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Genetic Diversity and Population Structure of Jordanian Durum Wheat (*Triticum turgidum* L. subsp. *durum*) Landraces As Revealed by RAPD Markers

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ABSTRACT

Genetic diversity and population structure of 20 durum wheat (*Triticum turgidum* L. subsp. *durum*) landrace populations collected from three eco-agricultural zones from Jordan were studied; using Random Amplified Polymorphic DNA (RAPD) markers. DNA from ten individuals (i.e. lines) per population was analyzed using 21 RAPD primers. A total of 148 reproducible bands were detected, of which 128 (86.5%) were polymorphic. Nei's genetic distance varied from 0.07 to 0.33. The unweighted pair-group method of arithmetic average (UPGMA) tree based on the genetic distance revealed that populations collected from northern and southern zones were grouped into two separate clusters in line with their putative geographic origins. Populations collected from the central zone were found mixed with populations collected from the two other zones, indicating that the villages located in the geographical center of the study area have a frequent exchange of seeds with other villages from northern and southern zones. In average, the proportion of polymorphic loci and Nei's gene diversity ranged among populations from 0.227 to 0.568 and from 0.131 to 0.218 respectively, implying that more chance to select individual lines with desirable traits from more diverse populations. Genetic variation was larger within (56.35%) than among (36.44%) populations; suggesting that collecting more genotypes within populations rather than collecting more populations within the same eco-agricultural zone is essential to capture the highest portion of genetic variability existing in Jordanian wheat landraces. The results indicate that Jordanian wheat landraces represent a valuable genetic resource for enlarging the genetic variation of durum wheat breeding programs.

Keywords: RAPD, Genetic Diversity, Durum Wheat Landraces, Population Structure.

INTRODUCTION

There is a need for broad-based germplasm pool as a mean of genetic improvement of major crops (Duvick, 1984). Wheat landraces undoubtedly, can significantly contribute towards the development of such germplasm pools (Srivastava *et al.*, 1988). A landrace is a heterogeneous population composed from a mixture of different genotypes and evolved by natural and farmer-directed selection under environmental conditions where they were grown (Harlan, 1975; Frankel *et al.*, 1995; Jaradat *et al.*, 2004). Although, yield potential of these landraces is low (Ehdaie *et al.*, 1988), their performance is usually stable and have better quality attributes than high-yielding cultivars under organic and low-input farming systems (van Lammerts Bueren *et al.*, 2003; Agorastos and Goulas, 2005). Durum wheat(*Triticum turgidum* L. subsp. *durum* conv. *durum* (Desf.) Mackey) landraces are important source of variation, which

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harbor a reservoir of useful genes for adaptation to arid and semiarid regions (Harlan, 1975; Jaradat, 1989, 1990 and 1991; Frankel *et al.*, 1995; Jaradat *et al.*, 2004; Abdel-Ghani, 2008). Previous studies revealed that wheat landrace collections from Jordan are highly variable for morphological, developmental traits, disease resistance and gene complexes for tolerance to abiotic stresses (Jaradat, 1989, 1990, 1991 and 1992; Abdel-Ghani, 2008). However, phenotypic variation does not reliably reflect the real genetic variation because of the genotype × environment interaction and the uncontrolled influence of the environmental factors on the expression of the traits (Smith and Smith, 1992). Molecular markers, unlike morphological markers, are stable and have been found to be very useful in population genetics studies to quantify accurately the extent of genetic diversity within and among populations (Fahima *et al.*, 1999; Fahima *et al.*, 2002; Ozkan *et al.*, 2005).

Among the various DNA marker systems (Vierling and Nguyen, 1992; Plaschke *et al.*, 1995; Fahima *et al.*, 2002; Khan *et al.*, 2005), RAPD markers were proved to be powerful tools in genetic diversity and population structure in the case of self-pollinating species such as wheat (e.g. Devos and Gale, 1992; Joshi and Nguyen, 1993 a and b; Bohn and Melchinger, 1999) and barley (e.g. Barua *et al.*, 1993; Russel *et al.*, 1997). RAPD markers have the advantages of simplicity and the ability to detect relatively small amounts of genetic variation and their use requires no previous sequence knowledge (Williams *et al.*, 1990). One frequently reported disadvantage associated with RAPD is poor levels of reproducibility if experimental conditions are not standardized carefully (Devos and Gale, 1992; Penner *et al.*, 1993; Penner, 1996). In wheat, the low reproducibility might be attributed to the large genome size and the high proportion of repetitive DNA sequences (Devos and Gale, 1992). Despite this fact, RAPD markers have provided informative data consistent with other markers especially at the intraspecific level and were effective for large-scale population genetic analysis (Dos santos *et al.*, 1994; Lerceteau *et al.*, 1997; Fahima *et al.*, 1999). Therefore, careful optimization and strict control of PCR conditions are essential for the application of the RAPD technique in wheat genetic studies (Joshi and Nguyen 1993, a and b; Penner, 1996).

This study used RAPD markers to investigate the distribution of genetic diversity in durum wheat landrace populations collected from three eco-agricultural zones in Jordan. The amounts and patterns of genetic variation are described with a major aim to provide basic genetic information relevant to the conservation and for designing breeding programs.

MATERIALS AND METHODS

Plant material

Field trips were organized in March 2007 to collect wheat landraces cultivated on farmers' fields. Two hundred genotypes (i.e. individual spikes) from twenty durum landrace populations were sampled from three eco- geographical zones from Jordan (Table 1). Each spike (representing one genotype or plant) was considered when separated at least by 1 m interval from other collected spikes. For RAPD analysis, each population was represented by ten individuals. The collection mission included the north districts (Irbid and Ajloun), the central districts (Maddaba, Karak and Dieban) and the south districts (Tafila, Ma'an and Shoubak). The collection sites represent a gradient of annual rainfall ranging from 250 to 540 mm and covered high (1430 m) – low (570 m) transects for altitude (Table 1). The geographical position of each field (latitude, longitude and altitude) was determined using the Global Positioning System (The Garmin® GPS 12 Personal Navigator®). Long-term average seasonal

rainfall and monthly temperature data were obtained from the Water Authority of Jordan and the Jordan Meteorological Department.

Table 1 Eco-geographical information about the 20 wheat landrace populations collected from Jordan during June 2007

No.	District	The nearest village	Abbreviation	Latitude N	Longitude E	Altitude (m)	Long-term average rainfall (mm)
1	Irbid	Hoson	IR	32° 30' 01"	35° 52' 55"	570	360
2	Ajloun	Saqra	AS	32° 20' 19"	35° 46' 43"	1050	540
3	Karak1	Qaser-East	KQE	31° 17' 07"	35° 45' 09"	870	250
4	Karak2	Quase-West	KQW	31° 18' 10"	35° 43' 04"	890	300
5	Karak3	Wasia	KW	31° 13' 26"	35° 43' 38"	910	300
6	Karak4	Rakeen -East	KRE	31° 13' 53"	35° 43' 27"	880	320
7	Karak5	Mutah-East	KME	31° 08' 37"	35° 43' 13"	1240	300
8	Karak6	Mutah-west	KMW	31° 07' 55"	35° 43' 03"	1260	330
9	Karak7	Rakeen -west	KRW	31° 41' 48"	35° 40' 50"	890	330
10	Maddaba	Team	MT	31° 43' 26"	35° 46' 20"	780	320
11	Dieban1	Dohaiba-west	DDW	31° 56' 16"	35° 43' 26"	740	330
12	Dieban2	Mleeh	DM	31° 44' 09"	35° 48' 58"	750	280
13	Tafila1	Al-Rashadia-west	TAW	30° 41' 45"	35° 39' 01"	1260	250
14	Tafila2	Al-Rashadia-East	TAE	30° 42' 25"	35° 35' 32"	1240	250
15	Dieban 3	Dohaiba-East	DDE	31° 35' 45"	35° 50' 27"	765	280
16	Karak8	Mazar	KM	31° 01' 35"	35° 40' 41"	1360	330
17	Ma'an1	Petra	MP	30° 17' 29"	35° 37' 39"	1240	240
18	Ma'an2	Basta	MB	30° 13' 57"	35° 37' 10"	1400	250
19	Ma'an3	Eil	ME	30° 13' 13"	35° 35' 47"	1360	250
20	Shouback	Ghair	SG	30° 20' 31"	35° 41' 40"	1430	275

Polymerase chain reaction

Genomic DNA was isolated from fresh dried ground leaves using CTAB (Cetyl Trimethyl Ammonium Bromide) method as described by Saghai Maroof *et al.* (1984). The presence of high-molecular weight genomic DNA was verified using 0.8% agarose gel in 0.5× TBE buffer. The purity and quantity of the isolated DNA were measured by DNA spectrophotometry (Biochrom, London, U. K.). The purity of DNA was also checked by absorbance ratio; 260/280 that should be 1.8-2.0, while the DNA concentration was calculated assuming 1 O.D. at 260 nm corresponding to 50 µg ml^{-1}. The DNA suspension was diluted to a concentration of 50 ng μl^{-1} and used for RAPD-PCR amplification.

A total of 62 decamer primers were initially screened for polymorphisms on a subset of 20 leaf samples representing all populations sampled. Primers were selected from Operon Technologies (Alameda, Ca,

USA) and University of British Columbia (Vancouver, Canada). A negative control to which water was added instead of template DNA was used for each primer in each run to ensure no contamination with foreign DNA was occurred. Reactions were repeated at least twice and only reproducible RAPD markers were scored. Twenty one decamers that produced highly reproducible polymorphic markers were selected for RAPD analysis.

Polymerase chain reactions (PCR) conditions were optimized by varying concentrations of $MgCl_2$ concentration and different annealing temperatures. Mixtures for RAPD PCR (25 µl) reactions contained 50 ng genomic DNA, 2.5 µl of 10× PCR buffer (10 mM Tris HCL pH 8.8, 50 mM KCl and 15 mM $MgCl_2$), 250 nM of each primer, 200 nM dNTPs, 1U Taq polymerase, 25 mM $MgCl_2$ and nuclease free water was added to make up the final volume of 25 µl. Amplification was performed on a MJ-Research thermal cycler (MJ Research PTC-200 Thermo Cycler). The thermal cycler was programmed for a preliminary 2-minute denaturation step at 94 ^oC, followed by 45 cycles of denaturation at 94 ^oC for 1 min, annealing at 35-38 ^oC for 1 minute and extension at 72^o C for 2 minutes and finally 10 min at 72 ^oC for one cycle. Approximately 10 µl of the reaction was loaded onto a 1.5% agarose gel containing ethidium bromide (0.5 µg ml^{-1}) and PCR fragments were separated by electrophoresis for 2 h at 120 V (Labenet, Taiwan). RAPD fragments were illuminated under UV light and images were captured with UV illuminator system (Alphainnotech, USA).

Data scoring and analysis

Each individual was scored for the presence or absence of each band, with 1 = present, 0 = absent and dot (.) = missing data. Only those major bands which showed reproducible variation between genotypes were scored. The identification of 148 bands led to the construction of a 200 genotypes × 148 bands data matrix which was analyzed for variability within and between populations as well as between eco-geographical zones. Genetic distances between populations were computed, following Nei (1972). Percentage of polymorphic loci and Nei's (1973) and gene diversity index (*He*) were calculated using the POPGENE program, version 1.31 (Yeh *et al.*, 1997). NTSYS-pc (version 2.1, Exeter software, Setauket, USA; Rohlf 2000) was used for dendrogram construction using unweighted pair-group method of arithmetic average (UPGMA) method. Analysis of molecular variance (AMOVA) (Excoffier *et al.*, 1992) was performed based on Arlequin program version 2.000 (Schneider *et al.*, 2000). The total variation was partitioned among individuals within populations, between populations within eco-geographical zone, and between eco-geographical zones.

RESULTS

Initial screening of 62 RAPD primers resulted in the identification of 21 primers which yielded informative and polymorphic products resolvable by gel electrophoresis (Table 2). Usually, products below 300 bp or above 4000 bp gave faint or non-reproducible bands; hence most of the scored products were in the range of 300-3000 bp (Table 2). The 21 selected RAPDs primers generated a total of 148 bands (loci) that ranged in size from 300 to 5000 base pairs (bp) across all wheat landrace populations. The primers yielded 4 to 10 bands, with an average of 7.05 bands per primer. Among the 148 bands, 128 (86.5%) were polymorphic.

Table 2 List of the selected informative primers and the degree of polymorphism obtained among collected durum wheat landrace accessions

Primer	name	sequence	Range	Total No. of bands	No.of polymorphic bands	Polymorphism%
2	OPA-19	CAAACGTCGG	1.40-3.83	6	5	83.33
4	OPV-14	AGATCCCGCC	1.06-2.13	4	3	75.00
6	UBC-493	TGATGCTGTC	1.11-2.15	6	4	66.67
8	OPB-07	GGTGACGCAG	1.01-2.27	8	7	87.50
9	OPC-02	GTGAGGCGTC	1.04-2.40	4	3	75.00
10	OPC-07	GTCCCGACGA	1.20-2.93	6	5	83.33
11	OPC-18	TGAGTGGGTG	0.68-2.30	8	8	100.00
14	OPD-07	TTGGCACGGG	1.34-4.28	6	5	83.33
16	OPO-20	CAGTGCTGTG	0.79-2.31	10	8	80.00
18	OPA-12	TCGGCGATAG	0.84-2.22	8	6	75.00
29	OPA-10	GTGATCGCAG	0.50-2.26	5	4	80.00
34	OPB-01	GTTTCGCTCC	0.74-1.95	6	6	100.00
36	OPB-03	CATCCCCCTG	0.34-2.42	7	7	100.00
37	OPB-04	GGACTGGAGT	0.55-1.75	5	5	100.00
40	OPB-08	GTCCACACGG	0.30-1.70	10	10	100.00
44	OPB-12	CCTTGACGCA	0.38-2.01	9	7	77.78
45	OPB-18	CCACAGCAGT	0.63-1.21	6	6	100.00
50	OPC-10	TGTCTGGGTG	0.26-2.70	8	8	100.00
51	OPC-11	AAAGCTGCGG	0.38-1.38	7	4	57.14
52	OPC-16	CACACTCCAG	0.30-5.00	10	9	90.00
60	OPZ-18	AGGGTCTGTG	1.11-2.71	9	8	88.89
	Total			148	128	-
	Mean	-	-	7.05	6.10	85.86

Nei's genetic distance and clustering analysis

Nei's genetic distance was calculated for paired comparisons of the 20 populations (Table 3), based on the normalized identity of all loci between populations (Nei, 1978). The mean value of genetic distance was 0.20, range 0.07 to 0.33. The highest genetic distance (0.33) was obtained between populations collected from Karak4 and Shoubak, while the most similar populations were at Ma'an2 and Ma'an3 with a genetic distance of 0.07. The UPGMA dendogram based on Nei's genetic distance revealed the existence of two major clusters (Figure 1). Populations collected from the north and the south were grouped in two separated clusters, while those collected from the central zone were found mixed with populations collected from the northern and southern zones.

Percentage of polymorphic loci, and Nei's gene diversity index

A summary of the genetic data for each population is

given in Table 4. Mean levels of the proportion of polymorphic loci, *P* (5%), and the gene diversity, *He* of the 20 populations were 0.567 and 0.167, respectively. The highest percentage polymorphic loci, *P* (5%) was obtained for samples from Karak2 (*P*=56.76%), followed by samples from Karak6 (*P* = 54.73%) and Ajloun (*P* = 52.03%), while samples from Tafila2 and Tafila1 showed the least percentage polymorphic loci (*P* = 22.78 and 34.46% respectively). The range of variation in *He* between populations was wide, ranging from 0.131 to 0.218 (Table 4). Samples from Karak2, Karak6 and Ajloun were the most diverse (*H* = 0.218, 0.208 and 0.200 respectively), while samples from Shoubak (*H* = 0.131) and Tafila1 (*H* = 0.137) were the least diverse.

Table 3 Nei's genetic distance based on RAPD showing the variability among 20 durum wheat landrace populations collected from Jordan during June 2007

No.	Site	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19
1	Irbid																			
2	Ajloun	0.08																		
3	Karak1	0.17	0.12																	
4	Karak2	0.22	0.15	0.11																
5	Karak3	0.22	0.20	0.21	0.14															
6	Karak4	0.22	0.24	0.23	0.19	0.09														
7	Karak5	0.22	0.23	0.24	0.21	0.13	0.09													
8	Karak6	0.24	0.23	0.21	0.20	0.14	0.15	0.11												
9	Karak7	0.24	0.22	0.23	0.21	0.18	0.17	0.19	0.09											
10	Maddaba	0.22	0.20	0.20	0.18	0.13	0.18	0.20	0.09	0.09										
11	Dieban1	0.29	0.22	0.23	0.18	0.21	0.25	0.21	0.18	0.21	0.16									
12	Dieban2	0.28	0.23	0.23	0.19	0.19	0.22	0.20	0.16	0.16	0.14	0.12								
13	Tafila1	0.22	0.20	0.20	0.16	0.21	0.22	0.22	0.16	0.17	0.18	0.17	0.12							
14	Tafila2	0.24	0.16	0.20	0.16	0.23	0.26	0.27	0.21	0.21	0.22	0.18	0.16	0.11						
15	Dieban3	0.31	0.22	0.22	0.16	0.22	0.23	0.24	0.21	0.23	0.21	0.20	0.18	0.14	0.10					
16	Karak8	0.24	0.22	0.18	0.15	0.20	0.21	0.23	0.16	0.18	0.17	0.22	0.19	0.13	0.15	0.11				
17	Maan1	0.27	0.25	0.20	0.16	0.21	0.22	0.27	0.18	0.23	0.20	0.21	0.20	0.17	0.19	0.17	0.09			
18	Maan2	0.28	0.23	0.19	0.17	0.24	0.25	0.28	0.20	0.23	0.20	0.20	0.22	0.21	0.17	0.16	0.14	0.09		
19	Maan3	0.26	0.23	0.23	0.19	0.23	0.24	0.26	0.21	0.24	0.20	0.23	0.24	0.21	0.19	0.19	0.14	0.12	0.07	
20	Shouback	0.27	0.21	0.22	0.18	0.28	0.33	0.29	0.23	0.26	0.22	0.20	0.23	0.22	0.17	0.17	0.17	0.16	0.15	0.19

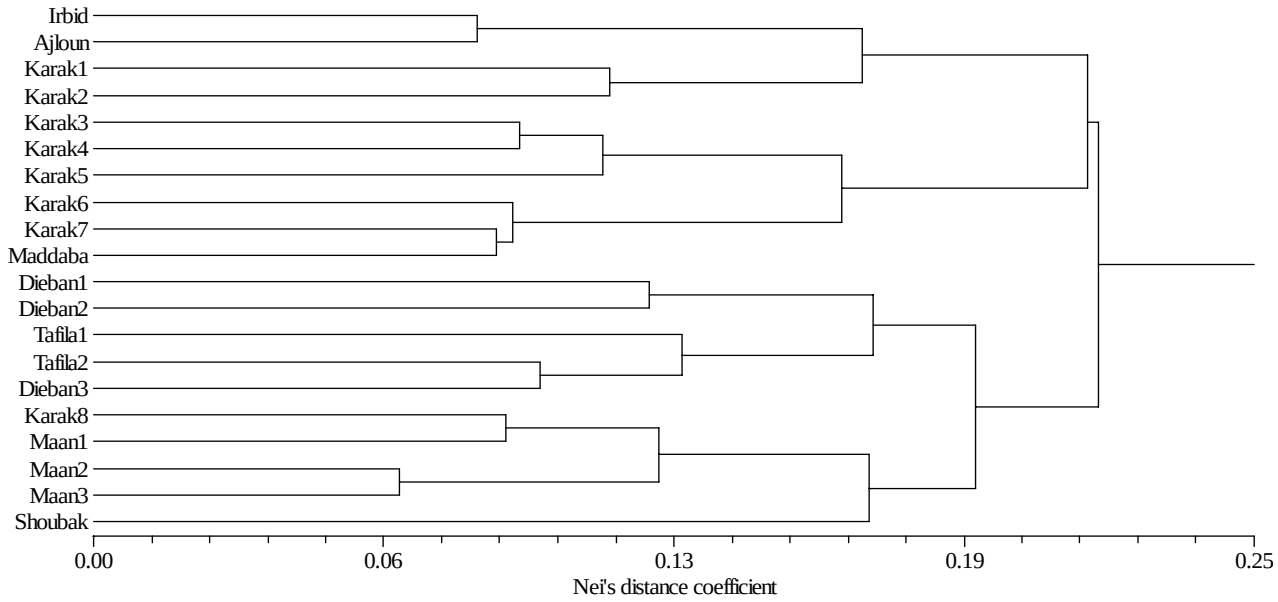

Figure 1 UPGMA derived dendrogram of the 20 durum wheat landrace populations based on Nei's genetic distance

Table 4 Summary of genetic variation based on 150 RAPD loci in 20 populations of wheat landraces from Jordan

No.	Site	No. of polymorphic loci[a]	RAPD proportion (%) of polymorphic loci (*P*)[b]	RAPD gene diversity *He*[c]
1	Irbid	63	42.57	0.174
2	Ajloun	77	52.03	0.200
3	Karak1	75	50.68	0.180
4	Karak2	84	56.76	0.218
5	Karak3	72	48.65	0.188
6	Karak4	70	47.3	0.175
7	Karak5	60	40.54	0.153
8	Karak6	81	54.73	0.208
9	Karak7	59	39.86	0.150
10	Maddaba	67	45.27	0.170
11	Dieban1	67	45.27	0.164
12	Dieban2	62	41.89	0.150
13	Tafila1	51	34.46	0.137
14	Tafila2	63	22.78	0.153
15	Dieban 3	62	41.89	0.149
16	Karak8	66	44.59	0.171
17	Ma'an1	60	40.54	0.150
18	Ma'an2	76	51.35	0.173

No.	Site	No. of polymorphic loci[a]	RAPD proportion (%) of polymorphic loci (*P*)[b]	RAPD gene diversity *He*[c]
19	Ma'an3	55	37.16	0.139
20	Shoubak	56	37.84	0.131
	Mean	66.3	43.81	0.167
	Range	51-84	22.78-56.76	0.131-0.218

[a] Polymorphic bands out of 60 scorable bands over populations

[b] *P*= Proportion of polymorphic loci (5%)

[c] *He* = Equivalent to the expected heterozygosity under panmixia (Nei 1978)

Analysis of molecular variance (AMOVA)

The partitioning of the genotypic variance among individuals within populations, among populations within eco-geographical zones, and between eco-geographical zones was assessed by AMOVA (Table 5). The components of AMOVA were highly significant ($P < 0.001$): 56.35% of the genetic variation was within populations, while the between-populations component was 34.44% and 7.2% between the eco-agricultural zones.

Table 5 Analysis of Molecular Variance (AMOVA, Excoffier *et al.*, 1992) for 200 genotypes (i.e. individual spikes) from twenty durum landrace populations sampled from three eco-geographical regions of Jordan (northern, central and southern zones), employing 160 reproducible RAPD fragments. Degrees of freedom (d.f.), sum squares and significance (*P*) of the variance components are shown

Source of variation	Degrees of freedom (d.f.)	Sum of squares	Variance components		*P-value**
			Absolute	% of total	
Among eco-geographical zones	2	203.942	0.90697	7.20	<0.001
Among populations within eco-agricultural zones	17	900.908	4.58974	36.44	<0.001
Among genotypes within populations	180	1277.500	7.09722	56.35	<0.001
Total	199	2382.350			

*The probability value (*P*-value) of a statistical hypothesis test

Discussion

RAPD markers used in this study generated a sufficient number of polymorphism to determine genetic relationships among wheat landrace populations. Knowledge of genetic divergence between populations was widely used to implement strategies for germplasm conservation (e.g., Fahima *et al.*, 1999; Fahima *et al.*, 2002; Ozkan *et al.*, 2005) and to provide information for effective uses of genetic resources in breeding programs (e.g., Souza and Sorrells, 1989; Barbosa-Neto *et al.*, 1996; Bohn *et al.*, 1999; Utz *et al.*, 2001; Jordan *et al.*, 2003; Kotzamanidisa *et al.*, 2008). Therefore, the results obtained in this study were discussed in relevant to the conservation strategies and to their possible practical

importance in plant breeding programs.

Populations collected from northern and southern zones were grouped in two separated clusters. Therefore, it could be concluded that populations at greater distances are more genetically differentiated by genetic drift than those closed geographically. Interestingly, results revealed that populations sampled from villages located in the geographical center of the study area has frequent exchange of seeds with farmers from north and south zones, this conclusion comes from the fact that populations collected from the central zone were found mixed with those collected from the northern and southern zones. In nature, isolation by distance is the result of limited gene flow, where the probability of gene flow between two populations is a function of the geographical distance between them (Slatkin, 1993) and the likelihood of exchange of genes between populations decreases exponentially with distance of separation (Epperson, 1990; Parzies *et al.*, 2004). For inbred cultivated wheat where little to no pollen flow occurs (Hucl, 1996), gene flow must occur by seed movement, specifically seed exchange between farmers. Genetic differentiation among landrace populations (i.e. farmers' varieties) might be related to the heterogeneity in environmental conditions among the collection sites and/or to the farmers' selection pressure and preferences for certain wheat types within eco-geographical zone.

The pattern of diversity and the genetic relationship among the populations might be related to the altitude and rainfall that vary sharply among the collection sites (Table 1). Landraces under cultivation might undergo evolutionary change; such change might be occur if farmers keep growing their own old seeds under where they grown. Indigenous farming communities in Syria and Jordan contributed for millennia, to the evolution, enrichment and *in situ* conservation of many crop landraces, such as wheat (Jaradat 1989, 1990 and 1991) and barley (Ceccarelli, *et al.* 1987).

The population genetic structure of landraces is influenced by various factors, including gene flow and mating system (Schaal *et al.*, 1998). Estimates of genetic variability between populations of inbred species based on AMOVA derived by analyzing RAPD markers have usually been > 70% (Nybom and Bartish, 2000; Koebner *et al.*, 2002). However, this might not accurate in autogamous crops where there is a high gene flow represented by seed exchange between farmers. Consequently, high variation (56.35%) found within wheat landrace populations might be due to seed exchange (gene flow) between farmers or to anticipate admixtures and only to an inconsiderable extent to outcrossing with foreign pollens (Hucl, 1996). A strong genetic differentiation (36.44%) among wheat landraces might be also due to the effect of natural or farmers' directed selection pressures focused on the adaptation of landraces to certain environmental conditions. The considerable level of variation within and among populations are in accordance with previous studies which revealed extensive genetic diversity within and between Jordanian durum wheat landraces based on developmental and morphological characters (Jaradat, 1989, 1990 and 1991; Abdel-Ghani, 2008). Similarly, other studies reported considerable genetic diversity among and within populations of primitive and wild tetraploid wheat from Fertile Crescent using RAPDs (Dawson *et al.*, 1993; Reddy and Soliman, 1997; Fahima *et al.*, 1999; Tanyolac, 2003).

Information on current levels of genetic diversity of germplasm at gene bank is essential for implementing strategies for Jordanian wheat landraces conservation. While most genetic variation is apportioned among individuals within populations (56.35%) and less variation due to differences among populations within wheat growing zones (36.44%), collecting as many

genotypes within sampling fields rather than collecting more populations (farmers seed samples) within the same eco-agricultural zone can be a good strategy to capture the largest proportion of genetic variability. According to the results of the present study, the high genetic diversity for populations collected from Karak2, Karak6 and Ajloun indicate that the most effective strategy for preserving genetic variation would be to conserve a large number of individuals from highly diverse populations.

Results showed that breeders may rely on Jordanian wheat landrace germplasm for designing breeding programs since sufficient genetic variability exists within and among populations. Results obtained in this study indicate that the heterogenous nature of wheat landraces; wheat landraces are typically mixtures of a high number of homozygote genotypes. Therefore, Jordanian wheat landraces contain a large amount of genetic variation within adapted genetic background. Multi-line varieties such as wheat landraces have enough population plasticity to enhance phenotypic stability by reducing vulnerability to diseases, pests and environmental stresses (Ceccarelli *et al.*, 1992; de Boef *et al.*, 1996). The existence of high level within populations' heterogeneity led to extraction of high yielding genotypes from locally grown landraces grown by farmers in several self pollinated crops including wheat (Tesemma *et al.*, 1993), barley (Weltzien, 1988; Jaradat *et al.*, 2004) and sesame (Bayder *et al.*, 1999). The high genetic diversity in Karak2 and Karak6 and Ajloun populations revealed that more chance to target selection of individual lines with desirable traits from these populations. Genetic variability estimated by means of RAPD markers might complement morphological evaluations in the selection of optimal parental cross combinations. The genetic distance based on DNA markers between populations might be useful for description or establishment of heterotic groups in various crops, and to assign inbred lines to those groups in self pollinated crops such as wheat (Barbosa-Neto *et al.*, 1996), oat (Souza and Sorrells, 1989) and sorghum (Jordan *et al.*, 2003). Moreover, it might be useful to predict genetic variance of segregating populations (Bohn *et al.* 1999; Utz *et al.* 2001; Kotzamanidisa *et al.*, 2008). Therefore, crosses between more distantly individuals/populations are expected to perform better than closely related individuals/populations and could lead to superior performance of F_1 hybrids compared to their parental inbreds. From this perspective, performing crossing between populations collected from Karak4 and Shoubak might give higher F_1 performance and more genetic variance in segregating progenies compared to closely related ones.

It would be suggested that collecting more individuals with fewer populations, rather than more populations within eco-agricultural zones, can be a good strategy to represent the entire variability in Jordanian wheat gene pool. Furthermore, breeders can rely on Jordanian wheat landraces for designing breeding programs since sufficient genetic variability exists within and among wheat landrace populations.

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التنوع و التركيب الوراثي لمجتمعات القمح القاسي من الأردن (*Triticum turgidum* L. subsp. *durum*) باستخدام المعلمة الوراثية RAPD

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ملخـص

تهدف هذه الدراسة الى دراسة التنوع و التركيب الوراثي لعشرين عشيرة من سلالات القمح القاسي المجموعة من ثلاث مناطق بيئية زراعية من الأردن باستخدام المعلمة الوراثية RAPD . تم تحليل الحامض الرايبوزي منقوص الأكسجين من عشرة أفراد من كل عشيرة باستخدام 21 من RAPD . تم تحديد 148 مؤشرا حيث أظهر 128 (86.5%) اختلافا. تراوحت المسافة الوراثية ما بين العشائر من 0.07 الى 0.33. أظهرت الشجرة الوراثية UPGMA المعتمدة على المسافة الوراثية ان العشائر المجموعة من المناطق الشمالية و الجنوبية قد تجمعت في مجاميع منفصلة بينما وجدت العشائر المجموعة من وسط المملكة مندمجة مع تلك المجموعة من المناطق الأخرى. تدل نتائج البحث على وجود تبادل للبذور ما بين الوسط من جهة وقرى الشمال والجنوب من جهة اخرى. تراوحت نسبة المؤشرات التي أظهرت اختلافا و قيمة التباين الوراثي المعتمد على Nei مابين العشائر من 0.227 و 0.568 و ما بين 0.131 و 0.218 على التوالي مما يعطي دلالة على امكانية انتخاب سلالات ذات صفات مرغوبة من العشائر الأكثر تنوعا. كان التباين الوراثي اكبر داخل العشائر مقارنة مع التباين مابين العشائر مما يدل على ضرورة جمع عدد أكبر من الأفراد داخل العشيرة بدلا من جمع عدد أكبر من العشائر داخل المناطق البيئية كاستراتيجية جيدة للحصول على أعلى مستوى من التباين الوراثي. يمكن الاستنتاج أن عشائر القمح القاسي الأردنية هي مصدر مهم لتوسيع القاعدة الوراثية في برامج التحسين الوراثي للقمح القاسي.

الكلمات الدالة: RAPD، سلالات القمح القاسي، تركيب العشائر، التركيب الوراثي.

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