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Seed yield variation and its relation with phenotypic characteristics in populations of cocksfoot (*Dactylis glomerata*) grown in Hamadan, Iran

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ABSTRACT

In order to study the genetic variation and relationships between seed yield and its components 36 populations of cocksfoot (*Dactylis glomerata* L.), were sown using complete block design with three replications in Hamadan agricultural research station. Iran in 2010. Analysis of variance showed significant differences among populations for dry matter (DM) yield, plant height, seed yield, panicle number, 1000-grain weight, heading date, flowering date, panicle length and harvest index. The estimates of broad sense heritability for the various traits were low to high ($h^2b=0.17$ to 0.90). The results of phenotypic correlation showed a positive correlation between seed yield with DM yield, panicle number and harvest index. Using principal component analysis, the most important variables were identified. The first three independent components accounted for 46, 21 and 10% of total variation. The relative magnitude of eigenvectors from the first principal component axis, indicates that heading date, flowering date, plant height, panicle number, DM yield and panicle length were the important traits for classifying accessions into clusters. From the second principal component axis, seed yield and harvest index were important variables. 1000 grains weight had high eigenvectors in the third principal component axis. Based on Ward clustering method, 36 were grouped into three clusters. Populations in cluster 1 were known as late maturity group couple with lower yield. Populations in clusters 2 were defined as mid season group plus with higher seed production and cluster 3 averaged well above the overall mean for DM yield couple with early maturity. It was concluded that there was moderate to high heritability for most traits in the cocksfoot populations and selection for DM yield could result in increase in seed yield

Key words: Cocksfoot (*Dactylis glomerata*), Seed yield, Correlation, PCA, Cluster analysis

INTRODUCTION

Cocksfoot is naturally growing in rangeland of Zagros and Alborz Mountains area of Iran [12]. Distribution of cocksfoot related to region with altitude of 500 to 3000 m from the sea and precipitation of more than 300 mm [7].

Cocksfoot is growing in range of 12-22°C. The optimum temperature for its growth is 21°C. The habitat growth of cocksfoot will be reduced at over 22°C but it has favorable growth on early spring and late autumn, therefore this species is nominated as cool season-grass [1].

The beneficial economic importance of cocksfoot is in its ability to be high yielding forage for livestock as pasture, hay and silage. It is a commercially available grass because it has high level of palatability when harvested or grazed in the vegetative stage. Its establishment and fast growth are the qualities that make it a high yielding forage crop. These qualities allow it to withstand greater grazing pressure than other grass species [3]

In forage breeding program, the knowledge of correlations between traits of interest is useful in designing an effective breeding program. Complex plant characters, such as yield, are quantitatively inherited and influenced by genetic as well as genotype by environment interaction effects. Therefore, selection for seed yield alone may not be the best criterion to improve seed production. Hence, it is also important to study correlations between agronomic traits, which may have high heritability, and seed yield, which has low heritability [4].

Cocksfoot breeding programs is focused much on improved DM yield, the knowledge of new varieties seed production and its relationships with forage yield are very important. The published data for seed yield of forage grasses are different. Nguyen and Sleper [10] in tall fescue showed that DM yield had strong positive correlation with seed production, Secer and Yunus [13] in *Bromus inermis* found negative correlation of both 1000 grains weight and panicle density on seed yield. Jafari [7] in cocksfoot showed a positive correlation between seed yield with panicle number, seed number panicle, seed weight panicle and harvest index, while a negative correlation values were obtained between seed yield and 1000 grains weight. The results of stepwise regression analysis also showed significant effects of DM yield, seed weight per panicle, heading date and harvest index on seed production [7].

Assessment of genetic divergence between populations is a vital to the success of plant breeding programs designed to exploit gene recombination. Strong positive relationships have been found between genetic distance and heterosis in broad range of crop species [5, 11]. Measure of genetic distance should have more value to breeding when based on a broad range of traits relevant to breeding objectives. Therefore, PCA and cluster analysis are effective tools for heterosis and producing synthetic varieties.

Despite key and important role of cocksfoot in forage production and also livestock productivity, little breeding has been done on this species, and the information on its breeding behavior especially in Iran climate conditions is less. Therefore, this research project was conducted to 1) study variability among 36 populations for seed yield, and morphological traits and 2) determine pattern of variation for seed yield and its components to identify groups of accessions through a multivariate approach.

MATERIALS AND METHODS

The present research was carried out at Hamadan agricultural station in Hamadan province, in west of Iran (34°52' N and longitude 48°33' E) at altitude 1730 m. The mean annual rainfall is 305 mm and the mean annual temperature is 10.3°C. The average maximum temperature is 22.9°C in August and average minimum temperature is -2.9°C in January. The soil texture was generally loam with alkaline pH =7.8 and the soil had no salinity problem $E_c=0.55$.

The cocksfoot genotypes utilized in this study were derived from Iranian natural resource gene bank. They were collected from slopes of Alborz altitude in north and Zagros altitude in west of country. Seeds of 21 domestic and 16 foreign populations in total 36 populations were sown in plots with four drilled lines as long as 2 m with 25 cm distance in sward condition using randomized complete block design with three replications in autumn 2009. Irrigation was made according to the plant requirement. Weeds were controlled mechanically and fertilizer application rates were 50 nitrogen (N) at sowing time followed by 50 kg/h for the second year. Field was irrigated once a week during summer. In establishment no data were recorded. The first harvest of the second year was assessed for seed yield and its components.

The data were collected and analyzed for the following traits: 1) Heading date and flowering date were recorded based on number of days from March 21, when at least 3 ears were visible/or pollinated. 2) Panicle number plant⁻¹ was counted as the number of fertile tillers. 3) Plant height (cm) measured from the ground to the top of the mean of 3 tallest panicles of each plant. 4) Panicle length (cm) recorded from mean of 10 selected stems from the base of lower to the top of the upper panicles. 5) 1000 grains weight determined for each plot. 6) Seed yield (Kg/ha⁻¹) determined by harvesting all panicles, then they were dried, threshed and the seed were cleaned and weighted. 7) Harvest index was estimated as ratio of seed yield/DM yield. 8) For DM yield, the remainder of panicles and stems of each plant was air dried and weighted as Ton.ha⁻¹.

Analysis of variance was computed on collected data for each trait. Variance components were used to estimate of broad sense heritability (h^2_b) according to Falconer and Mackay [4]. Phenotypic correlations among characteristics were estimated for all pair-wise combinations. All of variables were used in principal component and cluster analysis. The variables were standardized for cluster analysis (Ward method). The SAS software (SAS institute Inc.) was used for ANOVA and Minitab 15 for multivariate analysis.

RESULTS AND DISCUSSION

The results of analysis of variance (ANOVA) showed significant differences among populations for all of traits (Table 1). Estimates of components of genetic variance (S^2_g) and error variance (MSe) and broad sense heritability values (h^2_b) are summarized in Table 1. The genetic variances were significant for all of traits at the 1% level, except for 1000 grains weight at the 5% level (Table 1). The estimates of heritability for the various traits were low to high ($h^2_b=0.17$ to 0.90), (Table 1). The heritability estimates were based on individual year and they were relatively high for most of traits. This is expected, since, heritability estimates based on one year are inflated if genetic \times environment interaction variance was significant.

Mean, maximum, minimum standard error, standard deviation and coefficient of variation (CV%) of morphological traits and seed yield are given in Table 2. A range of 110 to 557 kg h⁻¹ and 717 to 2613 kg h⁻¹ were obtained for seed and DM yield in the first cut, respectively (Table 2).

Table 1. ANOVA of traits and estimates of components of genetic variance (S^2_g) and broad sense heritability (h^2_b) for 36 populations of cocksfoot evaluated in Hamadan, Iran in 2010.

S.O.V	DF	Heading date (day)	Flowering date (day)	Plant height (cm)	Panicle number	Panicle length (cm)	DM yield (Ton/ha)	Seed yield (kg/ha)	Harvest index	1000 Grain Weight
Populations	35	18.0**	32.3**	200.5**	337.5**	2.64**	0.612**	29529**	49.2 **	0.037*
Blocks	2	14.2**	17.6	94.6	83.5	0.73	0.703**	2271	48.1 **	0.038
Error	70	3.13	10.15	44.92	82.94	0.613	0.061	1096	10.01	0.0233
CV%		4.2	4.9	5.9	27.2	5.8	12.9	10.5	18.3	15.2
S^2_g		4.95**	7.39**	51.86**	84.84**	0.676**	0.184**	9478**	13.11**	0.0048*
h^2_b		%61	%42	%54	%51	%52	%75	%90	%57	%17

*, ** = Corresponding MS significant at 5%, 1%, respectively.

Table 2 summary of descriptive statistics for each trait for seed yield and seed components.

Traits	Mean	St Dev	SE Mean	Minimum	Maximum	CV
Heading date (day)	42.55	2.44	0.408	38.16	47.13	5.75
Flowering date (day)	65.62	3.28	0.547	59.66	72.00	5.00
Plant height (cm)	112.70	8.17	1.360	93.13	131.00	7.25
Panicle number	33.52	10.61	1.770	7.37	50.63	31.65
Seed yield (kg/ha)	315.50	99.20	16.50	101.50	557.30	31.44
Panicle length (cm)	13.31	0.938	0.156	11.67	15.78	7.05
DM yield (Ton/ha)	1.901	0.452	0.075	0.717	2.613	23.76
Harvest index	0.171	0.040	0.007	0.103	0.260	23.61
1000 Grain weight	1.003	0.112	0.019	0.797	1.200	11.140

The results of phenotypic correlation showed a positive correlation between seed yield with DM yield, panicle number and harvest index (Table 3), suggesting that selection for one would improve the other, It was in agreement with Jafari [7] for cocksfoot and Jafari et al [8] for tall fescue, Whereas, DM yield were positively correlated with plant height, panicle number, panicle length and 1000 grains weight, and were negatively correlated with heading date, flowering date and harvest index (Table 3). Similar to present study, strong negative relationships between heading date with DM yield were reported by Jafari et al [8] in tall fescue and Martiniello [9] in other grasses.

Table 3. Correlation analysis between seed yield and yield components in 36 populations of Cocksfoot in evaluated in Hamadan province, Iran in 2010.

Traits	Heading date (day)	Flowering date (day)	Plant height (cm)	Panicle number	Panicle length (cm)	DM yield (Ton/ha)	Harvest index	1000 Grain Weight
Flowering date (day)	0.75 **							
Plant height (cm)	-0.65**	-0.50**						
Panicle number	-0.58 **	-0.46**	0.52**					
Panicle length (cm)	-0.47**	-0.53**	0.47**	0.34*				
DM yield (Ton/ha)	-0.68**	-0.52**	0.80**	0.69**	0.36*			
Harvest index	0.44**	0.46**	-0.46**	-0.29	-0.39**	-0.34*		
1000 Grain weight	-0.25	-0.24	0.13	0.12	0.13	0.31*	0.09	
Seed yield (kg/ha)	-0.11	0.04	0.21	0.32*	-0.09	0.50**	0.62**	0.28

*, ** = significant at the 0.05 and 0.01 probability level, respectively.

Multivariate analysis has been used in several cross fertilized forage species to group accessions and varieties into cluster [2, 5]. Principal component analysis is often used prior to cluster analysis to determine the relative importance of classification of variables [6].

Using principal component analysis, the most important variables for seed yield characters were identified. First three independent components accounted for 72% of total variation. Eigenvalues from the first, second and third principal component axes, respectively, accounted for 46, 21 and 10 of total variation (Table 4). The relative magnitude of eigenvectors from the first principal component axis, indicates that heading date, flowering date, plant height, panicle number, DM yield and panicle length were important traits for classifying accessions into clusters. From the second principal component axis, seed yield and harvest index were important variables. 1000 grains weight had high eigenvectors in the third principal component axis (Table 4).

Table 4. Eigenvectors from the first three principal component axes for 9 variables used to classify 36 populations of Cocksfoot.

Traits	PC1	PC2	PC3
Heading date (day)	-0.425	0.027	0.076
Flowering date (day)	-0.384	0.148	0.256
Plant height (cm)	0.407	0.025	0.233
Panicle number	0.360	0.145	0.320
DM yield (Ton/ha)	0.424	0.241	0.175
Panicle length (cm)	0.309	-0.200	-0.216
Seed yield (kg/ha)	0.093	0.691	0.153
Harvest index	-0.266	0.539	-0.071
1000 Grain weight	0.148	0.300	-0.816
Eigenvalue	4.194	1.882	0.939
Proportion	0.466	0.209	0.104
Cumulative	0.466	0.675	0.779

The underlined and bold data has higher values in the PCA axes.

Based on Ward clustering method, 36 entries for 9 variables were subjected to cluster analysis. A distance coefficient of 12.00 arbitrary was chosen to separate the accessions into 3 cluster groups in a dendrogram (Fig. 1 and Table 5). Accessions from a defined geographic area tended to cluster, but some accessions from particular area were spread across several cluster groups.

In comparison means of clusters, the populations in cluster 1 averaged well above overall mean for both heading date and flowering date and known as late maturity groups. These populations had lower values for both seed and herbage production (Table 6). Ten domestic populations and two foreign populations that originated from USA were allocated in this cluster (Table 5). Populations in clusters 2 and 3 averaged well above the overall mean for seed yield and DM yield, respectively (Table 6). Cluster 2 had the higher accessions number (n=16), they were defined as midseason group. The populations in cluster 3 with five Iranian and 3 foreign populations originated from Kyrgyzstan, Russia and USA had the higher forage production couple with early maturity and taller stems, higher panicle number and panicle length (Tables 5 and 6).

Based on cluster distance the highest value was obtained between populations of 1557-Russia and 540-Karaj-Iran (data not shown). The result suggests the presence of a good variation within germplasm. According to Peters and Martinelli [11], by crossing between such genotypes with higher genetic distance, it is expected to obtain more heterosis

Table 5. Codes and origin of cocksfoot populations split into 3 clusters

Cluster 1 (n=12)	Cluster 2 (n=16)	Cluster 3 (n=8)
265-Gazvin-Ir*	1053-Karaj-Ir	1761-Oromia-Ir
255-Marand-Ir	411-Ardebil-Ir	412-Ardebil-Ir
1773-Sari-Ir	499-Zanjan-Ir	628-Bijar-Ir
197-Karaj-Ir	10112-Karaj-Ir	10155-Gene bank
10505-Gorgan-Ir	1455-Malayer-Ir	1250-Gene bank
455-Tabriz-Ir	10095-Sari-Ir	1555-Kyrgyzstan
783-Gazvin-Ir	1453-Hamadan-Ir	1557-Russia
2310-Zanjan-Ir	1072-Karaj-Ir	1261-USA
540-Karaj-Ir	10113-Karaj-Ir	
1094-Gene bank	1668-USA	
1058-USA	1715-USA	
1634-USA	1551-Russia	
	1609-Netherland	
	1556-Astoni	
	1054-Spanish	
	199-Gene bank	

* Ir=Iran

Table 5. Means of traits used in classification of the 3 clusters.

Traits	Heading date (day)	Flowering date (day)	Plant height (cm)	Panicle number	Panicle length (cm)	DM yield (Ton/ha)	Seed yield (kg/ha)	Harvest index	1000 Grain Weight
Cluster 1 (n=12)	44.55 a	67.76 a	107.04 b	23.71 b	12.48 c	1.48 c	277.1 a	0.19 a	0.93 b
Cluster 2(n=16)	42.58 b	66.17 a	112.39 b	36.21 a	13.49 b	1.99 b	358.7 a	0.18 a	1.05 a
Cluster 3(n=8)	39.52 c	61.33 b	121.79 a	42.83 a	14.22 a	2.35 a	286.9 a	0.13 b	1.02 ab

Means of clusters with the same letter are not significantly different ($p < 0.05$).

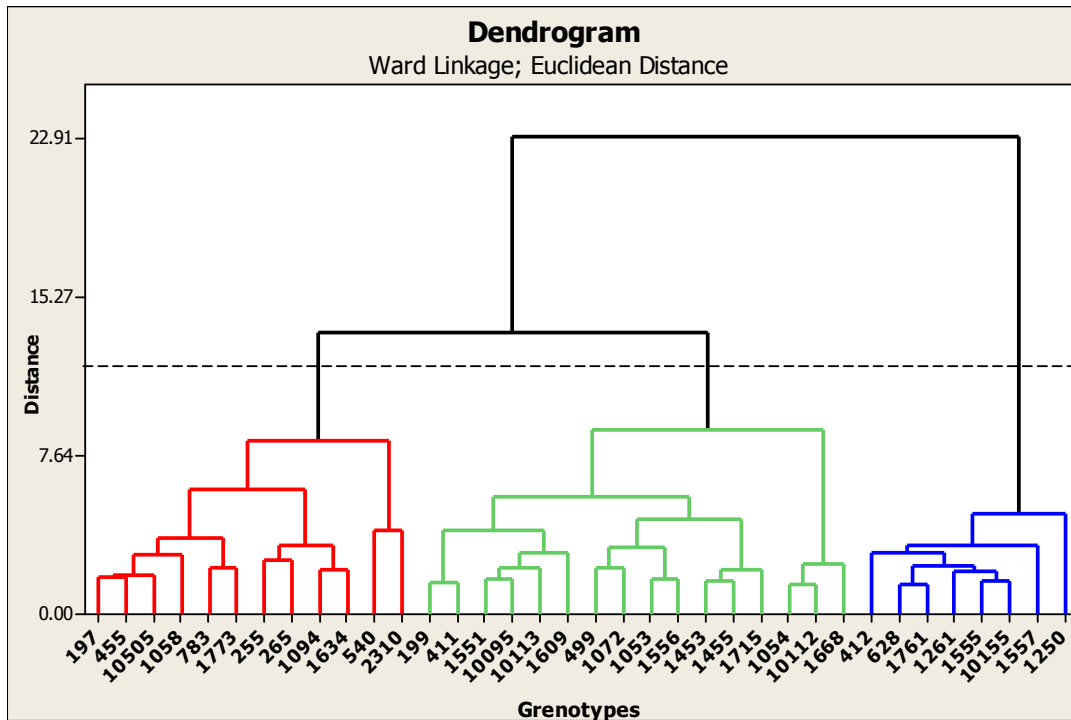


Figure 1. Dendrogram of 36 populations of cocksfoot by analyzing 9 morphological variables using Ward cluster analysis method.

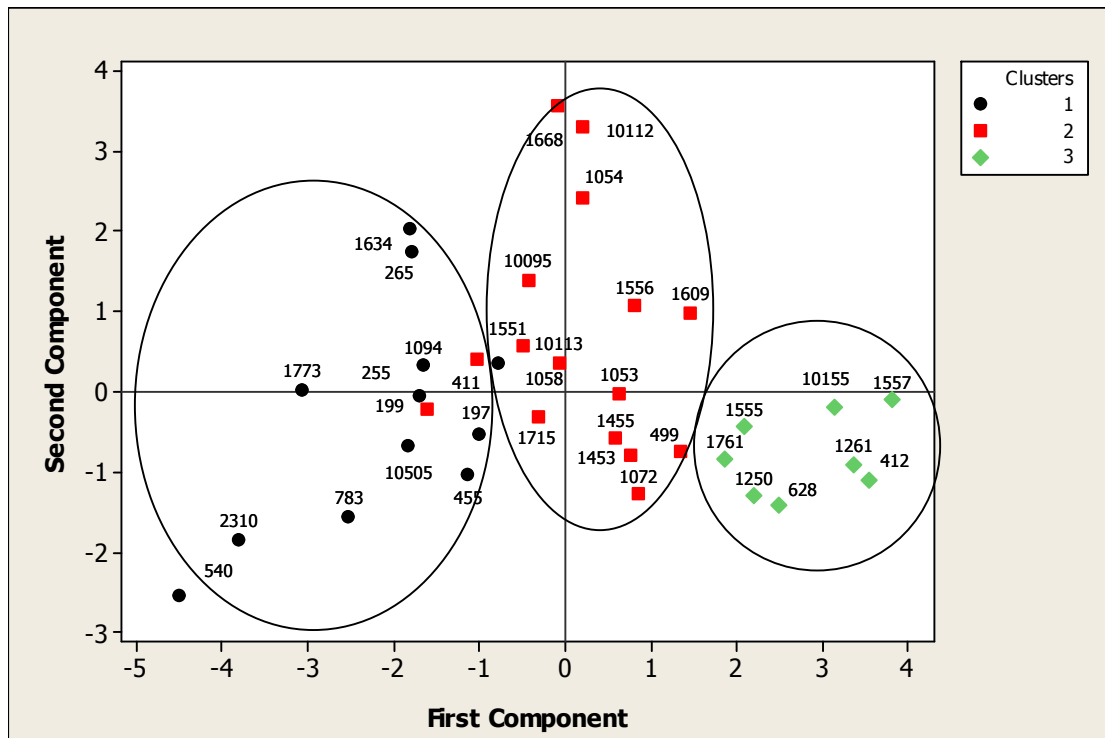


Figure 2. Scatter plot of 36 populations of cocksfoot for the first two principal components.

Fig. 2 shows graphically how accessions are classified into three clusters according to the first two principal components. The first component separated clusters 1 and 2 from 3 with trend of low to high DM yield (Fig. 2). The second component did not separated clusters, but it separated the two populations of 1668-USA and 10112-Iran with average values of 557 and 555 Kg ha⁻¹, respectively. These two populations had the highest seed production than other populations (data not shown). Distribution of accessions based on first component scores are in agreement with cluster analysis.

CONCLUSION

We concluded that there was significant variation and moderate to high heritability for most traits in the cocksfoot populations evaluated to improve seed yield and selection for DM yield could result in increase in seed yield

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