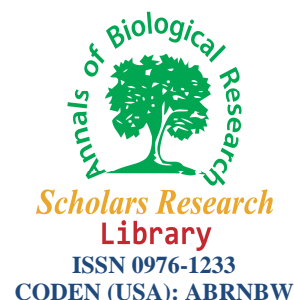




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## Evaluation of the forage yield and quality in some accessions of *Dactylis Glomerata* under irrigated conditions

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### ABSTRACT

In order to evaluate the forage quality and yield, 36 accessions of *Dactylis Glomerata* were investigated by using randomized complete block design with three replications. Traits such as the forage dry matter yield (DMY) and quality were measured. The results of the variance analysis indicated a significant difference between the heritability (Hb) and other traits studied. Among the quality traits studied, the crude protein (CP) indicated positive and significant correlation with ashes percent (AP) and significant negative correlation with water solution carbohydrates (WSC) and the crude fiber (CF). The cluster analysis and mean comparison among groups resulting from the cluster analysis verified these results. By using factor analysis, three factors could be identified after Varimax rotation. These independent factors accounted for 83.63% of total variance. The first and the second factors were markers of the forage quality. The third factor indicated the FDM. According to the mean comparison and the factor analysis, accessions 1, 8 and 11 had greatest values for quality traits. Accession 32 had greatest amount of the digestibility dry matter (DDM) and the CP based on mean comparisons. But this accession was too weak to produce FDM. Although, the greatest value of the FDM was observed in accessions 3 and 33. Based on the mean comparison and factor analysis, the optimum values of the quality traits were only observed in accessions 21 and 28. Consequently, accessions 9,8,11,32,3,33,21,28 could be introduced and suggested to produce artificial cultivars in breeding program under irrigated condition in Kermanshah province.

**Keywords:** *Dactylis Glomerata*, Quality Traits, Factor Analysis, forage dry matter.

### INTRODUCTION

One of the most important forage is *Dactylis Glomerata* which is native to Europe, Asia and Mediterranean areas [14]. This plant can be grown in poor and shallow soils. Therefore, it can be recommended producing and growing it for pasture establishment and reclamation [13].

Feeding value of pasture is the product of voluntary feed consumption and the digestibility of nutrients consumed [12]. The ADF, CP and the DDM which was measured to determine and improve the forage quality [1]. In livestock need to have high amount of the water solution carbohydrates to supply energy for biochemical reactions. Some studies indicated that the increasing the digestible percent of fibers and the ratio of the digestible fibers to indigestible fibers could improve the water solution carbohydrates values [6]. In *Dactylis Glomerata*, the WSC are increasing during growing seasons [3]. *Dactylis Glomerata* has high nutritional value for livestock [11]. The protein percent of the *Dactylis Glomerata* and the DDM content were 61.3% and 8.2 respectively during flowering stage [4].

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's plant genetic diversity [5]. The classification of the genotypes based on the genetic distance is effective when we study numerous traits

simultaneously [9]. In different studies on many accessions of *Dactylis Glomerata*, the genetic diversity was observed for many traits such as maturity, disease resistance, plant height, leaf size and DMY [2,14]. Finally, the genetic diversity for the forage quality among various genotypes was obtained and positive correlation of DDM with protein content and negative correlation with the CP and ADF were reported [11].

The aim of this study is to investigate about the genetic diversity of 36 accessions of *Dactylis Glomerata* with regard to the forage yield and quality. At first step, we estimated the genetic diversity by using the variance analysis and factor analysis. In the follow, by using mean comparisons and multivariate statistical analysis, we could choose and introduce accessions which were more efficient than other accessions.

## MATERIALS AND METHODS

In this study, 36 accessions of the *Dactylis Glomerata* were selected from the gene bank (Table 1) of the Research Institute of Forest and Rangeland of Iran. This study was carried out at the Kermanshah Research Center of Agriculture and Natural Resources, (46°, 59' E longitude; 34° 08' N latitude; 1260m above sea level; mean annual rainfall of 400mm; the mean temperature of 20°C; at loamy soil). The highest amount of the rainfall occurs in February. Also, we observed the lowest variation of the rainfall in April. Each plot consists of four 2<sup>m</sup>- rows. The interval between two plots was 75<sup>cm</sup>. 100<sup>cm</sup> distance between two replications were determined. This study was carried out under irrigated condition during spring and summer (once a week) since 2008 until 2009. Weeding was carried out mechanically. After harvesting, the dry weight yield of the forage was measured and calculated per hectare. The quality traits such as DDM, CPP, ADF, AP, CF and WSC were measured and calculated. All experiment was carried out by using NIR (Jafari et al, 2003).

By using Msg and Mse, GCV, PCV and Hb were estimated. These parameters were analyzed by using SPSS, SAS and Excel software.

**Abbreviations:** ADF- acid detergent fiber; DDM- digestibility dry matter; CP- crude protein ; AP- ash percent; CF- crude fiber; WSC; water solution carbohydrates; Msg- mean square of genotype; Mse- mean square of error; GCV- genotypic coefficient of variation; PCV- phenotypic coefficient of variation; Hb- heritability, DMY- dry matter yield

Table 1. 36 accessions of the *Dactylis glomerata* were used in current study

Entry, Origin, Name	Entry, Origin, Name
1, Karaj, 197	19, Hamadan, 1453
2, Gen Bank, 199	20, Malayer, 1455
3, Marand, 255	21, Russia, 1551
4, Ghazvin, 265	22, Kirghizian, 1555
5, Ardabil, 411	23, Stonia, 1556
6, Ardabil, 412	24, Russia, 1557
7, Tabriz, 455	25, Netherland, 1609
8, Zanzan, 499	26, USA, 1634
9, Sirachal, 540	27, USA, 1668
10, Bijar, 628	28, USA, 1715
11, Ghazvin, 783	29, Ourmieh, 1761
12, Karaj, 1053	30, Sari, 1773
13, Spain, 1054	31, Zanzan, 2310
14, Hispanica, 1058	32, Karaj, 10112
15, Karaj, 1072	33, Karaj, 10113
16, Gen Bank, 1094	34, Gen Bank, 10155
17, Gen Bank, 1250	35, Gorgan, 10505
18, USA, 1261	36, Sari, 10095-10

## RESULTS AND DISCUSSION

According to the variance analysis among accessions (Table 2), there were significant differences between the FDM and WSC ( $p \leq 0.01$ ) and among DDM, CP and ADF ( $p \leq 0.05$ ). The highest value of Hb was observed for the FDM and WSC. For the CF, the lowest value of Hb was obtained. The great significant differences were observed among accessions studied for all traits. The great significant differences among genotypes cause to improve the efficient of the traits in breeding program [11]. Also, the optimum value of the Hb was 62.77% for all traits especially for FDM. In other study, the value of the Hb was observed 63.89% among 21 accessions of the *Dactylis Glomerata* for DMY [10]. 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 [8] obtained that the heritability values of the quality traits of *Festuca arundinacea* ranged from the average to high amount.

Table 2. Analysis of variance

Characters	Mean square			CV (%)		Hb(%)
	Msp	Msg	Mse	GCV	PCV	
FDM	429716 <sup>**</sup>	269717	159999	27.28	21.01	62.77
DDM	5.32 <sup>*</sup>	0.96	4.35	1.91	4.06	18.09
CP	1.75 <sup>*</sup>	0.3	1.45	3.7	8.13	17.18
WSC	1.47 <sup>**</sup>	0.78	0.69	7.15	6.74	52.95
ADF	6.99 <sup>*</sup>	1.17	5.82	3.05	6.8	16.74
AP	1.16 <sup>ns</sup>	0.16	1.0	5.65	14.33	13.47
CF	8.66 <sup>ns</sup>	0.35	8.32	1.38	6.79	3.99

\*\* Significant at 1% level of probability, \* significant at 5% level of probability, ns non-significant

The mean comparison among all accessions based on Duncan multiple range' test (Table 3) reflected that accessions 1, 2, 3, 6, 8, 11, 12 and 13 produce more FDM, accessions 28,10,21,12,32 have higher DDM, accessions 4, 32, 21, 8, 15 and 17 can produce more CP, accessions 1, 7, 20, 36 and 28 can make more WSC, while accessions 10, 12, 28, 7 produce less ADF, and accessions 28, 18, 17, 21, 3 have more AP and also accessions 21, 27, 24, 4 and 28 had less CF in comparison with other accessions studied.

Table 3. Mean performance of 36 accessions for different characters

accessions	FDM	DDM	CP	WSC	ADF	AP	CF
1	3374ab	52.85abcde	15.29abcde	11.07jkl	34.12abcde	6.09abcd	42.25ab
2	2280cf	52.68abcde	13.65cde	14.47cdefghk	33.71abcde	6.84abcd	41.86ab
3	3797a	49.73de	14.74abcde	11.26ghijkl	38.03ab	7.83ab	41.21ab
4	1532abcde	50.34bcde	16.55a	11.24hijkl	37.13abcd	7.69abc	39.94b
5	2126defg	50.67bcde	14.42abcde	12.12defghijkl	37abcd	6.99abcd	42.43ab
6	2181cdeg	50.98bcde	15.19abcde	11.86efghijkl	34.86abcde	5.97bcd	44.49ab
7	1899defgh	50.98bcde	14.63abcde	14.2ab	33.34bcde	5.36d	44.64ab
8	2877bc	52.90abcde	15.95abc	12.26defghijkl	34.09abcde	6.9abcd	41.62ab
9	1808defgh	51.91abcde	14.22abcde	13.39abcde	34.38abcde	6.55abcd	41.82ab
10	1556efgh	54.27ab	14.40abcde	14.63a	31.18e	5.94bcd	42.18ab
11	2316cde	51.65abcde	15.61abcd	12.92bcdefg	35.54abcde	7.06abcd	41.11ab
12	2569cd	53.66abcd	15.37abcde	11.67ghijkl	32.62de	5.74cd	45.52ab
13	1494fgh	51.53abcde	15.14abcde	12.64bcdefghij	36.35abcd	7.48abc	41.15ab
14	1827defgh	50.64bcde	13.68cde	12.6bcdefghij	35.75abcde	6.87abcd	43.77ab
15	1957defgh	50.63bcde	15.75abc	12.26defghijkl	36.20abcd	6.78abcd	43.23ab
16	1863defgh	49.82cde	14.64abcde	12.14defghijkl	36.86abcd	6.89abcd	43.81ab
17	1619efgh	51.08bcde	15.74abc	11.37ghijkl	37.36abcd	7.92ab	40.47b
18	1868defgh	49.55de	15.11abcde	10.89kl	38.26a	7.93ab	41.36ab
19	1613efgh	52.43abcde	15.62abcde	11.73fghijkl	35.13abcde	7.35abcd	42.1ab
20	1678efgh	52.11abcde	13.28de	14.1abc	33.97abcde	6.66abcd	43.68ab
21	1606efgh	54abc	16.24ab	12.47cdefghijk	33.98abcde	7.85abcd	39.77b
22	1619efgh	51.63abcde	13.95bcde	13.49abcde	35.35abcde	6.51abcd	44.23ab
23	1574efgh	51.80abcde	13.73cde	12.58bcdefgh	34.49abcde	6.95abcd	41.43ab
24	1544efgh	52.27abcde	15.22abcde	12.92bcdefg	34.55abcde	7.77abc	39.87b
25	1743efgh	48.69e	14.56abcde	10.61l	38.46a	7.24abcd	42.44ab
26	1311h	50.10bcde	14.26abcde	12.78bcdefghi	36.23abcd	5.94bcd	45.26ab
27	1388gh	51.45abcde	15.06abcde	11.16ijkl	34.22abcde	7.44abc	39.81b
28	1161h	55.30a	14.96abcde	13.57abcd	32.82cde	8.12a	40.32b
29	1732efgh	49.86cde	14.48abcde	12.83bcdefghi	36.46abcd	6.49abcd	43.95ab
30	1770efgh	50.29bcde	13.63cde	12.24defghijkl	37.69abc	7.55abc	42.31ab
31	1482fgh	51.94abcde	15.6abcd	12.04defghijkl	35.31abcde	7.52abc	43.44ab
32	1560efgh	53.47abcd	16.34ab	11.05jki	34.5abcde	7.6abc	40.94ab
33	2899bc	48.70e	15.59abcd	12.27defghijkl	38.35a	7.28abcd	40.76ab
34	1710efgh	49.71de	14.14abcde	11.42ghijkl	37.30abcd	7.15abcd	43.98ab
35	1578efgh	52.10abcde	14.46abcde	11.77fghijkl	35.39abcde	7.08abcd	44.19ab
36	1645efgh	50.67bcde	12.96e	13.92abc	35.13abcde	5.75cd	46.45a

By using ward method, all accessions were grouped based on desirable traits (Fig 1). In the follow, Duncan multiple range' test was employed to compare these groups (table 4). The first group (C<sub>1</sub>) including accessions 19, 31, 35, 11, 15, 21, 32, 13, 24, 27 and 28 indicated higher content of the water solution carbohydrates than other groups. The second group (C<sub>2</sub>) including 1, 8, 6, and 12 was observed that have greater dry weight yield, DDM, the CP and the CF and have lower ADF than other groups, the third group (C<sub>3</sub>) including accessions 3, 33, 4, 17, 18 and 25 showed that higher value of the DMY, CP, ADF and lower DDM, WSC and the CP in comparison with other groups by using Duncan' test for. The fourth group (C<sub>4</sub>) consists of accessions 5, 30, 34, 10, 29, 14 and 26 that only indicated the highest CF content and the average amount of the water solution carbohydrates and ADF in comparison with other groups, these accessions were too weak for other traits. The fifth group (C<sub>5</sub>) including accessions 7, 34, 9, 22, 20, 2, 23 and 10 showed lower DMY, the CP, ADF and AP as well as higher, DDM, WSC and CF than other

groups. The second group (including accessions 1, 8, 6 and 12) resulting from cluster analysis can be introduced as the best group on the forage yield, DDM, CP and WSC. The other groups couldn't produce considerable amount of the forage yield in spite of showing greater values of the quality traits. As the result of the factor analysis and Varimax rotation, data structure could be determined. The first factor indicated high value of the CP and AP and low amount of the, CF and the second factor indicated the high values of DDM, WSC and ADF. Both these factors were determined as the quality factors. But the DMY was studied by the third factor. These factors accounted for 83.63% of total variations.

Phenotypic correlation of traits indicated (table 5) that there wasn't any significant association between the dry weight yield and each of the quality traits. Only DDM indicated the negative correlation ( $p \leq 0.01$ ) with ADF. On the other hand, there was negative correlation ( $p \leq 0.01$ ) between CP and WSC. The CP indicated the positive correlation with the AP ( $p \leq 0.05$ ). The analysis of the phenotypic correlation of the traits indicated that there wasn't any significant association between the DMY and the quality traits. According to this analysis it's very hard to choose both the forage yield and quality simultaneously in breeding program. The study of the numerous researches indicated that there weren't significant association between the forage yield and the quality traits specific heritability (Hb) for DDM, ADF and high Hb for other quality traits. Expressing the important of the non additive gene and additive gene respectively. Also, we didn't observe any correlation among different quality traits. For example, there was positive correlation between CP and AP. Also negative correlation was between CF and WSC. On the other way, the DDM had negative correlation with ADF. Therefore, because of these variation associations, it's too hard to select desirable traits. A classification based on the cluster analysis and Duncan' test verified this variation.

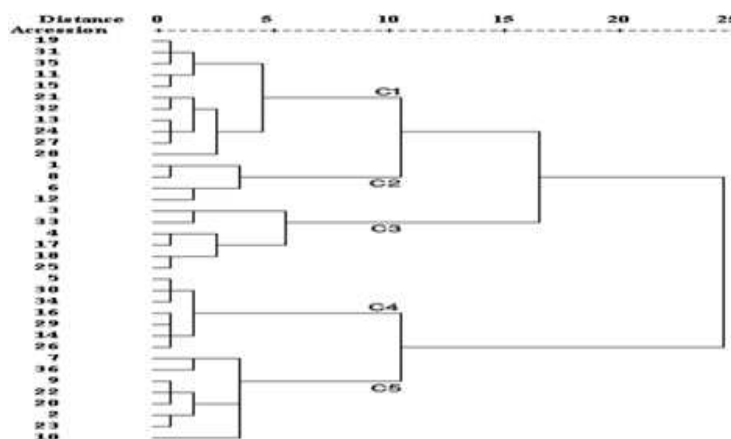


Fig 1. Dendrogram based on cluster analysis of the accessions studied by using ward method for desirable traits.

Table 4. The mean comparison of the traits based on Duncan' test ( $p=0.05$ ) for groups resulted from cluster analysis of the accessions studied

Group	DMY	DDM	CP	WSC	ADF	AP	CF
C1	1609c	52.43a	15.45a	12.23b	34.91c	7.46a	41.45b
C2	2743a	52.6a	15.45a	11.71bc	33.93c	6.38b	43.47a
C3	2243ab	49.68b	15.38a	11.27c	37.93a	7.65a	41.03b
C4	1763bc	50.15b	14.18b	12.31b	36.76b	6.84b	43.64a
C5	1757bc	52a	13.85b	13.63a	33.94c	6.32b	43.41a

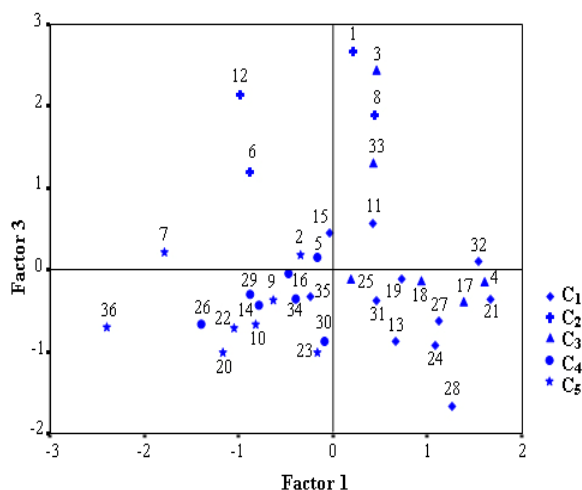
In order to determine the diversity among accessions for desirable traits, factor analysis was used (table 6). Three factors were accounted for 83.62% of total variance that showed gene values greater than 1. After Varimax rotation, factor coefficients detected that the first factor showed the high amount of the CP and AP and low amount of the CF, while the second factor indicated high value of the DDM and low value of ADF, But the third factor showed high forage dry weight yield. The similarity of all traits in three factors was great except for WSC and the CP. Therefore, we can't employ water solution carbohydrates for each of all these factors. Jafari et al, [9] investigated the genetic diversity of the different components of the yield of the *Agropyron desertorum* by using factor analysis. They reported the association between the first and the second factor with the grain yield. By using diagram of the distribution of the first and the third factors, we could realize that accessions 1,8,3,33,11 and 32 produced greater amount of the forage yield and AP than other accessions in spite of the CF was observed in lower amount. Also, we could find out that accessions 1, 8, 4, 12, 11, 32, 2 and 7 could produce the forage yield in optimum amount, DDM and WSC in greater amount, in spite of the ADF. Therefore, the diagram of the distribution of the first and the second factors could be named as diagram of the distribution of the quality traits. Hence, accessions 19, 31, 35, 11,

21, 32, 24, 27 and 28 of the cluster 1 and accessions 1, 8 of the cluster 2 are known as efficient accessions for quality traits. Cluster analysis was more affected by the quality traits.

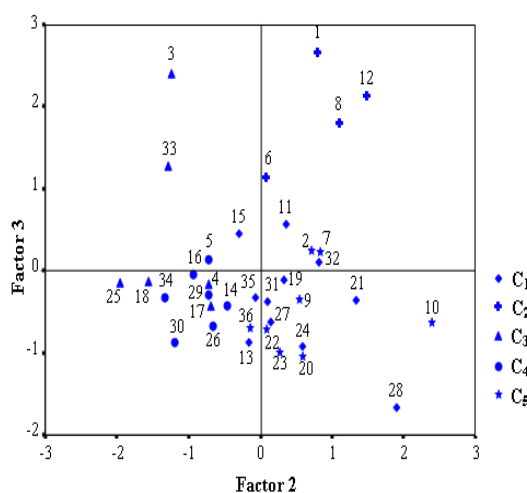
**Table 5. The phenotypic correlation of the traits studied**

Characters	DMY	DDM	CP	WSC	ADF	AD
DDM	-0.150					
CP	0.134	0.199				
WSC	-0.274	0.315	-0.475**			
ADF	0.141	-0.864**	0.035	-0.534**		
AD	-0.062	0.013	0.423*	-0.507**	0.404*	
CF	-0.019	-0.207	-0.538**	0.286	0.079	-0.797**

According to Fig 2, cluster 1 including 11, 32 cluster 2 including accessions 1, 8 and cluster 3 including 3, 33 indicated higher values for the DMY and while lower of CF than other accessions. Distribution diagram based on these three factors indicated that accessions 1, 8, 6 and 12 of the second cluster, accessions 11, 38 of the first cluster and accessions 2 and 7 of the fifth cluster had greater amount of the forage yield and DDM and lower values ADF in comparison with other accessions. In Fig 4, the distribution diagram of all accessions based on the first factor (high CP and AP and low CF) and the second factor (high DDM and low ADF) factors was showed. According to Fig 4, all accessions of the cluster 1 except for accession 13, 15 and accession 1, 8 of the cluster 2 can be introduced as accessions which had optimum values of the forage quality without any regard to the forage yield.



**Fig 2. Distribution diagram of accessions in regard to the first and the third factors based on traits studied**



**Fig 3. Distribution diagram of accessions in regard to the second and the third factors based on traits studied.**

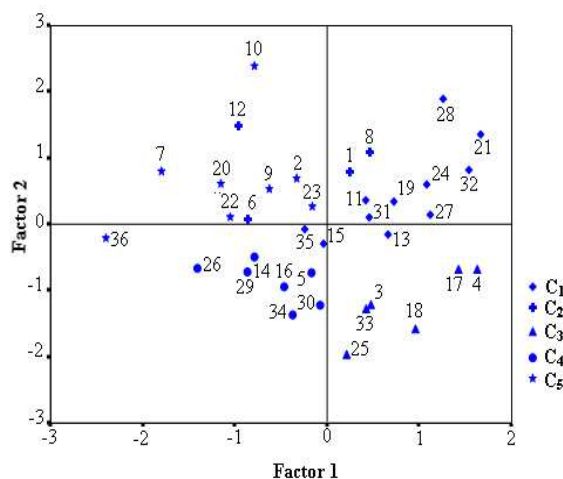


Fig 4. Distribution diagram of accessions in regard to the first and the second factors based on traits studied.

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

Characters	Factor1	Factor2	Factor3	Similarity rate
DMY	-0.030	-0.092	0.920	0.86
DDM	0.203	0.939	-0.067	0.93
CP	0.737	0.146	0.355	0.69
WSC	-0.551	0.501	-0.409	0.72
ADF	0.183	-0.962	0.042	0.96
AD	0.891	-0.246	-0.167	0.88
CF	-0.896	-0.086	0.066	0.81
Eigen values	2.767	2.014	1.073	
Variance%	39.523	28.775	15.328	
Cumulative Variance	39.523	68.298	83.626	

## CONCLUSION

Based on factor analysis and mean comparisons, it could be concluded that accessions 1, 8 and 11 were more efficient in quality traits and the forage yield than other accessions of the *Dactylis Glomerata*. However, accession 32 just indicated the largest amount of the DDM and the CP. Accessions 3, 33 in spite of accessions 21, 28 indicated the highest values of forage yield, but they couldn't produce considerable amount of the quality traits.

## REFERENCES

- [1] H. Arzani, M. Mosayyebi, A. Nikkhah, *Iranian. J. Natural Res*, **2006**. 58(4):251-260.
- [2] MD. Casler, *Theor. Appl. Genet.* **1991**. 81: 253-264
- [3] N. Charehsaz, AA. Jafari, H. Arzani, AN. Hossin, *Rang*, **2010**, 4: 121-129.
- [4] BR. Christie, AR. McElroy, second ed., *Forages*, Iowa State University Press, Iowa, USA. **1995**, 357-372
- [5] M. Farshadfar, E. Farshadfar, *J. Applied Sci.*, **2008**. 8: 1867-1874.
- [6] PC. Hoffman, KM. Lundberg, LM. Bauman, RD. Shaver, *Focus on Forage*, **2003**. 5: 1-3
- [7] AA. Jafari, V. Connolly, A. Frolich, EJ. Walsh, *Irish J. of Agricultural and Food Research*, **2003**. 42: 293-299.
- [8] AA. Jafari, SH. Javersineh, *Iranian J. of Rangelands and Forests Breeding and Genetic Research*, **2005**. 13(1):99-124.
- [9] AA. Jafari, R. Seyedmohammadi, N. Abdi, *Iranian J. of Rangelands and Forests Breeding and Genetic Research* **2007**.15(3):211-221.
- [10] R. Mohammadi, M. Khayyam-Nekouei, AF. Mirlohi, KH. Razmjoo, *Iranian J. of Rangelands and Forests Plant Breeding and Genetic Research*, **2008**.16(1): 14-26.
- [11] P. Moradi, AA. Jafari, *Iranian J. of Rangelands and Forests Breeding and Genetic Research*, **2006**, 12(2): 183-193.
- [12] PL. Peri, RJ. Lucas, DJ. Moot, *Agroforest Sys*, **2007**.70(1):63- 79
- [13] MA. Sanderson, RH. Skinner, GF. Elwinger, *Crop Science*, **2002**. 42: 224-230.
- [14] E. Santen, DA. Slepser, *Orchadgrass. Cool-season forage grasses*. American Society of Agronomy. Crop Science Society of America. Soil Science Society of America. AMA/CSSA/SSSA. Madison, WI (USA). **1996**. P. 503-534