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Investigation on genetic diversity in *Triticum turgidum* L. var. *durum* using agro-morphological characters and molecular markers

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Abstract

The present study was carried out to assess the genetic diversity in durum wheat genotypes under rainfed and irrigation conditions in dryland agricultural research institute (DARI) during the 2011-13 cropping seasons. Results of multivariate analysis revealed that the number of fertile spikes, number of grain per spike and days to physiological maturity were highly effective on grain yield under both conditions. A clustering analysis based on both agro-morphological and molecular characters indicated a good level of genetic diversity. Low correlation was found between the diversity obtained by markers and the agro-morphological traits. The Sardari genotype had the maximum genetic distance from other genotypes in the agro-morphological analysis. The average polymorphic percentage for inter simple sequence repeat (ISSR) primers was 83.46%. Primers, IS6, IS25, IS14 and IS27 had the highest resolving power. Maximum genetic distance among the genotypes with the Jaccard similarity (0.314) was between G6 (19E-M84859) and G17 (19E-M142070). The findings would help selecting suitable genotypes for enhancing the yield of durum wheat.

Key words: Durum wheat, agro-morphological traits, ISSR marker, genetic diversity, multivariate statistics methods

Introduction

Durum wheat (*Triticum turgidum* L. var*. durum*) is the second important crop under dryland condition in many countries; it is a major source of human food in the world (Kahrizi et al. 2010). It has gained importance due to the production of semolina flour used in the food industry, especially pasta (Khayatnezhad et al. 2010). This crop constitutes about 10% of the world's wheat production and cultivated on 21 million hectares of lands worldwide, including approximately 11 million hectares in the Mediterranean regions (Karimizadeh et al. 2013). In Iran, about two-thirds of rainfed wheat areas occupy arid and semi-arid regions. Drought stress is one of the most important factors to affect the production of durum wheat (Mohammadi et al. 2011; Khayatnezhad et al. 2010; Alaei et al. 2011). Developing new cultivars with suitable advantages under water stress conditions is a basic challenge for wheat improvement programmes (Moayedi et al. 2010). The genetic diversity among wheat genotypes is very important in reducing genetic vulnerability to various diseases. Most of genetic diversity investigations have been mainly devoted to agro-morphological traits (Marti and Slafer 2010). Morphological traits can be measured easily; they also have variable heritability. Multiple linear regression method is used to determine the role of yield components in increasing the yield (Farshadfar 2004). Factor analysis is an effective statistical method for justifying the existing diversity in plant population (Johnson and Wichern 1992). The cluster analysis is useful for classifying the genotypes based on phenotypic and genotypic diversity. The euclidean distance coefficient and the unweighted paired group method with arithmetic (UPGMA) can show the similarity among individuals better than other methods (Mohammadi and Prasanna 2003). Wolde et al. (2016) classified 68 durum wheat genotypes into five groups by cluster analysis, where 4 principal components accounted 75.9% of the total variation. Mengistu et al. (2016) showed that durum wheat landraces manifested larger genetic diversity. Genetic diversity analysis based on the molecular data has many applications nowadays as it has become an excellent

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tool for obtaining genetic information (Salahvarzi et al. 2013). DNA markers are widely used in agriculture because of their development and discrimination capability as well as their certainty and frequency. ISSR markers may be considered as worthwhile tools to analyze durum wheat genome due to the high length of primers, high annealing temperature and the simplicity of the method (Ammiraju et al. 2001). ISSR markers have been widely implemented for genetic variability studies by many researchers in wheat (Najaphy et al. 2012; Sofalian et al. 2009; Zamanianfard et al. 2015 and Sadigova et al. 2014) and other crops (Durgesh et al. 2005; Singh et al. 2016). Based on ISSR markers, Tarinejad et al. (2016) grouped 20 bread wheat cultivars displaying a high average polymorphism and efficiency. Etminan et al. (2016) also evaluated durum wheat germplasm to study genetic variation using ISSR markers and reported high levels of polymorphism which indicated that these markers are useful tools for detection of genetic variation in durum wheat. The objectives of this study were to use agro-morphological traits and ISSR markers to assess genetic diversity levels among durum wheat genotypes.

Materials and methods

Plant materials and station description

The study was conducted in the experimental station of Sararoud Dryland Agricultural Research Institute (DARI), which is located in Kermanshah province during the 2011-13 growing seasons (geographical coordinates; longitude of 47° 16' 48" and latitude of 34° 19' 12" and altitude of 1351 meteres above sea level with an average rainfall of 425 mm). In this research, the yield (g/m^2) of 17 wheat genotypes, including Saji, Zardak and Sardari genotypes, as control in irrigation and rainfed conditions (two times irrigations in flowering stage for the maturity of each stage as 25 mm) were investigated by randomized complete block design (RCBD) with three replications. Each genotype was cultivated in six rows of six meteres at 20 cm spacing. The names of wheat genotypes with their origins are given in Table 1.

Measurement of agro-morphological traits and statistical analysis

The pertinent traits and measuring units with the abbreviation of names have been given in Table 2. Various types of statistical analysis, including multiple linear regression, factor analysis and cluster analysis has been performed on morphological data. Euclidean

Table 1. Name, pedigree and mean yield of 17 durum wheat genotypes

No.	Name/pedigree	Mean yield (g/m^2)
G1	Saji	763.13
G2	Zardak	569.80
G3	Sardari	703.08
G4	19E-TOPDY	611.53
G5	19E-RASCON	560.80
G6	19E-M84859	557.87
G7	19E-M141979	661.14
G8	19E-M141982	713.23
G9	19E-M141994	685.64
G10	19E-M141995	798.14
G11	18E-M142005	678.32
G12	19E-M142017	818.09
G13	19E-M142025	608.83
G14	19E-M142038	730.05
G15	19E-M142045	662.18
G16	19E-M142069	710.53
G17	19E-M142070	669.78

Table 2. The studied traits and measuring units with the abbreviation of names

Row	Trait	Measuring units	Abbre-viation of names
1	Plant height	cm	PH
2	Spike length	cm	SL
3	Peduncle length	cm	PL
4	Peduncle extrusion	cm	PE
5	Flag length	mm	FL
6	Thousand kernels weight	g	TKW
7	Grain yield	g/m^2	GY
8	Biological yield	g/m^2	BY
9	Harvest index	%	HI
10	Number of grain/spike	-	NSPS
11	Total number of tillers	-	NTT
12	The number of fertile spikes	-	NFS
13	The number of non-fertile spikes	-	NNFS
14	Straw yield	g/m^2	SY
15	Days to physiological maturity	day	DM
16	Days to heading	day	DH
17	Days to booting	day	DB
18	Days to anthesis	day	DA
19	Canopy temperature	centigrade	CT
20	Chlorophyll fluorescence (*Fv*/*Fm*)	$m^{-2}s^{-1}$ mmol	CHF
21	Stomatal conductance	$m^{-2}s^{-1}$ mmol	SC
22	Relative water content	g	RWC
23	Relative water loss	g	RWL
24	SPAD	SPAD	SPAD
25	Relative growth rate	g/g.gdd	RGR

distance formed the distance matrix and (UPGMA) had been used for genotypes classification. Next, the related dendrograms were drawn and finally the cophenetic matrix was obtained to test the matching of dendrograms and the distance matrix. To determine the correlation between the similarity matrix and cophenetic, the mantel test was performed. Statistical analysis was conducted by using SPSS 20 and NTSYS-pc2.02e software.

DNA extraction, ISSR amplification and data analysis

A leaf sample of 0.12g was ground and DNA was extracted by a modified cetyltrimethylammonium bromide (CTAB) method according to Saghai- Maroof et al. (1984). The DNA content was measured fluorometerically. The 31 sequence ISSR primers were designed by bioinformatics tools. DNA amplifications were performed in a T100 Bioradat Thermal cycler with 20 µl reaction volume containing 10 µl master mix of Sinaclon Co. 2 µl genomic DNA, 2 µl primer and 6 µl ddH_2O. The PCR reaction conditions consisted of 4 min at 94^oC for initial denaturation, followed by 10 cycles of polymerization reaction, each consisting of a denaturation step of 30s at 94^oC, an annealing step of 45s at primer's annealing temperature+5^oC (annealing temperature was reduced by 0.5^oC in each of the 10 cycles), and a polymerization step of 2 min at 72^oC. The next 25 cycles consisted of 30s at 94^oC, an annealing step of 45s at primer's annealing temperature, and a polymerization step of 2 min at 72^oC, followed by a final polymerization step of 7 min at 72^oC. A total of 16 primers were used for PCR amplification. The samples (8 µl) was loaded on 1.5% agarose gels with 1X TBE buffer and bands visualized under gel documentation system. ISSR-amplified fragments were scored for band presence (1) or absence (0) and a binary qualitative data matrix was constructed. Polymorphic information content (PIC) for each locus was obtained by the formula suggested by Botstein et al. (1980). Marker index (MI) was calculated by the formula according to Kumar et al. (2009). Resolving power was obtained by Altintas et al. (2008). Clustering analysis for grouping the genotypes was performed by the FIND method based on the Jaccard similarity coefficient (Jaccard 1908) by NTYSYS-pc ver 2.02 software. Similarity matrix was used for the clustering analysis. It was conducted SAHN via UPGMA (Rohlf 1998) and the results were presented as dendrograms. The similarity and cophenetic matrixes were compared by using MxComp of the software package NTYSYS-pc according to the Mantel test procedure (Mantel 1967). Principle coordinate analysis was performed by the similarity matrix.

Results and discussion

Stepwise linear regression

The results of the regression analysis of 17 genotypes of durum wheat under rainfed condition in the 2011-12 crop year indicated that the number of grains per spike, the total number of fertile spikes (fertile ear bearing tillers) and thousand kernel weight had the highest effect on grain yield (explaining 95% of yield variation) facilitating selection to achieve higher yield. While under irrigation condition canopy temperature had a negative effect on yield and genotypes and hence the selection was based on days to physiological maturity and total numbers of fertile spikes (explaining 83% of yield variation) with highest efficiency. Rastegar (2008) reported the genotypes with high canopy temperature lose more water because of more evaporation and respiration which finally cause the yield decline under irrigation condition. Similar to the result of present study, Taghizadegan et al. (2014) and Ahmadizadeh et al. (2011) reported that the number of grains/ spike, the number of spikes/unit area, spike length and thousand kernel weight as the most effective traits for stable yield.

Since the grain yield is a polygenic quantitative trait, the selection based on grain yield alone is generally not effective. Hence, it is important to diagnose the traits with a close relationship to grain yield for increasing the efficiency of plant breeding programmes (Singh and Singh 1973). According to the present study under rainfed condition in the 2012-13, the number of fertile spikes, number of grains/ spike, and days to physiological maturity had the highest effect on grain yield (explaining 89% of yield variation). Under irrigation condition, days to physiological maturity had negative effect on yield and the genotypes with this trait were not good candidates for selection and hence the selection based on the traits *viz*., number of fertile ear bearing tillers and the number of grains/spike (explaining 62% of yield variation) would be more efficient. Therefore, under irrigation condition, selection for reduction of maturity period would increase the yield by increasing some components of yield. Mollasadeghi and Shahryari (2011) observed that number of spikes per unit area and grain weight/spike are important parameters in selecting high yielding genotypes. Kavyani et al. (2013) and Pour Siahbidi et al. (2013) indicated that, days to

physiological maturity, number of grain per spike and number of fertile spikes were the most effective traits contributing to higher yield in durum.

Factor analysis

The factor analysis was performed for 17 genotypes of durum wheat under the rainfed condition during 2011-12. The 25 traits decreased to five new factors (justified 81% of variation), so that the assessment of genotypes based on these factors can increase the efficiency of selection. The selection based on factors 1 to 5 increases the yield and influence the peduncle length, harvest index, yield components, biological yield, days to maturity and spike length concurrently; this illustrated the existence of wide range of variation for most of the traits among durum wheat genotypes. Under irrigation condition, the results classified variables to five new variables (justified 83% of variation). The selection based on new factors 1 to 5 can increase the yield, plant height, spike length, thousand kernel leaf weight, florescence chlorophyll and flag leaf length simultaneously. Khayatnezhad et al. (2010) and Ahmadizadeh et al. (2011) introduced first and second factors as the most effective factors under normal and moisture stress for selection of superior genotypes. In the present analysis we classified 25 traits into six new factors (justified about 86% of variation), under rainfed condition in the 2012-13 crop year and thus selection based on the first to sixth factors may increase the grain yield, yield components, early maturity and reduced plant height simultaneously.

Early maturity should be considered in genotypic selection, particularly in dry regions, because precocious genotypes can escape from the stress especially, the terminal heat stress. But, there is an inverse relationship between early maturity and plant yield, because these genotypes have low production due to the lack of enough time for developing carbohydrates in stems. So, based on these six factors, genotypes which can attain spike stage after spring coldness make the optimal use of growth period and humidity should be selected for higher yield. Considering the harvest problems in dry regions, dwarf genotypes are not appropriate as also reported by Rastegar (2008). Under irrigation condition in the 2012-13 crop year, the selection based on first to sixth factors (justified about 86% of variation) would increase the value of yield components, biological yield as well as physiological properties at the same time. The increase in the grain yield results from the increased biological yield and harvest index. Selection based on stomatal conductance and chlorophyll fluorescence increases plant photosynthetic efficiency and consequently improves plant yield. With more openness of stomata, stomatal conductance increases and photosynthetic efficiency improves under irrigation condition (Koocheki and Sarmadnia 1999).

Cluster analysis

The Mantel test based on the factor analysis under rainfed condition in the year 2011-12 showed a good fit of the cophenetic values to the similarity matrix (r = 0.83). The cut of dendrogram (mean = 3.008) classified 17 genotypes into five groups. Under irrigation condition in the 2011-12, the correlation was high (r = 0.84) and the genotypes were also grouped into 5 clusters with similar mean value. Under both irrigation and rainfed conditions the genotypes *viz*., G1(Saji), G9(19E-M141994), G4(19E-TOPDY), G11(18E-M142005), G12(19E-M142017), G17(19E-M142070), G13(19E-M142025) and G15(19E-M142045) were placed in first group and so were G7(19E-M141979) and G8 (19E-M141982) placed in the first group under the rainfed condition. However, under irrigation condition an independent second group was formed with high yield. Also, G10 (19E-M141995) and G16 (19E-M142069) were placed in the first group under rainfed condition but they formed the second independent group with the highest yield under irrigation condition. G2 (Zardak) was placed in the first group under the rainfed condition and placed in the fourth independent group with lowest yield under irrigation condition. G6 (19E-M84859) formed an independent first group under the rainfed condition and had the highest yield under irrigation condition. G5(19E-RASCON) formed the third group with the lowest yield under the rainfed condition and was placed in the first group under irrigation condition. G14 (19E-M142038) formed the independent second group with a mean yield under rainfed condition; it was placed in the first group under irrigation condition. G3 (Sardari) formed an independent fourth group with low yield under the rainfed condition and was placed in the fifth group under irrigation condition. The group with G3 (Sardari) had the highest genetic distance compared to other groups. Similar to the present study, Tahmasebi et al. (2013) and Taghizadegan et al. (2014) investigated durum wheat genotypes for agro-morphological traits, where cluster analysis showed that some groups have values higher than mean yield. Similarly, Wolde et al. (2016) conducted a study to assess the genetic diversity and cluster analysis in 68 durum wheat

accessions and genotypes and grouped them into five clusters. The distance between clusters was highly significant which enhances the probability select potential genotypic groups upon crossing. In the present study, the correlation between the similarity and copheneticmatrix was 0.72 under rainfed condition in the year 2012-13.

The cut of dendrogram (mean = 3.35) classified 17 genotypes into four groups and the correlation coefficient was 0.79 under irrigation condition. With the similar cut of dendrogram (mean = 3.35) the genotypes were grouped into five groups in other environment. G1(Saji), G12 (19E-M142017), G4 (19E-TOPDY), G10 (19E-M141995), G16 (19E-M142069), G17 (19E-M142070), G8 (19E-M141982), G11 (18E-M142005), G15 (19E-M142045) and G14 (19E-M142038) were grouped in first class in both the conditions. G6 (19E-M84859) and G7 (19E-M141979), which were in the first group in the rainfed condition, constituted independent second group under irrigation condition with low yield as compared to other groups. G5 (19E-RASCON) which was in the first group under the rainfed condition, with G2 (Zardak) also classified in the second group under the rainfed condition and constituting an independent fourth group with low yield as compared with other groups under irrigation condition. G13 (19E-M142025) placed in the second group under the rainfed condition was transferred displaying to the first group under the irrigation condition. Similarly, G9 (19E-M141994), placed in the third group under rainfed condition had the lowest yield as compared to other groups however, showed highest yield while retaining its independent group under irrigation condition. G3 (Sardari), constituted in the last group under the rainfed condition with higher yield, fell in last group under the irrigation condition while retaining its high yield showing highest genetic distance from other groups making useful from other groups hence suitable in future plant breeding programmes. Sabaghnia et al. (2014), Ajmal et al. (2013) and Aharizad et al. (2012) carried out cluster analysis for agro-morphological traits and classified wheat genotypes into many groups and some of them were identified to be good candidates for genetic improvement. Dehghan et al. (2011) classified 102 durum wheat lines using cluster analysis into four groups. Rainfall and temperatures in the dryland area of Iran show unpredictable fluctuations within cropping seasons. Considering the ability of durum genotypes to produce high and satisfactory yield over a wide range of stress, grouping of genotypes for the improvement of a crop's productivity under stressed conditions is very important in order to full fill the food needs of the country.

Molecular analysis

Out of 31 ISSR primers, 16 produced a total of 156 bands among the genotypes with an average of 9.75 bands for each primer ranging from 7 (IS9 and IS15) to 15 (IS25) bands. The most number of bands were produced by G2(Zardak) (119 bands) and the least by G17(19E-M142070) (79 bands). The total number of polymorphic markers and the average of percentage of polymorphism were 130 (average of 8.12 bands for each primer) and 83.46%, respectively with a range from 57.1for primer IS15 to 100% for primers IS4 and IS14 (Table 3) indicating considerable diversity at the DNA level. The ISSR marker profile produced by primer IS27 in the agarose gel is given in Fig. 2. The average resolving power (RP) index for primers was 6.98. The mean MI and PIC for the used primers are 2.32 and 0.28, respectively. The primers *viz*., IS6, IS25, IS14 and IS27 produced high amount of MI so indicate more resolving power of these primers as compared to others. Guasmi et al. (2012) examined genetic diversity in barely using ISSR markers and reported an average of polymorphic percentage and resolving power index. Generally, the MI index can be used as a general criterion for the forecasting efficiency of the marker in a set of germplasm (Powell et al. 1996). The PIC criterion determines the resolving power of each primer by the number of alleles at a locus and the relative frequency of alleles. The higher magnitude of PIC in double allele loci is 0.5, which occurs only when the frequency of alleles is equal in the population (Mateescu et al. 2005). The marker index also applies the number of genetic polymorphic loci results from the primers to evaluate their efficiency and resolving power (Powell et al. 1996). The higher amount of MI and PIC for the primers, IS6, IS25, IS14 and IS27 indicated the proper selection and high efficiency of these primers to distinguish and examine the genetic relationships among the durum wheat genotypes so that they can be used as a potential marker for screening wheat genotypes to be utilized in future studies,

Cluster analysis based on the ISSR markers grouped 13 genotypes in group I and the remaining four genotypes *viz*., G6(19E-M84859), G14(19E-M142038), G9(19E-M141994) and G17(19E-M142070) were classified independently in II group as depicted in Fig. 3. Considerable distances between the groups and the genotypes indicated that durum wheat genotypes are also diverse at molecular level. The

Table 3. Primer name and sequence along efficiency and number of polymorphic markers produced by ISSR primers used in 17 durum wheat genotypes

Primer name and sequence	Annealing temp.	No. of total bands	No. of polymorphic bands	Polymorphism %	Resolving power index (Rp)	PIC	MI
IS1(DBDACACACACACACACA)	52,1	13	8	61.53	4.58	0.26	2.10
IS3 (GACAGACAGACAGACA)	49,2	9	8	88.89	7.04	0.28	2.27
IS4(AGAGAGAGAGAGAGAGYT)	52,5	8	8	100.00	6.34	0.29	2.36
IS5(ACACACACACACACACC)	52,8	8	6	75.00	4.95	0.28	1.73
IS6(GAGAGAGAGAGAGAGARC)	54,8	12	11	91.67	13.75	0.34	3.76
IS7(CTCTCTCTCTCTCTCTG)	52,8	9	8	88.89	9.18	0.29	2.33
IS9(CACACACACACACACAG)	52,8	7	6	85.71	4.42	0.27	1.62
IS11(ACACACACACACACACYA)	52,5	9	9	100.00	12.24	0.29	2.68
IS12(GTGTGTGTGTGTGTGTYG)	54,8	9	8	88.89	4.11	0.22	1.82
IS13(GAGAGAGAGAGAGAGAYC)	54,8	10	7	70.00	5.21	0.27	1.95
IS14(AGAGAGAGAGAGAGAGT)	50,4	10	10	100.00	10.55	0.30	3.09
IS15(ACACACACACACACACYG)	54,8	7	4	57.14	4.47	0.32	1.30
IS23(CTCTCTCTCTCTCTCTRC)	54,8	8	6	75.00	2.66	0.19	1.14
IS25(CACACACACACACACARG)	54,8	15	12	80.00	11.28	0.31	3.72
IS27(TGTGTGTGTGTGTGTGRC)	54,8	11	9	81.81	6.42	0.30	2.73
IS28(TCTCTCTCTCTCTCTCG)	52,8	11	10	90.90	4.49	0.24	2.47
Mean		9.75	8.1	83.46	6.98	0.28	2.32

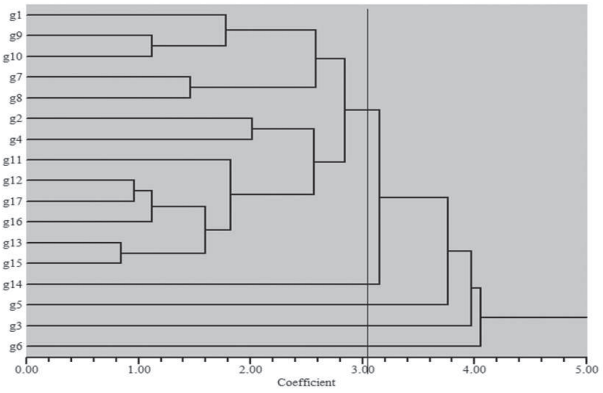

Fig. 1. Cluster analysis under rainfed condition based on agro-morphological characters

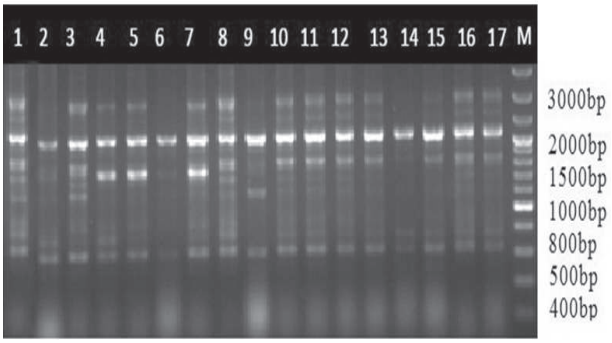

Fig. 2. Banding pattern of amplified DNA from 17 wheat genotypes by IS27

most distance among genotypes with the similarity amount of 0.314 was between G6(19E-M84859) and G17(19E-M142070) facilitating researchers to select suitable parent to create variability in order to select high yielding genotypes. The mean similarity index observed was 0.59. The dendrogram generated using Jaccard's similarity index showed that the observed genetic diversity among promising durum wheat materials collected from the western region of Iran are differentially structured. Sofalian et al. (2009) reported a good amount of genetic diversity at molecular level among Iranian landraces collected from the north-west regions indicating that ISSR markers can determine the genetic variation in wheat germplasm. The molecular analysis carried out by Sadigova et al. (2014) using molecular markers is useful for genetic differentiation of wheat accessions, making selection strategies and the genetic improvement of crops. In the present study, principle coordinate analysis was performed using NTSYS spc 2.02 and the first two components only justified approximately 70% of variance and therefore, two dimentional graph placed the genotypes in different sections (Fig. 4). The results indicated that the first ten components justify 90% of

data variance and the used primers showed acceptable polymorphisms and thus pointing out that the ISSR markers can effectively be used to study the genetic diversity of wheat cultivars. The present study further indicated that ISSR markers were highly effective for assessing the diversity in promising durum wheat genotypes by grouping the genotypes by both the methods of clustering and principle coordinate analyses. Sadigova et al. (2014), Zamanianfard et al. (2015) and Azizi et al. (2014) reported that, ISSR markers were superior to other markers in revealing more informative bands in a single amplification and are more specific due to the longer SSR-based primers. The higher primer annealing temperature might have enabled higher-stringency and greater band reproducibility amplifications. It can be emphasized that the use of ISSR markers must be the technique of choice for the first estimation of the genetic diversity in durum wheat germplasm. The genotypes showed diverse agro-morphological traits and distinct ISSR marker patterns (Figs. 1 and 3) suggesting the

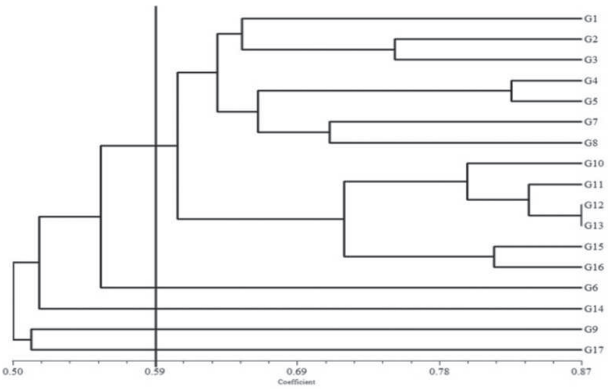

Fig. 3. Cluster analysis based on ISSR markers

importance of the evaluation of genotypic performance and to identify the best genotypes for a particular conditions. The analysis of both agro-morphological and molecular characters classified the 17 durum wheat genotypes into five groups and the results revealed that the genotypes differed from morphological characters and ISSR markers. It may indicate the effect of the conditions on the performances of the materials. Both methods of similarly index grouped G1(Saji), G4(19E-TOPDY), G11(18E-M142005), G12(19E-M142017) and G15(19E-M142045) together. Low correlation was found between the diversity obtained by molecular markers and agro-morphological traits. Mart´nez et al. (2005) pointed out the molecular markers

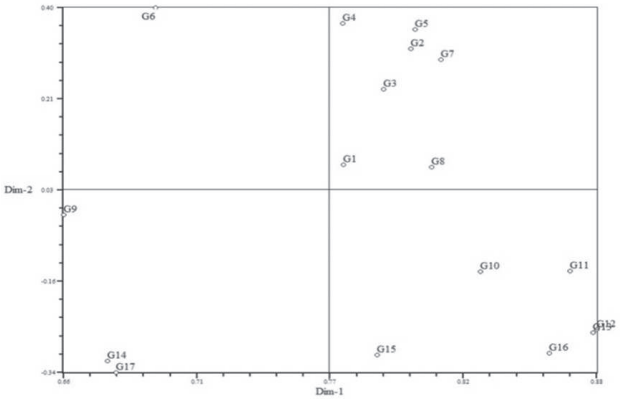

Fig. 4. Two-dimensional graph results from the principle coordinate analysis based on the Jaccard similarity matrix

and morphological traits necessarily do not have closely matching results. It is legitimate because molecular markers cover a larger proportion of the genome than the morphological markers and should survey more morphological characters and molecular markers for coordinating the results of these two methods. In this regard, Najaphy et al. (2012) showed that ISSR markers provided sufficient polymorphism and reproducible fingerprinting profiles for evaluating the genetic diversity of wheat genotypes. The results of present investigation demonstrated the usefulness of the methods by determining the genetic diversity in durum wheat. It could be concluded that studied durum wheat genotypes were diverse both under rainfed and irrigated conditions. This property of genetic diversity should be exploited for enhancement of yield and resistance to drought stress in durum wheat, especially terminal drought under rainfed conditions. The molecular diversity assessed in the present study in conjunction with agro-morphological characters of durum wheat can be useful in breeding programmes which largely depends on the magnitude of genetic diversity.

Authors' contribution

Conceptualization of research (RA, SH); Designing of the experiments (RA, RH, SH); Contribution of experimental materials (RA, SH); Execution of field/ lab experiments and data collection (RH, SH); Analysis of data and interpretation (SH, RA, RH); Preparation of the manuscript (SH, RA).

Declaration

The authors declare no conflict of interest.

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