INTERNATIONAL JOURNAL OF AGRICULTURE & BIOLOGY
ISSN Print: 1560–8530; ISSN Online: 1814–9596
15–720/2016/18–5–1049–1055
DOI: 10.17957/IJAB/15.0206
http://www.fspublishers.org

Full Length Article

Genetic Diversity of Bread Wheat Lines Based on Agro-morphological Traits

Hafsa Naheed[1*], Fida Mohammad[1], Quahir Sohail[2], Sana Abid[1] and Nadia Khan[1]
[1]*Department of Plant Breeding and Genetics, The University of Agriculture Peshawar, Pakistan*
[2]*Winter Wheat Breeding Program, ICARDA, Ankara, Turkey*
[*]For correspondence: hafsaa.naheed@gmail.com

Abstract

Twenty spring bread wheat genotypes (G) from eleven research centers in Pakistan were included in national uniform wheat yield trial (NUWYT) conducted at the Agriculture Research Farm of The University of Agriculture, Peshawar, in 2010–2011. The experiment was conducted using randomized complete block design with four replications. Statistical analysis showed significant differences among 43 traits of the 20 genotypes. The descriptive statistics of different traits of the 20 genotypes averaged over replications showed high variability among the genotypes for the traits. The highest coefficient of variation was observed for lodging followed by grain-weight: chaff-weight ratio, non-productive tillers, chaff weight, spike filling rate, vegetative: reproductive periods ratio, kernel filling rate and crop growth rate during seed fill duration. Euclidean distances as measure of genetic diversity were calculated using 51 agronomic and physiological traits for 190 possible pairs of the 20 genotypes. Euclidean distances ranged from 4.37 for G2-G6 pair to 16.80 for G12-G16 pair.

Keywords: Genetic diversity; *Triticum aestivum*; Cluster analysis; Phylogenetic tree

Introduction

Genetic variation or diversity is the basis for crop improvement and important for successful breeding and development of new cultivars (Franco *et al*., 2001; Liu *et al*., 2014). Genetic diversity is important for tolerance to biotic stresses like insect, pests and diseases, for increasing yield and to achieve genetic gain in a breeding program. Genetic diversity in populations is estimated to analyze genetic variability in cultivars (Cox *et al*., 1986), and to identify diverse genotypes for hybridization to generate progenies with more genetic variation for further selection (Barrett and Kidwell, 1998). The level of genetic diversity among parents of a cross determines the genetic variance among the segregating populations to be acted upon by breeders to develop better pure lines in varietal development programs. Evaluation of genetic diversity is important to introgress wanted genes from distinct germplasm into the existing genetic base (Thompson and Nelson, 1998) and to predict the response to selection. Information on grouping based diversity calculated from agronomic characters will be useful for wheat breeders to plan crosses in hybridization program to create greater and useful variation for plant improvement (Najaphy *et al*., 2012). Greater genetic diversity coupled with high yield potential of genotypes and useful yield components may be used in varietal development.

Different data sets are used for estimation of genetic diversity in crop plants including pedigree data (Van Hintum and Haalman, 1994), biochemical markers (Hamrick and Godt, 1997), agro-morphological traits (Bar-Hen *et al*., 1995) or molecular markers. Morphological traits have been effectively used for estimation of genetic diversity and varietal development. Many researchers used agronomic traits to calculate genetic diversity (Ali *et al*., 2008; Khodadadi *et al*., 2011; Aharizad *et al*., 2012; Pordel-Maragheh, 2013; Siahbidi *et al*., 2013; Fahim, 2014; Sabaghnia *et al*., 2014; Verma *et al*., 2014). Genetic diversity between two individuals can be computed by a number of statistical methods depending upon data sets (Mohammadi and Prasanna, 2003). Selection of an appropriate genetic distance measure is a critical part in assessment of genetic diversity among genotypes. Euclidean distance based on quantitative data is generally used for estimating genetic diversity among genotypes (Mohammadi and Prasanna, 2003). As defined by Nei (1973) genetic distance is "that difference between two entities that can be described by allelic variation."

Salem *et al*. (2008) carried out genetic diversity analysis based on SSR markers and morphological characters of seven wheat varieties. They reported lower genetic diversity ranging from 0.42 to 0.63 with mean

To cite this paper: Naheed, H., F. Mohammad, Q. Sohail, S. Abid and N. Khan, 2016. Genetic diversity of bread wheat lines based on agro-morphological traits. *Int. J. Agric. Biol.*, 18: 1049–1055

diversity of 0.53 based on SSR markers and higher genetic diversity ranging from 8.51 to 38.46 with an average of 23.49 based on morphological characters. They suggested that classification or diversity studies based on genetic markers and morphological traits would be helpful for breeders to plan hybridization programs for productive results. Najaphy *et al*. (2012) determined genetic diversity of 30 bread wheat accessions using agro-morphological traits and molecular markers. Both methods categorized the 30 wheat accessions into five groups with slight disagreements. They found no correlation between the dissimilarity measurements identified using molecular markers and quantitative traits. Aharizad *et al*. (2012) clustered 96 bread wheat lines on the basis of agronomic traits. These wheat genotypes were classified into three groups using squared Euclidean distance and Ward's method. Khodadadi *et al*. (2011) carried out cluster analysis based on Ward's method and squared Euclidean distances which grouped 36 winter wheat genotypes into seven groups. Autrique *et al*. (1996) in their genetic diversity study of 113 durum wheat landraces and cultivars by means of morpho-physiological traits, restriction fragment length polymorphism and coefficient of parentage reported lower genetic distances for cultivars and some of the landraces while greater genetic distances for most of the landraces by both morpho-physiological traits and restriction fragment length polymorphism. Maric *et al*. (2004) assessed genetic diversity of 14 wheat cultivars and efficiency of RAPD markers in comparison with pedigree data and morphological characters for evaluation of genetic diversity. They reported no significant correlation between genetic distances obtained through molecular and morphological data. They suggested that if data on more morphological traits are included in the study, there is a possibility of better correlation between morphological traits and RAPD markers diversity. Semagn (2002) stated two reasons for the general lack of correlation between molecular and morphological variation: (1) Molecular markers cover a large proportion of the genome, including coding and non-coding regions, and (2) molecular markers are less subjected to artificial selection compared with morphological markers. Correspondence between molecular and agronomic diversity might be improved by analyzing more morphological and DNA markers.

An understanding of genetic relationships among inbred lines or pure lines can be particularly useful in planning crosses, in assigning lines to specific heterotic groups, and for precise identification with respect to plant varietal protection (Hallauer and Miranda, 1988).

The objective of this study was to use a large number of morphological and agronomic characters to assess genetic variability and diversity among promising advanced lines of spring bread wheat from different research centers in Pakistan tested in NUWYT trial in 2010–2011. Another objective was to propose some ideas for using diversity based on many agronomic and physiological traits, grain yield, yield components and biological yield to generate a ranging of the pairs of genotypes for hybridization program to develop improved wheat varieties.

Materials and Methods

Site Characteristics

This study was conducted at Agriculture research farm of The University of Agriculture, Peshawar, in 2010–2011 under irrigated condition. The experimental site is located at 34.01º N latitude, 71.35° E and 359 m above sea level and has a continental type of climate.

Plant Materials

Nineteen advanced wheat lines from various national wheat breeding programs in Pakistan and a check cultivar (Janbaz) were evaluated in the study; the details of the lines and locations of the breeding programs are given in Table 1.

Methods

The study was conducted using randomized complete block design with four replications. Each genotype was grown in six rows of 5 m length with 30 cm row to row distance and thus the plot size for each genotype was 9 m^2. The experiment was planted on Nov 11, 2010 using seed rate of 128 kg/ha. The calculated seed per plot was uniformly distributed in six rows. Nitrogen and phosphate were applied at the rate of 136 and 57 kg/ha, respectively from urea and DAP. DAP and half of the urea were applied at the time of seed bed preparation and the rest of urea was applied with second irrigation on February, 5. Standard cultural practices were followed to raise the crop.

Primary data were recorded on days to heading (DTH), days to maturity (DTM), plant height (PH), stem length (SL), peduncle length (PL), peduncle extrusion (PE), spike length (SpL), flag leaf auricle height (FLAH), flag leaf node height (FLNH), flag leaf sheath length (FLSL), flag leaf blade length (FLBL), flag leaf blade width (FLBW), productive tillers (PT), non-productive tillers (NPT), percent lodging (L), spike weight (SpW), grain yield per spike (GYPSp), grains per spike (GPSp), tiller vegetative mass (TVM), 1000 kernel weight (TKW), grain yield (GY) and biological yield (BY).

Secondary data on seed fill duration (SFD), vegetative: reproductive periods ratio (V: RP R), per cent peduncle extrusion (PPE), plant height: peduncle length ratio (PH:PL R), plant height: spike length ratio (PH:SL R), peduncle length: spike length ratio, (PL: SL R), peduncle length as % of stem length (PL%SL), flag leaf area (FLA), leaf blade length: sheat length ratio, leaf length: width ratio, leaf length: peducle extrusion ratio, total tillers m^{-2}, per cent productive tillers, chaff weight (CW), grains: chaff ratio, grains m^{-2} (GPSqM), spike filling rate (mg/spike/day)

Table 1: Details of the bread wheat advanced lines from wheat breeding programs in Pakistan

NUWYT No.	Code	Line/Entry	Institution/Station	Pedigree and selection history
G1	WHTSD 10007	V-07067	AARI-Faisalabad	V-87094/AUQAB (Pb.30459-2A-3A-0A-10A-0A)
G2	WHTSD 10011	V-07096	AARI-Faisalabad	PB96/V-87094/MH97 (Pb.30332-0A-0A-0A-9A-27A)
G3	WHTSD 10017	V-08173	AARI-Faisalabad	ATTILA/3*BCN//BAV92/3/PASTOR (CMSS97MO4165-040Y-040M—020Y-030M-015Y-14M-3Y-3M)
G4	WHTSD 10021	V-07076	AARI-Faisalabad	BABAX/4/BOW/CROW//BUC/PVN/3/VEE#10/5/BABAX/6/LU26/HD2179 (Pb.31068-0A-0A-43A-0A)
G5	WHTSD 10029	V-08171	AARI-Faisalabad	MILAN/587230//BABAX (CMSS97M03689T-040Y-030M-020Y-030M-015Y-030M-3Y-1M)
G6	WHTSD 10031	V-05BT014	AARI-BIOTECH.	BR 83/UFAQ02//FBD 83/3/HORK (BIOTECH-0R4-1R1-2R7-3RK-0R)
G7	WHTSD 10035	DN-92	ARI-D.I.Khan	CROC 1/AE.SQUARROSA (224)//OPATA/3/KAUZ∗2/ (CMSS95Y03317T-055M-4Y- 010M-010Y-010M-20Y-0Y
G8	WHTSD 10041	V-76309	RARI-Bahawalpur	CAL/NH/H 567-71/3/SERI/4/CAL/NH/H 567-71/5/ (CMSS 97M05788-020Y-030M-020Y-040M-99Y-3M-0Y
G9	WHTSD 10049	V-76377	RARI-Bahawalpur	CNDO/R-143//ENTE/MEXI-2/3/ (CMSS 99M-00451S-040M-030Y-030M-9Y)
G10	WHTSD 10053	V-15	NIFA-Peshawar	PRL/PASTOR//2236
G11	WHTSD 10054	CT-04192	NIFA-Peshawar	KAUZ/PASTOR (CMSS93B00025S-48Y-010M-010Y-010M-5Y-0M-0KBY-0KBY-0M)
G12	WHTSD 10059	TW96007	AZRI-Bh;akkar	XIANG 820261x2-KAUZ/MILVUS (3-1T-3T-6T-0T)
G13	WHTSD 10060	HB-10	WRI-Sakrand	CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/3/VEE#7/ (CMSS93B01854T-040Y-08Y- 010M-010Y-010M-8Y-0M-5KBY
G14	WHTSD 10069	HB-11	WRI-Sakrand	FLAKE∗2/BISU/3/CHEN/AEGILOPS SQUARROSA (TAUS) (CMSS95Y01596S-4Y-010M- 010Y-010M-09Y-0Y)
G15	WHTSD 10072	PR-102	CCRI Pirsabak	CS/TH.SC//3∗PVN/3/MIRLO/BUC/4/MILAN/5/TILHI (CMSS97M04005T-040Y-020Y- 030M-020Y-040M-28Y-3M-0Y)
G16	WHTSD 10083	BGWS-4	BIOCENTURY GUARD	[(82 cb x M84)x27]x[(N182 x B791)]xZ9
G17	WHTSD 10085	QS-III	QAARI-Larkana	W462//VEE/KOEL/3/PEG//MRL/BUC
G18	WHTSD 10091	NR-378	NARC-Islamabad	WHEAR//INQALAB91∗2/TUKURU (CGSS04Y00076S-099Y-099M-099Y-099M-5WGY-0B)
G19	WHTSD 10099	NR-379	NARC-Islamabad	WHEAR//2∗PRL/2∗PASTOR (CGSS03B00090T-099Y-099M-099Y-099M-6WGY-0B-1B)
G20	Local check	Janbaz	-	Gen*2//Buc/Filk/3/Buchin (CMSS96M0308S-12M-010SY-010M-010SY-3M-0Y)

(SFR), total tiller weight (g) (TW), tiller partitioning to reproductive parts, kernel filling rate, straw yield (SY), harvest index (HI), straw: grains ratio, vegetative crop growth rate – planting to heading (g m^{-2} day) (VCGR), crop growth rate during seed fill duration (g m^{-2} d^{-1}) (CGRDSFD), and average crop growth rate – planting to maturity (ACGR) – were derived from the primary data (Sayre *et al.,* 1997; Van Ginkel *et al.,* 1998; Paigham Shah, 2003a and b).

Statistical Analysis

To test the significance of differences among the 20 genotypes, the data for each trait were subjected to analysis of variance technique appropriate for RCB design. Using mean values of the 20 genotypes average, minimum, maximum, variance, standard deviation and coefficient of variation were calculated for the 51 traits.

Euclidean distances as measure of genetic diversity were calculated for 190 pairs of the 20 wheat genotypes using mean values of 51 agronomic and physiological traits. Euclidean distance is the square root of the sums of squared differences between different traits of a pair of genotypes. As the data had different units, the data were statistically standardized and the distances were calculated using the following formula (Teknomo, 2011).

$$D_{ij} = \sqrt{\sum_{k=1}^{n} \left(\left(X_{ik} - X_{jk} \right)^2 \right)}$$

SAS program was used for clustering the genotypes and to generate dendrogram.

Results

A high degree of variation was observed among genotypes for most of the agronomic and physiological traits studied; F values for genotypes of 43 traits were significant, only eight of the 51 traits were not significant (Table 2). The genotypic differences for majority of the traits (29 out of 51) were very highly significant (probability of less than 0.001). The F-value for grain yield was significant at the 5% level of probability. Descriptive statistics of the studied traits showed high variability among the genotypes. The highest CV was observed for lodging followed by grain-weight: chaff-weight ratio, non-productive tillers, chaff weight, spike filling rate, vegetative: reproductive periods ratio, kernel filling rate and CGR in SFD – which indicate more variation among genotypes for these traits (Table 2). Grain yield ranged from 285 to 419 g m^{-2} with an average of 374 (g m^{-2}).

Table 2: Descriptive statistics of various traits of 20 bread wheat genotypes, significance of F values from ANOVA and correlation with yield of the traits recorded in the study

Trait (unit)	Mean	Min	Max	Var	SD	CV	Sig.	Cor.
Days to 50% heading (d)	122	114	128	13.6	3.7	3.0	***	0.079
Days to maturity (d)	162	160	164	1.6	1.3	0.8	Ns	-0.034
Plant height (cm)	90.6	72.1	100.0	39.2	6.3	6.9	***	0.219
Peduncle length (cm)	32.2	25.8	37.2	9.9	3.1	9.8	***	-0.001
Peduncle extrusion (cm)	14.9	10.0	18.7	5.3	2.3	15.5	***	-0.017
Stem Length (cm)	80.5	63.5	89.8	32.2	5.7	7.0	***	0.262
Spike length (cm)	10.1	8.4	12.4	1.1	1.1	10.5	***	-0.104
Flag leaf auricle height (cm)	24.4	18.3	29.4	6.2	2.5	10.2	***	-0.074
Flag leaf node height (cm)	24.4	18.3	29.4	6.2	2.5	10.2	***	-0.073
Flag leaf sheath length (cm)	1.6	1.4	2.0	0.0	0.2	9.6	***	-0.042
Flag leaf blade length (cm)	65.6	53.4	73.9	21.7	4.7	7.1	***	0.328
Flag leaf blade width (cm)	48.3	37.6	57.9	19.3	4.4	9.1	***	0.339
Productive tillers m^{-2} (number)	312	242	416	1975	44	14	***	0.369
Non-productive tillers m^{-2} (number)	38	16	63	154	12	33	Ns	0.059
Lodging (per cent)	6.8	0.0	26.3	68.5	8.3	122.2	Ns	0.426
Spike weight (g)	2.43	2.01	3.13	0.09	0.30	12.24	**	0.222
Grain yield per spike (g)	1.91	1.65	2.56	0.05	0.23	11.98	*	0.214
Grains/spike (number)	45	38	54	22	5	11	**	0.363
Tiller vegetative mass (g)	1.27	0.89	1.60	0.04	0.21	16.28	Ns	0.149
1000 grain weight (g)	37.53	31.61	42.94	11.44	3.38	9.01	***	-0.103
Grain yield (g m^{-2})	249.6	190.3	279.56	379.8	19.49	7.81	*	1.000
Biological yield (g m^{-2})	733.3	608.3	841.67	3461.6	58.84	8.02	***	0.676
Harvest index (%)	34.2	30.1	38.3	4.5	2.1	6.2	Ns	0.389
Straw yield (g m^{-2})	725.6	592.8	886.5	5155.7	71.8	9.9	**	0.424
Seed fill duration (d)	39.5	23.5	46.0	24.9	5.0	12.6	***	-0.036
Vegetative: reproductive periods ratio	3.17	2.48	5.44	0.41	0.64	20.14	***	0.021
Relative peduncle extrusion (per cent)	46.0	38.8	52.7	11.5	3.4	7.4	***	-0.033
Plant height: peduncle length ratio	2.84	2.53	3.35	0.05	0.21	7.55	***	0.206
Plant height: spike length ratio	9.06	7.83	10.48	0.56	0.75	8.28	***	0.350
Peduncle length: spike length ratio	3.21	2.76	3.74	0.10	0.32	10.02	***	0.144
Peduncle length as % of stem length	40.0	33.1	44.4	8.7	2.9	7.4	***	-0.229
Flag leaf area (cm^2)	34.6	23.0	44.8	22.9	4.8	13.8	***	-0.059
Leaf blade length: leaf sheath length ratio	1.42	1.20	1.69	0.02	0.14	9.52	***	-0.128
Leaf length: leaf width ratio	15.12	11.53	17.24	2.51	1.58	10.47	***	-0.074
Leaf length: peduncle extrusion ratio	1.69	1.27	2.29	0.07	0.27	15.68	***	-0.054
Total tillers m^{-2} (number)	351	268	479	2664	52	15	**	0.332
Per cent productive tillers (%)	;90	85	96	6.0	2.4	2.7	Ns	0.113
Chaff weight (g $tiller^{-1}$)	0.52	0.19	0.79	0.02	0.13	24.93	**	0.131
Grains: chaff ratio	4.40	2.94	9.69	3.08	1.75	39.84	*	-0.138
Grains m^{-2} (number in 100s)	139	106	181	377	19.4	14	*	0.610
Spike filling rate (mg $spike^{-1}$ d^{-1})	50	39	88	117	11	22	***	0.098
Total tiller weight (g)	3.70	3.08	4.67	0.22	0.47	12.58	**	0.208
Tiller partitioning to spike (%)	65.9	60.6	71.6	8.2	2.9	4.3	Ns	0.010
Kernel filling rate (mg $kernel^{-1}$ d^{-1})	0.97	0.78	1.64	0.03	0.18	18.86	***	-0.057
Straw:grains ratio	1.96	1.64	2.37	0.04	0.20	9.95	Ns	-0.402
Vegetative crop growth rate (g m^{-2} d^{-1}) planting to heading	5.96	4.66	6.92	0.34	0.58	9.77	**	0.418
Vegetative RGR (mg g^{-1} d^{-1})	54.1	50.1	57.7	3.1	1.8	3.3	***	0.157
Crop growth rate during seed fill duration (g m^{-2} d^{-1})	9.7	6.5	15.6	3.3	1.8	18.6	***	0.392
Average crop growth rate planting to maturity (g m^{-2} d^{-1})	6.8	5.7	7.9	0.3	0.5	7.9	**	0.692
Yield per day from planting (g m^{-2} d^{-1})	13.9	10.6	15.7	1.2	1.1	7.9	*	0.995
Yield per day from heading (g m^{-2} d^{-1})	58	39	94	117	11	19	***	0.392

Discussion

A phylogenetic tree was constructed based on the 43 agronomic and physiological traits showing considerable diversity. The 20 wheat genotypes could be divided into 2 major clades (A and B); both the clades had two main branches designated as A1, A2, B1 and B2 (Fig. 1). Clade B had 12, while clade A had 7 genotypes.

One genotype (16) was an outlier; it is interesting to note that this genotype is developed by a private

Table 3: Euclidean distances between all possible pairs of the 20 genotypes

G†	Code	G1	G2	G3	G4	G5	G6	G7	G8	G9	G10
G1	WHTSD 10007	0.0									
G2	WHTSD 10011	6.0	0.0								
G3	WHTSD 10017	10.2	9.8	0.0							
G4	WHTSD 10021	6.8	6.5	8.7	0.0						
G5	WHTSD 10029	9.0	8.7	9.9	9.2	0.0					
G6	WHTSD 10031	5.2	4.4	9.7	7.1	8.2	0.0				
G7	WHTSD 10035	6.3	7.9	8.8	6.2	8.6	7.0	0.0			
G8	WHTSD 10041	10.7	10.1	7.8	7.7	10.4	10.2	7.6	0.0		
G9	WHTSD 10049	7.9	6.9	10.3	5.0	8.7	8.7	8.6	10.0	0.0	
G10	WHTSD 10053	8.0	8.9	12.6	8.0	9.7	9.6	9.3	10.4	7.4	0.0
G11	WHTSD 10054	7.3	9.6	10.6	8.1	10.3	10.4	7.1	10.2	8.2	8.2
G12	WHTSD 10059	10.9	10.0	12.5	8.3	11.8	10.8	10.7	8.8	8.9	7.2
G13	WHTSD 10060	9.6	9.2	10.6	8.6	9.4	9.1	8.6	7.3	9.4	10.9
G14	WHTSD 10069	6.2	7.2	8.8	7.2	9.7	5.8	6.0	10.0	10.0	11.3
G15	WHTSD 10072	7.7	8.2	11.0	7.7	7.3	8.3	8.0	10.4	8.2	10.3
G16	WHTSD 10083	14.2	14.4	12.8	13.2	14.6	16.4	14.3	15.9	11.7	15.6
G17	WHTSD 10085	5.9	8.6	12.2	7.7	10.3	9.0	5.9	9.7	8.3	6.8
G18	WHTSD 10091	8.7	8.8	12.4	8.7	12.9	9.3	8.0	10.0	9.7	10.1
G19	WHTSD 10099	7.1	10.1	9.2	8.4	10.6	8.1	5.3	9.3	11.3	12.1
G20	Janbaz (check)	8.0	8.1	10.6	5.5	8.2	7.9	7.1	9.3	6.5	7.4

Table 3: Continued

G†	Code	G11	G12	G13	G14	G15	G16	G17	G18	G19	G20
G11	WHTSD 10054	0.0									
G12	WHTSD 10059	10.8	0.0								
G13	WHTSD 10060	10.3	10.4	0.0							
G14	WHTSD 10069	9.8	11.7	10.0	0.0						
G15	WHTSD 10072	9.2	11.1	7.3	8.6	0.0					
G16	WHTSD 10083	11.1	16.8	16.3	15.0	13.5	0.0				
G17	WHTSD 10085	6.4	9.8	9.6	8.8	8.8	14.6	0.0			
G18	WHTSD 10091	11.3	11.8	11.0	10.2	11.7	16.7	7.1	0.0		
G19	WHTSD 10099	10.1	13.2	9.6	5.2	9.5	16.1	8.4	9.6	0.0	
G20	Janbaz (check)	9.7	8.0	9.8	8.9	8.7	14.8	7.8	9.0	9.8	0.0

†G is the abbreviation used for genotype, the details of the genotypes studied is given in Table 1

company, while the origins of rest are mainly from International and National Research Centers. Three lines (G7, G13 and G14) are synthetically derived lines, but did not show any similarity; may be due to the fact the parents are not the same. The lines G2 and G6 showed highest similarity with one another. Euclidian distances, (measure of genetic diversity), between all 190 possible pairs of the 20 genotypes were calculated (Table 2); a summary of the distances is given in Table 3. Euclidean distances of all possible pairs ranged from 4.37 for G2-G6 pair to 16.80 for G12-G16 pair. The standardized distances revealed great genetic diversity among genotypes with a mean Euclidean distance of 0.522 (Table 3). The mean distance calculated in this study is slightly less than reported by Sohail *et al*. (2011), the reason for the difference may be the use of synthetic wheat lines created by crossing durum wheat with *Ae. tauschii*, the D genome donor of the bread wheat. Synthetic wheat lines were created with the objective to create more variability that is why they had more diversity. Genotypes 12 and 16 exhibited maximum diversity followed by genotypes 16 and 18, 6 and 16, and 13 and 16 (Table 3), indicating that the members of these pairs of genotypes are genetically more diverse than other pairs of genotypes, this information is important for breeder if they plan to use any of these lines in their crossing blocks. Hybrids of genotypes with genetic diversity results in transgressive segregates (Rahim *et al*., 2010), and thus breeders have greater probability to get high yielding lines in the segregating generations. These genotypes can be used in hybridization programs to attain maximum heterosis. Genotypes with minimum distances can be used in backcross programs (Khodadadi *et al*., 2011). Minimum distance was observed between genotype 2 and 6, the genotypes 4 and 9, 14 and 19, and 1 and 6 had comparatively lower genotypic diversity (Table 3). These genotypes can be used in backcross methods in future breeding programs to transfer specific characters from one member to the other member of the pairs more easily.

Most of the primary and secondary data showed reasonable amount of diversity. The primary and secondary data of the 2 major clades (A and B) and the main groups (A1, A2, B1 and B2) were compared. Some of the important traits had similar data among the genotypes of each group. For yield group A1 had an average of 2296 g, A2, 2313 g, B1, 2293 g and B2 had 2218 g. Group A1 had the highest average and the genotype (G11) having the highest yield (2480 g) also belong to this group. Interestingly, group A1 on the average required the

Table 4: Mean Euclidean distance and details of the seven smaller and seven greater Euclidean distances among all possible pairs of 20 wheat genotypes

Seven greater distances			Seven smaller distances		
Genotypes	Distance	Rank	Genotypes	Distance	Rank
G12 – G16	16.8	1	G2 – G6	4.4	190
G16 – G18	16.7	2	G4 – G9	5.0	189
G6 – G16	16.4	3	G14 – G19	5.2	188
G13 – G16	16.3	4	G1 – G6	5.2	187
G16 – G19	16.1	5	G7 – G19	5.3	186
G8 – G16	15.9	6	G4 – G20	5.5	185
G10 – G16	15.6	7	G6 – G14	5.8	184
Mean Euclidean distance of all the pairs of genotypes				9.5	
Other pairs with distances greater than mean + 2 SD are					
G14 - G16, G17 - G20, G5 - G16, G16 - G17, G2 - G16, G7 - G16					

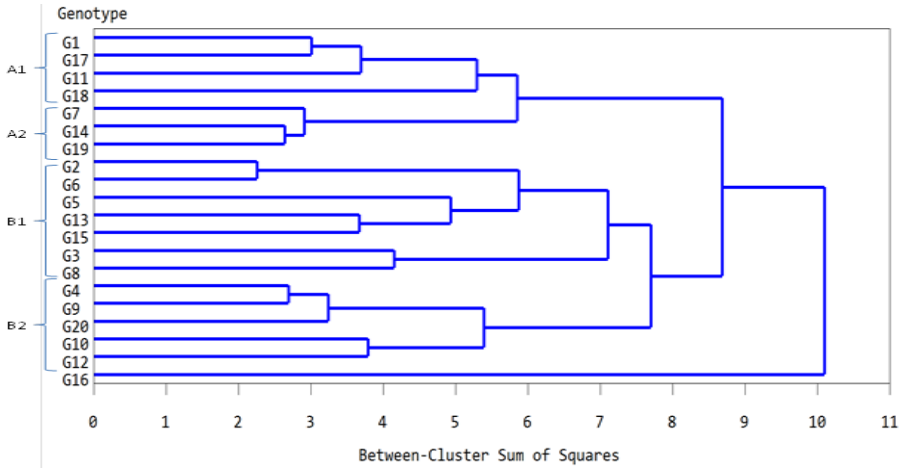

Fig. 1: Phylogenetic tree of the 20 bread wheat lines constructed using agro-morphological traits

maximum number of days (125) for 50% heading and the genotype requiring the most day for 50% heading (126) was the overall highest yielder. The leaf area of the genotypes ranged from 40 to 19 cm^2. The average leaf area ranged from 31 cm^2 (group B2) to 35 cm^2 (group A1) demonstrating that genotypes of group A1 had high photosynthesis leading to high yield. Many other traits showed similar trends.

Conclusion

Genotypes 2 and 6, 4 and 9, 14 and 19, and 1 and 6 genotypes has lower genetic diversity and thus can be used in backcross methods in future breeding programs to transfer specific characters from one member to the other member of the pairs more easily. Genotypes 12 and 16, 16 and 18, 6 and 16, and 13 and 16 exhibited higher genetic diversity and can be used in hybridization programs to generate variability for selection and to attain maximum heterosis.

References

Aharizad, S., M. Sabzi, S.A. Mohammadi and E. Khodadadi, 2012. Multivariate analysis of genetic diversity in wheat (*Triticum aestivum* L.) recombinant inbred lines using agronomic traits. *Ann. Biol. Res.*, 3: 2118–2126

Ali, Y., B.M. Atta, J. Akhtar, P. Monneveux and Z. Lateef, 2008. Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm. *Pak. J. Bot.*, 40: 2087–2097

Autrique, E., M.M. Nachit, P. Monneveux, S.D. Tanksley and M.E. Sorrells, 1996. Genetic diversity in durum wheat based on RFLPs, morphological traits and coefficient of parentage. *Crop Sci.*, 36: 735–742

Bar-Hen, A., A. Charcosset, M. Bourgoin and J. Cuiard, 1995. Relationships between genetic markers and morphological traits in maize inbred lines collection. *Euphytica*, 84: 145–154

Barrett, B.A. and K.K. Kidwell, 1998. AFLP-based genetic diversity assessment among wheat cultivars from the Pacific Northwest. *Crop Sci.*, 38: 1261–1271

Cox, T.S., J.P. Murphy and D.M. Rodgers, 1986. Changes in genetic diversity in the red winter wheat regions of the United States. *Proc. Natl. Acad. Sci. (USA)*, 83: 5583–5586

Fahim, M.G., 2014. Grouping of promising agronomic traits of genotypes and lines of bread wheat using cluster analysis and detection function. *Ind. J. Fund. Appl. Life Sci.*, 4: 182–185

Franco, J., J. Crossa, J.M. Ribaut, J. Betran, M.L. Warburton and M. Khairallah, 2001. A method for combining molecular markers and phenotypic attributes for classifying plant genotypes. *Theor. Appl. Genet.*, 103: 944–952

Hallauer, A.R. and J.B. Miranda., 1988. Quantitative Genetics in Maize Breeding, 2nd ed. Iowa State University Press, Ames, Iowa, USA

Hamrick, J.L. and M.J.W. Godt, 1997. Allozyme diversity in cultivated crops. *Crop Sci.*, 37: 26–30

Khodadadi, M., M.H. Fotokian, and M. Miransari, 2011. Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. *Aust. J. Crop Sci.*, 5: 17–24

Liu, Y., J. Guo, D. Zhang, Y. Zhao, L. Zhu, Y. Huang and J. Chen, 2014. Genetic diversity and linkage disequilibrium estimation among the maize breeding germplasm for association mapping. *Int. J. Agric. Biol.*, 16: 851–861

Maragheh, F.P., 2013. Assess the genetic diversity in some wheat genotypes through agronomic traits. *Eur. J. Zool. Res.*, 2: 71–75

Maric´, S., S. Bolaric´, J. Martinc˘ic, I. Pejic´ and V. Kozumplik, 2004. Genetic diversity of hexaploid wheat cultivars estimated by RAPD markers, morphological traits and coefficients of parentage. *Plant Breed.*, 123: 366–369

Mohammadi, S.A. and B.M. Prasanna, 2003. Analysis of genetic diversity in crop plants—salient statistical tools and considerations. *Crop Sci.*, 43: 1235–1248

Najaphy, A., R.A. Parchin and E. Farshadfar, 2012. Comparison of phenotypic and molecular characterizations of some important wheat cultivars and advanced breeding lines. *Aust. J. Crop Sci.*, 6: 326–332

Nei, M., 1973. Analysis of gene diversity in subdivided populations. *Proc. Natl. Acad. Sci. (USA)*, 70: 3321–3323

Paigham Shah, 2003a. *Designing Experiments* – Training manual for curriculum based teachers training course (Jan 6–11, 2003) sponsored by HEC, Islamabad, Pakistan

Paigham Shah, 2003b. *Conducting Experiments on Crops and Experimental Techniques* – Training manual for curriculum based teachers training course (Jan 13-18, 2003) sponsored by HEC, Islamabad, Pakistan

Rahim, M.A., A.A. Mia, F. Mahmud, N. Zeba and K.S. Afrin, 2010. Genetic variability, character association and genetic divergence in Mungbean (*Vigna radiate L. Wilczek*). *Plant Omics J.*, 3: 1–6

Sabaghnia, N., M.J. Mohammadi, A. Bashiri and R.A. Shirghan, 2014. Genetic variation of several bread wheat (*Triticum aestivum* L.) genotypes based on some morphological traits. *Annales*, 1: 44–54

Salem, K.F.M., A.M. El-Zanaty and R.M. Esmail, 2008. Assessing wheat (*Triticum aestivum* L.) genetic diversity using morphological characters and microsatallite markers. *World J. Agric. Sci.*, 4: 538–544

Sayre, K.D., S. Rajaram and R.A. Fischer, 1997. Yield potential progress in short bread wheats in northwest Mexico. *Crop Sci.*, 37: 36–42

Semagn, K., 2002. Genetic relationships among ten endod types as revealed by a combination of morphological, RAPD and AFLP markers. *Hereditas*, 137: 149–156

Siahbidi, M.M.P., A.P. Aboughadareh, G.R. Tahmasebi, M. Teymoori and M. Jasemi, 2013. Evaluation of genetic diversity and inter relationships of agro-morphological characters in durum wheat (*Triticum durum desf.*) lines using multivariate analysis. *Intl. J. Agric. Res. Rev.*, 3: 184–194

Sohail, Q., T. Inoue, H. Tanaka, A.E. Eltayeb, Y. Matsuoka and H. Tsujimoto, 2011. Applicability of *Aegilops tauschii* drought tolerance traits to breeding of hexaploid wheat. *Breed. Sci.*, 61: 347–357

Teknomo, K., 2011. *Similarity Measurement.* http://people.revoledu.com/kardi/tutorial/Similarity (Accessed April 7, 2011)

Thompson, J.A. and R.L. Nelson, 1998. Core set of primers to evaluate genetic diversity in soybean. *Crop Sci.*, 38: 1356–1362

Van Ginkel, M., D.S. Calhoun, G. Gebeyeho, A. Mirenda, C. Tain-you, R.P. Lara, R.M. Trethowan, K. Sayre, J. Crossa and S. Rajaram, 1998. Plant traits related to yield of wheat in early, late or continuous drought conditions. *In: Wheat: Prospects for Global Improvement – Proceeding of the 5th International Wheat Conference, 10–14 June, Ankara, Turkey*, pp: 167–197. Braun, H.J., F. Altay, W.E. Kronstad, S.P.S. Beniwal and A. McNab (eds.). Academic Publishers, Dordrecht, The Netherlands

Van Hintum, T.J.L. and D. Haalman, 1994. Pedigree analysis for composing a core collection of modern cultivars, with examples from barley (*Hordeum vulgare*). *Theor. Appl. Genet.*, 88: 70–74

Verma, P.N., B.N. Singh, G. Singh, M.K. Singh and T.L. Setter, 2014. Genetic diversity analysis for yield and other agronomic traits in bread wheat under water logged sodic soil condition. *J. Wheat Res.*, 6: 51–58

(Received 08 August 2015; Accepted 25 June 2016)