

## DETECTING GENETIC DIVERSITY AMONG BARLEY LANDRACES GROWN IN THE WEST-BANK, PALESTINE IN 2010-2011

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### ABSTRACT

Fifteen barley landraces were collected from different localities in the West-Bank,-Palestine during 2009. A field experiment was conducted at the Faculty of Agriculture-An Najah National University to evaluate several agronomical traits of these landraces in 2010-2011 growing season. Cluster analysis was performed using the complete-linkage method, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability ( $H^2$ ), and genetic advance (GA) were calculated for the quantitative traits. Significant diversity was exhibited among the landraces regarding days to 90% heading, 100- grain weight, number of grains per spike, spike length, and awns length. The Cluster analysis showed high genetic diversity among the collected landraces with dissimilarity ranging from 0.26 to 0.75. The fifteen landraces were grouped into four clusters. Genotypic coefficient of variation ranged from 6.1 to 22.9, whereas phenotypic coefficient of variation ranged from 6.6 to 41.8 with maximum phenotypic and genotypic variability observed for number of fertile tellers, number of grains per spike and spike length. Moderate to high heritability (broad sense) estimates (70-87%) were found for most of the characters. The genetic advance was highest for number of grains per spike (39.4%), followed by spike length (37.2%). High positive significant correlations were found among the different studied traits with correlation coefficient ranging from 0.395 to 0.536. The results of this study indicated high genetic diversity among barley landraces in Palestine, which make them potential sources for selection and hybridization programmes.

**Key words:** Barley landraces, Genetic diversity, Heritability, *Hordeum vulgare*.

### INTRODUCTION

The evaluation of genetic variability is among the main issues in the conservation and utilization of plant genetic resources. Another important issue is where to find genetic variability. Barley (*Hordeum vulgare* L.) is one of the main cereal crops worldwide (Dakir *et al.* 2002). Large germplasm collections of cultivated (*Hordeum vulgare subsp. vulgare*) and wild (*Hordeum vulgare subsp. spontaneum*) barleys are available in several gene banks, e.g. ICARDA (Syria) and IPK-Gatersleben (Germany) that encompass enormous genetic diversity. However, it is worth to evaluate the level of genetic variability maintained in small scale farming systems in developing countries, like Palestine. Cultivated barley was domesticated from its wild relative, *Hordeum spontaneum* around 7,000 BC. This crop originated in the 'Fertile Crescent' (Badr *et al.* 2000; Azhaguvel and Komatsuda 2007). The Fertile Crescent includes parts of Jordan, Lebanon, Palestine, Syria, South-eastern Turkey, Iraq and Western Iran. The wild progenitor of cultivated barley (*Hordeum vulgare subsp.*

*spontaneum*) is still widely distributed along the Fertile Crescent, particularly in the driest areas (Harlan and Zohary 1966). The domestication of barley is assumed to have taken place from two-rowed wild barley *Hordeum vulgare* L. subsp. *spontaneum* in the Near East (Harlan and Zohary 1966). The genetic diversity among and within landraces makes them a valuable resource as potential donors of genes for the development and maintenance of modern crop varieties and for direct use by farmers (Soleri *et al.* 1995). The knowledge and understanding of this genetic diversity serve as a basis for making decisions related to the conservation and the use of the germplasm collection in genetic improvement. However, morphological variability is limited to some stages of plant growth and might be affected by environment. Other studies of the genetic diversity of barley germplasms were based on isozymes (Liu *et al.* 2000) and seed storage proteins (Yin *et al.* 2003). The present study was undertaken with the objective to evaluate genetic diversity of cultivated Palestinian barley germplasm based on agro-morphological traits

## MATERIALS AND METHODS

**Plant collection:** Grains of fifteen barley landraces collected from farmers in different regions in the West Bank-Palestine during 2009 (Table 1) were used in this study. Grain samples were collected as a mixture from farmers who used to grow the same landrace from generation to generation. These landraces are well adapted to local conditions. Farmers were chosen based on geographical distribution across the governorates of the West-Bank.

**Experimental Site:** Field experiment was conducted at the experimental farm of the Faculty of Agriculture, An-Najah National University, Tulkarm (Khadouri), Palestine (32.31519° N, 35.02033° W and altitude of 75 m) during the 2010/2011 growing season in a heavy clay soil. The climate of the region is hot humid during summer and warm in winter with an average annual rainfall of 600 mm. All landraces were sown at the 1<sup>st</sup> of November 2010 in three complete randomized blocks. Each accession was represented by three rows (10–15 seeds per row), 1 m long per replicate.

**Data collection:** During the growing season, days to heading (number of days from planting the seeds until 90% of the plants per accession gave flowering) was recorded for each landrace. At maturity, five randomly selected plants from the central rows of each landrace were harvested and the following measurements were taken: plant height, number of fertile tillers per plant, spike length (for five random spikes), awns length (for five random spikes), number of grains per spike (average of five plants), and 100-grain weight.

**Statistical analysis:** Analysis of variance (ANOVA) was conducted using PROC GLM procedure of SAS/STAT software, version 9.0 for Windows (SAS institute 2002). Multiple comparisons among pairs of lines were performed using the REGWQ-test. Cluster analysis was performed using the complete-linkage method. Genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability ( $H^2$ ), and potential genetic advance (PGA) were estimated for quantitative traits based on partitioning the total variance into between-landraces (MSB) and within-landraces (MSW) components of variance as follows:

$$GCV = \frac{\sqrt{V_g}}{M} \times 100\%$$

$$PCV = \frac{\sqrt{V_p}}{M} \times 100\%$$

$$H^2 = \frac{V_g}{V_p}$$

$$PGA = \frac{i\sqrt{V_p}H^2}{M} \times 100\% \quad \text{Where,}$$

$V_g$  is the genetic variance = (MSB- MSW)/r

$V_p$  is the phenotypic variance = [(MSB- MSW)/r] + MSW

M = mean value of the trait

r = number of replications per treatment

i = 2.06 (selection intensity at 5%)

## RESULTS AND DISCUSSION

**Yield and yield related traits:** Significant differences (P < 0.05) were observed among the different accessions for all studied traits except for number of fertile tillers (P > 0.05); (Table 2). These results are in agreement with those of Talebi *et al.* (2009) who found significant differences among genotypes in spike length and number of grains per spike.

Means of morphological and production characters for studied genotypes are in Table 3. Mean plant height ranged from 80.38 cm (HV-15) to 109.80 cm (HV-3), mean spike length ranged from 4.93 cm (HV-8) to 9.10 cm (HV-9) and mean awn length ranged from 9.0 cm (HV-11) to 15.15 cm (HV-13). Awn length is alleged to have a positive contribution for drought tolerance. Martin *et al.*, (1976) reported that awns function in transpiration and photosynthesis.

Accessions HV-11 and HV-15 showed significantly the lowest number of days to 90% heading (88 and 89 days, respectively; Table 3), indicating that these are early producing genotypes. On the other hand, HV-5 could be considered as late producing accession (mean of 112 days). Mean number of fertile tillers ranged from 3.10 (HV-15) to 8.73 (HV-6). Accession HV-12 showed the lowest 100-grain weight (mean of 4.13 g) while HV-11, HV-7, and HV-13 (HV-7 and HV-11 are two-row accessions while HV-13 is six-row) showed the highest 100-grain weights (means of 6.04, 6.14, and 6.16 g, respectively) These same three accessions showed low number of grains per spike (25.67, 26.80 and 35.2 grains) but HV-7 and HV-11 had long spikes (means of 9.03 and 8.67 cm, respectively) while HV-13 had the shortest spikes (mean of 5.17 cm). In selection for high yield it is preferred to have genotypes with large number of fertile tillers, long spikes, large grains and high number of grains per spike. Ram and Singh (1989) found that spike length, number of grains per spike and grain weight, were the main characters contributing to yield in barley, while Nessa *et al.* (1998) observed that tiller number, spike length and plant height were the main characters contributing to yield in barley. These traits could be utilized efficiently for tailoring a new plant variety and assist in conservation of desirable gene pool, and its

utilization in breeding program for specific plant traits (Yahyaoui *et al.* 1997; Babu and Hanchinal 1998).

**Genetic similarities among genotypes:** The cluster analysis confirmed the high genetic diversity in the collected landraces with dissimilarity ranging from a minimum of 0.26 between landraces HV-1 and HV-4 to maximum of 1.75 between HV-1 and HV-11. The clustering dendrogram (Figure 1) proposed three groups. The first group (cluster-I) included two accessions (HV-7 and HV-11) which was most likely grouped based mainly on row number (both are two-row) and also on high 100-grain weight, small number of grains per spike and high spike length. The second group (cluster-II) consisted of four landraces (HV-8, HV-10, HV-13 and HV-15) grouped mainly based on similarities in plant height, 100-grain weight, and number of grains per spike. The third group (cluster-III) can be divided into two sub-clusters, the first one consisted of three landraces (HV-5, HV-9 and HV-12) grouped together based on the highest number of grains per spike and high spike length and the second consisted of four landraces (HV-8, HV-10, HV-13 and HV-15) grouped for low number of grains per spike and low number of fertile tillers.

The landraces have been grouped in a particular cluster on the basis of greater morphological trait similarities, thus representative landraces from a cluster of particular group could be chosen for hybridization programs. Some potentially important traits have been identified and these can be exploited for specific trait improvement and assembly of core collection from a bulk genetic stock.

**Coefficients of variation, heritability and potential genetic advance:** There were significant differences among genotypes for all the traits under study (Table 2). Genetic and phenotypic measures of variation, heritability (broad sense) and potential genetic advance as percentage of trait means are in Table 4. Genotypic coefficients of variation ranged from 6.1 to 22.9 whereas phenotypic coefficients of variation ranged from 6.6 to 41.8. The maximum phenotypic and genotypic variability were observed for number of fertile tillers, number of grains per spike and spike length (Table 3). Similar findings were reported for wheat (Waqar *et al.* 2008), rice (Akhtar *et al.* 2011) and field pea (Singh and Singh 2006).

**Table 1. Barley (*Hordeum vulgare* L.) landraces collected from different regions in Palestine**

Accession	Collection site	Province	Latitude	Longitude	Altitude
HV-1	Ras Atya	Qalqilya	32°9'33.35''N	34°59'30.20''E	70
HV-2	Imatin	Qalqilya	32°11'34.53''N	53°9'34.25''E	390
HV-3	Bayt Iba	Nablus	32°14'24.10''N	35°12'43.66''E	350
HV-4	Beta	Nablus	32°8'17.54''N	35°17'1.09''E	520
HV-5	Tayasir	Tubas	32°20'33.24''N	35°23'47.42''E	250
HV-6	Jayus	Qalqilya	32°12'2.29''N	35°2'2.71''E	240
HV-7	Sinjil	Ramallah	32°2'7.02''N	35°15'52.19''E	690
HV-8	Qabatiya	Jenin	32°24'42.83''N	35°16'48.41''E	260
HV-9	Silat Al-Dahr	Jenin	32°19'1.32''N	35°11'21.53''E	340
HV-10	Shuweka	Tulkarm	32°20'8.52''N	35°2'6.19''E	150
HV-11	Tubas	Tubas	32°19'21.30''N	35°22'6.44''E	400
HV-12	Azun	Qalqilua	32°10'38.25''N	35°3'19.96''E	220
HV-13	Anabta	Tulkarm	32°18'29.01''N	35°7'11.44''E	160
HV-14	Tel Albeida	Tubas	32°22'53.33''N	35°30'22.71''E	-20
HV-15	Ni'lin	Ramallah	31°56'57.36''N	35°1'16.37''E	260

**Table 2. Analysis of variance of agro-morphological characters in barley accessions**

Sources	df	Mean square						
		DH (days)	100GW (g)	PH (cm)	NFT (number)	SL (cm)	AL (cm)	NGS (number)
Block	2	21.07**	0.006	117.44	11.64 <sup>ns</sup>	0.439	0.939	22.14
Genotypes	14	110.32***	1.127***	313.96**	8.59 <sup>ns</sup>	6.77***	8.42***	414.80***
Error	28	5.45	0.177	137.88	4.21	0.73	0.594	52.64

DH: Days to heading; 100GW: 100-grain weight; PH: Plant height; NFT: Number of fertile tillers; SL: Spike length; AL: Awn length;

NSS = number of grains per spike

\*\*\* and \*\* significant at p = 0.01 and p = 0.05, respectively.

Heritability estimate is an important parameter which helps the breeder to select a plant trait that is high heritable as compared to a trait which is less heritable. High heritability (broad sense) estimates (70-87%) were found for all the characters, except number of fertile tillers and plant height (26% and 30% respectively). These results are in agreement with the results obtained by Eid (2009). Potential genetic advance (as a percentage of trait means) ranged from 8.8% for plant height to 39.4% for number of grains per spike. Waqar *et al.* (2008) have also reported high heritability values coupled with high genetic advance for number of grains per spike.

The moderate to high estimates of heritability and potential genetic advance found for spike length, 100-grain weight and number of grains per spike suggest that selection based on phenotype would be effective for these traits (Masood and Chaudhry 1987; Sharma *et al.* 1986; Firouzian *et al.* 2003). Low potential genetic advance as for plant height indicates slight chances of

improvement of this trait in subsequent generations as discussed by Firouzian *et al.* (2003).

**Phenotypic correlations among characters:** Simple correlation coefficients between the studied characters are presented in Table (4). Significant positive correlations were found for number of grains per spike with plant height (0.536), and days to heading (0.45), and for spike length with number of fertile tillers (0.426). Eid (2009) reported that there is a high correlation between days to heading and number of grains per spike. Spike length was negatively correlated with awns length (-0.602). Significant negative correlations were also found for 100-grain weight with number of grains per spike (-0.734), with days to heading (-0.378) and with plant height (-0.384). These correlations should be taken into consideration in selection programs to avoid any antagonistic effects.

**Table 3. Production and morphological characters of 15 barley accessions**

Accession	Production characters				Morphological traits		
	DH	100GW	NGS	NFT	PH	SL	AL
HV-1	96.33 <sup>cde</sup>	5.03 <sup>cde</sup>	54.80 <sup>ab</sup>	6.60	113.02	5.93 <sup>cd</sup>	14.01 <sup>ab</sup>
HV-2	99.67 <sup>bcd</sup>	4.72 <sup>cde</sup>	54.20 <sup>ab</sup>	4.67	107.93	7.02 <sup>abcd</sup>	12.91 <sup>b</sup>
HV-3	96.33 <sup>cde</sup>	4.63 <sup>de</sup>	49.60 <sup>ab</sup>	7.00	109.80	5.87 <sup>cd</sup>	13.34 <sup>ab</sup>
HV-4	95.00 <sup>cdef</sup>	5.33 <sup>abcd</sup>	50.13 <sup>ab</sup>	5.87	109.67	5.41 <sup>d</sup>	13.68 <sup>ab</sup>
HV-5	112.33 <sup>a</sup>	5.07 <sup>cde</sup>	64.90 <sup>a</sup>	4.43	99.62	8.07 <sup>abc</sup>	12.19 <sup>bc</sup>
HV-6	93.00 <sup>defg</sup>	5.10 <sup>bcde</sup>	53.40 <sup>ab</sup>	8.73	99.67	6.25 <sup>bcd</sup>	12.27 <sup>bc</sup>
HV-7	96.33 <sup>cde</sup>	6.14 <sup>a</sup>	26.80 <sup>c</sup>	8.33	95.13	9.03 <sup>a</sup>	10.40 <sup>cd</sup>
HV-8	98.67 <sup>bcd</sup>	5.01 <sup>cde</sup>	44.00 <sup>abc</sup>	4.33	94.33	4.93 <sup>d</sup>	13.21 <sup>ab</sup>
HV-9	101.00 <sup>bc</sup>	4.51 <sup>de</sup>	60.25 <sup>a</sup>	4.67	103.27	9.10 <sup>a</sup>	12.13 <sup>bc</sup>
HV-10	91.00 <sup>efg</sup>	5.72 <sup>abc</sup>	44.42 <sup>abc</sup>	4.20	87.77	5.17 <sup>d</sup>	11.98 <sup>bc</sup>
HV-11	88.00 <sup>g</sup>	6.04 <sup>ab</sup>	25.67 <sup>c</sup>	8.00	87.80	8.67 <sup>ab</sup>	9.00 <sup>d</sup>
HV-12	95.33 <sup>cdef</sup>	4.13 <sup>e</sup>	62.80 <sup>a</sup>	5.33	91.47	7.92 <sup>abc</sup>	9.60 <sup>d</sup>
HV-13	93.33 <sup>defg</sup>	6.16 <sup>a</sup>	35.20 <sup>bc</sup>	4.53	82.87	5.17 <sup>d</sup>	15.15 <sup>a</sup>
HV-14	102.00 <sup>b</sup>	5.32 <sup>abcd</sup>	49.40 <sup>ab</sup>	5.73	102.93	7.20 <sup>abcd</sup>	13.81 <sup>ab</sup>
HV-15	89.00 <sup>fg</sup>	5.64 <sup>abc</sup>	43.85 <sup>abc</sup>	3.10	80.38	5.28 <sup>d</sup>	12.39 <sup>bc</sup>

DH = days to heading. 100GW = 100-grain weight. NGS = number of grains per spike. NFT = number of fertile tillers. PH = plant height. SL = spike length. AL = Awn length.

Means in the same column with different superscripts are significantly different ( $P \leq 0.05$ ) using REGWQ test for multiple comparisons.

**Table 4. Estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability ( $H^2$ ), and potential genetic advance (PGA) for different characters of 15 barley accessions**

Character	PCV (%)	GCV (%)	$H^2$	PGA (%)
DH	6.6	6.1	0.87	11.7
100GW	12.9	11.1	0.74	19.7
PH	14.4	7.9	0.30	8.8
NFT	41.8	21.2	0.26	22.2
SL	24.6	21.1	0.73	37.2
AL	14.4	13.0	0.81	24.2
NGS	27.5	22.9	0.70	39.4

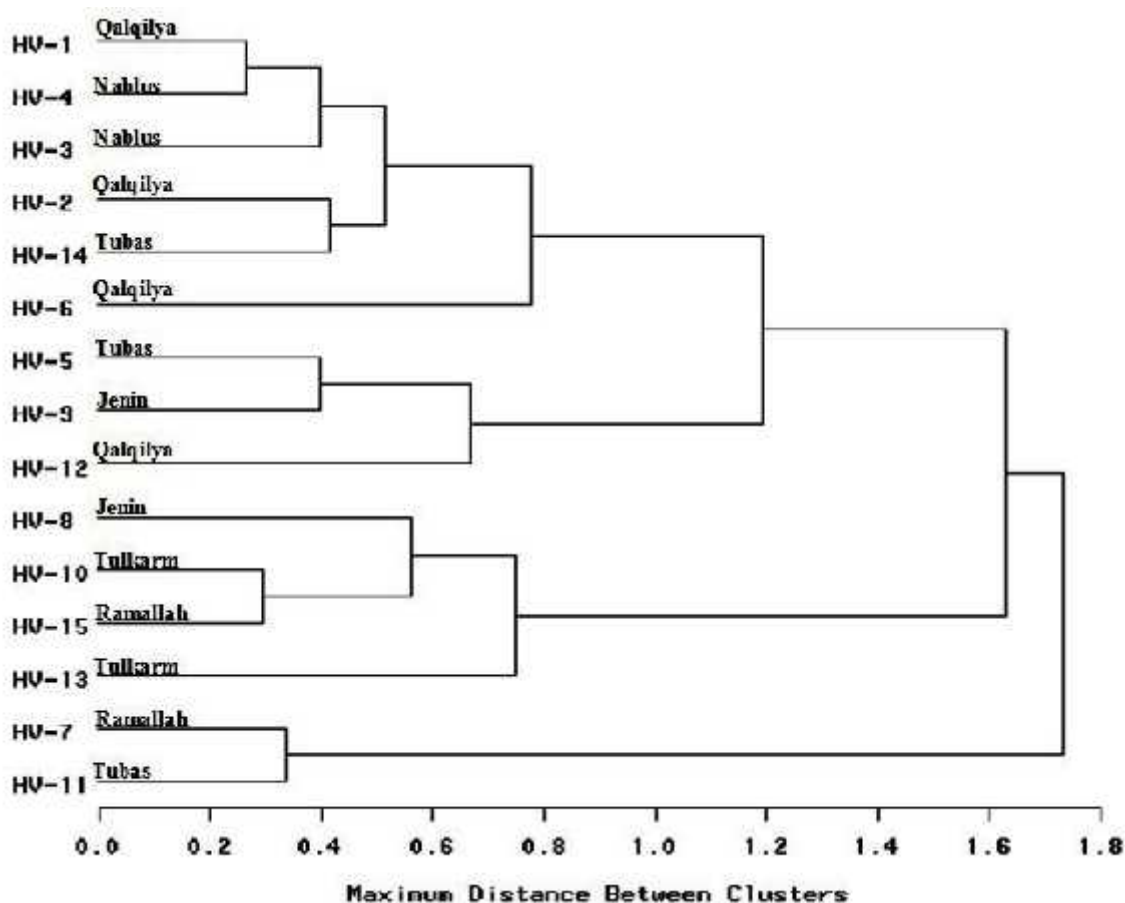
DH = days to heading. 100GW = 100-grain weight. PH = plant height. NFT = number of fertile tillers. SL = spike length. AL = Awn length. NGS = number of grains per spike.

**Table 5. Correlation coefficients for six agronomic characters of fifteen barley genotypes grown in 2010/2011.**

	DH	100GW	PH	NFT	SL	AL
100GW	-0.378**					
PH	0.143 <sup>ns</sup>	-0.384***				
NFT	-0.259 <sup>ns</sup>	0.053 <sup>ns</sup>	0.395***			
SL	0.239 <sup>ns</sup>	-0.145 <sup>ns</sup>	0.275 <sup>ns</sup>	0.426***		
AL	0.229 <sup>ns</sup>	0.038 <sup>ns</sup>	0.169 <sup>ns</sup>	-0.236 <sup>ns</sup>	-0.602***	
NGS	0.45***	-0.734***	0.536***	-0.020 <sup>ns</sup>	0.178 <sup>ns</sup>	0.152 <sup>ns</sup>

DH: Days to heading; 100GW: 100-grain weight; PH: Plant height; NFT: Number of fertile tellers; SL: Spike length; AL: Awn length, NGS = number of grains per spike

\*\*\* and \*\* significant at p 0.01 and p 0.05, respectively.

**Figure 1. Dendrogram of 15 barley landraces**

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