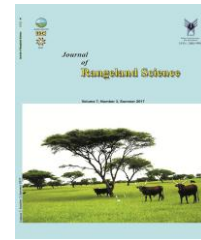


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**Research and Full Length Article:**

## Diversity and Relationships of Yield and Quality Traits in Cocksfoot (*Dactylis glomerata* L.) Genotypes

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**Abstract.** Cocksfoot (*Dactylis glomerata* L.) is an important cool season grass species in the moderate climate of Iran. In order to evaluate the yield and quality traits, an experiment was conducted in irrigation conditions using 36 accessions of *Dactylis glomerata* using a randomized complete block design with three replications in Islamabad, Kermanshah province, Iran in 2010. Characters such as forage dry matter (DM) yield and quality traits were measured. There were significant differences between genotypes for yield and all of quality traits. Results of correlations between traits showed that Crude protein (CP) was positively correlated with total ash and negatively correlated with both water soluble carbohydrates (WSC) and the crude fiber (CF). There were strong negative correlations between digestibility dry matter (DDM) and both acid detergent fiber (ADF). Using Cluster analysis (Ward method), the accessions were classified into five groups. Factor analysis after Varimax rotation revealed that three factors explained 83.63% of total variance. The first and the second factors were related to the forage quality. The third factor was correlated with DM yield. Based on factor analysis and means comparisons, it was concluded that the accessions Karaj197, Zanjan499 and Ghazvin783 were more efficient for both forage yield and quality traits than other accessions of the *D. glomerata*. However, accession Karaj10112, Russia1551, USA1715 had higher values of the quality traits but lower production. In spite of high forage yield, accessions Marand 255, and Karaj 10113 had a poor quality. Therefore, the accessions with higher forage yield and quality indices were introduced for improving the synthetic varieties.

**Key words:** *Dactylis glomerata*, Quality characters, Forage yield, Variability

## Introduction

Cocksfoot (*Dactylis glomerata* L.) is one of the most important forage grasses which are native to Europe, Asia and Mediterranean climate (Santen and Sleper, 1996). It can be grown in weak and shallow soils and cultivated to pasture establishment and reclamation in rainfall climate (Sanderson *et al.*, 2002).

Feeding values of pastures are assessed based on the amount of feed voluntarily consumed by animal and the digestibility of nutrients consumed (Peri *et al.*, 2007). The Acid Detergent Fiber (ADF), Crude Protein (CP) and the Digestible Dry Matter (DDM) are important traits to determine and improve the forage quality (Arzani *et al.*, 2006). High amount of the Water Soluble Carbohydrates (WSC) is necessary to supply energy for biochemical reactions in livestock. Some studies reported that increasing the digestible fibers and the ratio of the digestible to indigestible fibers could improve the WSC (Hoffman *et al.*, 2003). In *D. glomerata*, the WSCs are increasing during the growing seasons till grain filling period (Charesaz *et al.*, 2010). *D. glomerata* has a high nutritional value for livestock (Salehi Shanjani *et al.*, 2012). The CP and DDM contents of the *D. glomerata* were 61.3% and 8.2%, respectively during the flowering stage (Christie and Mc Elory, 1995).

Plant genetic resources are the basis of global food security. They comprise diversity of genetic material contained in traditional varieties, modern cultivars, crop wild relatives and other wild species. To meet the need for more food, it would be necessary to make better use of a broader range of the world plant genetic diversity (Farshadfar and Farshadfar, 2008). The classification of the genotypes based on the genetic distance is effective when we study numerous traits simultaneously (Jafari *et al.*, 2007; Yan *et al.*, 2016). In different studies on many genotypes of *D.*

*glomerata*, the genetic diversity was observed for many traits such as maturity, disease resistance, plant height, leaf size and DM yield (Casler, 1991; Santen and sleper, 1996). In other forage grasses, the genetic diversity for the forage quality among various genotypes was obtained. DDM was positively correlated with CP and negatively correlated with Crude Fiber (CF) and Acid Detergent Fiber (ADF) (Moradi and Jafari, 2006). The objectives of this research were to study the variation of DM yield, quality traits and their relationships in cocksfoot (*D. glomerata* L.)

## Materials and Methods

In this experiment, 36 accessions of the *D. glomerata* were provided from Natural Resources Gene Bank of Iran of Research Institute of Forest and Rangeland (Table 1). This study was carried out at Islamabad agricultural station, Kermanshah province, Iran during 2009-2010 (46°59' E longitude and 34°08' N latitude; 1260 m above sea level; mean annual rainfall of 485mm; the mean temperature of 20°C; loamy soil). Each plot consists of four rows with 2m length, 30 cm between rows and the distance between plots was 75 cm. Experiment was set up based on the Randomized Complete Block Design (RCBD) with three replications.

This study was carried out under the irrigated conditions during spring and summer (once a week). After harvesting, the forage Dry Matter (DM) yield was measured. The quality traits such as digestibility Dry Matter (DDM), Crude Protein (CP), Acid Detergent Fiber (ADF), total ash, Crude Fiber (CF) and Water Soluble Carbohydrates (WSC) were measured. All quality traits were measured using NIR (PERTEN8620) (Jafari *et al.*, 2003).

The collected data were subjected to analysis of variance. Accessions means comparisons were made using Duncan method. Phenotypic correlations among

characteristics were determined for all pair-wise combinations. Genetic parameters such as GCV (genotypic coefficient of variation, PCV (phenotypic coefficient of variation) and  $H_b$  (broad sense heritability) were estimated. Finally, all variables were used in correlation analysis, factor analysis and cluster analysis. Data were analyzed by MINTAB software.

## Results

Results of analysis of variance are shown in Table 1. Significant differences were

observed among accessions for DM yield, DDM, WSC, ADF, ASH and CF ( $P < 0.05$ ). The greatest values of broad sense heritability ( $H_b$ ) were observed for the DM yield (62.77%) and WSC (52.95%). The lowest  $H_b$  value belonged to CF (3.99%). The greatest GCV belonged to DM yield (27.28) and the lowest one was related to CF (1.38) trait (Table 1).

**Table 1.** Analysis of variance for quality traits

Characters	df	SS	MS	Sig.	GCV	PCV	H <sub>b</sub> (%)
DM yield	35	31999.8	159999	0.00	27.28	21.01	62.77
DDM	35	233.10	6.66	0.40	1.91	4.06	18.09
CP	35	78.58	2.24	0.65	3.7	8.13	17.18
WSC	35	105.92	3.026	0.07	7.15	6.74	52.95
ADF	35	33425.29	955.09	0.40	3.05	6.8	16.74
ASH	35	51.59	1.47	0.08	5.65	14.33	13.47
CF	35	327.37	9.35	0.33	1.38	6.79	3.99

GCV= Genotypic Coefficient of Variation; PCV= Phenotypic Coefficient of Variation; H<sub>b</sub>= Heritability

Means comparison among 36 accessions using Duncan Multiple Range' Test (DMRT) (Table 2) indicated that the accessions 1, 2, 3, 6, 8, 11 and 12 with the range of 2128 to 3797 kg<sup>-1</sup> had higher DM yield productions, the accessions 28, 10, 21, 12, 32 had higher DDM%, the accessions 4, 32, 21, 8, 15

and 17 produced higher CP%, the accessions 1, 7, 20, 36 and 28 could make more WSC% whereas the accessions 10, 12, 28, 7 produced lower ADF%, and the accessions 28, 18, 17, 21, 3 had higher total ash and also the accessions 21, 27, 24, 4 and 28 had less CF% in comparison with other studied accessions (Table 2).

**Table 2.** Means comparison of 36 accessions for different traits based on DMRT

Accessions name	Code code	DM yield (Kgh <sup>-1</sup> )	DDM (%)	CP (%)	WSC (%)	ADF (%)	ASH (%)	CF (%)							
1.Karaj	197	3374	ab	52.85	b-e	15.29	a-e	11.07	jkl	34.12	b-e	6.09	a-d	42.25	ab
2.Gen Bank	199	2280	b-e	52.68	bcd	13.65	cde	14.47	c-k	33.71	b-e	6.84	a-d	41.86	ab
3.Marand	255	3797	a	49.73	de	14.74	a-e	11.26	h-k	38.03	ab	7.83	ab	41.21	ab
4.Ghazvin	265	1532	e-h	50.34	b-e	16.55	a	11.24	h-l	37.13	a-d	7.69	abc	39.94	b
5.Ardabil	411	2126	d-g	50.67	b-e	14.42	a-e	12.12	e-k	37.00	a-d	6.99	a-d	42.43	ab
6.Ardabil	412	2181	c-f	50.98	b-e	15.19	a-e	11.86	e-k	34.86	b-e	5.97	bcd	44.49	ab
7.Tabriz	455	1899	d-h	50.98	b-e	14.63	a-e	14.20	ab	33.34	b-e	5.36	d	44.64	ab
8.Zanjan	499	2877	bc	52.90	bcd	15.95	ac	12.26	e-k	34.09	b-e	6.9	a-d	41.62	ab
9.Sirachal	540	1808	d-h	51.91	bcd	14.22	a-e	13.39	b-f	34.38	b-e	6.55	a-d	41.82	ab
10.Bijar	628	1556	e-h	54.27	ab	14.40	a-e	14.63	a	31.18	e	5.94	bcd	42.18	ab
11.Ghazvin	783	2316	cde	51.65	bcd	15.61	a-d	12.92	b-f	35.54	b-e	7.06	a-d	41.11	ab
12.Karaj	1053	2569	cd	53.66	a-d	15.37	a-e	11.67	h-k	32.62	de	5.74	cd	45.52	ab
13.Spain	1054	1494	fgh	51.53	bcd	15.14	a-e	12.64	c-i	36.35	a-d	7.48	abc	41.15	ab
14.Hispanica	1058	1827	d-h	50.64	b-e	13.68	cde	12.60	c-i	35.75	b-e	6.87	a-d	43.77	ab
15.Karaj	1072	1957	d-h	50.63	b-e	15.75	abc	12.26	e-k	36.20	a-d	6.78	a-d	43.23	ab
16.Gen Bank	1094	1863	d-h	49.82	cde	14.64	a-e	12.14	e-k	36.86	a-d	6.89	a-d	43.81	ab
17.Gen Bank	1250	1619	e-h	51.08	b-e	15.74	abc	11.37	h-k	37.36	a-d	7.92	ab	40.47	b
18.USA	1261	1868	d-h	49.55	de	15.11	a-e	10.89	kl	38.26	a	7.93	ab	41.36	ab
19.Hamadan	1453	1613	e-h	52.43	bcd	15.62	a-e	11.73	f-k	35.13	b-e	7.35	a-d	42.10	ab
20.Malayer	1455	1678	e-h	52.11	bcd	13.28	de	14.10	abc	33.97	b-e	6.66	a-d	43.68	ab
21.Russia	1551	1606	e-h	54.00	abc	16.24	ab	12.47	d-j	33.98	b-e	7.85	a-d	39.77	b
22.Kirghizian	1555	1619	e-h	51.63	bcd	13.95	b-e	13.49	b-e	35.35	b-e	6.51	a-d	44.23	ab
23.Stonia	1556	1574	e-h	51.80	bcd	13.73	cde	12.58	b-g	34.49	b-e	6.95	a-d	41.43	ab
24.Russia	1557	1544	e-h	52.27	bcd	15.22	a-e	12.92	b-f	34.55	a-e	7.77	abc	39.87	b
25.Netherland	1609	1743	e-h	48.69	e	14.56	a-e	10.61	kl	38.46	a	7.24	a-d	42.44	ab
26.USA	1634	1311	h	50.10	b-e	14.26	a-e	12.78	b-h	36.23	a-d	5.94	bcd	45.26	ab
27.USA	1668	1388	gh	51.45	bcd	15.06	bcd	11.16	i-l	34.22	bcd	7.44	abc	39.81	b
28.USA	1715	1161	h	55.30	a	14.96	bcd	13.57	a-d	32.82	cde	8.12	a	40.32	b
29.Ourmieh	1761	1732	e-h	49.86	cde	14.48	bcd	12.83	b-h	36.46	a-d	6.49	a-d	43.95	ab
30.Sari	1773	1770	e-h	50.29	b-e	13.63	cde	12.24	e-k	37.69	abc	7.55	abc	42.31	ab
31.Zanjan	2310	1482	fgh	51.94	bcd	15.60	a-d	12.04	e-k	35.31	bcd	7.52	abc	43.44	ab
32.Karaj	10112	1560	e-h	53.47	a-d	16.34	ab	11.05	jki	34.50	bcd	7.60	abc	40.94	ab
33.Karaj	10113	2899	bc	48.70	e	15.59	a-d	12.27	e-k	38.35	a	7.28	a-d	40.76	ab
34.Gen Bank	10155	1710	e-h	49.71	de	14.14	bcd	11.42	h-k	37.30	a-d	7.15	a-d	43.98	ab
35.Gorgan	10505	1578	e-h	52.10	bcd	14.46	bcd	11.77	f-k	35.39	bcd	7.08	a-d	44.19	ab
36.Sari	10095	1645	e-h	50.67	b-e	12.96	e	13.92	abc	35.13	bcd	5.75	cd	46.45	a

Means of each column followed with the similar letters has no significant differences based on Duncan Method

Phenotypic correlation between traits (Table 3) indicated that there was no significant association between DM yield and other quality traits. DDM was negatively correlated with ADF ( $p \leq 0.01$ )

and WSC ( $p \leq 0.05$ ). Similarly, there was a negative correlation ( $p \leq 0.01$ ) between CP and WSC. The CP had a positive correlation with total ash ( $p \leq 0.05$ ).

**Table 3.** The phenotypic correlation of the quality traits

Characters	DM yield	DDM	CP	WSC	ADF	ASH
DDM	-0.150					
CP	0.134	0.199				
WSC	-0.274	0.335*	-0.485**			
ADF	0.141	-0.864**	0.035	-0.534**		
ASH	-0.062	0.013	0.423*	-0.507**	0.404*	
CF	-0.019	-0.207	-0.538**	0.286	0.079	-0.797**

\* and \*\*= significant at 5% and 1% probability levels

Using cluster analysis Ward method, cocksfoot accessions were grouped to five clusters (Fig. 1 and Table 4). Means comparisons were made

between cluster groups for different traits (Table 5). The first cluster (C<sub>1</sub>) included the accessions 1, 6, 8, 11, 12, 15, 19, 31 and 35. It had the highest DM yield, CP

and DDM. The second group (C<sub>2</sub>) contained the accessions 1, 7, 9, 10, 14, 20, 22, 23, 26 and 36. This group had a lower CP and higher mean value for WSC. The third group (C<sub>3</sub>) included the accessions 3, 4, 17, 18, 25 and 33. It showed a higher value of the CP and DM

yield. The fourth group (C<sub>4</sub>) consisted of the accessions 5, 16, 29, 30 and 34 had a moderate DM yield but lower quality. The fifth group (C<sub>5</sub>) included the accessions 13, 21, 24, 27, 28 and 32 had the lowest DM yield but higher values for DDM and CP than other groups.

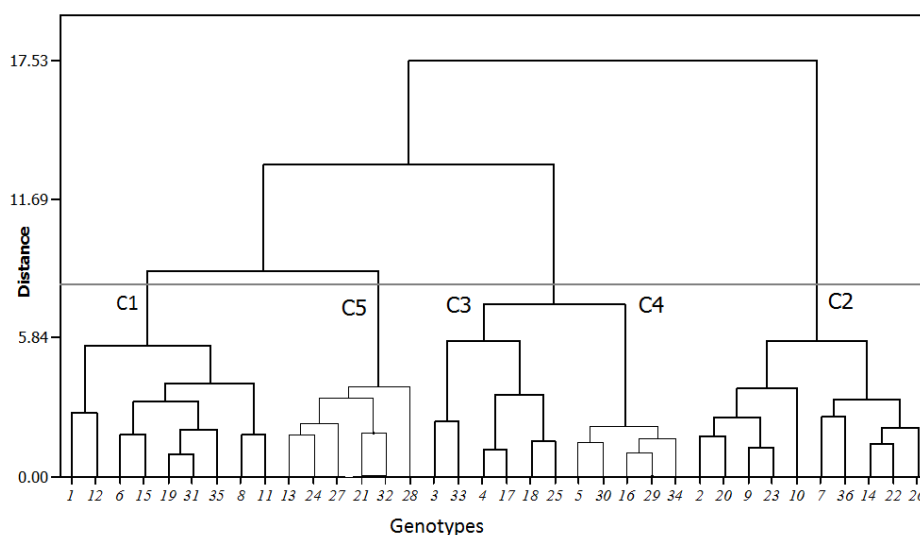


Fig. 1. Dendrogram based on cluster analysis of the studied genotypes

Table 4. The accession names within each group of clusters

Cluster1	Cluster2	Cluster3	Cluster4	Cluster5
1.Karaj	2.Gen Bank	3.Marand	5.Ardabil	13.Spain
6.Ardabil	7.Tabriz	4.Ghazvin	16.Gen Bank	21.Russia
8.Zanjan	9.Sirachal	17.Gen Bank	29.Ourmieh	24.Russia
11.Ghazvin	10.Bijar	18.USA	30.Sari	27.USA
12.Karaj	14.Hispanica	25.Netherland	34.Gen Bank	28.USA
15.Karaj	20.Malayer	33.Karaj		32.Karaj
19.Hamadan	22.Kirghizian			
31.Zanjan	23.Stonia			
35.Gorgan	26.USA			
	36.Sari			

Table 5. Means comparison of clusters for different quality traits

Cluster	Genotype No	DM yield(kgh <sup>-1</sup> )	DDM (%)	CP (%)	WSC (%)	ADF (%)	ASH (%)	CF (%)
1	9	2216.3 a	52.13 a	15.43 a	11.95 b	34.81 b	6.72 b	43.11 a
2	10	1719.7 ab	51.68 ab	13.88 b	13.62 a	34.35 b	6.34 b	43.53 a
3	6	2243.0 a	49.68 c	15.38 a	11.27 b	37.93 a	7.65 a	41.03 b
4	5	1840.2 ab	50.07 bc	14.26 b	12.15 b	37.06 a	7.01 ab	43.3 a
5	6	1458.8 b	53.0 a	15.49 a	12.30 b	34.40 b	7.71 a	40.31 b

Means of clusters followed with the similar letters has no significant differences based on Duncan Method

Result of the factor analysis using Varimax rotation showed three factors that explained 83.5% of total variation (Table 6). The factor coefficients revealed that the first factor was related

to high CP and ASH and low amount of the CF whereas the second factor indicated high value of the DDM and low value of ADF, but the third factor was related to high forage DM yield. Using

Biplot of the first and second factors, the accessions were scattered. Based on Factor1 axis, the accessions in clusters 3 and 5 had higher CP than that for clusters 4 and 2. In contrast, based on Factor 2 axis, the clusters 4 and 3 had higher forage production than other clusters whereas clusters 1, 2 and 5 had higher mean values for WSC and DDM. This finding was in agreement with data of cluster means comparisons in Table 5.

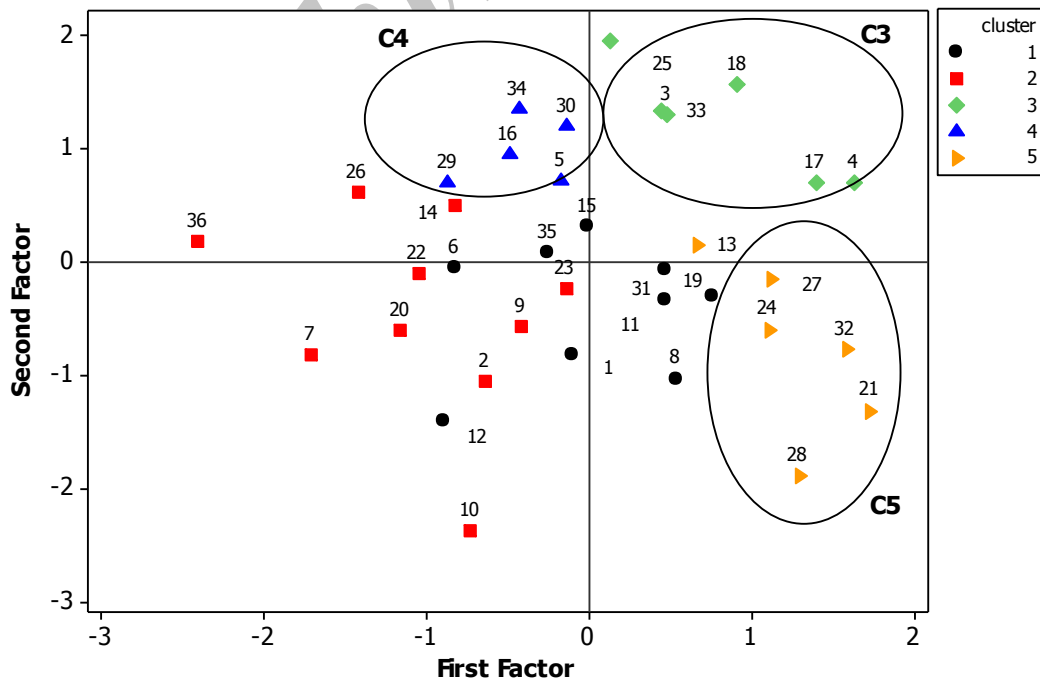
The genotypes within cluster 3 including Marand 255, Ghazvin265, Gen Bank1250, USA1261, Netherland1609

and Karaj10113 had higher values for forage production and CP. These accessions could be used for breeding improved synthetic varieties. Accessions of cluster 5 (Spain1054, Russia1551, Russia1557, USA1668, USA1715 and Karaj 10112) that were originated from other countries had a good potential for higher quality traits such as DDM and WSC but lower DM yield. This accession and domestic accession could transfer useful gens to local accessions and improve new varieties.

**Table 6.** The matrices of factor coefficients after Varimax rotation

Variable	Factor1	Factor2	Factor3	Similarity rate
CP	<b><u>0.75</u></b>	-0.12	0.40	0.74
ASH	<b><u>0.86</u></b>	0.27	-0.26	0.89
CF	<b><u>-0.88</u></b>	0.09	0.07	0.80
WSC	<u>-0.53</u>	<b><u>-0.54</u></b>	-0.40	0.72
DDM	0.21	<b><u>-0.94</u></b>	-0.06	0.93
ADF	0.17	<b><u>0.97</u></b>	0.03	0.96
DM yield	-0.06	0.10	<b><u>0.90</u></b>	0.81
Eigen values	2.44	2.20	1.19	
Variance%	34.90	31.50	17.10	
Cumulative Var %	34.90	66.40	83.50	

Bold and underlined data had significant effects in the relevant factors



**Fig. 2.** Distribution diagram of accessions in regard to the first and second factors

## Discussion

The significant differences among accessions caused to improve the efficiency of the traits in breeding program (Moradi and Jafari, 2006). In another study, the value of the  $H_b$  was observed as 63.89% among 21 accessions of the *D. glomerata* for DM yield (Mohamadi *et al.*, 2008). The existence of high value of heritability and the genetic diversity are used as proper parameters to improve traits in breeding program. Jafari and Javarsineh (2005) found the heritability values of the quality traits of *Festuca arundinacea* ranged from the average to high amounts.

In present study, the third group ( $C_3$ ) included the accessions 3, 4, 17, 18, 25 and 33 showing higher mean values of the CP and DM yield; therefore, it can be introduced as the best group for breeding programs. The analysis of the phenotypic correlation between traits indicated that there was no significant correlation between the DM yield and the quality traits. According to this analysis, it is hard to choose both the forage yield and quality (DDM and WSC) simultaneously in breeding program. Similar to present study, there are numerous researches indicated that no significant association was found between the forage yield and the quality traits (Azhir *et al.*, 2011; Arzani and Majidi, 2009; Jafari, 2002).

In our study, higher values of  $H_b$  for DM yield and WSC were obtained expressing the importance of the non-additive gene and additive gene, respectively. There was a positive correlation between CP and ASH percent. Also, there was a negative correlation between CF and WSC. On the other way, the DDM had a negative correlation with ADF. Therefore, because of these variation associations, it is hard to select desirable traits. A classification based on the cluster analysis and Duncan' test verified this variation as well.

The similarity rate of WSC and CP was less than the other traits.

Therefore, it does not recommend employing them to discriminate these factors. Jafari *et al.* (2007) investigated the genetic diversity of different components of the yield of *Agropyron desertorum* using factor analysis. They reported the association between the first and second factors with the grain yield. The first factor indicated high values of the CP and ASH percent and low amount of the CF, and the second factor showed high values of DDM, WSC and ADF. Both these factors were determined as the quality factors. However, the DM yield was expressed by the third factor.

Several researchers reported their results for yield and quality traits for *D. glomerata* and other forages. Skládanka *et al.* (2010) showed that *Festulolium* had the lowest CP in all year of cultivation. It was reported that digestibility in *D. glomerata* was lower than *Festuca arundinacea* (Prigge *et al.*, 1999). Baron *et al.* (2004) claimed that the quality of green and dead material remained relatively constant in winter. Turner *et al.* (2007) compared the establishment, productivity and feed qualities of four cocksfoot (*D. glomerata*) and four brome (*Bromus spp.*) cultivars under leaf stage based defoliation management. New cultivars showed more variation for the most traits. They revealed faster seedling emergence, tiller production, higher tiller density, lower ADF, higher CP and greater ME.

Jafari and Naseri (2007) estimated genetic parameters and correlation between DDM, WSC, and CP in 25 parents and half-sib (HS) family. They found significant variances between clonal parents for all traits except CP. The estimates of broad sense heritability were moderate to high for all traits. Chare-Saz *et al.* (2010) explained the amount of WSC in *Bromus tomentellus*, *D. glomerata* and *Agropyron intermedium* including 8.2, 9.4 and 13.8%, respectively. *Agropyron* had the

highest WSC (17.4%) during the complete growth stage; therefore, it could be applied for late season grazing. A positive linear relationship ( $R^2= 0.72$ ) between WSC and DM was reported (Rawnsley *et al.*, 2002). Some genetic parameters have been estimated for *Dactylis* as well (Dabkevičienė *et al.*, 2007; Zhao *et al.*, 2014; Madesis *et al.*, 2014; Salehi Shanjani *et al.*, 2012). Genetic diversity was assessed and the marker-trait associations for rust were examined using 18 EST-SSR and 21 SCoT markers in 75 cocksfoot accessions. A high level of genetic diversity was detected in cocksfoot with an average genetic diversity index of 0.369 (Yan *et al.*, 2016).

### Conclusion

Based on factor analysis and means comparison, it was concluded that the accessions Karaj197, Zanjan499 and Ghazvin783 were more efficient for both forage yield and quality traits than other accessions of the *D. glomerata*. However, the accessions of Karaj10112, Russia1551, and USA1715 had higher values of the quality traits but lower forage production. Accessions of Marand 255 and Karaj 10113 in spite of high forage yield, but their quality was poor. Therefore, the accessions with higher indices for both yield and quality traits were introduced for improving the synthetic varieties

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## مقایسه تنوع و ارتباط بین کیفیت و کمیت علوفه در ژنوتیپ‌های علف باغ (*Dactylis glomerata* L.)

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**چکیده.** به منظور مقایسه عملکرد و کیفیت علوفه و میزان تنوع، ۳۶ جمعیت علف باغ از گونه (*Dactylis glomerata*) در قالب طرح بلوک‌های کامل تصادفی تحت شرایط آبی با سه تکرار مورد بررسی قرار گرفت. صفات عملکرد علوفه خشک و کیفیت علوفه اندازه‌گیری شد. براساس تجزیه واریانس تنوع معنی‌دار در بین جمعیت‌های مورد بررسی مشاهده شد. بیشترین مقدار وراثت‌پذیری عمومی متعلق به وزن علوفه خشک با ۶۲/۷۷ درصد و قندهای محلول در آب (WSC) با ۵۲/۹۵ درصد و کمترین وراثت‌پذیری عمومی با ۳/۹۹ درصد مربوط به فیبر خام (CF) برآورد گردید. همبستگی فنوتیپی معنی‌دار بین عملکرد علوفه با صفات کیفی مشاهده نشد. ولی در صفات کیفی، پروتئین خام با خاکستر همبستگی مثبت ( $P < 0/05$ ) و با کربوهیدرات محلول و فیبر خام همبستگی منفی ( $P < 0/01$ ) معنی‌دار نشان داد. از طرف دیگر قابلیت هضم ماده خشک با فیبر نامحلول در شوینده اسیدی (ADF) همبستگی منفی نشان داد ( $P < 0/01$ ). در تجزیه کلاستر به روش Ward ژنوتیپ‌ها در پنج گروه قرار گرفتند. بر اساس تجزیه به عامل‌ها ۸۳/۵ درصد از واریانس موجود داده‌ها توسط سه عامل تبیین گردید. عامل اول و دوم به صفات کیفی و عامل سوم به عملکرد علوفه اختصاص یافت. در پراکنش ژنوتیپ‌ها و گروه‌ها بر اساس دو فاکتور اول و دوم بین تجزیه به فاکتورها و تجزیه کلاستر همخوانی وجود داشت. با توجه به نتایج، جمعیت‌های کرج ۱۹۷، زنجان ۴۹۹، و قزوین ۷۸۳ برای از لحاظ عملکرد علوفه و صفات کیفی برتر بودند. جمعیت‌های کرج ۱۰۱۱۲، روسیه ۱۵۵۱ و آمریکا ۱۷۱۵ دارای کیفیت علوفه بهتری بودند اما عملکرد علوفه ضعیفی داشت. جمعیت‌های مرنده ۲۵۵ و کرج ۱۰۱۱۳ دارای عملکرد علوفه بیشتری بودند، اما کیفیت علوفه مناسبی نداشتند. بنابراین جمعیت‌های که از لحاظ هر دو شاخص بهتر بودند به منظور تولید واریته‌های مصنوعی در برنامه‌های اصلاح نباتات قابل استفاده هستند.

**کلمات کلیدی:** علف باغ، عملکرد علوفه، کیفیت علوفه، تنوع ژنتیکی