Morphological Characterization of Barley Genotypes under Upland Rainfed Conditions

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ABSTRACT

The objective of this research was to assess the morphological characteristics of twenty five barley genotypes which were planted under field condition and their morphological traits were recorded. Analysis of variance indicated a significant difference for all of the measured traits in 25 barley genotypes which could be a result of the large variation among barley genotypes. The estimates of the coefficient of variation (CV) were high for spike length (66.2%), second internode length (38.5%), first internode length (25.4%) and seed yield (22.9%). The other remaining traits indicated moderate to low CV estimates, i.e. from 16.9% in straw weight of spike to 2.8% in harvest index of spike. The thousand seed weight ranged from 20.49 to 41.44 g and genotypes G10, G22, G23 and G24 exhibited high values. The seed yield varied from 751.1 (G3) to 170.9 (G17) kg ha⁻¹. The first internode weight, harvest index and thousand seed weight appeared to contribute on the barley seed yield. Also, the short plants with low values of plant height and regarding high values of the number of spikelet per spike and harvest index of spike could be useful as selection index for obtaining high seed yield in barley.

Keywords: Analysis of variance, morphological traits, seed yield, yield components

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INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the most important crops in world, it is widely adapted to diverse environmental conditions and is more stress tolerant than its close relative wheat. It is among the world's earliest domesticated crop species and today represents the fourth most abundant cereal in both area and tonnage harvested with a cultivated area of 46.92 million ha and a production of 141.28 million t year⁻¹ (FAO, 2016). Most of barley's global production is used for animal feed, some is malted for use in beverages, and a little as an ingredient in a range of food products while it remains a major food source in developing countries, maintaining

harvestable grain yield in harsh and marginal areas (Grando and Macpherson, 2005; Blake *et al.*, 2011). Barley is one of the most cultivated cereal crops of Iran and is produced about 2.9 million tons annually; with mean yield 1800 kg h⁻¹ from 1.6 million hectares of harvested area (FAO, 2016). The average global yield 3000 kg ha⁻¹, whereas Iran's average yield is only 60% of world's average, thus is a need to improve higher yielding cultivars to fulfill the large gap between world average yield and Iran's average yield for vertically increasing population.

Barley yield as a complex trait is the product of various contributing components and high yield is based on genetic diversity while about one-half of the accessions take the form of landraces (Parzies



et al., 2000). Yield is the result of physiological traits and is determined by number of spikes per plant, number of seeds per spike, and thousand seed weight (Ozturk et al., 2003). The yield improvement target may be reached on the basis of some yield components and selection of associated traits.

In cereal crops, yield components such as the number of spikes per plant, the number of seeds per spike, and the thousand seed weight have significant effect on seed yield and it has been found that approximately 72% of the cereal yield variations are explained by them (Ataei, 2006). The first yield component is the number of spikes per plant which causes to increase leaf area and capacity of sink while the second one is number of seeds per spike, which identifies reproductive stage and its increasing causes to decrease their weight.

Increasing the capacity of storage can help to achieve more yields and the factors, which act in the beginning of the growth season, affect the seed number. The third yield component of barley is the thousand seed weight, and the rate and length at seed filling period lead to increase its weight. Przulj et al. (2000) determined that seed yield increase results mainly from an increase of certain yield components consist on seed weight and number of seed per spike while Madic et al. (2005) found the seed yield increase results from an increase in total biomass or from harvest index improvement. According to Madic et al. (2009), the seed number per spike and the harvest index were found to be positively correlated with the seed yield but there was not any association between the seed weight per spike and seed yield. Ataei (2006) reported that number of spikes per plant, number of seeds per spike and thousand seed weight were the important traits in seed yield of barley. As late-terminal drought stress severity increased, yield components (number of spike per plant, number of seeds per spike and thousand seed weight), straw yield, seed yield and harvest index decreased significantly (Samarah et al., 2009). This study was undertaken as a practical trial in order to determine the characteristics of twenty-five Iranian genotypes of barley and the aim of this investigation is to help barley breeders, how to select suitable parental could be efficiently used in barley breeding programs.

MATERIALS AND METHOD

Twenty-five genotypes of barley were planted using based on a randomized complete block design with three replications and tillage of all plots was performed prior to sowing date and fertility is constrained by low organic matter. The experiment included 22 barley cultivars and three inbred lines, which represent a range of phenotypic variation in adaptation zone, yield potential and date of release (Table 1). The research was carried out in the experimental field of the University of Maragheh, Iran (37° 23' N, 46° I6' E). For chemical fertilization, 60 kg ha⁻¹ of nitrogen, 30 kg ha⁻¹ of phosphorus and 20 kg ha⁻¹ of potassium were applied and the weeds were controlled chemically by MCPA (2-methyl-4-chlorophenoxyacetic acid). Sowing was done by hand in plots with six rows 2.0 m in length and 0.25 m apart and the planted plot size was 3.0 m², plant density was 250-300 plants m⁻². Proper cultural practices were applied to the trial throughout the growing season according to local practices.

Table 1 The name and code of studied twenty five barley genotypes

Code	Name	Code	Name
G1	Yusef	G14	Valfajr
G2	Reyhan	G15	Makoee
G3	Ghohar	G16	Dasht
G4	Nik	G17	Shori4
G5	Karoun	G18	Afzal
G6	Torsh	G19	Kavir
G7	Nosrat	G20	Jonob
G8	Shirin	G21	Fajr30
G9	w-79-10	G22	Reyhan03
G10	D-10	G23	Aras
G11	Shori	G24	Nimroz
G12	Torkaman	G25	Sahra
G13	EH-83-7		

The harvested plot size was 1.5 m² and ten plants were tagged randomly to measure plant height (PH), first internode length (FIL), second internode length (SIL), spike length (SL), awn length (AL), stem diameter (SD), straw weight of spike (SWS), spike weight (SW), first internode weight (FIW), second internode weight (SIW), number of spikelet per spike (NSS), weight of seeds per spike (WSS), harvest index of spike (HIS), diameter of seed (DS) length of seed (LS) and seed number per spike (SNS). Also, harvest index (HI), thousand seed weight (TSW) and seed yield (SY) of each plot were recorded as well is possible. The obtained dataset was first subjected for normality test by the Shapiro-Wilk normality test via Minitab version 14.0 (Minitab, 2005). Analysis of variance (ANOVA) for all of the measured traits was performed with the conventional method using SPSS version13.0 (SPSS, 2004) statistical package. The least significant difference procedure (LSD) was used to carry out and compare mean differences.

RESULTS AND DISCUSSION

Analysis of variance indicated a significant difference (P < 0.01) for all of the measured traits in 25 barley genotypes (Table 2), such findings could be a result of the huge variation among studied genotypes and reflect their genetic differences. Such a considerable range of variations in morphological traits, yield components and yield performance provided a good opportunity for genetic improvement of barley grain seed. The estimates of the coefficient of variation (CV) were high for spike length (66.2%), second internode length (38.5%), first internode length (25.4%) and seed yield (22.9%). The other remaining traits indicated moderate to low CV estimates, i.e. from 16.9% in straw weight of spike to 2.8% in harvest index of spike (Table 2). Similar large CV amounts were reported for similar traits of the winter cereals by Ali et al. (2008). The development of different morphological traits in barley is a highly coordinated process; therefore, for an effective breeding program, it is necessary to consider all of the important traits that have a highly significant impact on seed yield performance of barley.

Table 2 Analysis of variance for measured traits of twenty five barley genotypes

sov	DF	ЬН	FIL	SIL	SL	AL	SD	SWS	SW	FIW	SIW
מ ני	2 2	2.55ns	9.44ns	21.31ns	26.11 ^{ns}	0.523ns	0.21902ns	0.00234ns	0.04293ns	0.00004 ^{ns}	0.00030
υш >	4 8 8	9.59 7.70	13.47 25.40	14.47 38.50	17.74 66.20	1.996	0.07766			~	0.00031 15.10
SOV	PF	NSS	WSS	HIS	rs	DS	SNS	포	TSW	SY	
<u>د</u>	2	64.29*	0.0666*	12.75ns	1.3698**	0.0027ns	5.05ns	10.41 ^{ns}	1.01 ^{ns}	12,0813.9ns	
Ŋ	24	141.60**	0.1990**	53.03**	1.5927**	0.2357*	68.53**	144.25**	87.33**	1,314,491.9**	
Ш	48	12.71	0.0139	4.63	0.1654	0.1150	5.79	8.70	7.29	226,267.4	
S		11.80	12.20	2.80	4.30	14.00	11.00	11.10	8.50	22.90	

Note: SOV, sources of variation; DF, degrees of freedom; CV, coefficient of variation

PH = plant height, FIL = first internode length, SIL = second internode length, SL = spike length, AL = awn length, SD = stem diameter, SWS = straw weight of spike, SW = spike weight, FIW = first internode weight, SIW = second internode weight, NSS = number of spikelet per spike, WSS = weight of seeds per spike, HIS = harvest index of spike, LS = length of seed, DS = diameter of seed, SNS = seed number per spike, HI = harvest index, TSW = thousand seed weight and SY = seed yield.

Mean values and their comparisons obtained using the LSD procedure for the measured traits of 25 barley genotypes are presented in Tables 3 and 4. According to the plant height, genotype G25 was the tallest genotype while G4, G10, G15, G19, G20 and G22 were the shortest genotypes, and plant height ranged from 29.35 to 73.32 cm with an average of 40.08 cm. Barley plant height shortening may lead to seed yield increase, but drastic stem height reduction would cause total biomass and therefore yield decrease (Przulj et al. 2000). Mahmood et al. (2006) obtained different results for plant height of wheat ranging from 62 cm to 110 cm, while Aliu and Fetahu (2010) reported a range from 71 to 79 cm for plant height in different bread wheat genotypes.

The first internode length (FIL) ranged from 7.53 to 28.13 cm with an average of 14.44 cm, and genotype G7 had the highest FIL value, while G3, G4, G5, G6, G8, G10, G14 and G15 were the thickest genotypes (Table 3). The results of this investigation indicated that genotype G7 was significantly longer (26.36 cm) than the other genotypes from second internode length (SIL) and the other studied genotypes had the lowest SIL (6.55 to 11.64 cm). According to the spike length (SL) trait (Table 3), genotype G7 had the maximum SL (24.02 cm), while all of the other remained genotypes had the minimum SL (3.88 to 8.36 cm). Similarly, in investigations of wheat genotypes, Fuma et al. (2005) found a high variation for all agronomic traits, especially spike length.

The awn length (AL) ranged from 7.12 to 15.89 mm and genotypes G4 and G14 exhibited the longest AL in contrast of genotypes G5, G8, G12, G13, G15, G16, G19 and G20 showed the shortest AL (Table 3). The stem diameter (SD) varied from 1.637 (G18) to 3.785 (G25) mm, while our genotypes showed relatively large variation (Table 3). As for the SWS (straw weight of spike), genotypes G8, G9 and G10 had the highest SWS, while genotypes G7, G15, G21 and G25 had the lowest SWS and it ranged from 0.1180 to 0.4165 g. (Table 3). The spike weight (SW) ranged from 0.6152 to 1.8548, and genotypes G10 and G11 had the maximum SW

while genotypes G7, G14, G21 and G25 had the minimum SW. In terms of the FIW (first internode weight), genotypes G1, G2, G9, G10, G11, G19 and G24 had the highest FIW while genotype genotypes G6, G14, G15, G21 and G25 had the lowest FIW (Table 3). The FIW varied from 0.0947 to 0.2301 g. As for the trait of the second internode weight (SIW) character (Table 3), genotypes G1, G9 and G24 (0.1464, 0.1747 and 0.1646 g, respectively) had the highest SIW, while genotypes G15 and G18 (0.0588 and 0.0862 g, respectively) had the lowest SIW.



Table 3 Mean comparison of measured traits (PH, FIL, SIL, SL, AL, SD, SWS, SW, FIW and SIW) in twenty five barley genotypes via least significant differences (LSD)

	DII		011	01	A.I.	0.0	0)4/0	0)4/	EDA/	ODA
	PH	FIL	SIL	SL	AL	SD	SWS	SW	FIW	SIW
G1	37.80	14.54	9.72	5.33	10.26	2.40	0.3076	1.5602	0.2080	0.1464
G2	39.26	14.90	9.62	4.39	10.01	2.56	0.3122	1.5751	0.1899	0.1382
G3	35.32	8.29	6.91	5.91	9.78	2.54	0.3060	1.4248	0.1503	0.1276
G4	29.35	12.01	7.87	5.37	15.89	2.67	0.2966	1.4576	0.1544	0.0997
G5	40.26	7.53	7.66	6.75	7.12	2.51	0.2972	1.2429	0.1422	0.1376
G6	41.03	13.38	8.48	6.03	9.83	2.06	0.2968	1.1350	0.1293	0.0971
G7	35.85	28.13	26.36	24.02	10.66	1.72	0.1852	0.8754	0.1761	0.0888
G8	44.06	10.59	8.31	6.50	8.05	2.55	0.3595	1.2433	0.1800	0.1386
G9	41.27	14.39	9.43	6.07	10.88	2.65	0.3620	1.2908	0.2138	0.1747
G10	32.80	13.55	7.81	5.83	10.66	2.53	0.4165	1.8548	0.2301	0.1435
G11	44.91	17.77	11.45	4.49	9.97	2.67	0.2626	1.7127	0.2073	0.1352
G12	37.40	14.07	8.11	5.05	8.61	2.49	0.2528	1.2756	0.1576	0.0953
G13	52.30	17.86	10.40	5.38	8.36	2.30	0.2085	1.2147	0.1717	0.1155
G14	37.48	9.60	6.55	7.53	14.24	2.78	0.2411	0.7894	0.1057	0.0886
G15	29.59	10.79	7.80	4.55	7.12	1.82	0.1737	0.8889	0.0947	0.0588
G16	40.70	16.44	9.99	3.88	8.75	2.50	0.2294	1.5033	0.1772	0.1245
G17	35.59	14.27	10.06	4.47	9.92	1.95	0.2125	0.9804	0.1463	0.1128
G18	35.65	14.22	9.29	5.28	10.88	3.79	0.2223	1.1516	0.1629	0.0862
G19	30.27	16.05	10.10	6.31	8.02	2.23	0.2509	1.3309	0.1894	0.1143
G20	31.59	14.15	9.24	4.85	8.53	2.04	0.2500	1.1317	0.1620	0.1071
G21	48.60	14.28	10.76	8.36	12.43	2.25	0.1902	0.8720	0.1277	0.0978
G22	31.49	13.63	9.75	6.05	9.60	2.46	0.2530	1.2335	0.1829	0.1418
G23	47.56	17.96	11.64	7.01	11.23	2.13	0.2453	0.8824	0.1780	0.1135
G24	48.42	18.89	10.93	5.25	9.99	2.46	0.2877	1.4859	0.2087	0.1646
G25	73.33	13.61	8.53	4.43	11.75	1.64	0.1180	0.6152	0.1255	0.0890
LSD	5.09	6.03	6.25	6.91	2.32	0.46	0.0724	0.2626	0.0420	0.0291

Note: PH = plant height, FIL = first internode length, SIL = second internode length, SL = spike length, AL = awn length, SD = stem diameter, SWS = straw weight of spike, SW = spike weight, FIW = first internode weight and SIW = second internode weight

The number of spikelet per spike (NSS) varied from 13.80 in G25 to 39.60 in G8 (Table 4), and genotypes G1, G2, G3, G5, G8, G9, G10, G11, G12 and G16 had the highest NSS but genotypes G14, G23 and G25 had the lowest NSS (Table 4). Genotypes G2, G10 and G11 had the high values of weight of seeds per spike (WSS) as 1.24, 1.41 and 1.43, respectively while genotypes G14 and G25 (0. 4823 and 0. 4887 g, respectively) had the lowest WSS. According to the harvest index of spike (HIS), genotypes G11, G13, G15, G16, G19 and G24 were the best genotypes while G14, was the worst genotype, and HIS ranged from 29.35 to 84.39% with an average of 65.40% (Table 4). The length of seed (LS) ranged from 8.41 to 11.04 mm with an average of 9.55 cm, and genotype G17 had the longest LS value, while genotype G16 had the shortest LS values (Table 4). The diameter of seed (DS) ranged from 1.885 to 2.839 mm with an average of 2.426 cm, and genotypes G2 and G11 had the highest LS value, while genotypes G14, G23 and G25 were the thinnest genotypes (Table 4).

The results of this investigation indicated that genotypes G2 and G11 had significantly high numbers (31.00 and 30.33, respectively) than the other genotypes from seed number per spike (SNS) and genotypes G14, G23 and G25 had the low numbers of SNS (13.33, 14.00 and 11.00, respectively). According to Madic et al. (2005), there is high correlation between seed number per spike and seed yield of barley indirectly through harvest index. According to the harvest index (HI) trait (Table 4), genotype G18 had the maximum HI (36.89%) followed by genotypes G4, G11, G17, G20 and G25, while genotypes G3, G5 and G12 had the minimum HI (12.15, 16.16 and 15.35%, respectively). The obtained results indicated the harvest index increase resulted in a more efficient redistribution of dry matter into seed and therefore in the seed yield increase, pointing to the possibility of using the harvest index in breeding programs for seed yield in early generations (Madic et al. 2009). The thousand seed weight (TSW) ranged from 20.49 to 41.44 g and genotypes G10, G22, G23 and G24 exhibited the heaviest TSW in contrast of

genotypes G3, G5 and G14 showed the lightest TSW (Table 4). The seed yield (SY) varied from 751.1 (G3) to 170.9 (G17) kg ha⁻¹, and our genotypes showed relatively large variation, as genotypes G1, G4, G10, G11, G13, G17, G20, G22 and G24 did not show any significant differences with the best genotype (Table 4). These favorable barley genotypes had high values of FIW, HI and TSW as well as low values of PH followed by high values of NSS and HIS.



Table 4 Mean comparison of measured traits (NSS, WSS, HIS, LS, DS, SNS, HI, TSW and SY) in twenty five barley genotypes via least significant differences (LSD)

	NSS	WSS	HIS	LS	DS	SNS	HI	TSW	SY
G1	35.70	1.1727	77.18	10.06	2.58	25.57	30.26	35.21	2739.2
G2	37.15	1.2447	79.52	8.66	2.56	31.30	30.90	30.84	2347.9
G3	39.45	1.1059	77.99	8.66	2.11	22.83	12.54	20.49	785.1
G4	32.70	1.1439	79.00	10.49	2.47	24.49	34.63	35.30	2803.6
G5	36.61	0.9304	75.21	8.75	1.89	24.81	16.16	23.45	1580.5
G6	29.70	0.8218	72.63	8.82	2.39	19.25	23.12	27.56	1634.9
G7	25.90	0.6856	77.77	9.70	2.03	17.10	22.14	31.23	1586.5
G8	39.60	0.9769	75.60	8.85	2.16	25.12	20.38	28.26	1533.5
G9	34.50	0.9428	72.66	9.54	2.25	24.63	18.78	26.17	1977.4
G10	35.90	1.4133	76.79	10.08	2.68	24.64	31.56	40.06	2848.6
G11	35.00	1.4281	84.39	9.23	2.68	30.47	33.55	32.49	3169.2
G12	34.20	1.0270	80.39	10.47	2.38	24.28	15.35	28.13	2169.2
G13	33.25	0.9883	82.17	9.73	2.74	24.41	27.86	31.10	2536.4
G14	19.40	0.4887	65.40	8.85	2.80	13.32	18.44	22.76	886.0
G15	26.05	0.7648	84.07	8.90	2.41	20.07	29.34	28.41	2115.5
G16	35.55	1.2089	82.32	8.41	2.46	22.13	22.10	31.63	1530.1
G17	25.90	0.6819	72.85	11.04	2.77	21.49	32.99	36.03	3170.9
G18	28.85	1.0634	78.58	9.76	2.44	20.76	36.90	31.95	1803.8
G19	33.30	1.0875	81.75	9.84	2.30	23.42	30.51	31.90	2232.6
G20	30.55	0.8683	77.16	10.45	2.27	22.35	33.04	35.25	2533.5
G21	22.20	0.6844	78.37	8.90	2.13	17.22	20.07	27.98	1463.4
G22	24.55	1.0017	80.64	9.30	2.52	19.28	31.24	38.34	2562.8
G23	17.65	0.6886	76.09	10.06	1.96	13.75	26.05	41.44	1962.0
G24	29.75	1.2265	81.80	10.48	2.84	22.25	31.52	38.54	2723.2
G25	13.80	0.4823	79.64	9.82	2.84	11.09	32.25	35.46	1338.1
LSD	5.85	0.1933	3.53	0.6677	0.5568	3.95	4.84	4.43	780.9

Note: NSS = number of spikelet per spike, WSS = weight of seeds per spike, HIS = harvest index of spike, LS = length of seed, DS = diameter of seed, SNS = seed number per spike, HI = harvest index, TSW = thousand seed weight and SY = seed yield

The results indicated high variability can be affected by various factors and selections made by breeders might be the reason for genetic differences among the origin of plant materials or due to natural selection. The results of present study indicated that some genotypes from the same origins close to each other are genetically similar to

each other and similar results on genetic diversity in the morphologic characterization of barley were reported by Ataei (2006) and Madic (2002) and in the molecular characterization were reported by Fernandez et al. (2002) and Malysheva-Otto et al. (2006). Previous investigations on cereals have demonstrated significant differences among landraces

and cultivars for seed yield, yield components and morphological traits (Joshi *et al.*, 2004; Dagustu, 2008). In general, some environmental factors such as rainfall, drought and biotic stresses influence yield as well as temperature and rainfall at flowering time while selection for higher yield may be effective by improving yield components traits, as it has been shown by Khaliq *et al.* (2004) and Anwar *et al.* (2009) in various studies. Such type of breeding program may lead to the improvement of the economic traits in general and farmers living in the semi–arid areas in particular.

The observed high variation among barley genotypes due to morphological traits would be reflecting their genotypic differences or can be explained on the basis of the environmental factors (Moriss, 2009). The morphological traits are subject to both natural and artificial selection, aside from their high environmental dependence and it is clear that if there is an association between the loci controlling the targeted morphological trait, the influence of

environmental factors will be low and there may be some reasons for the above problem; at first, selection based on one environment has not been performed long enough to determine the various genotypes, secondly, fitness responsible genes to one environmental condition are not unique to that environment and may confer fitness to the other environments, and thirdly, adaptation to a different environments is not based on accretion of random genes but rather on a limited set of specific genes (Malysheva–Otto et al., 2006).

CONCLUSIONS

The present study indicated that the first internode weight, harvest index and thousand seed weight appeared to contribute on the grain yield. Also, the short plants with high values for the number of spikelet per spike as well as harvest index of spike could be useful as selection index for obtaining high seed yield in barley.

REFERRENCES

- Ali, Y., B.M. Atta, J. Akhter, P. Monneveux and Z. Lateef. 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. Pak. J. Bot. 40: 2087–2097.
- Aliu, S. and S. Fetahu. 2010. Determination on genetic variation for morphological traits and yield components of new winter wheat (*Triticum aestivum* L.) lines. Not. Sci. Biol. 2: 121–124.
- Anwar, J., M.A. Ali, M. Hussain, W. Sabir, M.A. Khan, M. Zulkiffal and M. Abdullah. 2009. Assessment of yield criteria in bread wheat through correlation and path analysis. J. Animal Plant Sci. 19: 185–188.
- Ataei, M. 2006. Path analysis of barley (Hordeum vulgare L.) yield. Tarim Bilimleri Dergisi 12: 227–232.
- Blake, T., V. Blake, J. Bowman and H. Abdel-Haleem. 2011. Barley Feed Uses and Quality Improvement. pp 522–531. *In:* S.E. Ullrich, (Ed), Barley: Production, Improvement and Uses, Wiley-Blackwell, New Jersey, United States.
- FAO (Food and Agriculture Organization of the United Nations). 2016. FAOSTAT Available Source: http://www.fao.org/faostat/en/#data/QC, July 1, 2018.
- Fernandez, M., A. Figueiras and C. Benito. 2002. The use of ISSR and RAPD markers for detecting DNA polymorphism, genotype identification and genetic diversity among barley cultivars with known origin. Theor. Appl. Genet. 104: 845–851.



- Fuma, H., P. Stephen Baenziger, B.S. Beecher, R.A. Graybosch, K.M. Eskridge and L.A. Nelson. 2005. Genetic improvement trends in agronomic performances and en-use quality characteristics among hard red winter wheat cultivars in Nebraska. Euphytica 144: 187-198.
- Grando, S. and H.G. Macpherson. 2005. Food barley: importance, uses and local knowledge. pp 140–147. In: Proceedings of the International Workshop on Food Barley Improvement, Aleppo, Syria.
- Khaliq, I., N. Parveen and M.A. Chowdhry. 2004. Correlation and path coefficient analyses in bread wheat. Intern. J. Agric. Biol. 6: 633-635.
- Madic, M., D. Kneževic, A. Paunovic and V. Zečević. 2009. Inheritance of stem height and secondinternode length in barley hybrids. Genetika 41: 229-236.
- Madic, M., A. Paunovic, D. Đurovic and D. Kneževic. 2005. Correlations and path coefficient analysis for yield and yield components in winter barley. Acta Agric. Serb. 10: 3-9.
- Mahmood, Q., W.D. Lei, A.S. Qureshi, M.R. Khan, Y. Hayat, G. Jilani, I.H. Shamsi, M.A. Tajammal and M.D. Khan. 2006. Heterosis, correlation and path analysis of morphological and biochemical characters in wheat (Triticum aestivum L. Emp. Thell). Agric. J. 1: 180–185.
- Malysheva-Otto, L.V., M.W. Ganal and M.S. Röder. 2006. Analysis of molecular diversity, population structure and linkage disequilibrium in a worldwide survey of cultivated barley germplasm (Hordeum vulgare L.). BMC Genet. 7: 1-14.
- Minitab. 2005. Minitab User's Guide. version 14. Minitab Institute, Harrisburg, Pennsylvania, USA.
- Morris, J.B. 2009. Characterization of sesame (Sesamum indicum L.) germplasm regenerated in Georgia, USA. Genet. Resour. Crop Evol. 56: 925-936.
- Ozturk, A., O. Caglar and F. Sahin. 2003. Yield response of wheat and barley to inoculation of plant growth promoting rhizobacteria at various levels of nitrogen fertilization. J. Plant Nutrit. Soil Sci.166: 262-266.
- Parzies, H.K., W. Spoor and R.A. Ennos. 2000. Genetic diversity of barley landrace accessions (Hordeum vulgare ssp. vulgare) conserved for different lengths of time in ex situ gene banks. Heredity 84: 476-486.
- Przulj, N., V. Momčilović and V. Đurić. 2000. Good technological quality and stable yields the main objectives of barley breeding at the Novi Sad institute. A Period. Sci. Res. Field Veget. Crops 33: 151-162.
- Samarah, N.H., A.M. Algudah, J.A. Amayreh and G.M. McAndrews, 2009. The effect of late-terminal drought stress on yield components of four barley cultivars. J. Agron. Crop Sci. 195: 427-441.
- SPSS. 2004. SPSS User's Guide. SPSS Institute, Chicago, IL, USA.