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RESEARCH ARTICLE

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Breeding for drought tolerance in perennial ryegrass (*Lolium perenne* L.) and tall fescue (*Lolium arundinaceum* [Schreb.] Darbysh.) by exploring genotype by environment by management interactions

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Abstract

Background: Drought-tolerant turfgrass cultivars are becoming more important each year as landscape irrigation practices are becoming more restrictive.

Methods: In this study, we quantified the level of drought tolerance (DT) in perennial ryegrass and tall fescue genotypes across years under different mowing (MH) and fertility (FL) rates. A total of 48 ryegrass and 38 tall fescue genotypes were planted in 2011 at NexGen, Albany, OR. The trial was divided into three subtrials: (i) DT; (ii) MH and DT; and (iii) FL and DT.

Results: The results showed that there was significant genetic variance for most of the traits in both species. The genotype × year interaction was predominantly simple, indicating small changes in genotype ranking for both species. Lower MH improved DT in perennial ryegrass, whereas higher MH resulted in greater DT in tall fescue. For both species, higher MH improved the population mean for turf quality. Higher FL inputs led to higher turf quality for both species, but it did not affect the DT response.

Conclusions: Using a selection index, six genotypes for perennial ryegrass and four for tall fescue were selected.

KEYWORDS

drought stress, ryegrass, tall fescue, turf quality, turfgrass breeding

INTRODUCTION

Perennial ryegrass (*Lolium perenne* L.) and tall fescue (*Lolium arundinaceum* [Schreb.] Darbysh.) are two of the most planted turfgrass species in temperate and transition regions around the world. Both species are cool-season, self-incompatible, allogamous, and belong to the Poaceae family. Perennial ryegrass is a diploid ($2n = 2x = 14$) species native to Europe, Asia, and northern Africa (Cornish et al., 1979). Tall fescue is an allohexaploid ($2n = 6x = 42$) species native to Europe (Hoveland, 2009). Perennial ryegrass and tall fescue provide a rapid cover and are widely used for their diverse applications (sports fields, lawns, parks, etc.; Pornaro et al., 2020). Perennial ryegrass generally fails to thrive under water-stress conditions (Jiang et al., 2016; Rawnsley et al., 2009) and it has a poor ability to recover after drought. Although tall fescue shows better drought tolerance than other cool-season turfgrasses, improving drought tolerance in tall fescue would increase the persistence of this species under lower water inputs (Carrow & Duncan, 2003).

The development of cultivars with improved water stress tolerance is becoming more important each year as landscape irrigation practices are becoming more restrictive (San Antonio Water System, 2020; State of California, 2017; State of Georgia, 2020; State of Oregon, 2021). Plants have many drought stress mechanisms to withstand water stress, such as drought avoidance, tolerance, and scape (Turner, 1986). Drought tolerance is desirable

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for breeding resilient turfgrass cultivars for semiarid regions that could be exposed to longer water-stress periods. The identification and selection of improved turfgrass cultivars that can withstand water stress while maintaining superior/acceptable turf quality (TQ) can delay the need for supplemental irrigation and aid in the conservation of water resources (Karcher et al., 2008). This is especially beneficial in areas where rainfall is sporadic during the warm season, as the ability of the plant to maintain a favorable water balance until the next rainfall event could greatly minimize the need for supplemental irrigation, while maintaining acceptable TQ. The maintenance of green tissue is an important consideration in turfgrass systems, as a hydrated lawn provides many desirable benefits over a dormant lawn, including cooling and fire prevention (Beard & Green, 1994).

Several studies have documented the differences in drought tolerance between tall fescue and perennial ryegrass cultivars (Carrow & Duncan, 2003; Jiang et al., 2016; Pornaro et al., 2020; Richie et al., 2002). Unfortunately, most studies included a limited number of cultivars and/or breeding lines, preventing researchers from exploring genotype × environment × management interactions in these species. In addition, most studies focused only on drought tolerance (Carrow & Duncan, 2003; Karcher et al., 2008; Pornaro et al., 2020), without exploring the effect of additional turfgrass management practices. Fertilizer rate and mowing height can affect water-use efficiency in turfgrasses since it is linked to canopy height and plant growth rate (Goss, 2017). High nitrogen rates result in a taller canopy, and increasing the evapotranspiration, leading to increased water requirements (Barton et al., 2009). As mowing height increases, more water is necessary to maintain acceptable TQ (Harivandi et al., 2009). Techniques have been developed to assess the drought tolerance under prolonged water deficit stress (Karcher et al., 2008; Richardson et al., 2008), which include the evaluation of root systems in greenhouses and turf coverage in the fields during drought stress.

The interaction among turfgrass genotypes, drought stress, and management practices is poorly documented or understood, and a thorough understanding of mechanisms of turfgrass stress responses under various management practices is vital for the development of superior stress-tolerant cultivars. Cultivar development in turfgrass is based on data collected over several years, environments, and grown under various management practices, making the selection cycle slower when compared to annual plants. Therefore, advanced statistical methods are key to predict the genetic value of breeding lines as accurately as possible (Smith & Spangenberg, 2014). These statistical methods need to take into account the spatial variation and correlation within a trial, as well as the temporal correlation between repeated measures, to improve the accuracy in the selection process (Faveri et al., 2015; Gouveia et al., 2021). These methods can be even more relevant when it is intended to select genotypes under stress conditions, because the discrimination of tolerant/susceptible genotypes tends to be more difficult due to low heritability estimates and higher environmental variance (Hoffmann & Merilä, 1999).

Improvement of drought tolerance in perennial ryegrass and tall fescue is important to ensure sustainable turfgrass production, and it remains a critical research objective in turfgrass breeding. The objective of this study was to quantify the level of drought tolerance in a selected group of perennial ryegrass and tall fescue breeding lines and cultivars and select superior breeding lines for TQ traits and drought tolerance under different management practices.

MATERIALS AND METHODS

Plant material

The 44 experimental breeding lines for perennial ryegrass and 38 for tall fescue were developed by multiple cycles of phenotypic and/or genotypic recurrent selection by crossing parental lines selected from various sources: released cultivars, ecotype selections, and plant introductions from USDA-GRIN (Debra Hignight, NextGen, personal communication). The cultivars included as controls were (i) perennial ryegrass: APR 2225, APR 2105, APR 2106, Pop, APR 2186, APR 2104, Phenom, APR 2154, APR 2280, Integra II, APR 2212, APR 2201, APR 2198, APR 2208, APR 2149, Manhattan, and Radiance and (ii) tall fescue: ATF 1458, South Fork, ATF 1485, ATF 1434, Falcon IV, ATF 1402, ATF 1426, Rebel V, Crackle, ATF 1492, and ATF 1479.

Experimental design and crop management

Two field trials were planted in September 2011 at NexGen Plant Science Center, LLC, Albany, OR (44°33′ N, 123°08′ W). The entries were sown into a native soil. The soil was a Woodburn silt loam, fine silty, mixed superactive, mesic Aquultic Argixeroll, pH 5.6–6.5, organic matter 3%–5%. All entries were seeded into 1 m × 1 m plots at a 250 kg ha^{-1} seeding rate for perennial ryegrass and a 300 kg ha^{-1} seeding rate for tall fescue. Propiconazole was applied as needed for disease control from January to May and October to December of each year. Irrigation was carried out as needed from March to May. Fertilizer application and mowing height practices are summarized in Table 1. The subplots for both mowing height and fertility levels were created by dividing each plot in half, along orthogonal directions, as shown in Figure S1. The resulting dimensions of the mowing height subplots were 0.5 m × 1 m, while those for fertility levels were 1 m × 0.5 m.

The trials for perennial ryegrass and tall fescue were established in 2011 and conducted as a randomized complete block design (RCBD) with three replications. The trials were split into three subtrials, each one composed of 2 years of repeated measures. In the first subtrials (2012–2013), only the main effect of entries and year were evaluated. In the second subtrials (2014–2015), the plots were split into two different mowing height levels; therefore, the effect of entries, years, and

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TABLE 1 Summary of fertilizer (NPK 19-03-16) application (kg ha^{-1}) and mowing height (cm) practices by year.

Year	Fertilization		Mowing	
1 and 2 (2012–2013)	125 kg ha^{-1} in April 125 kg ha^{-1} in October		3.8 cm	
3 and 4 (2014–2015)	250 kg ha^{-1} in April		Low	High
	125 kg ha^{-1} in October		3.8 cm	7.6 cm
5 and 6 (2016–2017)	Low	High	3.8 cm	
	125 kg ha^{-1} in April	250 kg ha^{-1} in April		
	62.5 kg ha^{-1} in October	125 kg ha^{-1} in October		

mowing height were evaluated. In the third subtrials (2016–2017), two fertility levels were evaluated also in a strip plot and the effects of fertility, entries, and years were assessed (Table 1). To avoid carryout effects from the mowing height treatments to the fertility level treatments, the two levels of fertility were applied in a North–South direction of the plots, whereas the mowing height treatments were applied in the East–West direction (Figure S1). Each subtrial was analyzed separately using a mixed-model approach and the models for each subtrial are described in the following topics.

Drought stress and recovery evaluations

The experimental areas were irrigated each year in May to field capacity with 50 mm of irrigation per day for 3 consecutive days to eliminate dry areas and produce uniformly wet conditions across all plots in all years evaluated. Immediately thereafter, irrigation was withheld to allow for development of drought stress symptoms. The plots were evaluated weekly (Tables S1 and S2) until all plots had fallen below 25% green turf cover and the experimental area was saturated with 50 mm of irrigation to initiate drought recovery in September. Thereafter, the trials were irrigated weekly with 25 mm of water until the plots reached 100% green cover.

Digital image analysis

Low-resolution photographs were taken and analyzed for percent green cover and green color (Richardson et al., 2001). Photographs were taken using a Canon Power Shot SD1300 IS ELPH (Canon Corporation) camera. The camera was mounted on a custom-built hand-held light box designed for placement in the plots. The light box has four bulbs (TCP TruStart™ Springlamps® CFL Light Bulb, 6500-Kelvin, TCP 5800965K, 9w) mounted on the inside of the box to provide uniform light. Images were analyzed for percent green cover and green color as described by Karcher et al. (2018) and Karcher et al. (2017). This is a patent-pending system that was designed for objectively analyzing digital images of turfgrass to rate various parameters (e.g., percent green cover and green color) and to objectively measure overall quality (TQ). The system establishes thresholds (scores ranging from 1 to 9) and executes a series of steps to determine green coverage (Cover), turf color (TC), turf density (TD), and uniformity. The digital image analysis technique was also used to determine the entries' responses to drought by determining the percentage of green coverage of the plots weekly after the irrigation was withheld.

Statistical analysis

Drought tolerance estimation at the plot level

For each subtrial, the estimated number of days without irrigation (x_j) when plot green cover reached the 75%, 50%, and 25% thresholds under water stress followed a binomial generalized linear model (BGLM):

$$\eta_{ij} = \lg\left(\frac{\pi_{ij}}{1-\pi_{ij}}\right) = \alpha_j + \beta_j x_{ij},$$

where η_{ij} is the linear predictor associated with the observed percentage of green cover in plot j with i days without irrigation (p_{ij}), being $p_{ij} \sim \frac{\text{Binomial}(100, \pi_{ij})}{100}$; π_{ij} is the expected percentage of green cover in plot j with i days without irrigation; α_j is the intercept associated with plot j; β_j is the regression coefficient associated with plot j; and $\lg\left(\frac{\pi_{ij}}{1-\pi_{ij}}\right)$ is the logit link function.

From the adjusted BGLM, the values of x_j at the thresholds of 75%, 50%, and 25% coverage were estimated using the inverse of the logit link function: $\pi_{ij} = \frac{e^{\hat{\alpha}_j+\hat{\beta}_j x_{ij}}}{1+e^{\hat{\alpha}_j+\hat{\beta}_j x_{ij}}}$. The generalized model was adjusted using the *glm* function of the stats package in R version 4.1.1 (R Core Team, 2020). Thus, these x_j values at the thresholds of 75%, 50%, and 25% represent the drought response (DR) at DR75, DR50, and DR25, respectively, and they are directly related to the drought tolerance at the plot level. These values (DR75, DR50, and DR25) were later analyzed using a mixed-model approach.

Mixed-model approach to select breeding lines under drought

Percent cover (Cover), turfgrass genetic color (TC), turfgrass density (TD), turfgrass quality (TQ), and drought tolerance traits DR75, DR50, and DR25 were analyzed using a mixed-model approach in ASReml-R 4.0 (Butler et al., 2018). The variance components were estimated using the residual maximum likelihood (REML) method (Patterson & Thompson, 1971). The estimation of fixed effects (Best Linear Unbiased Estimates, BLUEs) and the prediction of random effects (Best Linear Unbiased Predictions, BLUPs) were obtained by solving Henderson's mixed-model equations.

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Residual modeling

For all trials and traits, different variance–covariance structures were tested for the residual matrix (**R**). First, four spatial variance–covariance structures were tested: $\mathbf{R} = \mathbf{I_s}\sigma_e^2 \otimes \mathbf{I_n}$, $\mathbf{R} = \mathbf{I_s}\sigma_e^2 \otimes \boldsymbol{\Sigma}_\mathbf{r}(\boldsymbol{\rho}_\mathbf{r}) \otimes \mathbf{I_c}$, $\mathbf{R} = \mathbf{I_s}\sigma_e^2 \otimes \boldsymbol{\Sigma}_\mathbf{c}(\boldsymbol{\rho}_\mathbf{c}) \otimes \mathbf{I_r}$, and $\mathbf{R} = \mathbf{I_s}\sigma_e^2 \otimes \boldsymbol{\Sigma}_\mathbf{r}(\boldsymbol{\rho}_\mathbf{r}) \otimes \boldsymbol{\Sigma}_\mathbf{c}(\boldsymbol{\rho}_\mathbf{c})$. After checking the best spatial structure, two variance–covariance structures related to years were tested and addressed in the **R** matrix: $\mathbf{R} = \sigma_e^2\boldsymbol{\Sigma}_\mathbf{s}(\boldsymbol{\rho}_\mathbf{s}) \otimes \boldsymbol{\Sigma}_\mathbf{r} \otimes \boldsymbol{\Sigma}_\mathbf{c}$; where $\mathbf{I_s}$, $\mathbf{I_n}$, $\mathbf{I_c}$, and $\mathbf{I_r}$ are identity matrices related to the years, error vector **e**, columns, and rows, respectively; $\boldsymbol{\Sigma}_\mathbf{r}(\boldsymbol{\rho}_\mathbf{r})$ and $\boldsymbol{\Sigma}_\mathbf{c}(\boldsymbol{\rho}_\mathbf{c})$ are first-order autocorrelation matrices for rows and columns associated with the error vector **e**; $\boldsymbol{\Sigma}_\mathbf{s}(\boldsymbol{\rho}_\mathbf{s})$ are first- and second-order autocorrelation matrices associated with years; and σ_e^2 is the error variance. The structure of the **R** matrix for the residuals was selected based on the Bayesian Information Criterion (Tables S3–S8).

First subtrial: Drought tolerance in Years 1 and 2

The statistical analyses were performed according to the model for an RCBD with multiple years:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zg} + \mathbf{e},$$

where **y** is the vector of the data; **β** is the vector of fixed effects (seasons and replications); and **g** is the vector of the effects of genotypes within the years, with $\mathbf{g} \sim N(0, \mathbf{G_s} \otimes \mathbf{I})$, where $\mathbf{G_s}$ is a variance–covariance genetic matrix across the years assuming a compound symmetry structure, in which the main diagonal is composed of the linear combination of variance components $\sigma_g^2 + \sigma_{gy}^2$, and nondiagonal elements represent the variance component related to genotype main effect, with σ_g^2 being the genetic variance associated with the main effect of genotypes and σ_{gy}^2 the variance associated with the genotype × year (G × Y) interaction. The symbol ⊗ is a Kronecker product; **e** is the vector of the residuals with $\mathbf{e} \sim N(0, \mathbf{R}\sigma_e^2)$; and **X** and **Z** are the incidence matrices associating fixed and random effects to the data.

Second subtrial: Mowing height in Years 3 and 4

In the second trial, the performance of genotypes was evaluated under two mowing height levels (Table 1). The analyses were performed using the following model for an RCBD and a split-plot treatment design with genotypes as the whole-plot factor and mowing height as the strip-plot factor, and further considering data collected in two different years:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zg} + \mathbf{e_1} + \mathbf{e_2},$$

where **y** is the vector of the data; **β** is the vector of fixed effects (years, replications, mowing height, and the year × mowing height interaction); and **g** is the vector of the effects of the genotypes within the mowing height and year, with $\mathbf{g} \sim N(0, \mathbf{G_t} \otimes \mathbf{G_h} \otimes \mathbf{I})$, where $\mathbf{G_t}$ and $\mathbf{G_h}$ are the compound symmetry covariance matrices of the genotype effects within the years and the mowing height levels. The main diagonal elements of the Kronecker product matrix of the $\mathbf{G_t}$ and $\mathbf{G_h}$ matrices are composed of the linear combination of the variance components $\sigma_g^2 + \sigma_{gt}^2 + \sigma_{gh}^2 + \sigma_{gth}^2$, the off-diagonal elements are the combinations $\sigma_g^2 + \sigma_{gt}^2$ and $\sigma_g^2 + \sigma_{gh}^2$, as well as the genetic variance component σ_g^2, where σ_g^2 is the genetic variance associated with the main effect of genotypes; σ_{gt}^2 is the variance associated with the G × Y interaction; σ_{gh}^2 is the variance associated with the G × H; and σ_{gth}^2 is the variance associated with the G × Y × H. The vector $\mathbf{e_1}$ is the residual associated with the whole plots, being $\mathbf{e_1} \sim N\left(0, I\sigma_{e_1}^2\right)$, and $\mathbf{e_2}$ represents the vector of residuals associated with the split plots, being $\mathbf{e}_2 \sim N\left(0, R\sigma_{e_2}^2\right)$. **X** and **Z** are incidence matrices associating fixed and random effects to the data.

Third subtrial: Fertility level in Years 5 and 6

In the third trial, two rates of fertility (Table 1) were used to evaluate the performance of the genotypes. The high fertility rate consisted of two applications, 250 and 125 kg ha^{-1}, applied in the spring and in the fall, respectively. For the low fertility rate, 125 and 62.5 kg ha^{-1} of NPK 19-03-16 were applied at the same time as the high fertility treatment. The model used in the analyses followed an RCBD and a split-plot treatment design with genotypes as the whole-plot factor and fertility level as the strip-plot factor, and further considering data collected in two different years:

$$\mathbf{y} = \mathbf{X\beta} + \mathbf{Zg} + \mathbf{e_1} + \mathbf{e_2},$$

where **y** is the vector of the data; **β** is the vector of fixed effects (years, replications, fertility level, and the year × fertility level interaction); and **g** is the vector of the random effects of the genotypes, with $\mathbf{g} \sim N(0, \mathbf{G_t} \otimes \mathbf{G_f} \otimes \mathbf{I})$, where $\mathbf{G_t}$ and $\mathbf{G_f}$ are compound symmetry covariance matrices of the genotype effects within the years and levels of fertility. The matrix generated by the Kronecker product between $\mathbf{G_t}$ and $\mathbf{G_f}$ provides the linear combinations of the variance components: σ_g^2, $\sigma_g^2 + \sigma_{gt}^2$, $\sigma_g^2 + \sigma_{gf}^2$, and $\sigma_g^2 + \sigma_{gt}^2 + \sigma_{gf}^2 + \sigma_{gtf}^2$, in the same way as reported in "Second subtrial: Mowing height in Years 3 and 4," where σ_g^2 is the genetic variance associated with the main effect of genotypes; σ_{gt}^2 is the variance associated with the G × Y interaction; σ_{gf}^2 is the variance associated with genotype × fertility level interaction (G × F); and σ_{gtf}^2 is the variance associated with G × Y × F interaction. The vector $\mathbf{e_1}$ is the residual associated with the whole plots (genotypes × replications), being $\mathbf{e_1} \sim N\left(0, \mathbf{I}\sigma_{e_1}^2\right)$, and $\mathbf{e_2}$ is the vector of residuals associated with the split plots, being $\mathbf{e_2} \sim N\left(0, \mathbf{R}\sigma_{e_2}^2\right)$. **X** and **Z** are

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incidence matrices associating the fixed and random effects to the data.

Significance of the variance components, heritability estimates, and genotype × trait biplot

In all subtrials, the REML ratio test was performed at a 5% probability level to infer the significance of the variance components. The broad-sense genotype mean-based heritability (H^2) was estimated according to the following estimator provided by Cullis et al. (2006):

$$H^2 = 1 - \frac{v_{\text{BLUP}}}{2\sigma_g^2},$$

where v_{BLUP} is the average of the variance of the difference between two BLUPs of genotypes; and σ_g^2 is the genetic variance of genotypes.

Caterpillar plots of the BLUP predictions of the genotypes were generated with the Student's *t*-test based prediction intervals at 95% probability using the R package *ggplot2* (Wickham, 2008). Additionally, principal component analyses (PCA) were performed to evaluate trait correlations and to identify genotypes showing drought tolerance and improved turf traits. PCA were fitted according to the following model:

$$\mathbf{g_{ij}} = \sum_{\mathbf{n}=1}^{2} \lambda_{\mathbf{n}} \boldsymbol{\xi}_{\mathbf{in}} \boldsymbol{\delta}_{\mathbf{jn}},$$

where g_{ij} is the BLUP prediction of the genotype *i* for the trait *j*; λ_n is the singular value associated with the principal component *n*; and $\boldsymbol{\xi}_{\mathbf{in}}$ and $\boldsymbol{\delta}_{\mathbf{jn}}$ are the elements of the eigenvectors of the principal component *n* associated with genotype *i* and trait *j*, respectively. The PCA were performed using the *prcomp* function of the stats R package (R Core Team, 2020). The genotype × trait biplots were generated using the scores of the first two principal components using the *ggfortify* R package (Tang et al., 2016).

Genotype selection

A multitrait selection was based on all traits evaluated. An additive index (AI) was applied to select the best breeding lines in both species using the method developed by Resende (2016):

$$AI_i = \sum_{j=1} \frac{\mu_j + g_{ij}}{\sigma_j},$$

where $\mu_j + g_{ij}$ is the overall mean of trait *j* added to the predicted genotypic value of genotype *i* at trait *j* and σ_t is the standard deviation for $\mu_j + g_{ij}$. For AI, a selection intensity of 20% was adopted and the selection direction was to increase the value of all evaluated traits.

RESULTS

Drought tolerance across years

The behavior of the regression lines for each plot subjected to drought stress over time showed a pattern between Years 1 and 2 (Figure S2). In Year 1, plots maintained greater plot coverage for a longer time than in Year 2 in both species. After imposing two mowing heights in Years 3 and 4, the lower mowing height maintained greater percent cover under drought stress in perennial ryegrass in Year 3; however, in Year 4, greater percent cover was associated with higher mowing height (Figure S2a). In tall fescue, both mowing heights produced similar responses for plot cover in Year 3, while the higher mowing height treatment maintained greater cover for a longer time in Year 4 (Figure S2b). For the two different nitrogen rates in Years 5 and 6, higher fertilization rates resulted in some accessions showing greater coverage, and there was no clear trend in tall fescue (Figure S2).

Assessing drought tolerance in Years 1 and 2

The genotypic variance was significant ($p < 0.05$) for all traits in both species, except for TD in perennial ryegrass (Table 2). There was also a significant variance associated with the effect of the cultivar × year interaction (σ_{gy}^2) for all traits in perennial ryegrass (Table 2). For the traits related to drought tolerance, cover, and TC, there was no significance variance for the G × Y interaction in tall fescue (Table 2).

Heritability estimates ranged from 0.11 (TD) to 0.89 (TC) for perennial ryegrass and from 0.27 (TQ) to 0.84 (TC) for tall fescue. For perennial ryegrass, the traits related to turfgrass performance (Cover, TC, and TQ) had the highest heritability estimates (> 0.79). In contrast, the traits related to drought tolerance (DR25, DR50, and DR75) showed moderate heritability estimates (< 0.68); these lower values of heritabilities can be associated with the greater σ_{gy}^2 for these traits (Table 2). A similar trend was observed for tall fescue, and the traits related to turfgrass performance (Cover, TC, and TD) showed higher heritability (> 0.73) than those related to drought tolerance (DR25 and DR50) (< 0.62), except for the trait DR75 (0.74) (Table 2).

The genotypes showed differential responses across years for all traits for perennial ryegrass, whereas for tall fescue, only TD and TQ showed differential responses through the years. Despite the significant interaction between genotypes and years, the ranking of genotypes did not change significantly among years, as the genetic correlations between years were high for most of the traits, indicating noncrossover interactions. However, the genetic correlations for TD (perennial ryegrass) and TQ (tall fescue) were low (0.08) to moderate estimates (0.50), respectively, indicating more changes in rank among the genotypes between the years (Table 2). Drought tolerance traits (DR25, DR50, and DR75) showed different results between the two species. Perennial ryegrass showed greater G × Y interaction than tall fescue (Table 2). Tall fescue had genetic

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TABLE 2 Estimates of variance components for the first trial, spatial, and temporal autocorrelations, and heritability estimate in 48 perennial ryegrass and 38 tall fescue genotypes for seven traits.

Species	Component	Cover	TC	TD	TQ	DR25	DR50	DR75
Perennial ryegrass	σ_g^2	0.043[a]	0.118[a]	0.003	0.080[a]	1.765[a]	1.156[a]	1.316[a]
	σ_{gy}^2	0.014[a]	0.021[a]	0.033[a]	0.009[a]	0.623[a]	0.518[a]	0.571[a]
	$\overline{\sigma_e^2}$	0.106	0.139	0.118	0.186	9.790	6.185	2.108
	ρ_{col}	0.36	0.36	0.22	0.34	0.24	0.29	0.25
	ρ_{row}	–	0.46	0.30	0.37	0.36	0.36	0.35
	ρ_{year}	0.30	0.18	0.31	0.42	–	–	–
	ρ_g	0.75	0.85	0.08	0.90	0.74	0.69	0.69
	H^2	0.75	0.89	0.11	0.78	0.56	0.58	0.68
Tall fescue	σ_g^2	0.034[a]	0.060[a]	0.034[a]	0.011[a]	26.258[a]	15.381[a]	7.442[a]
	σ_{gy}^2	0.002	0.0000	0.010[a]	0.011[a]	2.826	1.002	0.557
	$\overline{\sigma_e^2}$	0.064	0.070	0.068	0.087	64.468	30.465	12.897
	ρ_{col}	0.47	0.44	0.36	0.35	–	–	0.24
	ρ_{row}	–	0.18	–	–	0.16	0.14	0.32
	ρ_{year}	0.41	0.37	0.29	0.41	0.83	0.84	0.70
	ρ_g	0.96	1.00	0.77	0.50	0.90	0.94	0.93
	H^2	0.76	0.84	0.73	0.27	0.57	0.62	0.74

Abbreviations: Cover, percent cover; TC, turfgrass color; TD, turfgrass density; DR25, DR50, and DR75, days to reach 25%, 50%, and 75% of plot coverage under drought stress, respectively; σ_g^2, genetic variance; σ_{gy}^2, genotype × year interaction variance; $\overline{\sigma_e^2}$, mean error variance through the years; ρ_{col}, spatial autocorrelations between columns of the trial; ρ_{row}, spatial autocorrelations between rows of the trial; ρ_{year}, first autocorrelation through the years; ρ_g, genetic correlation between years; H^2, estimate of Cullis' heritability on the genotype-mean basis.

[a]Variance component different from zero by the likelihood ratio test at the 5% probability level.

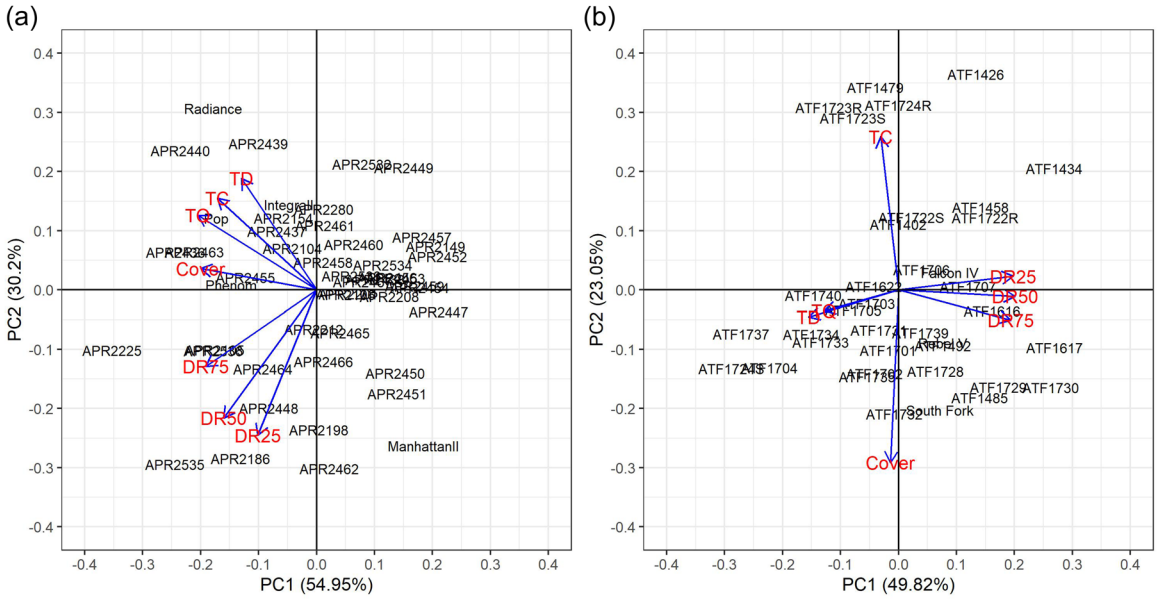

FIGURE 1 Genotype × trait biplot for percent cover (Cover), turf grass color (TC), turf density (TD), turf quality (TQ), and days to reach 25%, 50%, and 75% of coverage (DR25, DR50, and DR75) for perennial ryegrass (a) and tall fescue (b) in 2012 and 2013.

correlations higher than 0.90, indicating similar genotype performance in both years.

The genetic correlations between the day to reduce cover due to drought stress were high for both species (Figure 1a,b). There were differences in the correlation patterns between the two species for the turfgrass performance traits. These traits grouped together in a cluster for perennial ryegrass, indicating a high

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correlation between them (Figure 1a). For tall fescue, a high positive correlation was observed between TD and TQ, and a high negative correlation between TC and Cover, while TD and TQ were not correlated with TC and Cover (Figure 1b).

The general mean of the predicted values of the genotypes for TQ was higher in 2013 than in 2012 for both species. However, for DR50, the overall behavior of the genotypes was the opposite of that observed for TQ. This behavior might reflect the genotypes' limitations in recovering from prolonged drought stress (Figure 2a,b). Higher values in the first year compared to the second year were observed for the other traits evaluated (Figure S2).

Both species showed differences in drought tolerance (Figure 2b). Tall fescue showed a better overall performance compared to perennial ryegrass, in which the tall fescue genotypes took an average of 60 days (2012) and 47 days (2013) to lose 50% of their coverage, while for perennial ryegrass, it took 37 days (2012) and 24 days (2013) to lose the same percentage of coverage.

Evaluating drought tolerance under different mowing heights in Years 3 and 4

Genotypic variance was significant for most traits, except for TD in perennial ryegrass and cover and DR75 in tall fescue. For perennial ryegrass, there was significant G × Y interaction only for traits related to drought tolerance, while the interaction for genotype × mowing height was only significant for TD and TQ. There was significant G × Y interaction for most traits in tall fescue, except for TC, TD, and DR75. The interaction between genotype and mowing height was significant for traits, except Cover and DR75, in tall fescue (Table 3).

Heritability estimates varied from 0.31 (TD) to 0.93 (TC) in perennial ryegrass and between 0.00 (Cover) and 0.89 (TC) in tall fescue. For tall fescue, higher heritability estimates (> 0.80) were found for traits related to drought tolerance (DR25 and DR75), while higher heritability estimates (> 0.72) for turfgrass performance traits (Cover, TC, and TQ) were found in perennial ryegrass. The genotypes showed differential responses to the mowing heights for TD and TQ for perennial ryegrass (Table 3). Even though σ^2_{gh} was significant for these traits, the genetic correlation for TQ was high, providing evidence that there was no extensive reranking among genotypes (Table 3). For the other qualitative traits and drought tolerance traits, the genetic correlations (ρ_g) were high, indicating an absence of complex interaction (Table 3). For tall fescue, the magnitude of the mowing height × genotype interaction was medium to high, except for Cover, which was extremely low.

For perennial ryegrass, the genetic correlation between traits had similar results to the first trial (2012–2013). Traits related to turfgrass performance were highly correlated, and traits related to drought tolerance clustered together (Figure 3a). In tall fescue, DR75 showed a high positive correlation with Cover, which had a negative correlation with TC. The traits DR25 and DR50 showed a positive correlation, while they showed a negative correlation with TD and TQ (Figure 3b).

The high mowing height treatment resulted in higher TQ ratings for both species (Figure 4a). Tall fescue showed more changes in the genotype ranking for TQ between the two mowing height levels (Figure 4a). Similarly, the other turfgrass performance traits, except for TD, showed better turfgrass performance under the high mowing height level (Figure S2). For DR50, the low mowing height level retained greater coverage under drought in perennial ryegrass, while mowing tall fescue

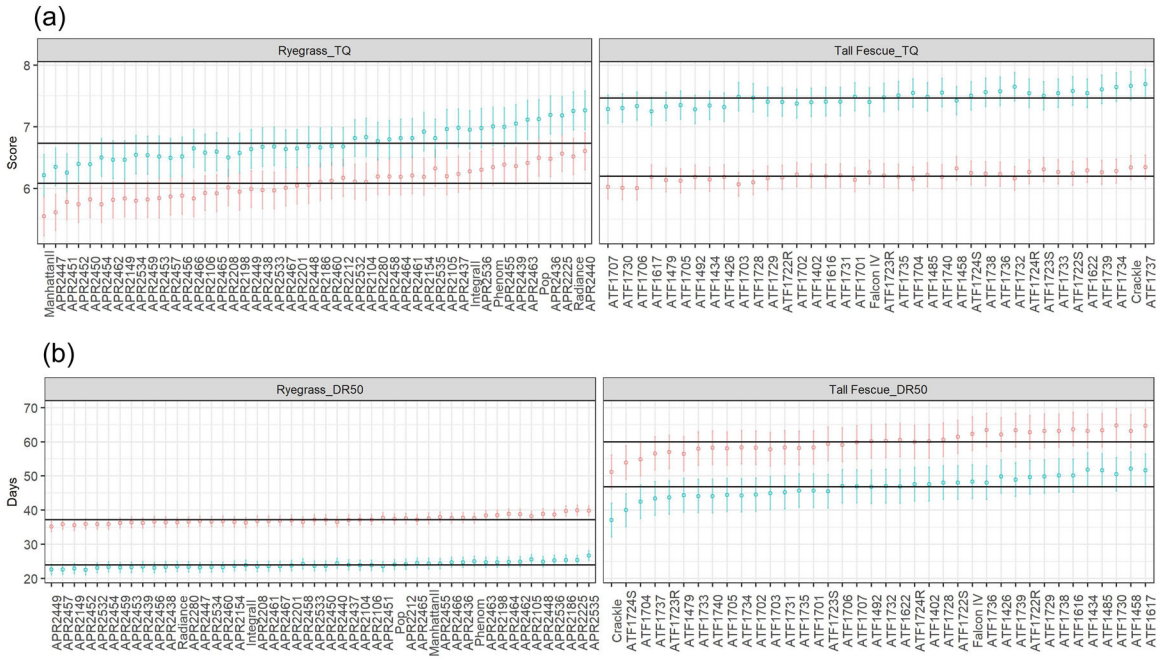

FIGURE 2 Predicted values (95% confidence interval) for 48 perennial ryegrass (left) and 38 tall fescue (right) genotypes phenotyped in 2012 (red) and 2013 (blue) for turf quality (a) and days to reach 50% of coverage under drought (DR50) (b).

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TABLE 3 Estimates of variance components for the second trial, spatial, and temporal autocorrelations, and heritability measured in 48 perennial ryegrass and 38 tall fescue genotypes for seven traits under two mowing heights.

Species	Component	Cover	TC	TD	TQ	DR25	DR50	DR75
Perennial ryegrass	σ^2_g	0.031[a]	0.150[a]	0.010	0.041[a]	4.548[a]	1.892[a]	1.826[a]
	σ^2_{gy}	0.008	0.005	0.000	0.004	1.530[a]	0.504[a]	1.176[a]
	σ^2_{gh}	0.002	0.000	0.018[a]	0.010[a]	0.000	0.038	0.336
	σ^2_{gyh}	0.004	0.004	0.000	0.000	0.084	0.149	0.000
	σ^2_{e1}	0.006	0.009	0.007	0.016	3.199	0.648	0.301
	$\overline{\sigma^2_{e2}}$	0.139	0.119	0.174	0.112	27.172	10.950	6.358
	ρ_{col}	–	–	0.13	–	0.49	0.34	–
	ρ_{row}	0.22	0.42	0.33	0.41	0.41	0.40	0.13
	ρ_{year}	0.33	0.36	–	–	0.35	0.26	–
	ρ_g	0.88	1.00	0.04	0.80	1.00	0.98	0.84
	H^2	0.72	0.93	0.31	0.85	0.57	0.58	0.75
Tall fescue	σ^2_g	0.000	0.088[a]	0.063[a]	0.058[a]	15.261[a]	3.672[a]	0.542
	σ^2_{gy}	0.022[a]	0.002	0.007	0.022[a]	2.001[a]	0.789[a]	0.030
	σ^2_{gh}	0.006	0.009[a]	0.032[a]	0.027[a]	3.433[a]	0.905[a]	0.155[a]
	σ^2_{gyh}	0.000	0.000	0.000	0.000	0.000	0.000	0.642
	σ^2_{e1}	0.004	0.025	0.049	0.041	1.835	5.446	0.220
	$\overline{\sigma^2_{e2}}$	0.121	0.097	0.113	0.166	2.478	8.697	5.878
	ρ_{col}	–	–	–	–	–	–	–
	ρ_{row}	0.26	0.20	0.35	0.27	0.40	0.39	0.35
	ρ_{year}	–	–	–	–	–	–	–
	ρ_g	0.00	0.91	0.66	0.68	0.82	0.80	0.77
	H^2	0.00	0.89	0.84	0.80	0.85	0.80	0.46

Abbreviations: Cover, percent cover; TC, turfgrass color; TD, turfgrass density; DR25, DR50, and DR75, days to reach 25%, 50%, and 75% of plot coverage under drought stress, respectively; σ^2_g, genetic variance; σ^2_{gy}, genotype × year interaction variance; σ^2_{gh}, genotype × mowing height interaction variance; σ^2_{e1}, plot error variance; $\overline{\sigma^2_{e2}}$, mean split-plot error variance through the years; σ^2_{gyh}, genotype × year × mowing height interaction variance.

[a]Variance component is different from zero by the likelihood ratio test.

at a higher height resulted in greater number of days to lose cover in response to drought.

Investigating the impact of fertility levels on drought tolerance in Years 5 and 6

The genetic variance component was significant for all traits in both species, as well as the σ^2_{gy}, indicating a differential response of the genotypes through the years. However, the G × F (σ^2_{gf}) variance component was not significant for all the traits evaluated in the two species (Table 4).

All traits showed moderate to high heritability in both species (Table 4). For perennial ryegrass, the values ranged from 0.58 (DR25) to 0.94 (TC), and for tall fescue, it ranged from 0.49 (TQ) to 0.87 (TC). For both species, traits related to turfgrass performance had higher heritability compared to traits associated with drought tolerance, except TQ in tall fescue.

For perennial ryegrass, the genetic correlations between traits followed the same pattern that was observed in the two first trials, with drought-tolerant traits clustering together and showing low correlation with turfgrass performance traits (Figure 5a). For tall fescue, high correlation was observed among drought tolerance traits (Figure 5b). For turf performance, there were differences compared to the first two trials. Turfgrass quality and color showed a high correlation, whereas there was a small correlation between TD, TQ, and TC, and Cover was negatively correlated with other traits related to turf performance (Figure 5b).

High fertility rates resulted in better performance for DR50 and TQ for both species (Figure 6). This better performance under the high fertility level was more expressive for turf performance traits than for those related to drought tolerance. There were no large differences in the genotype ranking between the two fertility levels (Figure 6).

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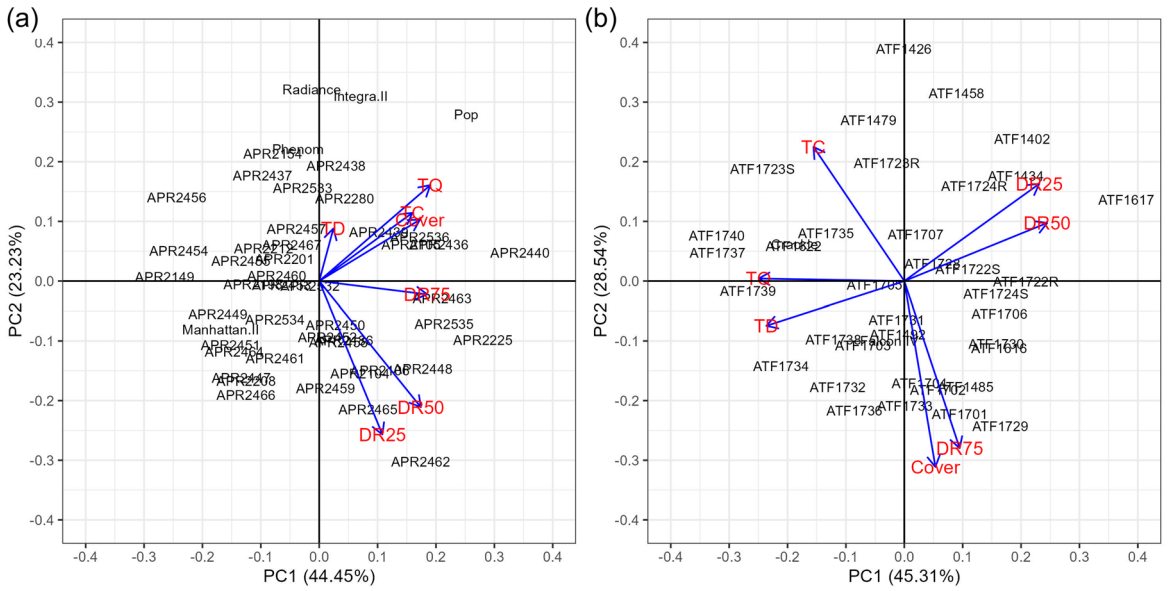

FIGURE 3 Genotype × trait biplot for coverage (Cover), turf color (TC), turf density (TD), turf quality (TQ), and days to reach 25%, 50%, and 75% of coverage (DR25, DR50, and DR75) for perennial ryegrass (a) and tall fescue (b) in 2014 and 2015. [Correction added on May 15, 2023, after initial online publication, Figure 3 was duplicated as Figure 5 and Figure 3 has now been updated with the correct Figure.]

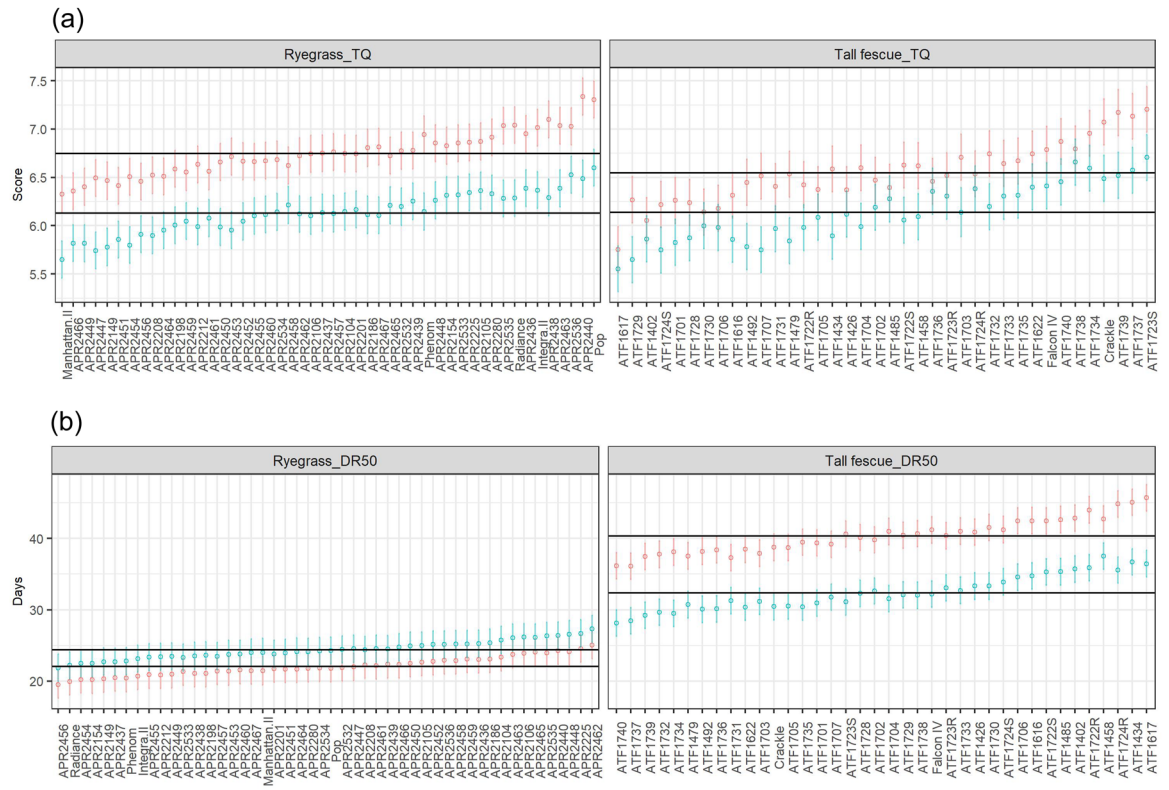

FIGURE 4 Predicted values (95% confidence interval) for 48 perennial ryegrass and 38 tall fescue genotypes in two levels of mowing height: high (red) and low (blue). Predicted values for turf quality (TQ) (a) and days to reach 50% of coverage (DR50) (b).

Selection index for drought and turfgrass performance traits

A selection index was used to rank breeding lines and compare their performance across all traits in both species, and the population mean was set as the threshold for selection. The index estimated a performance value for each genotype, calculated by summing the predicted value for each trait and dividing it by their standard deviation, which allowed the selection of the best genotypes considering all traits simultaneously. Although some controls had a higher value for the AI, most of the genotypes that exceeded the threshold of selection were breeding lines (Figure 7). In perennial ryegrass, six breeding lines showed greater performance than the population mean (APR2440, APR2463, APR2535, APR2436, APR2536, and APR2462), and four breeding lines performed better than the overall

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TABLE 4 Estimates of variance components for the third trial, spatial and temporal autocorrelations, and heritability measured in 48 perennial ryegrass and 38 tall fescue genotypes for seven traits in two levels of fertility.

Species	Component	Cover	TC	TD	TQ	DR25	DR50	DR75
Perennial ryegrass	σ^2_g	0.105[a]	0.212[a]	0.029[a]	0.113[a]	2.621[a]	1.269[a]	1.344[a]
	σ^2_{gy}	–	–	–	–	1.427[a]	0.789[a]	0.563[a]
	σ^2_{gf}	0.000	0.008	0.004	0.007	0.270	0.125	0.119
	σ^2_{gyf}	–	–	–	–	0.000	0.000	0.000
	σ^2_{e1}	0.034	0.000	0.031	0.036	1.227	0.511	0.525
	$\overline{\sigma^2_{e2}}$	0.102	0.092	0.094	0.086	14.326	6.887	4.308
	ρ_{col}	–	0.24	−0.11	–	0.40	0.35	0.32
	ρ_{row}	0.25	0.41	0.31	0.32	0.24	0.28	0.20
	ρ_{year}	–	–	–	–	0.35	0.32	0.18
	ρ_g	1.00	0.96	0.88	0.94	0.90	0.91	0.92
	H^2	0.87	0.94	0.67	0.89	0.58	0.57	0.70
Tall fescue	σ^2_g	0.067[a]	0.117[a]	0.063[a]	0.029[a]	7.431[a]	3.134[a]	0.990[a]
	σ^2_{gy}	–	–	–	–	3.778[a]	1.270[a]	0.508[a]
	σ^2_{gf}	0.010	0.004	0.000	0.007	1.069	0.043	0.184
	σ^2_{gyf}	–	–	–	–	0.000	0.000	0.061
	σ^2_{e1}	0.046	0.001	0.025	0.000	1.833	0.588	0.141
	$\overline{\sigma^2_{e2}}$	0.118	0.089	0.167	0.168	24.824	13.097	5.751
	ρ_{col}	–	–	–	–	0.37	0.45	0.35
	ρ_{row}	–	0.23	0.42	0.27	0.50	–	0.44
	ρ_{year}	–	–	–	–	0.50	0.45	0.41
	ρ_g	0.87	0.96	1.00	0.79	0.87	0.99	0.84
	H^2	0.73	0.87	0.71	0.49	0.69	0.59	0.75

Abbreviations: Cover, percent coverage; TC, turfgrass color; TD; turfgrass density; DR25, DR50, and DR75, days to reach 25%, 50%, and 75% of plot coverage under drought stress, respectively; σ^2_g, genetic variance; σ^2_{gy}, genotype × year interaction variance; σ^2_{gf}, genotype × fertility level interaction variance; σ^2_{gyf}, genotype × year × fertility level interaction variance; σ^2_{e1}, plot error variance; $\overline{\sigma^2_e}$, mean split-plot error variance through the years; ρ_{col}, autocorrelations between columns of the trial; ρ_{row}, autocorrelations between rows of the trial; ρ_{year}, first-order autocorrelation through the years; ρ_g, genetic correlation between the two levels of fertility; H^2, estimate of heritability on the cultivar-mean basis.

[a]The variance component is different from zero by the likelihood ratio test.

mean in tall fescue (ATF1722S, ATF1724R, ATF1722R, and ATF1617) (Figure 7). For both species, the number of breeding lines that surpassed the selection intensity threshold was greater than most of the checks (Figure 7).

DISCUSSION

Overall drought resistance

Plants show different adaptive strategies to survive in drought environments. There are three drought-resistance strategies: escape, avoidance, and tolerance (Turner, 1986). The first strategy, drought escape, is the ability of a plant to survive drought stress by becoming dormant during a drought episode. Drought avoidance is the ability of a plant to grow under drought stress by maintaining internal water status through a reduction in water loss from plant canopy or increasing water uptake of roots from the soil. Turfgrass species that possess drought avoidance mechanisms may survive or sustain growth and suitable esthetic characteristics during short-term drought until water is depleted in the soil. Drought tolerance in plants refers to their ability to maintain their metabolic processes even when there is a reduced amount of water in their cells. This mechanism is essential for plants to endure prolonged periods of drought, allowing them to survive and thrive in water-scarce environment (Turner, 1986).

These drought-resistance strategies are not mutually exclusive, and the same species may have more than one strategy when adapting to drought stress (Nilsen & Orcutt, 1996). In this study, we can infer about drought avoidance and drought tolerance, since perennial ryegrass and tall fescue did not show dormancy when subjected to drought stress. The mechanism to avoid drought can be more related to the DR75 trait, as this point is closer to the plateau in logistic regressions

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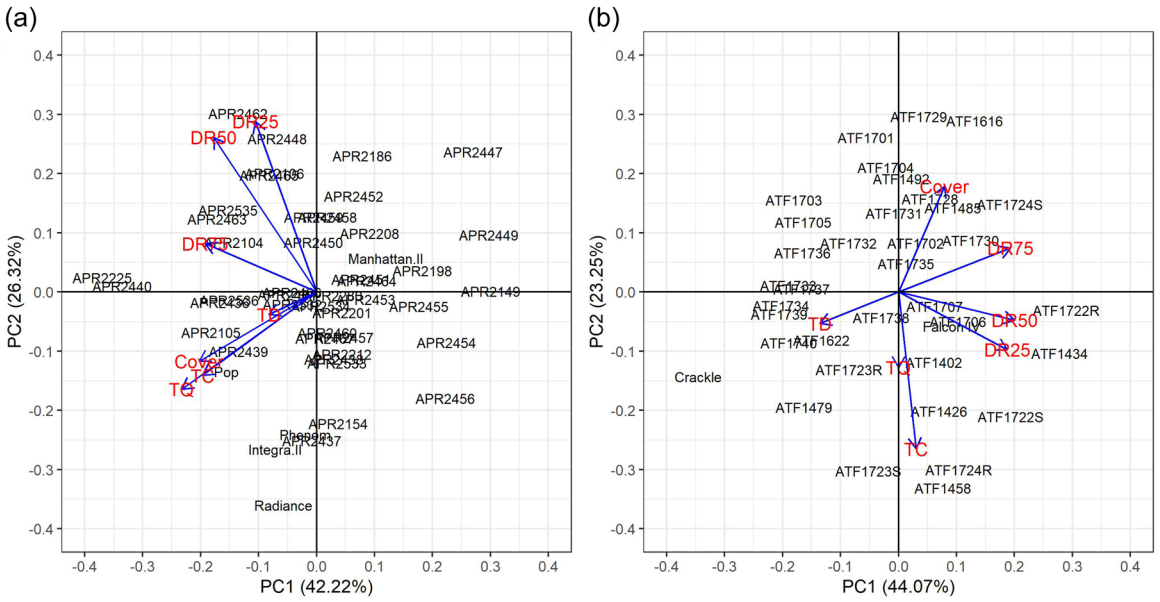

FIGURE 5 Genotype × trait biplot for coverage (Cover), turf color (TC), turf density (TD), turf quality (TQ), and days to reach 25%, 50%, and 75% of coverage (DR25, DR50, and DR75) for perennial ryegrass (a) and tall fescue (b) in 2016 and 2017.

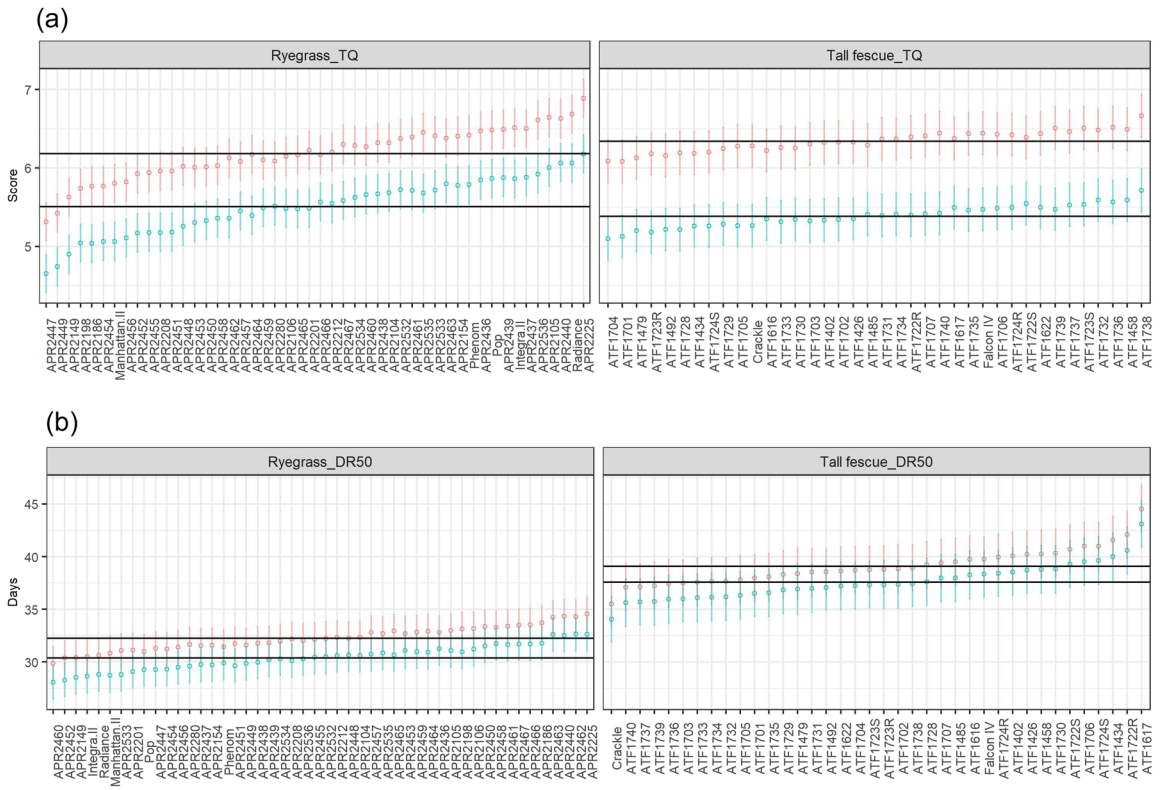

FIGURE 6 Predicted values (95% confidence interval) for 48 perennial ryegrass and 38 tall fescue genotypes in two levels of fertility: high (red) and low (blue). Predicted values for turf quality (TQ) (a) and days to reach 50% of coverage (DR50) (b).

(Figure S2). The DR75 stage showed the length of time for which the plants were able to maintain vegetation cover before a sharp fall, which occurred in a short period of time. The other two traits (DR25 and DR50) can represent the ability of plants to conserve vegetative cover for prolonged periods of drought, which relates to the drought tolerance mechanism.

Given the above information, tall fescue managed to maintain vegetative coverage for longer periods when exposed to drought stress. It is possible to observe the formation of a plateau with a small variation in the vegetative cover over time in all the years evaluated (Figure S2b), that is, tall fescue used the avoidance strategy to face drought stress. White et al. (1993) and Carrow (1996) suggested that drought avoidance mechanisms associated with deep rooting are more important than drought tolerance aspects for overall drought resistance in tall fescue.

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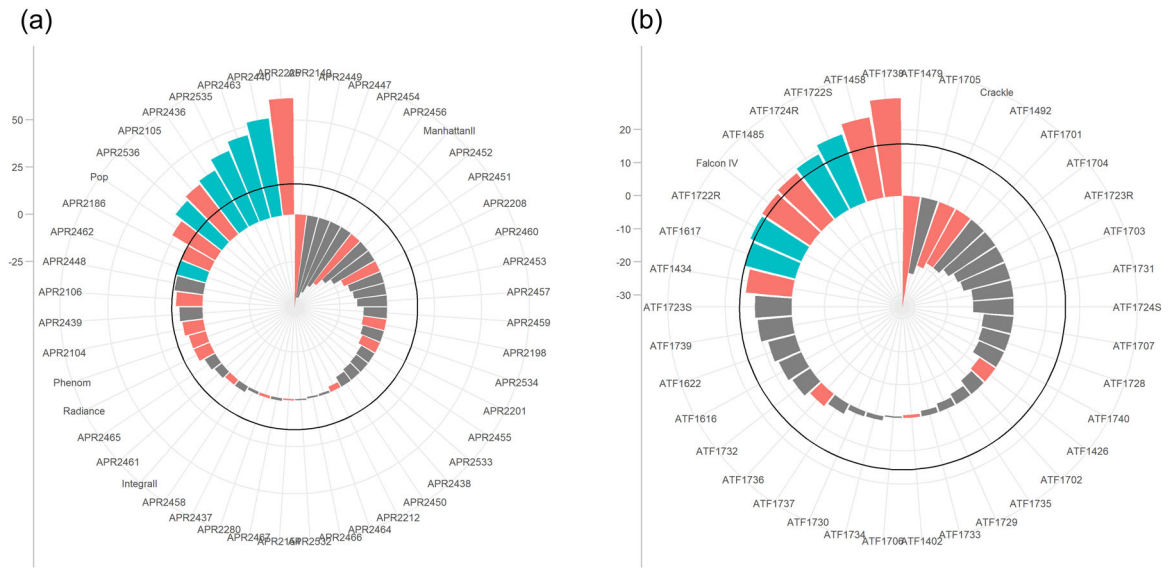

FIGURE 7 Ranked checks (red) and breeding lines (blue and gray) by the additive index, in which blue breeding lines are the selected genotypes, and the solid black line represents the selection intensity (20%).

For perennial ryegrass, the presence of this plateau in the logistic regression was pronounced in the first year of evaluation (Figure S2a), demonstrating that this species had a decay in vegetative coverage already in the first days after drought stress was imposed, that is, drought avoidance was probably not the main mechanism used by this species. Sugiyama and Nikara (2004) studied the relative importance between the two strategies (avoidance and tolerance) in perennial ryegrass, and the authors observed that drought tolerance had greater relative importance than drought avoidance in the composition of drought resistance in perennial ryegrass.

Although a direct comparison between the two species used in this study is not possible, because the trials were conducted separately, other authors concluded that tall fescue had greater drought resistance than perennial ryegrass (Aronson et al., 1987; Jiang & Huang, 2001). In this study, it is possible to observe a differential response to drought between both species, in which the decay of vegetative cover in tall fescue was slower than the decay observed in perennial ryegrass (Figure S2).

Genetic parameters and trait correlations

Climate change will have negative impacts on agriculture in the coming decades. According to the Intergovernmental Panel on Climate Change (2014), the most drastic consequences will be associated with fluctuations in precipitation (extended periods of drought and more intense rainfall). Therefore, agriculture must become more sustainable to minimize its effects on global warming, and plant breeders must focus efforts on developing cultivars that tolerate adverse abiotic stresses and that require less inputs (nutrient, water, and pesticides) (Carter et al., 2015; Tester & Langridge, 2010; Walther et al., 2002). Improving response to abiotic stresses is particularly challenging for turfgrass, where breeders must focus on selecting genotypes that respond to short- and long-term changes in stresses while maintaining superior esthetic value (Meyer et al., 2017). In this study, it was possible to observe that the breeding populations used in this study showed significant genetic variances for TQ and drought tolerance traits for species and all years. Therefore, it is expected that the selection of the best genotypes promotes gains with the selection and continuity of the breeding program in terms of selecting genotypes that are tolerant to drought and that have good quality in future selection cycles (Tables 1–3).

Regarding the estimation of heritability for breeding populations grown under stresses, it has been reported that the greater the level of stress to which the plants are subjected, the lower the heritability estimates (Fernandes Filho et al., 2021; Hoffmann & Merila, 1999; Mwadzingeni et al., 2017). Hence, it poses a challenge in selecting drought-resistant genotypes when they are subjected to long periods of drought. According to Hoffmann and Merila (1999), lower heritability is often found in stressful environments because of the high environmental variance found in these environments. However, high correlation between the different drought tolerance thresholds was observed in this study (Figures 1–5). Thus, the selection performed in the DR75 threshold had a highly correlated response in the other thresholds (DR25 and DR50, indicating that breeders could take advantage of selecting at lower thresholds of drought stress, since the heritability estimates were higher, and the discrimination among breeding lines is clearer. Furthermore, the high correlation between these thresholds indicates that long periods of drought stress are not necessary for selecting superior genotypes, as the ranking of genotypes did not change much among the thresholds. Falconer and Mackay (1996) proposed that the genotype × environment interaction can be considered a pleiotropic effect of a trait evaluated in various environments. Thus, the genetic correlation between environments indicates whether the same genes are being

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expressed in different environments (Gauch & Zobel, 1996). Based on this principle, the results obtained in this study showed that most of the genes that confer resistance to drought are expressed across the different stress levels (DR25, DR50, and DR75).

The heritability estimates for traits associated with turfgrass performance were high for both species, indicating that the phenotypic variance observed is mainly due to genetic variance (Tables 1–3). This fact indicates that selection gains for turfgrass performance can be obtained through cycles of recurrent selection. This information is of great importance in these species, since both species are sexually, cross-bred and self-incompatible, requiring several cycles of recurrent selection to develop more stable and uniform cultivars (Fribourg et al., 2009; Meyer et al., 2017).

Another important factor in the selection of genotypes for turfgrass is the correlation between traits, as these correlations can define the best strategy for selection in breeding programs. For perennial ryegrass, the correlations between the turf performance traits were high and followed the same pattern in all the evaluated trials, in which they were grouped into a single cluster (Figures 1, 3, and 5). This strongly indicates that the genes that control the expression of the traits Cover, TQ, TC, and TD are linked. Thus, selecting genotypes based on TQ would be sufficient, as this is the most important trait related to turfgrass performance. For tall fescue, the correlations between turf performance traits did not follow a pattern in the PCA (Figures 1, 3, and 5), indicating that the genes controlling these traits are not linked; thus, a suitable strategy to obtain gains for these traits together would be the implementation of a selection index.

G × Y, G × H, and G × F interactions

The simple G × Y interaction can be observed when there is heterogeneity of variances (Crossa et al., 2004) without changing in the genotype ranking, whereas the complex G × E interaction is found when there is a lack of genetic correlation between environments (Elias et al., 2016; Van Eeuwijk et al., 2016), that is, there is a change in ranking. Most of the traits evaluated in this study showed that the simple interaction was predominant, as the genetic correlations between years were high (Tables 1–3).

The development of a drought-tolerant cultivar in turfgrass requires several years, and changing cultural practices can be an efficient way to promote a better response of plants facing drought stress, without the need to invest in lawn renovations or changes in the irrigation technology (Milesi et al., 2005). Therefore, studies aiming to improve cultural practices are essential to optimize water-use efficiency in turfgrass. Turfgrass development is modified according to the mowing management, including root system development and water use (Harivandi et al., 2009). Better growth and a deeper root system are found under high mowing height management, leading to higher water-use rates. In contrast, turfgrass mowed shorter shows denser shoot and tight canopy, traits that lead to lower evapotranspiration. A balanced mowing practice promotes a depth root system and density, affecting drought tolerance (Harivandi et al., 2009).

The simple interaction was predominant for the G × H reported in this study. However, Ebdon and Gauch (2002) reported that mowing height was the covariate that mostly contributed to the genotype × environment interaction estimated for large populations of perennial ryegrass and Kentucky bluegrass (*Poa pratensis*) across multiple locations. In this study, the lower mowing height imposed on perennial ryegrass resulted in less genotypes showing stress caused by drought (Figure 4b). According to Colmer and Barton (2017), this happens due to lower evapotranspiration when most of the aerial part of the plant is eliminated. However, tall fescue showed greater drought tolerance under higher mowing height (Figure 4b). According to Qian et al. (1997), the main drought resistance mechanism for tall fescue is drought avoidance because the root system is deep. A lower mowing height results in shorter root systems (Harivandi et al., 2009), making them more susceptible to drought.

Nitrogen fertilization increases shoot growth, resulting in increased leaf area and higher irrigation requirements. However, under-fertilized turfgrass will lose more soil water to evapotranspiration because the reduced leaf area does not provide soil shading, longer soil water retention, or moderated soil temperatures during periods of drought (Bond & Willis, 1970). In the present study, the behavior of genotypes under contrasting fertility levels did not cause complex interaction in any of the measured traits. Low nitrogen levels negatively affected turfgrass quality, while drought tolerance was not significantly affected (Figure 6), in which, under lower nitrogen rates, genotypes showed a slight decrease in drought tolerance. Goss (2017) investigated the DR under different nitrogen fertilization levels in two cool-season and two warm-season turfgrass species; the author concluded that fertilized turf grass swards can maintain acceptable turfgrass quality with lower irrigation rates than swards receiving no fertilization.

Selection index

When selecting for multiple traits, the selection index is the most effective method of genotype selection (Hazel & Lush, 1942; Pesek & Baker, 1969). Independent culling levels are less effective than the selection index because, when strictly applied, it will not select genotypes below the threshold for only one trait despite being superior for all other traits, while the use of a selection index makes it possible to retain those individuals (Bernardo, 2010). The selection index is a method for estimating the genotypic value of a genotype by combining all relevant information available on the individual into a unique trait (Mrode, 2014). The AI proposed by Resende (2016) allowed the selection of superior breeding lines considering all the evaluated traits.

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CONCLUSIONS

Significant genetic variability for drought tolerance and turfgrass performance was estimated for the NexGen breeding program for the two species, making it possible to select tolerant genotypes that have good turfgrass quality. Based on the selection index, it was possible to select six breeding lines for perennial ryegrass (APR2440, APR2463, APR2535, APR2436, APR2536, and APR2462) and four breeding lines for tall fescue (ATF1722S, ATF1724R, ATF1722R, and ATF1617).

The G × Y interactions were predominantly simple, indicating a high correlated response between the years, reducing the need for multiyear trials if the environmental conditions remain constant, making the breeding process more efficient.

Lower mowing height positively improved drought tolerance in perennial ryegrass, but lower mowing height resulted in lower ratings for turfgrass performance. For tall fescue, high mowing height led to higher turfgrass quality ratings and greater drought tolerance. With regard to nitrogen fertilization, genotypes for both species showed improvement in turfgrass quality under higher nitrogen doses, while no significant effect was observed between the two nitrogen rates for drought tolerance.

AUTHOR CONTRIBUTIONS

Claudio C. Fernandes Filho: Data curation; formal analysis; validation; visualization; writing—original draft. **Mario H. Murad Leite Andrade**: Formal analysis; supervision; writing—review and editing. **Jose A. Rodrigues Nunes**: Supervision; validation; writing—review and editing. **Kevin Kenworthy**: Supervision; validation; writing—review and editing. **Joseph Wipff**: Conceptualization; data curation; investigation; methodology; writing—review and editing. **Debra L. Hignight**: Conceptualization; investigation; methodology; writing—review and editing. **Kenneth Hignight**: Conceptualization; data curation; investigation; methodology; writing—review and editing. **Esteban F. Rios**: Software; supervision; writing—review and editing.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

Data are available on request from the authors.

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