



<https://ijpb.ui.ac.ir/?lang=en>

Journal of Plant Biological Sciences

E-ISSN: 3041-9603

Vol. 17, Issue 4, No. 66, 2025, pp. 15- 26

Received: 2026/05/25 Accepted: 2026/07/22

(Research Paper)

Morphological variation, trait associations, and genotype assessment in tall fescue (*Festuca arundinacea* Schreb.) using biplot analysis

Ehsan Rahimi¹, Alireza Pourmohammad ^{*1}, Naser Sabbaghnia¹, Reza Mohammadi², Sezai Ercişli³

¹Department of Plant Production and Genetics, Faculty of Agriculture, University of Maragheh, Maragheh, Iran

²Branch for Northwest and West region, Agricultural Biotechnology Research Institute of Iran (ABRII), Agricultural Research, Education and Extension Organization (AREEO), Tabriz, Iran

³Department of Horticulture, Faculty of Agriculture, Ataturk University, 25240 Erzurum, Turkey

Abstract

As a perennial forage grass, tall fescue (*Festuca arundinacea* Schreb.) is cultivated in temperate regions due to its high adaptability, drought tolerance, and forage production potential. Current research assessed twenty-five tall fescue genotypes for morphological, phenological, and yield traits under field conditions in Tabriz, Iran. Traits assessed included plant height (PH), canopy width (CW), crown diameter (CD), fresh forage weight (FF), dry forage weight (DF), stem number (SN), seed weight (SW), days to heading (DH), and days to pollination (DP). Data were analyzed using a genotype-by-trait biplot model. The first two principal components explained 80% of the total variation, indicating the contribution of interactions. Biplot analysis indicated genotype 25 as superior for morphological and yield-related traits, while genotype 5 excelled in phenological traits. Trait discriminative power analysis identified CD and FF as the most effective traits for differentiating genotypes, followed by PH, CW, and DF, whereas DH and DP had the lowest discriminative ability. Ideotype-based analysis highlighted genotypes 24, 5, 7, 22, 6, 23, and 25 as closest to the ideal genotype, integrating high performance of all measured traits. Evaluation of DF indicated genotypes 25, 22, 23, 24, and 7 as highest-yielding. Genotypes 7, 22, 23, 24, and 25 were identified as top performers for seed weight. Morphological traits like PH, CW, CD, FF, DF, and SN were important contributors to forage and seed yield and can be utilized as early selection criteria in breeding efforts.

Keywords: Forage yield, Genotype by trait interaction, Seed weight, Ideotype selection

*Corresponding Author: pourmohammad@maragheh.ac.ir



Introduction

Tall fescue (*Festuca arundinacea* Schreb.) is a deeply rooted, perennial grass species distributed across many regions of the world. It tolerates a broad range of soil types as well as grows under diverse pH, temperature, rainfall, and moisture conditions (Wang et al., 2011; Satognon, 2024). The use of tall fescue has expanded after the release of the cultivars Alta and Kentucky-31, and it is now cultivated for forage and soil conservation properties in many temperate regions. Tall fescue is one of the main perennial forage crops naturally growing in the pastures and rangelands of the northern and western regions of Iran. It is used for hay production and grazing and serves as an important feed resource for livestock, while its species are found at altitudes ranging from sea level up to 2900 m in regions receiving more than 300 mm of annual precipitation (Saha, 2014). Its perennial nature exposes it to continuous natural selection pressures, contributing to its adaptability under different environmental conditions.

Increasing scarcity of water resources is a significant problem that threatens global agricultural systems. It poses the greatest constraints to animal husbandry in arid and semi-arid areas. Forage shortages are a limitation factor for animal husbandry, leading to poor animal productivity and limitations in animal protein supplies in Iran (Rad et al., 2015). Considering the importance of forage crops for the sustainable livestock system, strengthening and managing sustainable, resilient forages has become a major concern. Tall fescue, the more water-tolerant of common temperate grasses such as perennial ryegrass in persistence and productive capability, is a promising candidate for water-shortage environments.

Nevertheless, though the tolerance for drought for the plant is high, prolonged and severe water stress may be affecting its development, reproduction, and productivity. Availability of nutrients can affect plant attributes due to water and temperature—availability and nutrient status, as well as growth stage and genotype (Insua et al., 2018). Tall fescue grass has a wide utilization for the production of pasture, hay, and silage, with the boot stage regarded as the ideal growth stage for best quality forage. Compared with perennial ryegrass, tall fescue showed lower values of digestible content and simple sugars, but higher values for protein and fiber (Baert & Van Waes, 2014).

Genetic variation in agronomic traits is an essential prerequisite for developing efficient selection programs. Quantitatively inherited and influenced by genetic, environmental, and

interaction effects (Caradus & Chapman, 2025), making it possibly inefficient to select for only yield directly. Therefore, an indirect selection for a yield trait that has high heritability and is easily measured and highly correlated with the yield trait will offer better chances for success in breeding programs. Extensive variability in forage yield, plant height, seed production, and related agronomic traits has been reported among genotypes in tall fescue (Waldron et al., 2021; Tate et al., 2023; Pirnajmedin et al., 2025).

In the present study, many associations between morphological traits like plant height, fertility index, and harvest index and forage or seed yield showed that these simple and easily measured criteria would provide a useful guide to improve productive performance (Majidi et al., 2009). These morphological variances can reflect genetic variation between populations or be influenced by environmental factors for plant growth and development. In recent years, a huge amount of morphological variation in tall fescue has been noted. However, with overgrazing, erratic precipitation, and rangeland degradation in regions, considerable genetic resources useful for selection of productivity have been eroded in some cases (Lou et al., 2015). So, an efficient estimation of germplasm available and the informative traits would be helpful for efficient selection to improve productive varieties of tall fescue. Morphological traits are critical in selecting suitable parents for hybridization and breeding programs. is fundamental for effective selection in breeding programs. Despite its potential, the wide utilization of tall fescue is limited by traits such as leaf roughness and weak regeneration potential (Sun et al., 2013; Pirnajmedin et al., 2016). High-performing cultivars are expected not only to produce greater biomass but also to tolerate stressful conditions. Extensive tall fescue germplasm, including landraces, commercial cultivars, and breeding lines, is available, providing opportunities to improve the species for forage use. However, the genetic variation of morphological traits in tall fescue is not yet fully understood, and describing a large collection remains time-consuming and costly. Focusing on a smaller, well-characterized sample for detailed trait evaluation is therefore practical.

Assessing the relations with the genotype-by-trait biplot is a useful graphical method for depicting genotype value, relationships among traits, genotypic ranking, and trait discrimination. It is also beneficial in identifying superior genotypes for selection purposes and trait association, thus making a breeding program more effective. There have been many reports in

different plant species in which the genotype-by-trait biplot was used in evaluating accessions for their germplasm enhancement like *Carthamus tinctorius* (Ebrahimi et al., 2023), *Nigella sativa* (Mohebodini et al., 2024), *Anethum graveolens* (Farmanpour-Kalalagh et al., 2025), and *Beta vulgaris* (Sabaghnia et al., 2026), as this methodology was especially developed to assess a phenotypic variability and relationship between traits in populations. Some studies have studied genetic variation for forage yield, seed production, and morphological traits of tall fescue; however, they mostly applied traditional statistical analyses. To the best of our knowledge, genotype-by-trait biplot analysis has not yet been used to investigate traits of tall fescue. Thus, this study presents a unique multivariate analysis of tall fescue germplasm that jointly addresses all the analyzed traits to select outstanding genotypes, to recognize the more discriminative traits, and to exhibit relationships between genotypes and traits for efficient forage and seed productivity improvement. The objectives of the current research were to investigate the phenotypic diversity in morphological characteristics of tall fescue and to determine the structures of relationships among traits in some populations, with the goal of identifying promising breeding materials suitable for improving forage yield.

Materials and Methods

Seeds of 25 tall fescue genotypes (Table 1) were obtained from the seed bank of the Agricultural Biotechnology Research Institute (Branch for Northwest and West Region), Tabriz, Iran. The genotypes were evaluated in Tabriz, Iran (46°16'E and 38°06'N), with an altitude of 1354 m. According to the De Martonne climate classification, the region has a cold semi-arid climate. The mean yearly temperature is 10 °C, with average yearly maximum and minimum temperatures of 16 °C and 2.2 °C, respectively. The mean yearly precipitation is 327 mm, and the soil pH of the experimental area ranges from moderately to strongly alkaline. Five seeds were transplanted into 3-kg pots containing a growing medium that comprised 50% arable soil, 25% sand, and 25% well-decomposed animal organic fertilizer. Pots were kept in the greenhouse at a 16/8 hr light / dark photoperiod, a relative humidity ranging from 50 to 65%, and a temperature in the range of 20 to 28 °C.

In autumn, at the beginning of this season after germination, and at the start, five-leaf stage, plants from germination were relocated to the field for 7 days of acclimatization, following a randomized complete block scheme with four replicates. Each

row contained six plants, with 60 cm spacing between plants both within and between rows. The plants were irrigated after transplanting, on May 20 in 2015, followed by subsequent irrigations at 20-day intervals until harvest. Fertilization was applied once before the first irrigation, using urea at a rate of 80 kg ha⁻¹. Weed control was performed mechanically throughout the experiment. No significant pest or disease incidence was observed during the research. Tall fescue is a perennial species, so it needs vernalization to initiate reproductive growth; no data were collected during the first year to allow full establishment of the plants in the field. Data collection began in early April of the second year for the first harvesting operation, and was done on the central plants of each row, with the marginal plants removed to avoid border effects. The traits were obtained by averaging the values of two harvests during the second year and grouped into traits based on morphological, phenological, and yielding aspects.

In terms of morphological traits, plant height (PH), canopy width (CW), crown diameter (CD), and number of stems (SN) were measured. Dates to heading (DH) and date to pollination (DP) represent the phenological traits, and fresh forage weight (FF), dry forage weight (DF), and seed weight (SW) were measured for the yield traits. PH was recorded using a ruler, starting from the soil level up to the furthest apical vegetative growth. Canopy width was recorded at the widest section of the canopy of the plant by a ruler. Crown diameter was recorded by a caliper at the base of the plant. Stem number was counted per plant before harvesting by recording the number of tillers or stems. Phenology traits (DH and DP) were considered as the number of days after sowing, approximately until 50% of plants per plot displayed the heading and pollination phases. Yield-related traits are fresh forage weight (FF), dry forage weight (DF), and seed weight (SW). After harvesting forage, the fresh biomass per plot was weighed using a scale as FF, and collected samples were oven-dried until a constant weight and dried weights were recorded as DF. Seed weight was measured at the beginning of seed harvesting and after seed cleaning according to the plot harvest weight.

The dataset was analyzed via the genotype by trait (GT) biplot model, which provides a visual interpretation of patterns, facilitating the evaluation of relationships among genotypes and traits by GGEBiplot application. For more details about the GT biplot model, refer to Yan & Rajcan (2002). The cosine between two vectors represented their correlation: acute angles denoted positive associations ($\cos 0^\circ = +1$), and

right angles indicated independence ($\cos 90^\circ = 0$). Also, vector lengths reflected trait

importance, with longer vectors indicating greater discriminatory ability.

Table 1. The scientific name and characteristics of tall fescue genotypes.

#	Genotype	Characteristics
1	<i>Festuca arundinacea</i> -Kh1,2	Unknown foreign genotype
2	<i>Festuca arundinacea</i> -Kh1,2	Unknown Iranian genotype
3	<i>Festuca arundinacea</i> -83D+F2	Genotype Fariman, Khorasan
4	<i>Festuca arundinacea</i> -83D+F2	Unknown foreign genotype
5	<i>Festuca arundinacea</i> -Cham20-F1	Cultivar Rebel
6	<i>Festuca arundinacea</i> -Cham20-F1	Unknown Iranian genotype
7	<i>Festuca arundinacea</i> -83*Reb-F2	Unknown Iranian genotype
8	<i>Festuca arundinacea</i> -Hosh-F1	Unknown foreign genotype
9	<i>Festuca arundinacea</i> -Hosh-F1	Unknown Iranian genotype
10	<i>Festuca arundinacea</i> -43-Sh	Cultivar Mini Mustang
11	<i>Festuca arundinacea</i> -43-Sh	Unknown Iranian genotype
12	<i>Festuca arundinacea</i> -83*Reb-1-F2	Rebel $\times$ Fariman
13	<i>Festuca arundinacea</i> -Poa-Sh	Unknown foreign genotype
14	<i>Festuca arundinacea</i> -Poa-Sh	Unknown Iranian genotype
15	<i>Festuca arundinacea</i> -Poa-Sh	Unknown Iranian genotype
16	<i>Festuca arundinacea</i> -46-ShF1	Cultivar Fiesta2
17	<i>Festuca arundinacea</i> -46-ShF1	Unknown Iranian genotype
18	<i>Festuca arundinacea</i> -Abyane4+	Genotype Abyaneh, Isfahan
19	<i>Festuca arundinacea</i> -Abyane4+	Unknown Iranian genotype
20	<i>Festuca arundinacea</i> -30-Sh-F1	Unknown Iranian genotype
21	<i>Festuca arundinacea</i> -30-Sh-F1	Unknown Iranian genotype
22	<i>Festuca arundinacea</i> -Honjan2+	Genotype Hunejan, Isfahan
23	<i>Festuca arundinacea</i> -Ch-22-F1	Unknown Iranian genotype
24	<i>Festuca arundinacea</i> -83B+F2	Unknown Iranian genotype
25	<i>Festuca arundinacea</i> -30-ShF1	Cultivar Bonsai

Results

The first two PCs together explained 80% of the variation (Figure 1), with PC1 accounting for 59% and PC2 for 21%. Such findings were reported in forage crops like alfalfa (*Medicago sativa* L.) (Sayar et al., 2016) and sainfoin (*Onobrychis viciifolia* Scop.) (Sabaghnia et al., 2024), whereas interaction effects complicated indirect selection responses. Thus, the biplot model effectively described genotype and trait behavior, providing a robust visual representation of genotype performance. Figure 1 illustrated the spatial arrangement of tall fescue genotypes relative to traits. The traits days to heading (DH) and days to pollination (DP) were located in the section of genotype 5, identifying it as the leading genotype for these characteristics. The other remained traits; plant height (PH), canopy width (CW), crown diameter (CD), fresh forage weight (FF), dry forage weight (DF), stem number (SN), and seed weight (SW), corresponded most closely with

genotype 25, while it was better than the related genotypes (3, 7, 18, 20, 22, and 23) which were in this section. In contrast, the other vertex genotypes (1, 9, 11, and 24) were not identified as superior for any measured traits of tall fescue. These results suggested that both forage and seed yield performances in tall fescue are influenced by plant height, canopy width, crown diameter, and stem number rather than by phenological traits. This agrees with Biligetu et al. (2013) and Shanjani et al. (2023), who emphasized the contribution of most of these parameters to forage yield in some forage species. The applied biplot model provided clear insights into genotype responses and trait relationships, supporting the identification of superior genotypes like genotype 25, which can be used in future breeding programs.

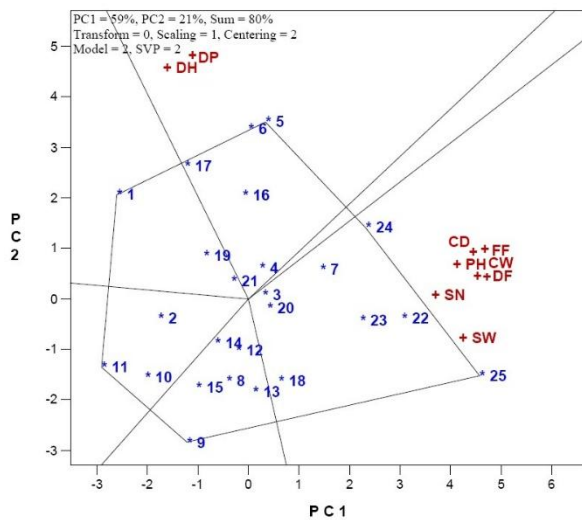


Figure 1. Polygon tool of genotype-by-trait biplot model, for identification of which tall fescue genotype wins which across which trait(s).

Traits were: PH, plant height; CW, canopy width; DH, days to heading; DP, days to pollination; CD, crown diameter; FF, fresh forage weight; DF, dry forage weight; SN, stem number; and SW, seed weight.

The structural relationships among traits were visualized by projecting vectors from the origin toward each variable (Figure 2). Strong positive relationships between DH and DP, and among CD, FF, PH, CW, and DF were found, while the positive relationships of SN and SW with CD, FF, PH, CW, and DF were relatively moderate

(Figure 2). Nearly perpendicular vectors between the phenological traits (DH and DP), with the other remained traits indicated weak or negligible correlations of phenological traits with yield and morphological traits of tall fescue. Majidi et al. (2009) found positive and significant associations of plant height, number of stems and shoots, and canopy width with dry forage yield of tall fescue, which aligns with the current findings of morphological traits (PH, CW, SN) correlated with yield-related traits (FF, DF, SW). In the study on naturalized tall fescue populations in semi-arid environments, plant height was shown to be useful to indirectly select for dry biomass production (Vega et al. 2021), which echoes morphology-yield relationships. However, the used biplot model captured 80% of the total variance, so relatively minor discrepancies between graphical and numerical correlations (Table 2) are expected, while the numerical correlation coefficients measure only pairwise associations, but the biplot model discovered the overall multivariate pattern among traits.

Table 2. The simple correlation coefficients for measured traits of tall fescue genotypes.

	PH	CW	DH	DP	CD	SN	SW	FF
CW	0.754**							
DH	-0.147 ^{ns}	-0.176 ^{ns}						
DP	-0.100 ^{ns}	-0.127 ^{ns}	0.960**					
CD	0.606**	0.794**	-0.129 ^{ns}	-0.033 ^{ns}				
SN	0.558**	0.511**	-0.173 ^{ns}	-0.126 ^{ns}	0.565**			
SW	0.610**	0.495*	-0.373 ^{ns}	-0.315 ^{ns}	0.640**	0.772**		
FF	0.786**	0.825**	-0.117 ^{ns}	-0.077**	0.782**	0.552**	0.707**	
DF	0.732**	0.742**	-0.196**	-0.165 ^{ns}	0.774**	0.569**	0.800**	0.972**

**, *, and ^{ns} were significant at 0.05 and 0.01 probability levels, and non-significant. Traits were: PH, plant height; CW, canopy width; DH, days to heading; DP, days to pollination; CD, crown diameter; FF, fresh forage weight; DF, dry forage weight; SN, stem number; and SW, seed weight.

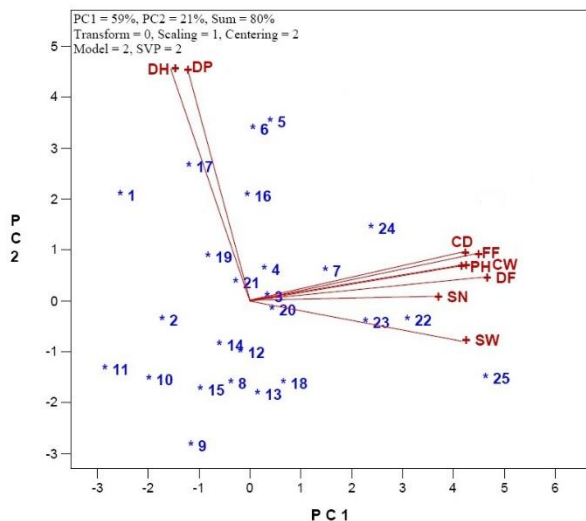


Figure 2. Ranking of tall fescue genotypes based on traits in genotype-by-trait biplot model.

Traits were: PH, plant height; CW, canopy width; DH, days to heading; DP, days to pollination; CD, crown diameter; FF, fresh forage weight; DF, dry forage weight; SN, stem number; and SW, seed weight.

The idea of an ideal genotype (Figure 3) permits assessment of the proximity of each genotype to a hypothetical genotype with optimal performance across all traits. Genotypes 24, following 5, 7, and 22, as well as genotypes 6, 23, and 25, were closest to this ideal point, indicating their superior performance. In contrast, genotypes 9, 10, and 11 were located farthest from the ideal position, reflecting weaker trait expression in them.

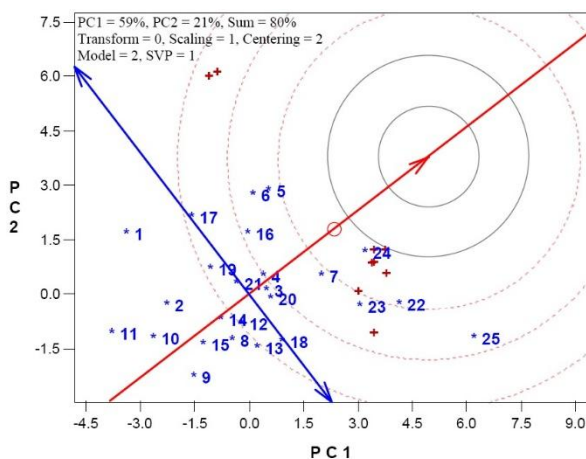


Figure 3. Ranking tall fescue genotypes according to discriminative and representativeness potentials.

Trait discriminative power reflected its ability to differentiate among genotypes and is proportional to its variability (Figure 4). In the current investigation, CD and FF, followed by PH, CW and DF, exhibited the highest discriminative potential,

emphasizing their effectiveness in distinguishing genotype performance. In contrast, DH and DP had the lowest discrimination capabilities, while all measured traits (Figure 4) displayed above-average discriminatory ability. Using such multi-trait indices for detection of the ideotype or ideal genotype as the reference for distance-based ranking is suggested by Behera et al. (2024), where the genotype closest to the ideotype in multi-trait space is considered best. It shows phenological attributes possess relatively weak discriminating power in contrast to morphological attributes and attributes related to yields, thereby playing a negligible part in discriminating between genotypes. This observation further supports the ideological idea of ideology-based breeding, which suggests prioritizing the traits or characters that mostly contribute to the objectives of breeding rather than stressing all the attributes studied. For complex relationships, Multivariate analysis methods become the best tools for comparing different genotypes and help breeders to distinguish the informative characters that play a discriminating role, resulting in faster selection of the best genotypes with the highest potential for agronomic activities.

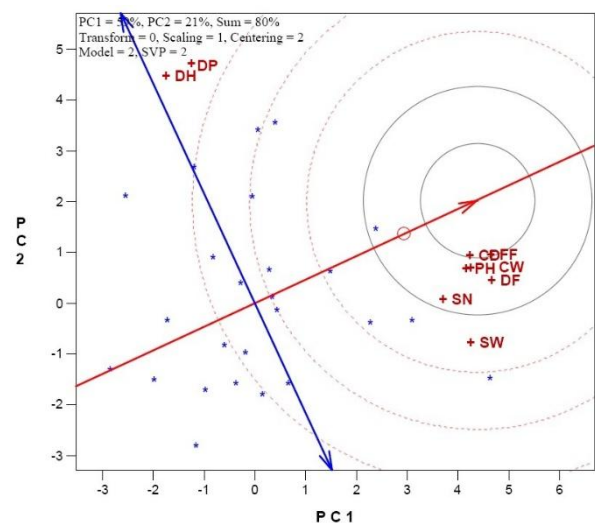


Figure 4. Ranking tall fescue traits based on discriminative and representativeness potentials.

Traits were: PH, plant height; CW, canopy width; DH, days to heading; DP, days to pollination; CD, crown diameter; FF, fresh forage weight; DF, dry forage weight; SN, stem number; and SW, seed weight.

Figure 5 presented the biplot of genotype performance relative to dry forage weight (DF), the primary target trait, whereas the horizontal axis represented DF, with the arrow showing the direction of increasing yield. Genotype 25, followed by genotypes 22, 23, 24, and 7, achieved

the highest dry forage weight, while genotypes 1, 10, and 11 recorded the lowest (Figure 5). The distance of each genotype from the horizontal axis indicated stability; shorter distances denote greater consistency. Accordingly, genotypes 3, 4, and 7 were identified as the most stable, whereas genotypes 5 and 6, despite their above-average DF, displayed high variability and lower reliability.

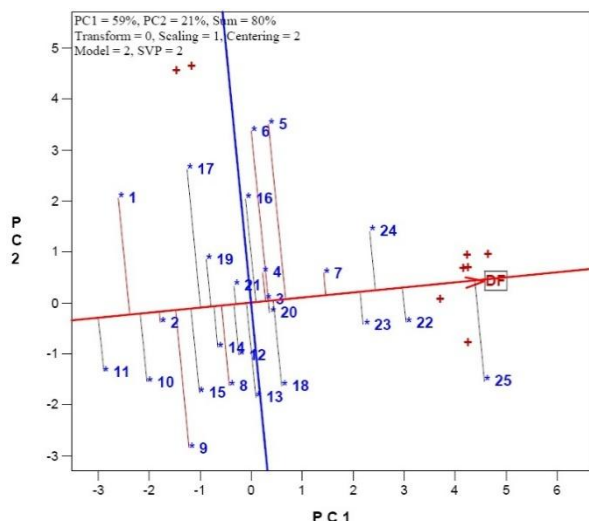


Figure 5. Testing the performance of dry forage weight (DF) across tall fescue genotypes.

The response of genotypes to seed weight (SW) is shown in Figure 6, whereas genotypes 7, 22, 23, 24, and 25 had the highest SW, indicating their good potential for seed yield production, whereas genotypes 1, 2, 10, 11, and 17 showed lower SW. Genotypes 5, 6, and 9 exhibited below-average SW and large distances from the horizontal axis, so they were the most unfavorable genotypes, which indicated high variability and low seed yield performance. These findings confirmed the efficiency of the biplot model in assessing the response of entries to seed yield performance.

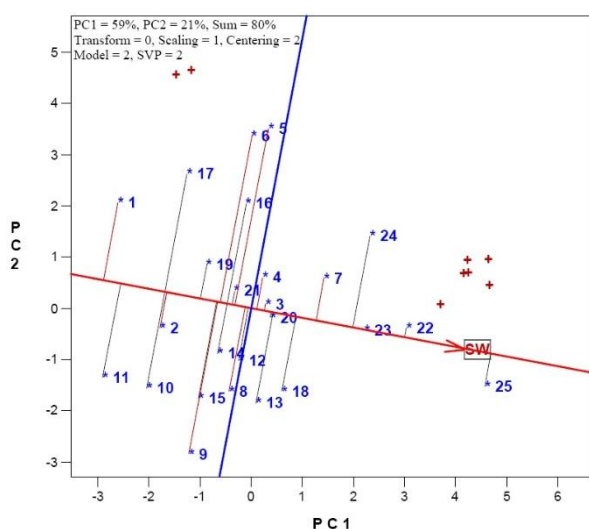


Figure 6. Testing the performance of/at seed weight (SW) across tall fescue genotypes.

Discussion

The current research indicated genetic variation among genotypes for the measured traits, highlighting the potential for selection and improvement in breeding programs targeting both forage and seed yield. Genotype 5 was associated with phenological traits, whereas genotype 25 aligned with morphological and yield-related traits. The superior performance of genotype 25 (cultivar Bonsai) across multiple yield-related traits suggested its potential as an advising cultivar for semi-arid regions and as a donor of favorable alleles in breeding programs. In contrast, genotypes 1, 9, 11, and 24 were not associated with high performance for any of the traits, showing the genetic variability in this germplasm and providing a basis for selection. The disparate genotype groups revealed by the GT biplot suggest heterogeneity between the different tall fescue materials. Genotypes in the different groups likely represent different parental contributions, and they may be evaluated in subsequent crosses in an effort to assess combining ability and possible heterotic effect.

The observed associations between morphological traits confirmed their utility as indirect selection criteria in tall fescue. Specifically, plant height, canopy width, crown diameter, and stem number showed strong correlations with fresh and dry forage yield performances. These results were consistent with findings from Wassie et al. (2018) and Tubritt et al. (2020), who found that morphological parameters significantly contribute to forage yield in perennial grasses. Similarly, Rahimi et al. (2020) demonstrated that plant height, stem number, and canopy width are positively associated with dry forage yield, suggesting that these traits can serve as reliable selection indices for early-generation screening. The current study confirmed that morphological traits play a significant role in increasing forage production potential, as the genotypes with the favorable traits, especially genotype 25, generally yielded better. This means that targeting morphological and yield-related traits through breeding methods may be more effective to enhance selection toward higher production yield. On the other hand, phenological traits revealed weak or no significant association with forage and seed yield, signifying that the variations in phenological traits were not the driving forces behind high yield production in the current germplasm of tall fescue under semi-arid conditions, similar to that previously performed on some populations of tall fescue assessed under semi-arid conditions (Żurek et al., 2018). However,

it is important to note that phenological traits also have a direct impact on environmental adaptation as they can modulate the length of the growing season, time for avoiding environmental stresses, and adaptation of performance to the season. Accordingly, using phenological traits for improving the yielding potential of the plant could be unreliable, whereas, in association with morphological and production-related traits, could serve to provide better results.

Strong positive correlations were observed among DF, FF, PH, CW, and CD, indicating that taller plants with broader canopies and larger crowns tend to accumulate greater biomass. Moderate positive associations were observed between SN and SW with the main morphological traits, suggesting that while stem number and seed weight contribute to yield, their influence is not as pronounced as that of other structural traits. These findings support the view that biomass accumulation in tall fescue is primarily driven by plant architecture rather than reproductive phenology (Kandel et al., 2016), and that morphological traits can serve as efficient predictors of forage yield. The genotypes that were the closest to the ideal point were genotypes 24, 5, 7, 22, 6, 23, and 25, which means that the combined characteristics are the most appropriate and desirable ones for the characteristics we analyzed, which allows breeders to integrate multiple traits simultaneously, facilitating ideotype-oriented selection. Similar methodologies have been applied in forage breeding programs to prioritize genotypes with balanced trait combinations, accelerating genetic gains (Kaplan et al., 2017). According to ideotype-based selection, a genotype with high plant height but low stem number may underperform in terms of biomass accumulation compared to a more balanced genotype. By such analysis, breeders can identify genotypes that not only perform well for individual traits but also exhibit harmonious combinations of structural and yield components, increasing the likelihood of generating superior progeny. In the current study, CD and FF exhibited the highest discriminative potential, followed by PH, CW, and DF, while DH and DP were the least discriminative. These results indicated that morphological traits were more informative for genotype differentiation and selection than phenological traits, aligning with prior research on multi-trait selection in forage

grasses (Behera et al., 2024). The high discriminatory power of morphological traits reinforced their use as early selection criteria, enabling breeders to efficiently screen large germplasm collections before conducting more resource-intensive evaluations of biomass or seed yield.

Genotype comparison in relation to the target traits such as DF was conducted through GT biplot analysis, with DF being selected as the main yield performance-related index, particularly for dry forage weight (DF), the primary target trait. Genotype 25 achieved the highest DF, followed by genotypes 22, 23, 24, and 7. Also, the correlation between morphological traits and DF suggested that early selection based on traits such as PH, CW, and CD can improve efficiency by identifying promising genotypes before extensive forage yield measurements. However, the non-additive genetic control and potentially low heritability of DF (Pirnajmedin et al., 2022) suggested that breeding strategies should also incorporate heterosis, combining ability, or family-based selection to maximize gains in biomass production. Seed weight (SW) analysis demonstrated variation among genotypes, with genotypes 7, 22, 23, 24, and 25 achieving the highest SW, indicating strong potential for seed yield. These results are consistent with past investigations reporting significant genotypic variation for seed yield in tall fescue (Ahmed & Escobar-Gutiérrez, 2022). Including SW as a selection criterion in breeding programs is particularly valuable for seed multiplication efforts, where consistent and high-quality seed yield is essential. Also, the positive association between SW and other morphological traits supported the use of indirect selection for seed yield, leveraging easily measurable vegetative traits to predict reproductive performance.

Ahn et al. (2023) mentioned that the ideal genotype concept offers a tool in ideotype breeding to manage multiple trait objectives within a single selection index. In this study, a graphical multivariate method for simultaneously considering genotypes on performance as well as differentiation of attributes could distinguish favorable genotypic combinations, supporting Selection of genotypes with appropriate combinations for an effective selection strategy based on both individual performance and traits' differentiability. This approach emphasizes the

balance of multiple attributes, as in a forage breeding program, total yield of forage would result from some interactions among traits (plant height, canopy width, crown diameter, dry forage yield, and biomass). GT biplot analysis of morphological traits might help breeders in recognizing a group of the selected genotypes with superior characteristic traits to continue further study, to establish as well as integrate these selected varieties for a breeding program. Morphological attributes were useful in discriminating genotypes as they were closely related to forage yield; thus, selecting genotypes based on these traits in an early step may be sufficient instead of evaluating very long lists of selection candidates based on dry forage performance tests. However, dry forage yield was a qualitative trait that might be influenced by non-additive gene action and, often, it has a very low heritability (Pirmajmedin et al., 2022), so breeders must also evaluate combined abilities, progeny selection, or family-based approaches to get highly accurate selection. The significant variation that was observed between genotypes is in agreement with many authors reporting higher variability in seed yield performance for many grass species, including the tall fescue genotype (Shahabzadeh et al., 2020; Ahmed & Escobar-Gutierrez, 2022). Since seed weight and its other traits as constituents have a moderate heritability, the selection of superior genotypes by using seed weight combined with stable yield performance will certainly improve efficiency for seed multiplication of improved lines (Guidalevich et al., 2025). Thus, seed weight also should be taken into account when forage grasses are managed as a seed production crop for further establishment.

The findings of the current study have several important implications for tall fescue breeding. Firstly, the identification of genotypes with favorable combinations of morphological and yield-related traits, particularly genotypes 25, 22, 23, 24, and 7, provided candidates for inclusion in breeding projects. Secondly, the founded correlations among morphological traits and yield components supported the use of indirect selection, enabling breeders to prioritize traits with high discriminative ability and strong influence on biomass or seed yield. Thirdly, the ideotype-based and multi-trait biplot approaches facilitated holistic

assessment, integrating performance and trait harmony, which is particularly valuable for complex traits influenced by non-additive effects. While some genotypes may exhibit high yield, their variability may limit their utility in breeding programs. Breeders will be able to improve accuracy in selection and increase the chance of getting better material by knowing which genotype(s) always have the same excellent combination of traits in the environment tested. The results obtained from this research can be used to assist tall fescue breeding. The identified promising genotypes 25, 22, 23, 24, and 7 had desirable morphological and yield performance, and these genotypes could be used as germplasm for further evaluation. Since morphological characteristics are highly correlated with forage yield, they can be used for indirect selection to improve forage yield efficiency through efficient screening of germplasm. It is also advantageous that this study allows the evaluation of genotype performance as well as relationships between traits using a combination of the GT biplot analysis and the ideotype approach simultaneously for complicated traits like forage and seed production performance to improve the selection of new varieties.

Conclusion

The biplot modeling of 25 tall fescue genotypes provided comprehensive insights into genotype performance, trait interrelationships, and selection potential. Morphological traits, PH, CW, CD, and SN, were associated with forage yield and exhibited high discriminative ability, while phenological traits were less informative. Genotypes 25 (cultivar Bonsai), 22 (Genotype Hunejan), 23 (Unknown Iranian genotype), 24 (Unknown Iranian genotype), and 7 (Unknown Iranian genotype) emerged as superior performers for both forage and seed yield, with favorable trait combinations. The ideotype-based approach facilitated the identification of genotypes with balanced multi-trait performance, supporting targeted selection in breeding programs.

Acknowledgement

The authors gratefully acknowledge Dr. W. Yan (Agriculture and Agri-Food Canada) for providing access to the GGEbiplot software.

References

- Ahmed, L.Q., & Escobar-Gutiérrez, A. J. (2022). Tall fescue (*Festuca arundinacea* Schreb.) shows intraspecific variability in response to temperature during germination. *Agronomy*, 12(5), 1245. <https://doi.org/10.3390/agronomy12051245>
- Ahn, E., Botkin, J., Curtin, S.J., & Zsögön, A. (2023). Ideotype breeding and genome engineering for legume crop improvement. *Current Opinion in Biotechnology*, 82, 102961. <https://doi.org/10.1016/j.copbio.2023.102961>
- Baert, J., & Van Waes, C. (2014). Improvement of the digestibility of tall fescue (*Festuca arundinacea* Schreb.) inspired by perennial ryegrass (*Lolium perenne* L.). *Grass and Forage Science*, 19, 172-174. <https://B2n.ir/mb8293>
- Behera, P.P., Singode, A., Bhat, B.V., Ronda, V., Borah, N., Verma, H., & Sarma, R.N. (2024). Genetic gains in forage sorghum for adaptive traits for non-conventional area through multi-trait-based stability selection methods. *Frontiers in Plant Science*, 15, 1248663. <https://doi.org/10.3389/fpls.2024.1248663>
- Biligtu, B., Schellenberg, M.P., McLeod J.G., & Wang Z. (2013): Seed yield variation in plains rough fescue (*Festuca hallii* (Vasey) Piper) populations and its relation with phenotypic characteristics and environmental factors. *Grass and Forage Science*, 68(4), 589-595. <https://doi.org/10.1111/gfs.12012>
- Caradus, J.R., & Chapman, D. (2025). Evaluating pasture forage plant breeding achievements: a review. *New Zealand Journal of Agricultural Research*, 68(6), 1146-1220. <https://doi.org/10.1080/00288233.2024.2395370>
- Ebrahimi, H., Sabaghnia, N., Javanmard, A., & Abbasi, A. (2023). Genotype by trait biplot analysis of trait relations in safflower (*Carthamus tinctorius* L.) at seedling stage. *Agrotechniques in Industrial Crops*, 3(2), 67-73. <https://doi.org/10.22126/atic.2023.8906.1086>
- Farmanpour-Kalalagh, K., Mohebodini, M., Sabaghnia, N., & Janmohammadi, M. (2025). Biplot analysis of the genetic variation in the essential oil profile of Iranian landraces of *Anethum graveolens*. *Biologija*, 71(4), 276-288. <https://doi.org/10.6001/biologija.2025.71.4.2>
- Guidalevich, V., Berro, I., Aparicio, A.G., Azpilicueta, M.M., López, A.S., Arias-Rios, J.A., & Marchelli, P. (2025). Genetic variation and heritability of agronomic traits in a native perennial forage species from drylands: breeding potential of *Festuca pallescens*. *Scientific Reports*, 15(1), 6896. <https://doi.org/10.1038/s41598-025-90875-7>
- Insua, J.R., Agnusdei, M.G., Utsumi, S.A., & Berone, G.D. (2018). Morphological, environmental and management factors affecting nutritive value of tall fescue (*Lolium arundinaceum*). *Crop and Pasture Science*, 69(11), 1165-1172. <https://doi.org/10.1071/CP18182>
- Kandel, T.P., Elsgaard, L., Andersen, M.N., & Lærke, P.E. (2016). Influence of harvest time and frequency on light interception and biomass yield of *festulolium* and tall fescue cultivated on a peatland. *European Journal of Agronomy*, 81, 150-160. <https://doi.org/10.1016/j.eja.2016.09.010>
- Kaplan, M., Arslan, M., Kale, H., Kara, K., & Kökten, K. (2017). GT biplot analysis for silage potential, nutritive value, gas and methane production of stay-green grain sorghum shoots. *Ciencia e Investigación Agraria*, 44(3), 230-238. <https://doi.org/10.7764/rcia.v44i3.1802>
- Lou, Y., Chen, L., Xu, Q., & Zhang, X. (2015). Genotypic variation of morphological traits in tall fescue (*Festuca arundinacea* Schreb.) accessions. *Hortscience*, 50(4), 512-516. <https://doi.org/10.21273/HORTSCI.50.4.512>
- Majidi, M.M., Mirlohi, A., & Amini, A. (2009). Genetic variation, heritability and correlations of agro-morphological traits in tall fescue (*Festuca arundinacea* Schreb.). *Euphytica*, 167(3), 323-331. <https://doi.org/10.1007/s10681-009-9887-6>
- Mohebodini, M., Sabaghnia, N., & Janmohammadi, M. (2024). Evaluation of phenotypic variation in some black cumin (*Nigella sativa* L.) landraces using the genotype by trait biplot model. *Journal of Organic Farming of Medicinal Plants*, 3(1), 7-15. <https://www.sid.ir/paper/1820478/en>
- Pirnajmedin, F., Majidi, M.M., Taleb, M.H., & Rostami, D. (2022). Genetic parameters and selection in full-sib families of tall fescue using best linear unbiased prediction (BLUP) analysis. *BMC Plant Biology*, 22(1), 293. <https://doi.org/10.1186/s12870-022-03675-w>
- Pirnajmedin, F., Majidi, M.M., & Gheysari, M. (2016). Survival and recovery of tall fescue genotypes: association with root characteristics and drought tolerance. *Grass and Forage Science*, 71(4), 632-640. <https://doi.org/10.1111/gfs.12231>
- Pirnajmedin, F., Majidi, M.M., & Safari, M. (2025). Genetic analysis of forage, seed, and turf quality in tall fescue: Unraveling inheritance patterns and interrelationships.

- Crop Science*, 65(1), e21447. <https://doi.org/10.1002/csc.2.21447>
- Rad, E.B., Mesdaghi M., Ahmad, N., & Abdullah, M. (2015). Nutritional quality and quantity of available forages relative to demand: a case study of the goitered gazelles of the Golestan National Park, Iran. *Rangelands*, 37(2), 68-80. <https://www.sciencedirect.com/science/article/pii/S0190052815000139>
- Rahimi, E., Mohammadi, R., Pourmohammad, A., & Aliloo, A. A. (2020). Identification of Effective Traits on Forage Yield in Tall Fescue (*Festuca arundinacea* Schreb.). *Plant Productions*, 43(3), 419-430. <https://doi.org/10.22055/ppd.2019.28151.1704> [In Persian]
- Sabaghnia, N., Moayed, F., & Janmohammadi, M. (2024). Assessment of genetic variation in sainfoin landraces based on agronomic characteristics using a genotype by trait biplot model. *Iranian Journal of Genetics and Plant Breeding*, 13(1), 51-59. <https://doi.org/10.30479/ijgpb.2024.20998.1381>
- Sabaghnia, N., Pourmohammad, A., Sayad, Y., & Fotouhi, K. (2026). Biplot analysis of morphological, quality, and disease resistance traits in sugar beet hybrids. *Agriculture and Forestry*, 72(2), 217-231. <https://www.agricultforest.ac.me/data/20260525-14%20Sabaghnia%20et%20al.pdf>
- Saha, M.C. (2014). Tall Fescue. In H. Cai, T. Yamada & C. Kol (Eds.), *Genetics, genomics and breeding of forage crops* (pp. 58-89). CRC Press. <https://doi.org/10.1201/b15564>
- Satognon, F. (2024). Advancements in tall fescue (*Festuca arundinacea*) in the US: origin, American introduction, development, and improvement. *Journal of Crop Improvement*, 38(6), 665-687. <https://doi.org/10.1080/15427528.2024.2389456>
- Sayar, M.S., Basbag, M., Cacan, E., & Karan, H. (2022). The effect of different cutting times on forage quality traits of alfalfa (*Medicago sativa* L.) genotypes and evaluations with biplot analysis. *Fresenius Environmental Bulletin*, 31(8), 9178-9190. <https://B2n.ir/gb6590>
- Shahabzadeh, Z., Mohammadi, R., Darvishzadeh, R., Jafari, M., & Alipour H. (2020). Investigation of genetic diversity of forage yield and morphological traits in tall fescue (*Festuca arundinacea* Schreb.) populations. *Iranian Journal of Rangelands and Forests Plant Breeding and Genetic Research*, 28(1), 17-36. <https://doi.org/10.22092/ijrfpbgr.2020.342243.1363> [In Persian]
- Shanjani, P.S., Rasoulzadeh, L., & Javadi, H. (2023). Evaluation of morphological traits in the populations of *Coronilla varia* L. *Journal of Rangeland Science*, 13, 52-71. <https://oiccpres.com/jrs/article/view/2375>
- Sun, J., Meyer, W., Cross, J., & Huang, B. (2013). Growth and physiological traits of canopy and root systems associated with drought resistance in tall fescue. *Crop Science*, 53(2), 575-584. <https://doi.org/10.2135/cropsci2012.05.0292>
- Tate, T.M., Cross, J.W., Wang, R., Bonos, S. A., & Meyer, W.A. (2023). Inheritance of summer stress tolerance in tall fescue. *Grass Research*, 3, 14. <https://www.maxapress.com/article/doi/10.48130/GR-2023-0014?viewType=HTML>
- Tubritt, T., Delaby, L., Gilliland, T. J., & O'Donovan, M. (2020). The relationship between the grazing efficiency and the production, morphology and nutritional traits of perennial ryegrass varieties. *The Journal of Agricultural Science*, 158(7), 583-593. <https://B2n.ir/wx5274>
- Vega, D.J., di Santo, H.E., Ferreira, V.A., Castillo, E.A., Bonamico, N.C., & Grassi, E.M. (2021). Evaluación fenotípica de poblaciones de *Festuca arundinacea* Schreber naturalizadas en ambientes subhúmedos semiáridos. *Cienciay Tecnología Agropecuaria*, 22(2), e1814. <http://revistacta.agrosavia.co/index.php/revista/article/view/1814>
- Waldron, B.L., Jensen, K.B., Peel, M.D., & Picasso, V.D. (2021). Breeding for resilience to water deficit and its predicted effect on forage mass in tall fescue. *Agronomy*, 11(11), 2094. <https://doi.org/10.3390/agronomy11112094>
- Wang, Q., Hu, T., Cui, J., Wang, X., Zhou, H., Han, J., & Zhang, T. (2011). Modelling of seed yield and its components in tall fescue (*Festuca arundinacea*) based on a large sample. *African Journal of Biotechnology*, 10(59), 12584-12594. <https://academicjournals.org/journal/AJB/article-full-text-pdf/BBEEC6B33084.pdf>
- Wassie, W.A., Tsegay, B.A., Wolde, A.T., & Limeneh, B.A. (2018). Evaluation of morphological characteristics, yield and nutritive value of *Brachiaria* grass ecotypes in northwestern Ethiopia. *Agriculture and Food Security*, 7(1), 89. <https://doi.org/10.1186/s40066-018-0239-4>
- Yan, W., & Rajcan, I. (2002). Biplot analysis of test sites and trait relations of soybean in Ontario. *Crop Science*, 42(1), 11-20. <https://doi.org/10.2135/cropsci2002.1100>
- Żurek, G., Prokopiuk, K., Martyniak, D., Rachwalska, A., Paszkowski, E., Woźna-

Pawlak, U., & Jurkowski, M. (2018). Seed yield and its components in three *Festuca* species. *Plant Breeding and Seed Science*, 77, 15-31. <https://www.cabidigitallibrary.org/doi/full/10.5555/20203478633>