an area of 1 m² at full flowering (50% inflorescence), followed by drying in an oven (70ºC) to constant mass, and b) seed productivity (kg ha^{-1}) measured by collecting seeds from the plots after physiological maturation.

Meteorological data, including total fortnightly precipitation from May to October for the four years of cultivation (2018, 2019, 2020, and 2021) were collected from the Frederico Westphalen/RS automatic station (A854) and presented graphically.

Statistical analysis

To identify interactions between genotypes and environment for the traits studied, joint analysis of variance (ANOVA) and the F test ($P<0.05$) were performed, using the statistical model below:

$$Y_{ijk} = \mu + G_i + A_j + GA_{ij} + B/A_{jk} + \varepsilon_{ijk} \tag{1}$$

where Y_{ijk} = observation obtained in the plot with *i-th* genotype in the *j-th* block, μ = general mean of the experiment, G_i = effect of the *i-th* genotype considered fixed, A_j effect of the *j-th* environment considered fixed, GA_{ij} = effect of the *i-th* genotype interaction with the *j-th* environment, B/A_{jk} = effect of the *k-th* block within the *j-th* environment, considered random and ε_{ij} = random error effect.

The genotype-environment interaction was decomposed into simple and complex using the methodology proposed by Cruz and Castoldi (1991): simple: $0.5(\sigma_1 \ \sigma_2)$, where σ_1 and σ_2 are the genotypic variance for the environments 1 and 2, and complex,

$$(\sqrt{(1-r)^3 Q_1 Q_2}) \tag{2}$$

where r is the correlation coefficient between the means of the genotypes from both locations, and Q1 and Q2 are the mean squares of the genotypes in environments 1 and 2.

Environments were grouped using the average Euclidean distance and the UPGMA clustering method. Data were analyzed using R software, version 4.0.2 (R Core Team, 2020) and the "metan" package (Olivoto & Lúcio, 2020).

Results and discussion

Joint analysis of variance revealed significant effects ($P \leq 0.05$) for genotypes, environment, and their interactions for total dry mass and seed productivity. The coefficients of variation were, respectively, 7.22% and 6.35% for the total dry mass and seed productivity, indicating reliable data. These results demonstrate variation in the response of the genotypes tested over the four years of cultivation. The occurrence of interactions between genotypes and environments makes the selection and recommendation of new cultivars more difficult (Silva *et al.*, 2011).

The fluctuation in the response of the genotypes to the years of cultivation can be seen in Figure 1. The year 2019 was the most favorable for total dry mass productivity, with averages exceeding the general average of the trial. The years 2020 and 2021 had averages lower than the general average (Fig. 1) due to the low volume of accumulated precipitation for the period from the second half of August to the second half of October (Fig. 2). The year 2021 was marked by a dry period, followed by another very rainy one, extreme conditions that harmed the growth of the genotypes. Plant phenology is influenced by water availability and air temperature (Oteros *et al.*, 2015), which can alter genotype performance and the rankings.

UFSMFW 2-07 line stood out in terms of total dry mass productivity, reaching more than 10,000 kg ha^{-1}. In terms of seed productivity UFSMFW genotypes showed potential, with the UFSMFW 2-07, reaching a seed productivity in 2019 exceeding 4,000 kg ha^{-1}. The highest productivities of total dry mass and of seeds were obtained in 2018 and 2019, while 2020 and 2021 showed lower values due to significant
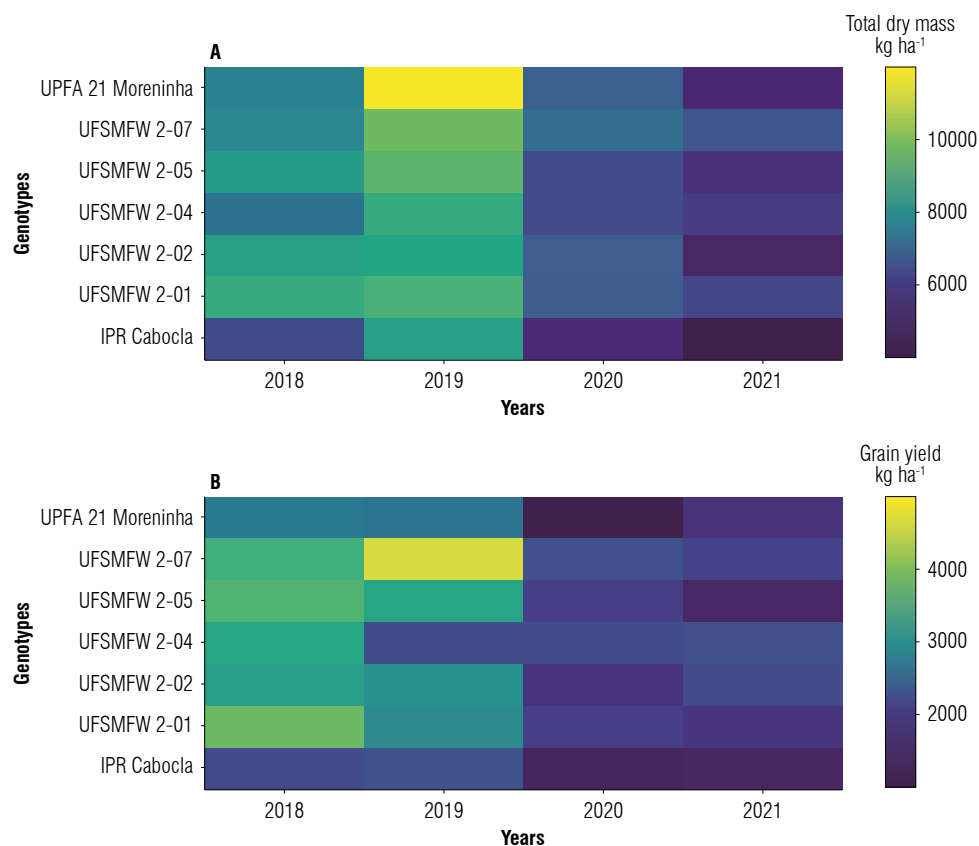
FIGURE 1. Overview of genotype-environment interaction for total dry mass (A) and seed productivity (B) of seven black oat genotypes cultivated in 2018, 2019, 2020, and 2021.
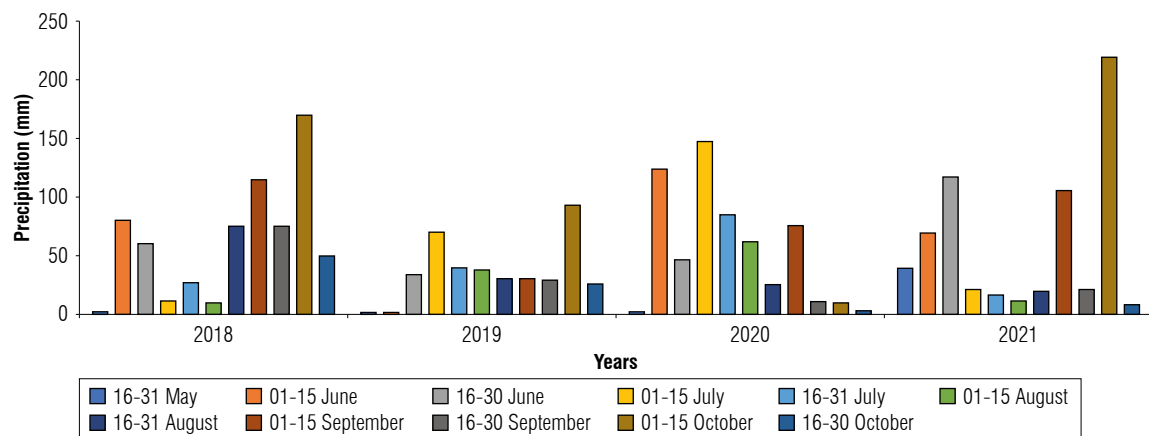
FIGURE 2. Accumulated biweekly precipitation, covering the months of May to October, in 2018, 2019, 2020 and 2021 in the municipality of Frederico Westphalen/RS, Brazil.

drought conditions (Fig. 2). Benin *et al.* (2005) emphasize that the production of white oats is highly influenced by the environment, which results in variable productivity over the years.

Cruz *et al.* (2012) classify genotype-environment interaction into simple and complex parts. The simple part reflects the different responses of genotypes to environmental variations without changes in the ranking of genotypes, while the complex part involves changes in the ranking. When a complex interaction occurs, a top-performing genotype in one environment may perform poorly in another. The fractionation of the interaction revealed a predominance of the complex type of interaction for the total dry mass characteristic, showing the inconsistency of the genotypes in relation to environmental variation, and a predominance of the simple type for the seed productivity characteristic (Tab. 1). Cargnin *et al.* (2006) found a predominance of the complex part of the interaction in wheat for the traits of days from emergence to heading, plant height, grain mass and grain yield.

Complex interaction values greater than 50% hinder genotype selection across environments (Sousa *et al.*, 2015). They also indicate the presence of genotypes adapted to specific environments (Costa *et al.*, 2015). In the same sense, according to Santos *et al.* (2016), in the presence of a complex interaction, the analysis of the interaction does not provide sufficient information about the performance of the genotypes studied. In view of the above and considering the results presented in Table 1, seed productivity was more influenced by the simple environmental effect, that is, constant conditions from one year to the next.

To simplify the environments according to the fraction of interaction, the environments were grouped using the Unweighted Pair-Group Method Using an Arithmetic Average (UPMGA), based on the correlation between environments for total dry mass and seed productivity following the method of Cruz and Castoldi (1991) (Figs. 3A and 3B, respectively). For total dry mass, the simple interaction showed a similarity between 2018 and 2021, grouped together, while 2019 and 2020 formed two separate groups.

TABLE 1. Pairs of environments, correlation between environments, percentage of the simple part of the interaction (SPI) and complex part of the interaction (CPI), resulting from the decomposition of the interaction between genotypes and environment pairs, according to the methodology of Cruz and Castoldi (1991), for total dry mass and seed productivity in black oat.

Environment pairs	Total dry mass			Seed productivity		
	Correlation	SPI	CPI	Correlation	SPI	CPI
2018 and 2019	0.36	51.87	48.13	0.61	52.59	47.41
2018 and 2020	0.60	36.91	63.09	0.88	83.10	16.90
2018 and 2021	0.39	22.14	77.86	0.56	69.16	30.84
2019 and 2020	0.84	87.96	12.04	0.66	76.80	23.20
2019 and 2021	0.32	48.88	51.12	0.23	66.20	33.80
2020 and 2021	0.71	46.56	53.44	0.61	51.76	48.24
Total	-	49.05	50.95	-	66.59	33.41
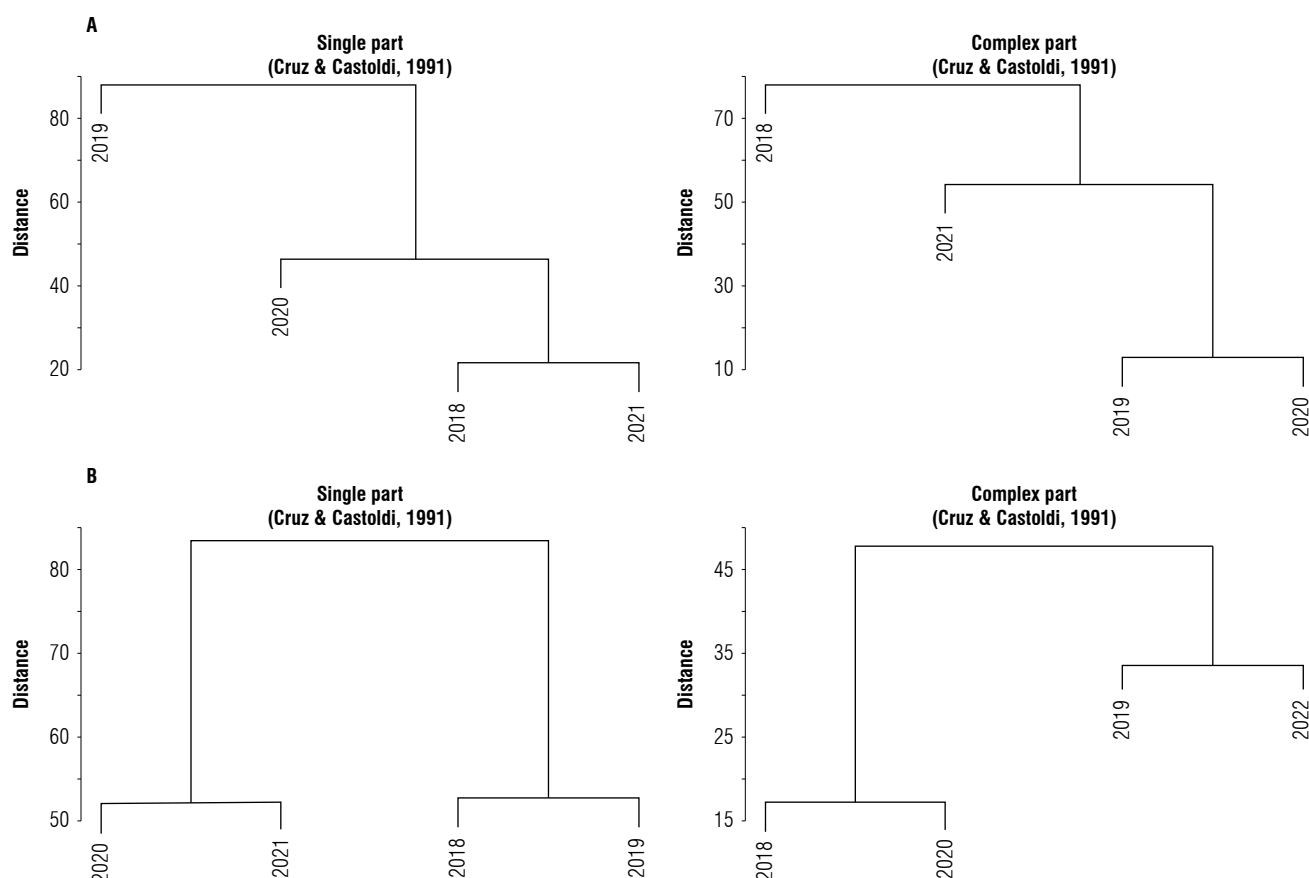
FIGURE 3. Clustering of the years 2018, 2019, 2020 and 2021 using the UPMGA method for total dry mass (A) and seed productivity (B).

In the complex part of the interaction, the clustering revealed similarity for the genotypes of the years 2019 and 2020, while in 2018 and 2021 they formed isolated groups.

For the seed productivity characteristic, the simple part of the interaction revealed the formation of two groups: 2018 and 2021 were in one group, and 2019 and 2020 in another group. When considering precipitation (Fig. 2), similarities were observed in the distribution of rainfall between the years 2018 and 2021 and between 2019 and 2020. As for the complex part, two groups were also formed: one for 2018 and 2020, and another for 2019 and 2021. These results indicate that environments can be similar for one characteristic, but different for another, making genotype-environment interaction studies difficult.

Conclusion

The results indicate variation in the responses of the genotypes across the years of cultivation, with genotype-environment interactions that make it difficult to select new cultivars. The decomposition of the interaction revealed a predominance of the complex part of the interaction for the total dry mass and the simple part of the interaction for the seed productivity trait. The grouping of the environments showed differences in the interactions, highlighting the complexity in the analysis of the effects of the genotype and the environment.

Conflict of interest statement

The authors declare that there are no conflict of interests regarding the publication of this article.

Author's contributions

VSM and LAK: conceptualization, methodology, resources, visualization, data curation, formal analysis, writing - original draft, writing - original draft, review, and editing. DM and TO: conceptualization, data curation, formal analysis, writing - original draft, review, and editing. DFO, CBF, TASL, KMK, and ECMI: conceptualization, and editing. All authors have read and approved the final version of the manuscript.

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