

# Inheritance of Summer Dormancy, Persistence and Productivity Using Half-sib Matting in Tall Fescue

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## Research article

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# **Inheritance of summer dormancy, persistence and productivity using half-sib matting in tall fescue**

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## **Abstract**

**Background:** The genetic basis and variability of persistence and summer dormancy and their association with forage production traits has been less investigated in tall fescue.

**Results:** High genotypic variation was found for all the measured traits in both parental genotypes and half-sib families. Incomplete summer dormancy was found for most of the evaluated genotypes. Summer dormancy index were negatively correlated with forage production and yield related traits. Half-sib families had higher persistence than parental genotypes, which can be due to the heterosis expression in progenies. Moderate narrow-sense heritability for persistence indicates that both additive and dominant gene action may play a role in the expression of this trait. Yield-related traits and summer dormancy showed moderate to high estimates of narrow sense heritability (0.63-0.73) indicates additive gene action for these traits. This suggest phenotypic recurrent selection can be successful to achieve genetic progress.

**Conclusion:** In conclusion, our results can enhance the knowledge of inheritance of summer dormancy and related traits which would be useful for future genetic studies. Based on the general combining ability and application of multivariate analysis, preferable genotypes for forage use (such as 21M and 1E) and turf application (such as 17M and 4E) were identified for future programs.

**Keyword:** Tall fescue, Persistence, Summer dormancy, Heritability, Polycross

## Background

The changes concerning rainfall distribution and its scarcity, increased drought, and global heating are considered as a major obstacle to agriculture production [1]. Many areas of the world face the challenge of heat and drought stresses during the summer, where the maximum daily temperatures can exceed 40C° [2, 3]. In many regions, grasslands are the major forage resources for animal farming and complementary forage crops are crucial to secure farming systems and increase productivity and stability of animal production. This emphasizes the need for plant species or genotypes that are able to persist and have favorable productivity under this condition. Among perennial species that can be used to create sustainable and persistent forage crops, tall fescue is of high interest because of wide distribution with a great genetic diversity [4-6].

Biomass productivity and persistence in grasses are the results of a complex combination of many variables that affect plant growth all over the growing periods. Persistence is defined as an ability to maintain a viable crown at the soil surface from which growth regenerates and to produce consistent high forage yield across several growing seasons [7, 8]. The difference in performance throughout the years can give an idea of persistence, especially in spaced plant material [9]. Besides, it is assumed to be linked with summer dormancy over successive summer droughts [10].

Summer dormancy is acknowledged as a combination of processes endogenously controlled that lead to cessation of leaf growth, senescence and reduction of herbage under non-limiting growth conditions in summer [11]. This trait express under subsequent long photoperiods and high temperatures of summer under full irrigation conditions [12]. The trait has been associated with summer survival and fast recovery following severe summer drought stress in most grass species [10, 12, 13]. Dormancy enables plant survival by reducing water loss and reallocation of energy and storage in meristems to keep the plant alive and to support regrowth [14-16]. Therefore, the correct recognition and ranking of the expression of summer dormancy have substantial implications for the management and improvement of perennial grass species. Several summer dormancy indices have been recommended based on comparison with control cultivars with a known level of summer dormancy in order to identify the level of dormancy in plants [11, 13].

Information on the inheritance and nature of genetic variability and correlation among traits requires for improving the efficiency of breeding programs and selecting superior genotypes [17]. In most forage species, half-sib mating such as topcross, polycross, and open-pollination are widely used to obtain quantitative genetic information in grasses [18]. Since genetic variance among half-sib families created by polycross or open-pollination is essentially equal with the additive genetic variance, estimation of genetic parameter based on half-sib family evaluation gives a good prediction of narrow-sense heritability [19, 20]. The heritabilities of different agro-morphological traits have been estimated in some forage grass species using various design and biometrical methods. Most of these studies reported low to a moderate value of heritability for forage yield and moderate to high values for yield-related traits such as plant height, crown diameter, and the number of stems per plant [21-24].

Little information is still available on genetic analysis of summer dormancy and persistence and their contribution to forage production of tall fescue. The current study aimed (1) to evaluate the genetic variation of tall fescue genotypes for agro-morphological traits, persistence, and summer dormancy, (2) to estimate inheritance, general combining ability, and the relationship of different traits, and (3) to identify suitable genotypes for the future programs.

## Results

### Analysis of variance and mean comparison of traits

Analysis of variance revealed that the effect of the genotype (parental genotype and half-sib families) and year were significant for all measured traits (Table S1).

In both parental and half-sib populations, the highest values of forage production were observed in the third year when compared with the second and fourth year (Fig. 1). After the establishment year (First year), spring cut had the highest values of dry forage yield in both parental genotypes and half-sib families during 3 years (2017-2019) (Fig. 1).

The values of summer dormancy index (SDI) and mean dry forage yield (MDFY) during the four years of the experiment are given in Table 3. The range of SDI was from 6.75 to 25.16 and from 1.78 to 8.49 in parental genotypes and half-sib families, respectively (Table 3). Mean dry forage yield in parental genotypes ranged from 21.07 to 58.20 and in half-sib families ranged from 79.84 to 256.65 (Table 3). Parental genotypes 3E, 4E, and 17M had the highest value of SDI and genotypes 1E and 21M had the highest value of MDFY. In contrast, genotypes 1E and 21M had the lowest value of SDI and genotypes 3E, 17M, and 4E had the lowest value of MDFY (Table 3). In half-sib families, 4E and 17M had the highest value of SDI and lowest value of MDFY. The lowest value of SDI and highest value of MDFY were identified for families 1E and 21M (Table 3).

The degree of persistence varied greatly between and within both parental genotypes and half-sib families (Fig. 2). Three out of sixteen parental genotypes had negative persistence, while none of the half-sib families had negative persistence (Fig. 2). Parental genotypes 1E and 21M showed higher values of persistence and genotypes 6L, 14E, and 3M showed lower values of this trait (Fig. 2). In half-sib families, the highest value of persistence was observed for families 17M and 4E, and the lowest one belonged to families 14E and 11M (Fig. 2).

### Narrow-sense heritability ( $h_n^2$ ) and general combining ability (GCA)

The range of estimated narrow-sense heritability was from 0.49 for autumn dry forage yield (AUDFY) to 0.73 for crown diameter (CD) (Table 4). The narrow-sense heritability values for persistence (Persis) and summer dormancy index (SDI) were 0.54 and 0.63, respectively (Table 4). The heritability of yield related traits consisted of plant height (PH), the number of stems per plant (NS), and CD was greater than the heritability of spring, summer and autumn dry forage yield (Table 4).

The results of general combining ability (GCA) showed a broad range of GCA for all evaluated traits (Table S2). The highest GCA for ADFY, PH, CD, and NS was observed for genotypes 1E and 21M and the lowest ones belonged to genotypes 17M and 4E (Table S2). Genotypes

1E and 21M had lower GCA for SDI in compared with the genotypes 17M, 4E and 1M (Table S2). The highest GCA for flowering time (FLO) was identified for genotypes 21M and 12L and the lowest one identified for genotypes 4E and 17M (Table S2). The GCA for persistence (Persis) varied from -271.27 for genotype 14E and to 332.70 for genotype 4E (Table S2).

### **Bi-plot analysis and association among traits**

The result of principal component analysis (PCA) revealed that the first two components justified more than 83% and 85% of the variation in parental genotypes and half-sib families of tall fescue, respectively (Fig. 3). In parental genotypes, the correlation coefficients and the acute angle between the PC vectors of the traits showed that the crown diameter (CD), plant height (PH), number of stems per plant (NS) and persistence (Persis) were positively correlated with dry forage yield at three cuts (Table S3 and Fig. 3). Whereas in half-sib families, CD, PH, and NS had also a positive correlation with dry forage yield at three cuts but, no significant association was observed for these traits with persistence (Table S3 and Fig. 3). In half-sib families, persistence showed a positive correlation with summer dormancy index. It is also remarkable that in both parental and half-sib populations, summer dormancy index was negatively correlated with SPDFY, SUDFY, AUDFY, ADFY, and yield components (Table S3 and Fig. 3). The result of PCA showed that selection based on the high PC1 and low PC2 values would lead to genotypes with high yield productivity, preferable persistence, and low summer dormancy in both parental genotypes and half-sib families. Based on the wide distribution of genotypes on the biplot of PCA, in both parental genotypes and half-sib families, genotypes 1E and 21 M had high values of yield productivity, with favorable persistence and low summer dormancy. In contrast, genotypes 4E and 17M had low values of yield productivity and a high level of summer dormancy (Fig. 3).

### **Discussion**

Productivity, persistence, and summer dormancy of grasses are greatly affected by climate conditions [25-27]; therefore, it is important to evaluate genotypes during consecutive years. In tall fescue breeding, it is important to assess genetic variability and inheritance of important traits such as productivity, persistence, and summer dormancy and identify superior genotypes for breeding programs.

Summer dry forage yield (SUDFY) was found to be lower than spring (SDFY) and autumn dry forage yield (AUDFY) in the evaluated germplasm during the years after establishment. Variation in summer dormancy index suggests low to moderate incomplete summer dormancy in this germplasm. Similar to our results, several researchers have reported the reduction of summer forage yield in some grass species which is likely due to the higher temperature and induction of summer dormancy [10-12; 28-29]. [Volaire and Norton \[15\]](#) and [Norton et al. \[8\]](#) demonstrated that perennial grass species with summer dormancy had less growth and yield production during summer seasons than during autumn and spring seasons despite irrigation, and they have a better chance to persist and recover through periods of extended hot and dry conditions.

In the current study, half-sib families had higher values of persistence than their corresponding parental genotypes. It seems that higher persistence in half-sib families can be due to the

heterosis expression (hybrid vigor) in polycross progenies which can open a new breeding opportunity. Saeidnia et al. [30, 31] documented that open pollination improved persistence in orchardgrass (*Dactylis glomerata* L.), while did not affect this trait in smooth brome grass (*Bromus inermis* L.).

One of the main objectives in the plant breeding programs is studying the inheritance of traits [32]. In the present study, the estimates of narrow-sense heritability for dry forage yield (DFY) were lower than the yield related traits and summer dormancy indices. Moderately high estimates of narrow-sense heritability for flowering time (FLO), summer dormancy index (SDI) and yield components including plant height (PH), crown diameter (CD) and the number of stems per plant (NS), indicated that phenotypic recurrent selection would be effective for these traits. Also summer dormancy had a negative correlation with dry forage yield and moderately positive correlation with persistence. Therefore, phenotyping selection for moderate summer dormancy and high yield components such as CD, PH and NS (positively correlated with DFY) may be effective for indirect selection to increase yield productivity and persistence of this plant, especially in hot regions. The moderate narrow-sense heritability for persistence indicates that both additive and dominant gene effects may control this trait and family recurrent selection might be more effective. Consistent with our findings, some previous studies in different forage grass species such as tall fescue have reported the moderate to high narrow-sense heritability for yield-related trait [22, 33, 34]. Pirnajmedin et al. [35] reported moderate to high values of heritability for persistence (0.54) and summer dormancy index (0.64) in orchardgrass (*Dactylis glomerata* L.). However, little literature is still available on the heritability of summer dormancy index and persistence in different perennial grass species.

Generally, based on the mean comparison of genotypes and biplot of PCA in both parental genotypes and half-sib families, genotypes 21M and 1E with high values of forage production, preferable persistence, and low level of summer dormancy were identified as suitable genotypes for forage use in the high-temperature region. Also, these genotypes had high GCA values for forage yield and its components and low values of GCA for summer dormancy indices. In contradiction, genotypes 17M and 4E had low yield production and a high level of summer dormancy. These genotypes also had high persistence than their parental genotypes. Since in turf grass systems, low forage production and high persistence would be suitable, therefore, these genotypes may be useful for turf application. However, further experiments would be required to assess turf related traits and their association with summer dormancy in this germplasm.

## Conclusion

Considerable genetic variability for yield productivity, its components, persistence, and summer dormancy index indicated that this germplasm has high potential for genetic improvement in tall fescue. The low values of summer forage yield than spring and autumn forage yields, suggest the presence of partial summer dormancy in the evaluated genotypes which confirmed by the range of summer dormancy index. Moderate narrow-sense heritability for persistence and dry forage yields at three cuts indicated that both additive and dominant gene action play an important role in the inheritance of these traits. However, the moderately high narrow-sense heritability for summer dormancy indicates that phenotypic recurrent

selection may be effective. Based on the general combining ability (GCA) and the biplot of PCA, genotypes 21M and 1E were identified as preferable genotypes for forage use in high-temperature region which can be used in other breeding programs. In contrast, genotypes 17M and 4E with low forage productivity and high persistence can be suitable for turf application. Further experiments are needed to assess turf related traits and their association with summer dormancy in this germplasm.

## Methods

### Experimental Site

This study was conducted at the research farm of the Isfahan University of Technology, Isfahan, Iran (32° 30' N, 51° 20' E, 1630 m asl). This area with an average annual precipitation of 122 mm and an average annual temperature of 17 °C faces with high temperatures and dry conditions throughout summers; with usually no rain in summer, irrigation is necessary for growing crops. Monthly temperature and rainfall information during 2016-2019 is given in [Table 1](#). The soil was clay loam (pH 7.5) with an average bulk density of 1.48 g/cm<sup>3</sup> in the top 60-cm layer of the soil surface.

### Plant Materials and Development of Progenies

The primary plant material was including 72 genotypes of tall fescue which were chosen from broad base germplasm and evaluated during 2011-2014 under normal and drought stress conditions at field experiment [[29](#), [36](#)]. From the 72 genotypes, sixteen parental genotypes with different range of forage productivity and more same flowering date were selected ([Table 2](#)). These genotypes were clonally propagated in a greenhouse and then transferred to a polycross field nursery according to a completely randomized block (RCB) design with 12 repetitions in February 2015. In June 2015, seeds from each of the 16 genotypes were harvested at the maturity stage separately and were grown in pots in a greenhouse during the fall and winter of 2016 to produce the 16 half-sib families. The clones of their corresponding parental genotypes along with established seedlings of each half-sib family, and control cultivar of tall fescue with incomplete summer dormancy (Flecha) were space planted in the field in March 2016 and were evaluated under normal irrigation condition according to the RCB design with three repetitions during 2016-2019. Each plot contained 12 clones of each parental genotype and 12 individual plants of each half-sib family, planted in two rows, 45 cm apart, with inter-row plant distance of 40 cm. No limitation of irrigation was conducted during the whole experiment. Irrigation was applied when 45% of the total available water was depleted from the root-zone. [[37](#)].

### Measurements

The above-ground biomass (forage) was harvested at three times in each year. The first harvest was in late spring after flowering, the second and third one was in late summer and autumn to assess complete growth, respectively. At each harvest, the grass was cut from 5 cm above the ground and the weight of dry forage yield per plant was recorded after drying at 72 °C for 48 h. The annual dry forage yield of each year (ADFY) was calculated by the sum of the spring (SPDFY), summer (SUDFY) and autumn (AUDFY) forage yield. Flowering time (FLO),

number of stems per plant (NS) and plant height (PH), and crown diameter (CD) were measured as recommended by Pirnajmedin et al. [29]. Persistence (Persis) was calculated based on the difference of annual forage yield from year four (2019) to year two after establishment (2017) [38].

Summer dormancy was assessed using summer dormancy index (SDI) as follow [13]:

$$\text{SDI} = [(\text{summer yield of Flecha}/\text{summer yield of genotype}) * 100]/10 \quad \text{Eq. (1)}$$

The higher and lower values of SDI indicated the high and low levels of summer dormancy, respectively.

### Statistical Analysis

After normality test, the analysis of variance were performed for all the measured traits using PROC Mixed in SAS v. 9.2 [39]. Variance components were estimated from mean squares of the ANOVA after being equated to their expected variance components [40]. Treatment means were compared using Fisher's LSD test ( $P < 0.05$ ). Narrow sense heritability ( $h^2_n$ ) on a phenotypic mean basis averaged over replications and years was estimated as described by Nguyen and Sleper [40] by the following formula:

$$h^2_n = \frac{\sigma_f^2}{\sigma_f^2 + \frac{\sigma_{fy}^2}{y} + \frac{\sigma_{fr}^2}{r} + \frac{\sigma_e^2}{ry}} \quad (\text{for DFY, PH, CD, NS, FLO, SDI, S/Sndc, and S/Sp traits}) \text{ Eq. (2)}$$

$$h^2_n = \frac{\sigma_f^2}{\sigma_f^2 + \frac{\sigma_e^2}{r}} \quad (\text{for persistence}) \text{ Eq. (3)}$$

where  $\sigma_{fy}^2$  is the family  $\times$  year interaction,  $\sigma_{fr}^2$  is the family  $\times$  replication interaction,  $\sigma_f^2$  is the family and  $\sigma_e^2$  is the residual variance, while r and y represent the replications and year, respectively.

General combining ability (GCA) was calculated as the deviation of the mean of the traits for each HS family from the mean of all families [19]. Principal component analysis (PCA) based on the correlation matrix was performed [41]; Stat Graphics v17.2 was used to create biplots [42].

## **Additional files:**

**Table S1** Analysis of variance for agro-morphological traits and summer dormancy index in parental genotypes (G) and half-sib families (F) of tall fescue assessed during four years (2016-2019). **Table S2** General combining ability (GCA) of measured traits in tall fescue genotypes. **Table S3** Correlation coefficients among traits in parental genotypes (above diagonal) and half sib families.

## **Abbreviations:**

Rep: replication, Y: year, G: parental genotypes, F: half-sib families, SPDFY: spring dry forage yield, SUDFY: summer dry forage yield, AUDFY: autumn dry forage yield, ADFY: annual dry forage yield, PH: plant height, CD: crown diameter, NS: number of stems per plant, FLO: flowering time, SDI: summer dormancy index (summer yield of dormant control cultivar/summer yield) Persis: persistence.

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## **Declarations**

### **Ethics approval and consent to participate**

Not applicable.

### **Consent for publication**

Not applicable.

### **Availability of data and material**

The data sets supporting the results of this article are included within the article and its additional files.

### **Competing interests**

All authors declare that they have no competing interests.

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## **Authors' contributions**

FP, MM, and SAMMM designed the study. FP and HT performed the research. FP analyzed the data and wrote the article. All authors reviewed and approved the manuscript.

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### **Figure legends:**

**Fig. 1.** Spring, summer, autumn and annual dry forage yield in parental genotypes and half-sib families of tall fescue evaluated under normal irrigation condition during 4 years (2016-2019) in the field.

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**Table 1** Information about monthly temperature and rainfall in experiment site during 2016-2019

Year	2016			2017			2018			2019		
	Rainfall (mm)	Min. Temp. (°C)	Max. Temp. (°C)									
Jan.	36.1	-11.6	16.8	2.8	-5.8	17.4	14	-4	9	16	-5.0	20.2
Feb.	8	-11.4	19.2	0.4	-5.2	23.4	14.7	-1.3	11.8	13.7	-3.6	18.4
Mar.	66.5	0	22.6	14	0	23.4	36.9	3.2	16.5	38.7	-2.8	22
Apr.	15.2	4	29	26.8	2.8	30.4	2.9	8	22.3	3.9	4.4	28.6
May	18.4	10.6	36	3.4	9.8	34.9	3.8	12.5	28.4	4.7	10	35.6
June	0	17	42.2	0	16	40.6	0	16.9	39.7	0	18.6	40.6
July	0	19.6	45.6	0	19.8	42.8	0	19.6	44.9	0	16.6	42.2
Ague.	0	16.4	40.2	0	16.8	39.05	0	18	40.7	0	18	39.4
Sep.	0	14.8	36.2	0	11.8	36.4	0.7	13.4	37.3	0.6	10.4	37.8
Oct.	9.1	5.8	32.4	0	6.2	31.8	13.7	8	35.1	14.0	7.4	31.8
Nov.	37.9	-2.8	19.2	0.2	-9.6	25.4	0	2.8	21.1	0	-1.4	20.2
Dec.	0.7	-3.8	16.8	37.3	-4.8	20.4	16.5	-1.5	18.1	17.9	-5.2	21.8

**Table 2** Names and origin of 16 tall fescue genotypes and control cultivar of Flecha (incomplete summer dormant) used in this study

<b>Genotype name</b>	<b>Origin</b>
1E	Iran, Isfahan, Yazdabad
3E	Iran, Isfahan, Mobarake
4E	Iran, Isfahan, Mobarake
9E	Iran, Isfahan, Fozve
10E	USA, New Jersey
14E	Hungary, unknown
1M	Iran, Isfahan, Yazdabad
3M	Iran, Yasuj
11M	Hungary, unknown
17M	Iran, Isfahan, Fozve
21M	Iran, Isfahan, Fozve
22M	Poland, unknown
23M	Poland, unknown
6L	Iran, Isfahan, Daran
12L	Hungary, unknown
20L	Iran, Isfahan, Fozve
Flecha (control cultivar)	Mediterranean

**Table 3** Summer dormancy index and mean dry forage yield in 16 parental genotype and half-sib families of tall fescue evaluated during 2016-2019

<b>Parental genotypes</b>	SDI	MDFY	<b>Half-sib families</b>	SDI	MDFY
<b>21M</b>	8.12	53.48	<b>21M</b>	1.81	240.23
<b>20L</b>	8.67	51.79	<b>20L</b>	2.63	181.96
<b>14E</b>	10.79	42.71	<b>14E</b>	3.03	156.72
<b>23M</b>	12.66	32.38	<b>23M</b>	3.26	149.57
<b>6L</b>	10.62	39.82	<b>6L</b>	4.92	112.58
<b>3M</b>	17.01	29.79	<b>3M</b>	3.81	138.71
<b>22M</b>	16.17	31.86	<b>22M</b>	3.49	145.65
<b>12L</b>	11.62	40.65	<b>12L</b>	2.94	172.82
<b>9E</b>	14.97	34.71	<b>9E</b>	4.14	118.02
<b>11M</b>	8.16	52.11	<b>11M</b>	2.31	205.64
<b>3E</b>	25.16	21.41	<b>3E</b>	3.68	141.17
<b>1M</b>	16.55	30.57	<b>1M</b>	5.58	111.73
<b>10E</b>	14.62	30.69	<b>10E</b>	3.58	152.06
<b>1E</b>	6.75	58.20	<b>1E</b>	1.78	256.65
<b>17M</b>	22.51	21.07	<b>17M</b>	7.51	85.14
<b>4E</b>	24.72	22.86	<b>4E</b>	8.49	79.84
<b>LSD</b>	0.98	1.58	<b>LSD</b>	0.23	4.45

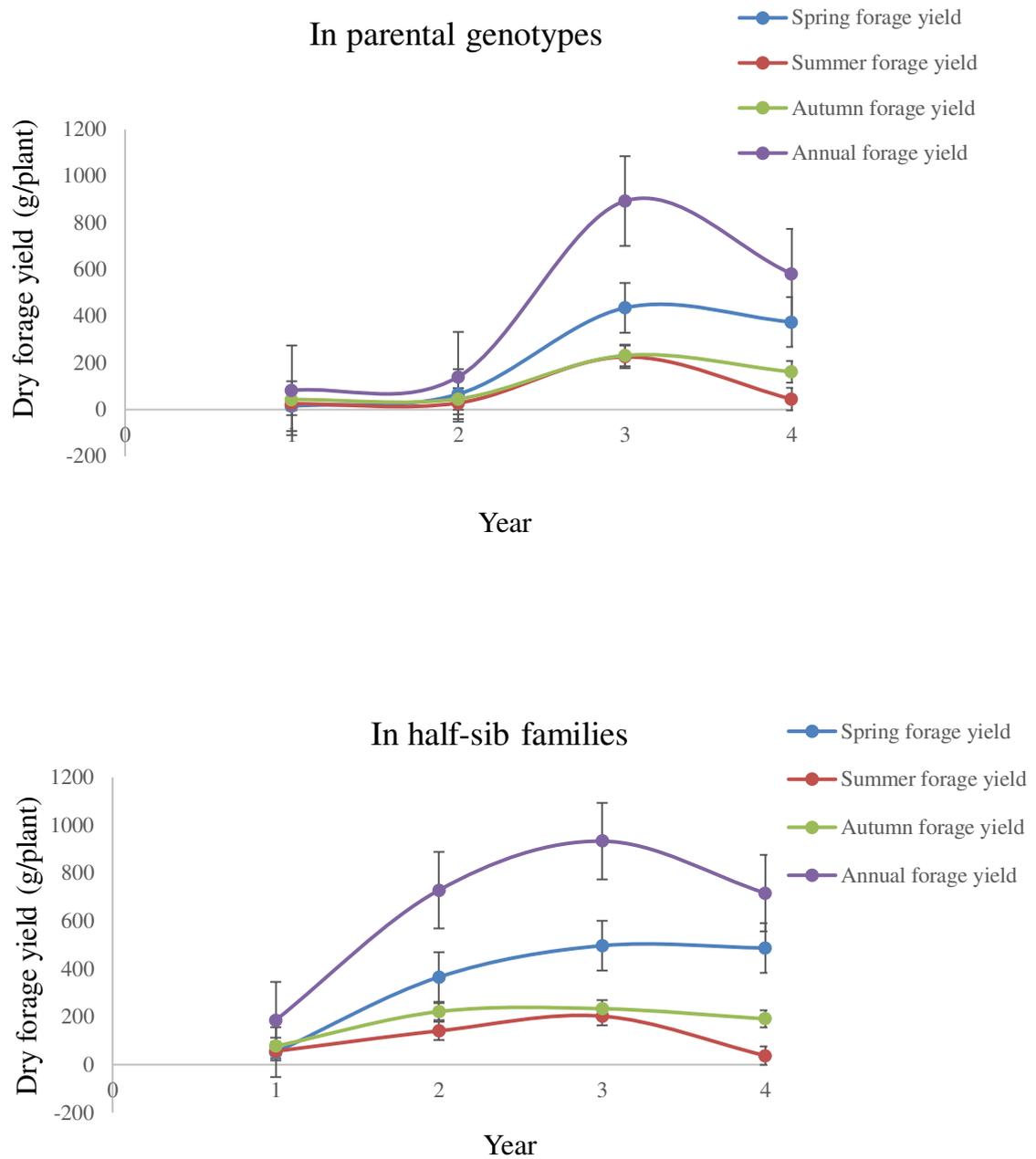
SDI: summer dormancy index (summer yield of dormant control cultivar/summer yield),  
MDFY: mean dry forage yield

**Table 4** Estimate of variance component and narrow-sense heritability of measured traits in half-sib families of tall fescue evaluated during years 2016-2019

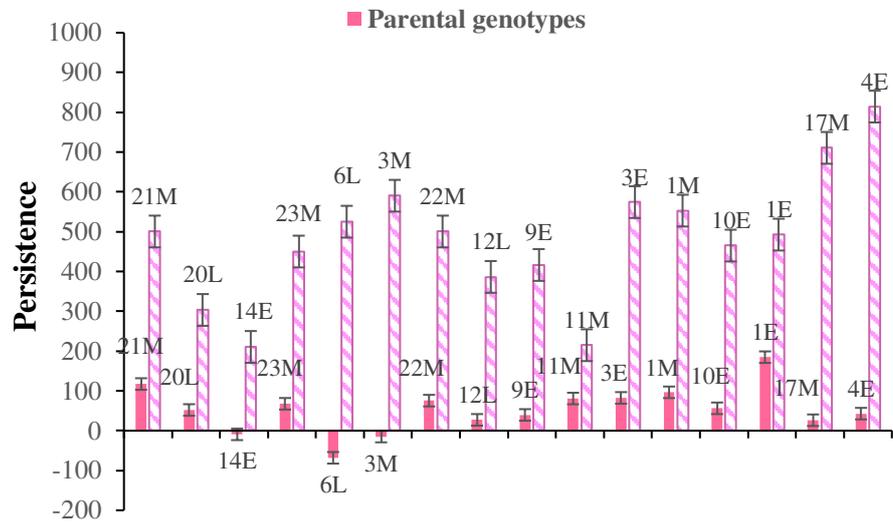
Variance component	$\sigma_f^2$	$\sigma_{fy}^2$	$\sigma_{fr}^2$	$\sigma_p^2$	$h_n^2$
SPDFY	1149.75	2124.6	41.67	2299.12	0.50
SUDFY	627.32	1273.05	246.63	1185.32	0.52
AUDFY	566.80	1663.57	120.58	1146.84	0.49
ADFY	3801.85	4250.09	1730.87	7086.08	0.53
PH	38.49	63.49	0.32	56.44	0.68
CD	6.90	4.88	1.85	9.39	0.73
NS	341.46	375.69	18.45	498.87	0.68
FLO	9.78	10.67	1.23	16.27	0.60
SDI	0.25	0.42	0.03	0.39	0.63
Persis	31559.85	-	-	34599.45	0.54

SPDFY: spring dry forage yield, SUDFY: summer dry forage yield, AUDFY: autumn dry forage yield, ADFY: annual dry forage yield, PH: plant height, CD: crown diameter, NS: number of stems per plant, FLO: flowering time, SDI: summer dormancy index (summer yield of dormant control cultivar/summer yield) Persis: persistence

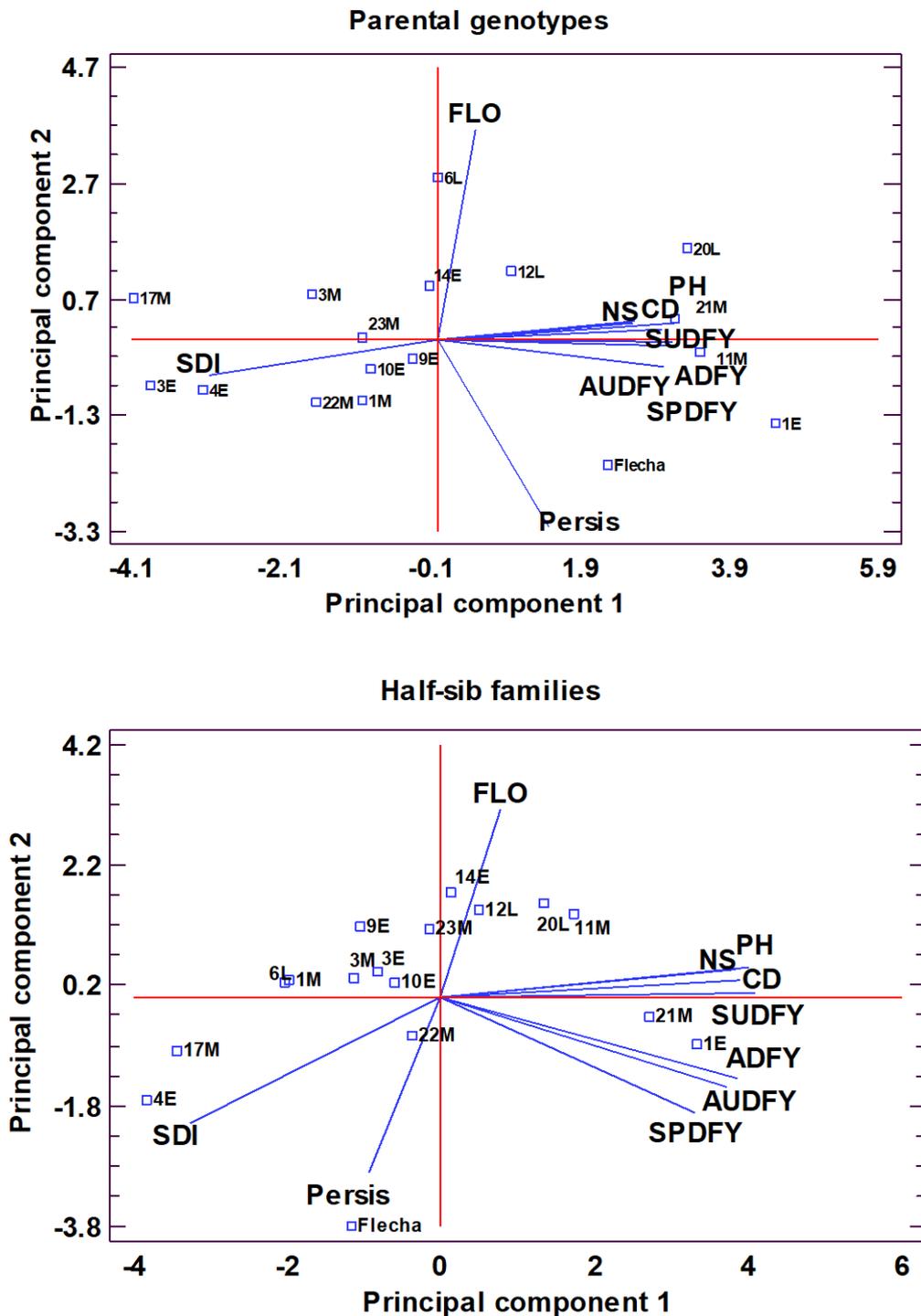
$\sigma_f^2$  family,  $\sigma_{fy}^2$  family  $\times$  year,  $\sigma_{fr}^2$  family  $\times$  replication, and  $\sigma_p^2$  phenotypic variance;  $h_n^2$  narrow-sense heritability.



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**Fig. 2** Persistence of 16 parental genotypes and half-sib families of tall fescue based on the difference of annual dry forage yield from year 4 to year 2 after establishment under normal irrigation condition



**Fig. 3** The biplot display of morphological traits, summer dormancy indices and persistence in parental genotypes and half-sib families of tall fescue. SPDFY: spring dry forage yield, SUDFY: summer dry forage yield, AUDFY: autumn dry forage yield, ADFY: annual dry forage yield, PH: plant height, CD: crown diameter, NS: number of stems per plant, FLO: flowering time, SDI: summer dormancy index (summer yield of dormant control cultivar/summer yield), Persis: persistence. The definition origin of the genotypes can be seen in Table 2.

# Figures

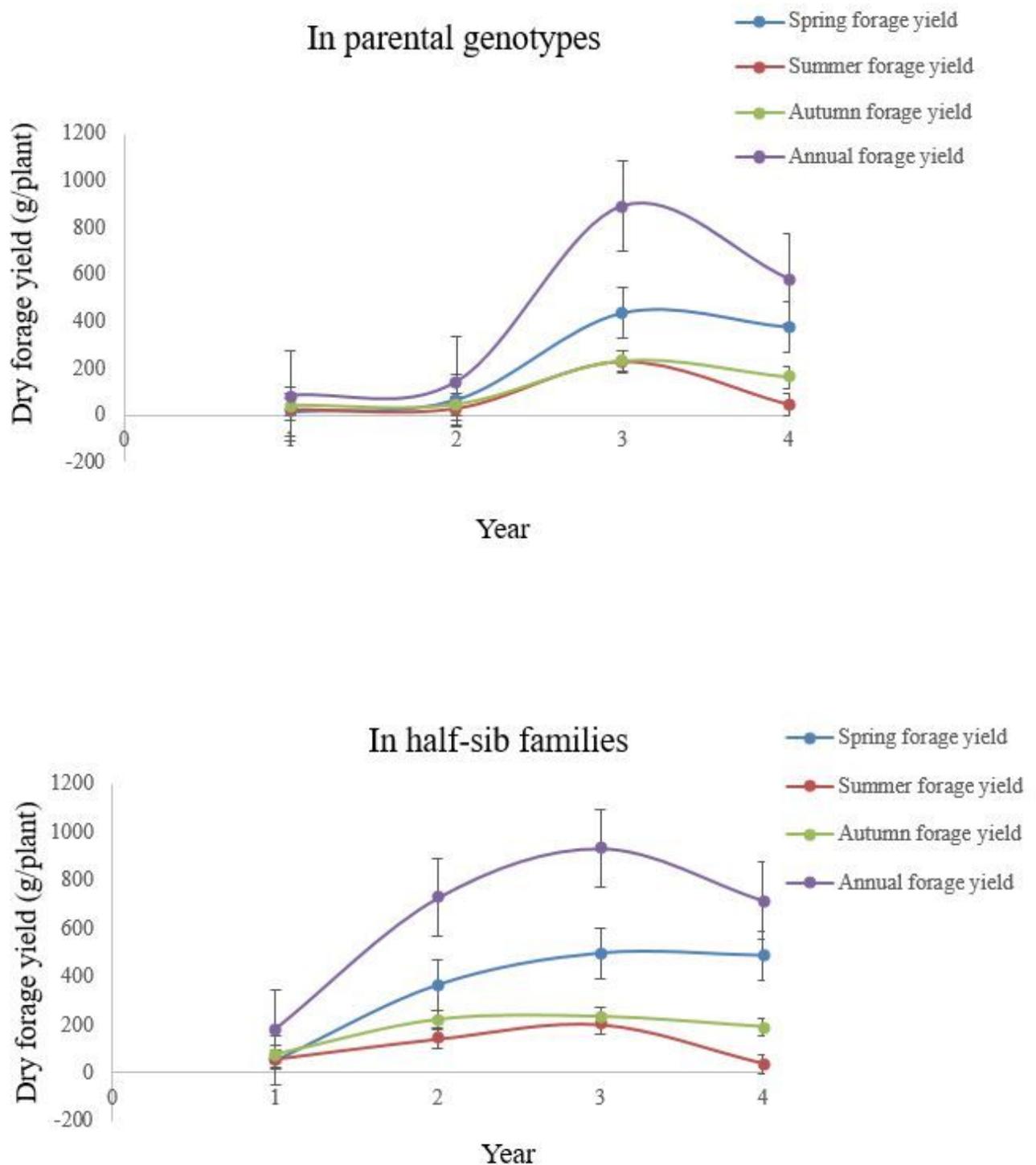
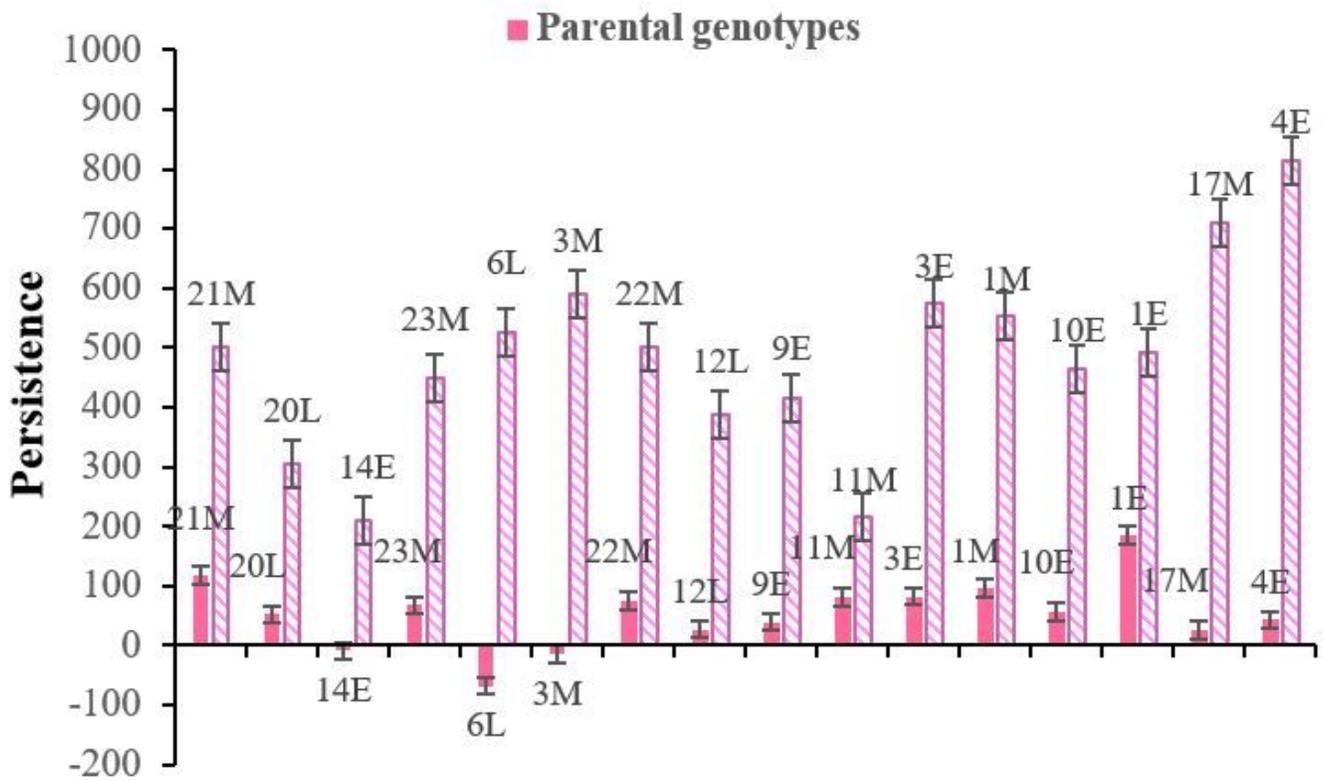


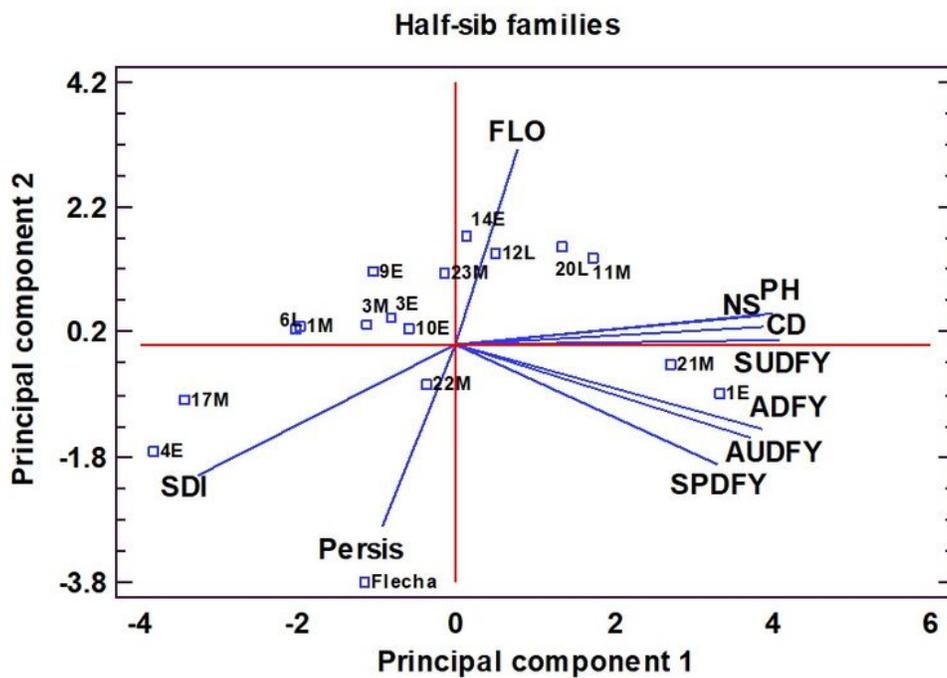
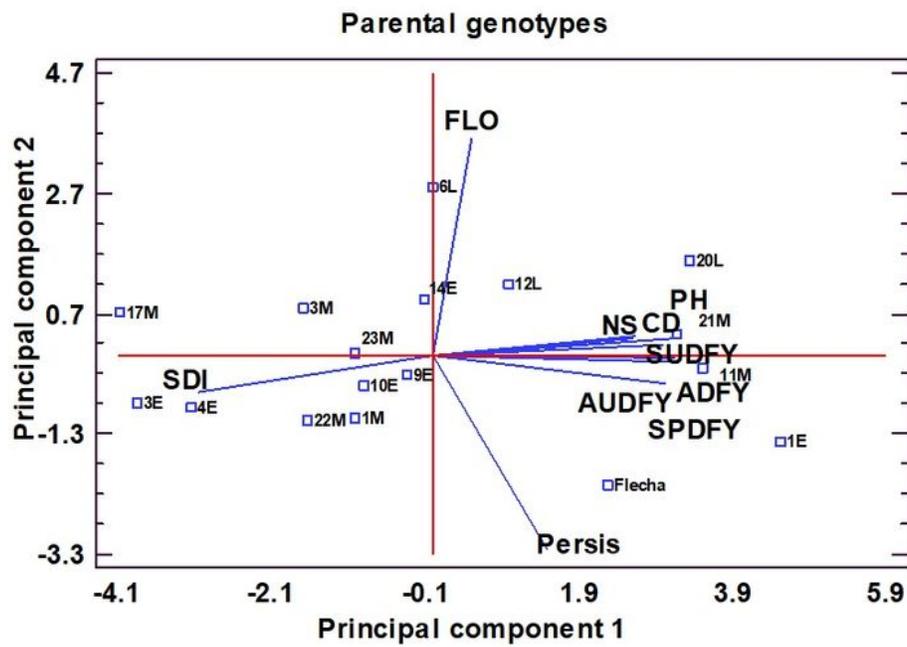
Figure 1

Spring, summer, autumn and annual dry forage yield in parental genotypes and half-sib families of tall fescue evaluated under normal irrigation condition during 4 years (2016-2019) in the field.



**Figure 2**

Persistence of 16 parental genotypes and half-sib families of tall fescue based on the difference of annual dry forage yield from year 4 to year 2 after establishment under normal irrigation condition.



**Figure 3**

The biplot display of morphological traits, summer dormancy indices and persistence in parental genotypes and half-sib families of tall fescue. SPDFY: spring dry forage yield, SUDFY: summer dry forage yield, AUDFY: autumn dry forage yield, ADFY: annual dry forage yield, PH: plant height, CD: crown diameter, NS: number of stems per plant, FLO: flowering time, SDI: Persis: persistence. The definition origin of the genotypes can be seen in Table 2.

## Supplementary Files

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