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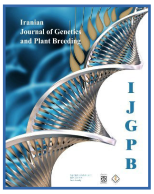

Assessment of genetic variation among bread wheat genotypes based on yield-related traits

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ABSTRACT

Genetic diversity is a base for the survival and improvement of crops. This experiment was conducted to evaluate genetic diversity among 400 bread wheat genotypes based on nine quantitative yield-related traits. The results of descriptive statistics showed that the highest and lowest amount of phenotypic variation belonged to kernel weight per spike (34.61%) and kernel length (7.61%), respectively. Correlation coefficient analysis showed a strong and positive correlation between kernel weight and spike weight (0.97) followed by the number of kernels per spike and number of kernels per spikelet (0.91). Principal component analysis reduced the nine traits into three principal components that explained 85 percent of the total variation. Factor analysis revealed three underlying factors that explained 86 percent of the variation. Cluster analysis based on all the studied traits divided the genotypes into four clusters. The first cluster included 145 genotypes and had the lowest means for most of the traits. The second cluster included 43 genotypes and had the highest mean for kernel length. The third cluster included 77 genotypes that had the highest means for spike weight, kernel weight per spike, kernel width, and thousand-kernel weight. The fourth cluster included 135 genotypes and had the highest means for spike length, number of spikelets, kernels per spikelet, and kernels per spike. The results of this study can contribute to the understanding of genetic diversity among bread wheat genotypes and can be used for bread wheat improvement programs.

Key words: Bread wheat, Genetic diversity, Morphological traits, Multivariate analysis.

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INTRODUCTION

Wheat is the most important cereal crop because of its domestication and significance as the world's primary staple food crop (Iqbal *et al*., 2021). According to the Food and Agriculture Organization in 2021, the global area under wheat cultivation reached 220 million hectares in the world and 6.5 million hectares in Iran, resulting in a reported wheat production of 770 million tons in the world and 10 million tones in Iran. Also, the average wheat yield was reported as 3.5 tons per hectare in the world and 1.5 tons per hectare in Iran (FAOSTAT, 2021).

Genetic diversity is a base for the survival of plants in nature and also for crop improvement. Diversity in plant genetic resources provides the opportunity for plant breeders to develop new and improved cultivars with desirable characteristics, which include both farmer-preferred traits (high yield potential, large grain yield, etc.) and breeder-preferred traits (pest and disease resistance, photosensitivity, etc.) (Franco *et al*., 2001; Liu *et al*., 2014; Bhandari *et al*., 2017).

Genetic diversity in populations is estimated to analyze genetic variability in cultivars and identify diverse genotypes for hybridization to generate progenies with more genetic variation for further selection. The level of genetic diversity among parents of a cross determines the genetic variance among the segregating populations to be addressed by breeders to develop better pure lines in varietal development programs. Evaluation of genetic diversity is important to introgress desired genes from distinct germplasm into the existing genetic base and to predict the response to selection (Naheed *et al*., 2016). Information on grouping-based diversity calculated from agronomic characters will be useful for wheat breeders to plan crosses in hybridization programs to create greater and more useful variations for plant improvement. Greater genetic diversity coupled with the high yield potential of genotypes and useful yield components may be used in varietal development (Najaphy *et al*., 2012).

Diversity analysis can be carried out using morphological, cytological, biochemical, and molecular characterizations. Initially, morphological markers were used for diversity analysis and are still in use. Morphological traits have been effectively used for the estimation of genetic diversity and cultivars development. Many researchers have used agronomic traits to calculate genetic diversity (Ali *et al*., 2008; Khodadadi *et al*., 2011; Aharizad *et al*., 2012; Maragheh, 2013; Siahbidi *et al*., 2013; Fahim, 2014; Sabaghnia *et al*., 2014; Verma *et a*l., 2014; Naheed *et al*., 2016; Mecha *et al*., 2017; Poudel *et al*., 2017; Singh *et al*., 2018; Adilova *et al*., 2020; Sharma *et al*., 2021; Hassani *et al*., 2022). The study of the genetic variability of grain yield and its component characters among different varieties provides a strong basis for the selection of suitable genotypes for the expansion of yield and other agronomic characteristics (Mangroliya and Sapovadiya, 2020).

Cluster analysis is a multivariate method, which aims to classify a sample of subjects based on a set of measured variables into different groups such that similar subjects are placed in the same group. (Cornich, 2007) It sorts genotypes into groups, or clusters, so the degree of association will be strong between members of the same cluster and weak between members of different clusters (Tiwari *et al*., 2017; Yadav *et al*., 2021).

The selection of an appropriate genetic distance measure is a critical part of the 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). Several authors have suggested the use of cluster and principal component analyses to study the genetic diversity and relationships of wheat genotypes (Adilova *et al*., 2020; Fouad, 2020). Another experiment was conducted at the Agricultural Research Farm of Shahed University, Tehran, Iran as a randomized complete block design with three replications. 36 winter wheat genotypes from different regions of Iran were selected. Cluster analysis based on squared Euclidean distance and Ward's method categorized the cultivars into seven groups (Khodadadi *et al*., 2011).

Principal Component Analysis (PCA) can reduce a large number of potentially correlated variables to a smaller number of variables known as principal components (Muaju and Chakauya, 2008). Principal components analysis is an important tool for finding regularities among data. Basically, PCA transforms the closely correlated data sets into a new system of traits and separates them from non-correlated components (Janmohammadi *et al*., 2014).

Factor analysis is usually applied to reduce the number of variables into some hidden factors, to recognize some chief components of yield, to group traits based on intra-relationships among them, and to study genetic diversity (Azizi *et al*., 2001).

The main purposes of this investigation were to evaluate the genetic variability of 400 genotypes of

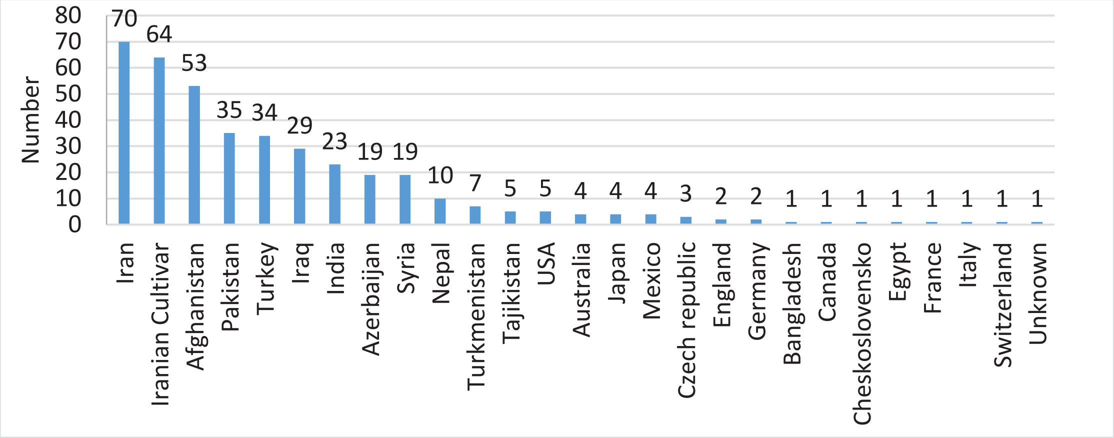

Figure 1. Origin of the studied bread wheat Genotypes.

wheat, utilizing cluster, and principal components analyses to determine genetic relationships among evaluated genotypes to be used for future breeding programs.

MATERIALS AND METHODS

In this study, a collection of 400 bread wheat genotypes from various geographical origins was evaluated. A detailed list of the evaluated genotypes can be found in Supplementary Table 1 and Figure 1. These genotypes were obtained from the Gene Bank of IPK-Gatersleben, Germany, the Gene Bank in the Czech Republic, the Gene Bank in ICARDA in Syria, and the Seed and Plant Improvement Research Institute (SPII), Cereal Research Department (CRD), in Iran. The experiment was conducted during the wheat cropping season of 2021-2022 in the research field of Gorgan University of Agriculture Sciences and Natural Resources in Iran. The seeds of each genotype (75 seeds) were sown by hand on two rows with two-meter lengths. The space between the seeds was 5 centimeters and 20 centimeters distance between the rows while there was a one-meter distance between the rows of different genotypes. The experiment was conducted based on an Augmented design with six common cultivars as controls in eight blocks in rain-fed conditions (Table 1).

Table 1. Name of the common wheat cultivars applied in the randomized complete blocks design.

Rain fed cultivars	Irrigated cultivars
Aftab	Kalate
Kohdasht	Ehsan
Qabos	Gonbad

Nine morphological traits including spike weight (gr), kernel weight per spike (gr), spikelet number per spike (number), spike length (cm), kernel number per spike (number), kernel length (cm), kernel width (cm), thousand-kernel weight (gr), and kernel number per spikelet (number) were measured. These quantitative traits were averaged and analyzed. Descriptive statistics such as mean, minimum, maximum, standard deviation, coefficient of variation (C.V.), plus correlation coefficients between traits were calculated to determine the genetic diversity among the studied genotypes, applying SAS.V.9.0 (Copyright (c) 2002 by SAS Institute Inc., Cary, NC, USA.) and MINITAB14 software. To determine the genetic diversity among the 400 studied genotypes, cluster analysis based on Ward's method using squared Euclidian distance was carried out. The tree diagram was drawn using SAS.V.9.0 and SPSS.V.16 software. Principal components analysis and factor analysis by principal components method and maximum likelihood were carried out, and for better interpretation, factors were rotated by the Varimax method using SAS.V.9.0 software.

RESULTS

Analysis of variance (ANOVA) for the common wheat cultivars on randomized complete blocks design showed that spike weight, kernel weight per spike, spikelet number per spike, kernel number per spike, and kernel width had significant differences between the common wheat cultivars while spike length, kernel length, thousand-kernel weight, and kernel number per spike had no significant difference. The blocks did not show any significant differences (Table 2), indicating that there was no need for data correction based on block variations. The C.V. was within the acceptable range of agricultural experiments. According to GOMES (2009), in field experiments, any C.V. less than 10% is considered low which means that the experiment has a high accuracy. From 10 to 20% the C.V. is considered medium, implying good precision. From 20 to 30% is considered high, meaning low precision. Finally, C.V.s above 30% considered very high, indicating very low precision. Histogram charts with the normal curve were plotted for all the studied traits of genotypes which can be used to check the normality (Figure 2). According to these graphs, there was no outlier data in this data set.

Descriptive statistics

Descriptive statistics including range, minimum, maximum, mean, standard deviation, and C.V. for the nine measured traits are shown in Table 3. As the table shows, kernel weight per spike exhibited the highest C.V. (34.61%) followed by spike weight. This result can be a reason for the greater diversity of these traits. Kernel length had the lowest C.V. (7.61%).

Correlation analysis

Pearson correlation coefficient analysis was conducted to examine the relationship between the measured traits among the studied genotypes. The results revealed a strong and significant positive correlation between spike weight and kernel weight per spike (r=0.97), followed by kernel number per spike and kernel number per spikelet (r=0.91). The detailed correlation coefficients are presented in Table 4.

Principal component analysis

Principal component analysis was performed based on the correlation matrix to reduce the dimensions of the data and identify the most important components explaining the variation. The PCA reduced the nine traits into three principal components, which accounted for a total of 85.2% of the total variation. The first principal component (PC1) had an eigenvalue of 4.95 and explained 49.52% of the variation. The PC2 and PC3 accounted for 22.81% and 12.95 variation, respectively, with eigenvalues of 2.28 and 1.29 (Table 5). Kernel weight per spike (0.439), spike weight (0.436), thousand-kernel weight (0.366), kernel width (0.362), kernel number per spike (0.329), and kernel weight per spikelet (0.329) had the highest loadings on PC1. Correspondingly, PC2 was characterized by significant positive loadings due to the number of kernels per spike (0.430), number of spikelets per spike (0.382), and number of kernels per spikelet (0.320) and negative loading due to kernel length (0.433), kernel width (0.366) and thousand-kernel weight (0.166). The traits that contributed the greatest to PC3 showed the highest factor loadings for spike length (0.707),

Table 2. Analysis of variance for the studied trait on the control bread wheat genotypes.

Source of variation	df	Mean of square								
		Kernel weight per spikelet	Thousand kernels weight	Kernel width	Kernel length	Kernel number per spike	Spike length	Spikelet number per spike	Kernel weight per spike	Spike weight
Block	7	0.19^{ns}	0.36^{ns}	0.48^{ns}	0.10^{ns}	31.33^{ns}	0.36^{ns}	0.48^{ns}	0.10^{ns}	0.19^{ns}
Genotype	5	1.10**	1.20^{ns}	6.23**	0.54*	230.26*	1.20^{ns}	6.23**	0.54*	1.10**
Error	35	0.23	0.87	1.72	0.15	78.87	0.87	1.72	0.15	0.23
Coefficient of variation (%)		13.66	7.93	6.35	14.63	14.82	7.93	6.35	14.63	13.66

*, ** and ns: significant at *P*<0.05, *P*<0.01 and non-significant.

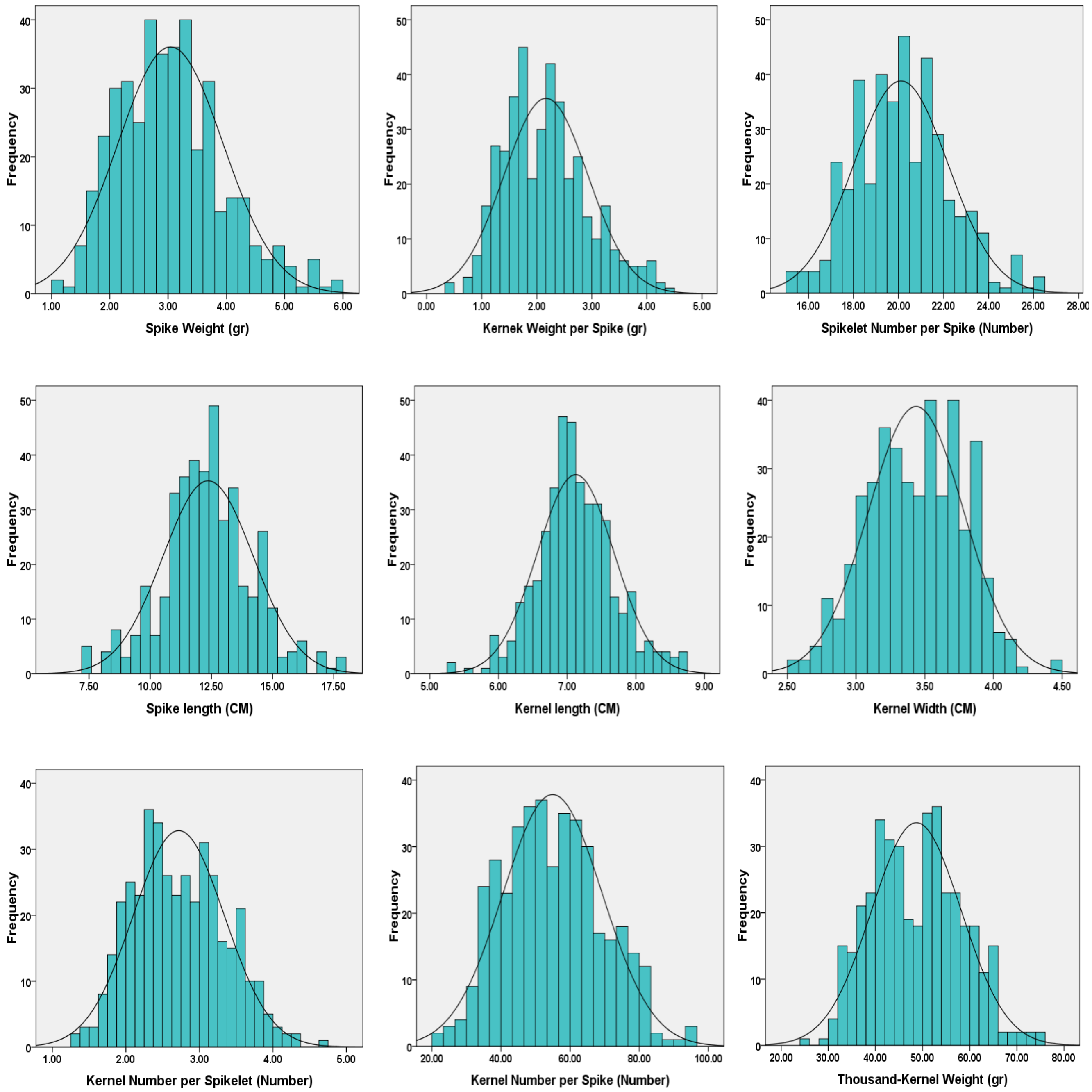

Figure 2. Histograms of the studied traits.

number of spikelets per spike (0.441), and kernel length (0.432).

According to the results of the correlation between the traits and the principal components, traits like kernel weight per spike, spike weight, thousand-kernel weight, kernel width, number of kernels per spike and number of spikelets per spike in the firth principle, number of kernels per spike and number of spikelet per spike in second principal and number of spikelets per spike and spike length in third principal had positive value. The number of spikelets per spike had equal values in the second and third principal components.

Factor analysis

Factor analysis for the nine studied traits on 400 bread wheat genotypes extracted three main factors. Factors with eigenvalues higher than 1 were selected for performing the loading factor matrix. After extracting the main factors, a Varimax orthogonal rotation was

Table 3. Descriptive statistics for the studied traits.

Traits	Range	Minimum	Maximum	Mean	Standard deviation	Coefficient of variation (%)
Spike weight (gr)	4.77	1.07	5.85	3.03	0.89	29.18
Kernel weight per spike (gr)	3.90	0.43	4.33	2.16	0.75	34.61
Spikelet number per spike (number)	11.40	15	26.40	20.11	2.05	10.18
Spike length (cm)	10.60	7.35	17.95	12.35	1.80	14.51
Kernel number per spike (number)	71.90	23.20	95.10	55	14.19	25.79
Kernel length (cm)	3.41	5.31	8.73	7.11	0.54	7.61
Kernel width (cm)	1.86	2.56	4.43	3.43	0.34	9.94
Thousand-kernel weight (gr)	50	25	75	48.72	0.49	19.52
Kernel number per spikelet (number)	3.41	1.30	4.71	2.72	0.61	22.53

Table 4. Pearson correlation coefficients between the studied traits.

Traits	Spike weight	Kernel weight per spike	Spikelet number per spike	Spike length	Kernel number per spike	Kernel length	Kernel width	Thousand-kernel weight	Kernel number per spikelet
Spike weight	1	**0.97****	0.37**	0.06^{ns}	0.79**	0.15**	0.69**	0.72**	0.75**
Kernel weight per spike		1	0.32**	0.006^{ns}	0.80**	0.13**	0.71**	0.72**	0.78**
Spikelet number per spike			1	0.32**	0.52**	-0.12**	0.04^{ns}	-0.04^{ns}	0.15**
Spike length				1	0.09^{ns}	0.07^{ns}	-0.17**	0.10**	-0.02^{ns}
Kernel number per spike					1	-0.21**	0.39**	0.24**	**0.91****
Kernel length						1	0.05^{ns}	0.50**	-0.19**
Kernel width							1	0.79**	0.44**
Thousand-kernel weight								1	0.30**
Kernel number per spikelet									1

*, ** and ns: significant at *P*<0.05, *P*<0.01 and non-significant.

Table 5. Principal Component Analysis for the studied traits of 400 bread wheat genotypes.

Traits	Principal component			Traits and principal correlation		
	PC1	PC2	PC3	1	2	3
Spike weight	0.436	0.086	0.070	0.972	0.130	0.080
Kernel weight per spike	0.439	0.079	0.002	0.978	0.116	0.002
Spikelet number per spike	0.123	0.387	0.441	0.275	0.585	0.502
Spike length	-0.007	0.186	0.707	-0.016	0.282	0.804
Kernel number per spike	0.329	0.430	-0.045	0.733	0.650	-0.051
Kernel length	0.085	-0.433	0.432	0.194	-0.654	0.492
Kernel width	0.362	-0.166	-0.192	0.806	-0.250	0.219
Thousand-kernel weight	0.366	-0.366	0.055	0.814	-0.553	0.062
Kernel number per spikelet	0.329	0.320	-0.250	0.733	0.483	-0.285
Proportion	0.495	0.228	0.129			
Cumulative	0.495	0.723	0.852			
Eigenvalue	4.95	2.28	1.29			

Table 6. Factor analysis for the nine studied traits of 400 bread wheat genotypes.

Traits	Factors			Communality
	F1	F2	F3	
Spike weight	0.827	0.515	0.151	0.973
Kernel weight per spike	0.844	0.509	0.076	0.978
Spikelet number per spike	0.425	-0.127	0.699	0.686
Spike length	-0.067	0.013	0.858	0.741
Kernel number per spike	0.954	-0.039	0.229	0.965
Kernel length	-0.344	0.764	0.194	0.740
Kernel width	0.580	0.616	-0.271	0.790
Thousand-kernel weight	0.340	0.920	-0.129	0.979
Kernel number per spikelet	0.927	0.021	-0.046	0.862
Proportion	0.507	0.229	0.129	
Cumulative	0.507	0.736	0.865	
Eigenvalue	3.98	3.22	1.45	

used and then the variance of uncorrelated variables was computed by the highest correlation coefficient in each array. The first three factors explained 86.57 percent of the total variation. Based on the result, the the Kaiser-Meyer-Olkin (KMO) index is equal to 0.664 which suggests that the data is appropriate for applying factor analysis. The first factor had an eigenvalue of 3.98 and accounted for 50.71% of the variation. The second and third factors accounted for 22.93 and 12.93% of variations and had eigenvalues of 3.22 and 1.45, respectively (Table 6). The number of kernels per spikelet, number of kernels per spike, kernel weight per spike, and spike weight contributed the most to the first factor. Therefore, the first factor can be called the “yield factor”.. Also, the second factor included thousand-kernel weight, kernel width, and kernel length with positive factor loadings, reflecting the “kernel structure” of the genotypes. Moreover, the third factor included spike length and spikelet per spike with positive factor loading which can be called the “spike structure factor”.

Cluster analysis

To group the wheat genotypes, cluster analysis based on Ward’s method was performed. The cubic clustering criterion values were estimated and shown as a CCC plot to determine the number of groups in the cluster analysis (Figure 3). Cluster analysis classified the genotypes into four clusters (Figure 4). The first cluster included 145 genotypes, mainly from Afghanistan, Iraq, Turkey, and Iran. The second cluster included 43 genotypes with diverse origins. This cluster had the highest mean for the trait kernel length. The third cluster included 77 genotypes, mainly from Pakistan and India, and

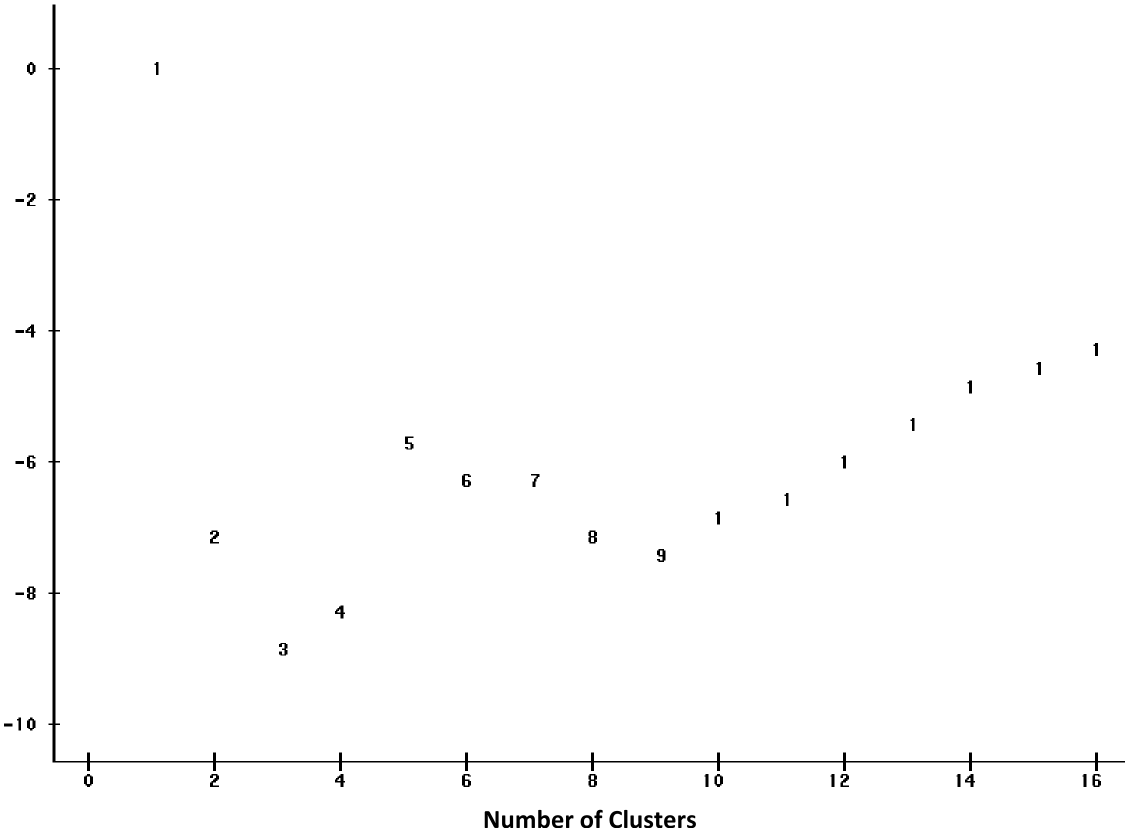

Figure 3. CCC plot to determine the number of groups in the cluster analysis.

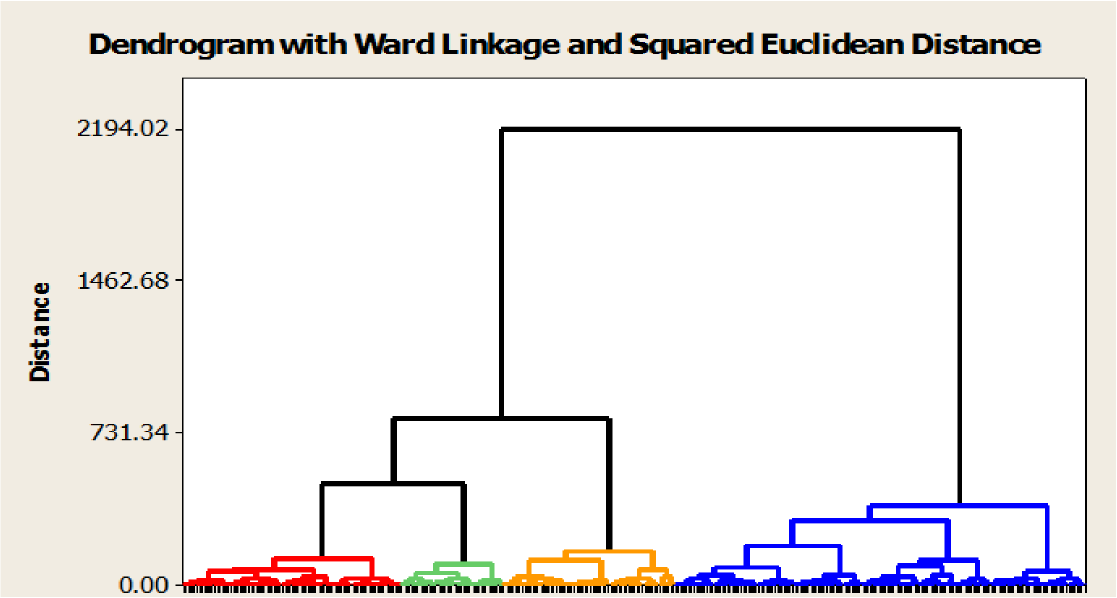

Figure 4. Dendrogram of cluster analysis using Ward's method and squared Euclidean distance as a measure of dissimilarity.

had the highest means in spike weight, kernel weight per spike, kernel width, and thousand-kernel weight. The fourth cluster included 135 genotypes, including Iranian cultivars as well as Indian, and Mexican genotypes. This cluster had the highest mean in the number of spikelets per spikelet, kernel number per spikelet, spike length, and kernel number per spike (Table 7).

Table 7. The mean of clusters for the studied traits of 400 genotypes.

Cluster	Spike weight	Kernel weight per spike	Spikelet number per spike	Spike length	Kernel number per spike	Kernel length	Kernel width	Thousand-kernel weight	Kernel number per spikelet
Cluster I	2.27	1.51	19.65	12.37	45.65	6.98	3.16	32.95	2.32
Cluster II	2.61	1.77	19.14	12.15	38.43	7.64	3.50	46.02	2.01
Cluster III	3.66	2.70	19.43	12.35	56.49	7.40	3.73	47.52	2.93
Cluster IV	3.61	2.67	21.26	12.43	68.83	6.94	3.54	38.47	3.25

DISCUSSION

In this study, significant diversity was observed among the studied genotypes and the descriptive statistics revealed consistent with previous findings in wheat crops (Singh *et al*., 2013; Singh, 2014; Tewari *et al*., 2015; Kumar *et al*., 2016). Naheed *et al*. (2016) and Antim *et al.* (2022), by studying similar traits to this research, reported a lower range and C.V. which indicates the existence of good diversity in the current study. Sufficient variability among genotypes provided ample scope for the selection of superior and desired genotypes by the concerned breeders (Lawati *et al*., 2021).

Knowledge of correlation is required to obtain the expected response of other traits when selection is applied to the trait of interest in a breeding program (Maqbool *et al.,* 2010). In this study, correlation analysis indicated a strong positive correlation between kernel weight and spike weight followed by the number of kernels per spike and the number of kernels per spikelet. Comparable correlations were reported in previous studies (Shahid *et al*., 2002; Saleem *et al*., 2006; Bahandari *et al*., 2017; Xhulaj and Koto 2022)., Similarly, Xhulaj and Koto (2022) reported positive significant correlations between the number of kernels per spikelet and the number of kernels per spike, and the weight of kernel per spikelet. They also reported a positive correlation between thousand kernel weight and kernel weight per spike. These traits exhibited a negative correlation with spike length. The number of kernels per spike is positively related to kernel weight per spike. Furthermore, Tsonev *et al*. (2021) have recorded a similar pattern of significant positive correlation for similar traits with this study.

Principal component analysis reduced the nine measured traits into three principal components, explaining 85% of the total variation. This result further confirmed the presence of ample genetic diversity for possible use in improvement programs. According to Mecha *et al*. (2017), 64 bread wheat genotypes were studied for similar traits, and five principal components (PC1, PC2, PC3, PC4, and PC5) exhibited eigenvalues greater than one that accounted for 72.78% of the total variation was detected. Another study by Qaseem *et al*. (2017) showed that the principal component analysis divided data into four main components accounting for 75.51% of the variation. The first principal component had an eigenvalue of 5.05 and accounted for 38.85% of the variation. The PC2, PC3, and PC4 accounted for 17.49% 10.87%, and 8.29% of variation and had eigenvalues 2.27, 1.41, and 1.07, respectively. Many researchers, (Tuhina-Khatun *et al*., 2015; Vandenberg *et al.,* 2019; Antim *et a*l., 2022; Xhulaj and Koto, 2022) have also attempted principal component analysis to obtain the percentage of variation explained by various characters studied.

Factor analysis revealed three underlying factors that explained 86% of the variation. Comparable findings have been documented, where factor analysis extracted five factors that were able to describe nearly 75% of the total variance (Babaie Zarch *et al*., 2013). Another factors analysis using principal components by Moetamadipoor *et al*. (2015) showed that seven factors had eigenvalues larger than 1 and these factors overall justified 87.7% of the variation in traits. The first two factors justified the total variation of traits as 17% and 16%, respectively and they were entitled as yield and yield components factor and maturity factor. Considering complex relationships between traits, a final judgment cannot be made based on simple correlation coefficients. Thus, it is necessary to use factor analysis techniques for a deeper understanding of the relationship between traits. Suitable factors can be used as selection criteria for use in wheat breeding programs.

Cluster analysis classified the genotypes into four groups. Cluster means revealed that significant variability existed for morphological traits. The lowest cluster means for thousand-kernel weight were recorded for cluster I. The highest cluster means for kernel length were recorded for cluster II, thus the genotypes in cluster II can be used for the improvement of kernel length. Cluster III had the highest cluster means for spike weight, kernel weight per spike, kernel width, and thousand-kernel weight, therefore the genotypes in cluster III can be used for the improvement of these traits, and cluster IV can be used for the improvement of traits including number of spikelet, spike length, number of kernels per spike and number of kernels per spikelet. Genotypes may be chosen from the particular groups for hybridization programs with other approved cultivars. This will aid in the identification, selection, and combining of genotypes to obtain important traits in one line with a broad genetic base.

The grouping of genotypes based on multivariate analysis has also been reported earlier by Singh (2014); Verma *et al*. (2014); Tewari *et al*. (2015); Kumar *et al*. (2016); Vora *et al*. (2017); Majid and Dar, (2020); Tanveer *et al*. (2021); Chaudhary *et al*. (2022); Abdelghany *et al*. (2023) and Chauhan *et al*. (2023). Also, Shashikala *et al*. (2006) grouped 169 wheat genotypes into 12 clusters based on morphological traits. Furthermore, Singh and Kumar (2017) and Yadav *et al*. (2023) reported that specific genotypes within a cluster exhibited high cluster means for various traits related to flowering, plant height, spike length, kernel weight, and yield.

The results of this study contribute to the understanding of genetic diversity among bread wheat genotypes and provide valuable insights for crop improvement programs. Genetic diversity among populations usually helps a plant breeder in choosing desirable parents for a breeding program. The identification of distinct clusters and their associated traits can aid in the selection of desirable genotypes for specific breeding goals. Future research should focus on exploring the genetic basis of these traits and investigating the potential for incorporating diverse genotypes from different clusters to enhance wheat breeding programs

CONCLUSION

In conclusion, the comprehensive analysis of 400 wheat genotypes in this study demonstrated significant variability in the measured traits. Grouping the genotypes by multivariate methods in this study has practical value for wheat breeders. Cluster means for the different traits showed that among all the clusters, cluster III and cluster IV exhibited the highest cluster means for the maximum number of the studied traits. The genotypes in these clusters could be selected directly based on these traits to be used in cross-based breeding programs. Finally, the findings of this study contribute to the understanding of the genetic diversity present within the wheat genotypes, providing valuable information for wheat improvement programs.

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SUPPLEMENTAL DATA

Supplementary Table 1. Genotype number and other characteristics of bread wheat according to Gene bank.

Number	Number in gene bank	Accession Number	Scientific Name	Origin	Number	Number in gene bank	Accession Number	Scientific Name	Origin
1	1	ATRI 519	*T. aestivum* L.	India	56	99	ATRI 2648	*T. aestivum* L.	Afghanistan
2	3	ATRI 527	*T. aestivum* L.	India	57	101	ATRI 2657	*T. aestivum* L.	Afghanistan
3	4	ATRI 530	*T. aestivum* L.	Australia	58	102	ATRI 2658	*T. aestivum* L.	Afghanistan
4	5	ATRI 532	*T. aestivum* L.	India	59	103	ATRI 2659	*T. aestivum* L.	Afghanistan
5	6	ATRI 533	*T. aestivum* L.	Australia	60	104	ATRI 2660	*T. aestivum* L.	Afghanistan
6	10	ATRI 537	*T. aestivum* L.	India	61	105	ATRI 2664	*T. aestivum* L.	Afghanistan
7	14	ATRI 541	*T. aestivum* L.	Australia	62	109	ATRI 2675	*T. aestivum* L.	Afghanistan
8	15	ATRI 542	*T. aestivum* L.	India	63	110	ATRI 2678	*T. aestivum* L.	Afghanistan
9	16	ATRI 571	*T. aestivum* L.	Australia	64	119	ATRI 2817	*T. aestivum* L.	England
10	17	ATRI 572	*T. aestivum* L.	Afghanistan	65	122	ATRI 2822	*T. aestivum* L.	Afghanistan
11	18	ATRI 723	*T. aestivum* L.	Turkey	66	127	ATRI 2846	*T. aestivum* L.	Afghanistan
12	19	ATRI 740	*T. aestivum* L.	Afghanistan	67	129	ATRI 2850	*T. aestivum* L.	England
13	21	ATRI 785	*T. aestivum* L.	India	68	131	ATRI 2852	*T. aestivum* L.	Afghanistan
14	22	ATRI 1494	*T. aestivum* L.	Turkey	69	135	ATRI 2877	*T. aestivum* L.	Afghanistan
15	23	ATRI 1495	*T. aestivum* L.	Afghanistan	70	136	ATRI 2899	*T. aestivum* L.	Italy
16	26	ATRI 1536	*T. aestivum* L.	Turkey	71	137	ATRI 2900	*T. aestivum* L.	Iran
17	28	ATRI 1541	*T. aestivum* L.	Turkey	72	140	ATRI 2912	*T. aestivum* L.	Afghanistan
18	29	ATRI 1543	*T. aestivum* L.	Afghanistan	73	141	ATRI 2916	*T. aestivum* L.	Iran
19	32	ATRI 1906	*T. aestivum* L.	Afghanistan	74	146	ATRI 2956	*T. aestivum* L.	Iran
20	33	ATRI 1922	*T. aestivum* L.	Turkey	75	149	ATRI 3157	*T. aestivum* L.	Iran
21	40	ATRI 2162	*T. aestivum* L.	Turkey	76	150	ATRI 3166	*T. aestivum* L.	Afghanistan
22	45	ATRI 2188	*T. aestivum* L.	Turkey	77	158	ATRI 3304	*T. aestivum* L.	India
23	47	ATRI 2198	*T. aestivum* L.	Afghanistan	78	161	ATRI 3405	*T. aestivum* L.	Afghanistan
24	49	ATRI 2202	*T. aestivum* L.	Turkey	79	164	ATRI 3559	*T. aestivum* L.	India
25	51	ATRI 2205	*T. aestivum* L.	Afghanistan	80	166	ATRI 3572	*T. aestivum* L.	Iran
26	54	ATRI 2221	*T. aestivum* L.	India	81	170	ATRI 3945	*T. aestivum* L.	Afghanistan
27	55	ATRI 2222	*T. aestivum* L.	Afghanistan	82	175	ATRI 3995	*T. aestivum* L.	Afghanistan
28	57	ATRI 2430	*T. aestivum* L.	Afghanistan	83	180	ATRI 5427	*T. aestivum* L.	Iraq
29	58	ATRI 2434	*T. aestivum* L.	Afghanistan	84	183-1	ATRI 5489	*T. aestivum* L.	Iran
30	59	ATRI 2436	*T. aestivum* L.	Afghanistan	85	183-2	ATRI 5489	*T. aestivum* L.	Iran
31	60	ATRI 2437	*T. aestivum* L.	Nepal	86	185-1	ATRI 5498	*T. aestivum* L.	Iran
32	61	ATRI 2439	*T. aestivum* L.	Afghanistan	87	185-2	ATRI 5498	*T. aestivum* L.	Iran
33	63	ATRI 2442	*T. aestivum* L.	Nepal	88	191	ATRI 5550	*T. aestivum* L.	Iran
34	64	ATRI 2443	*T. aestivum* L.	Afghanistan	89	192	ATRI 5555	*T. aestivum* L.	Iran
35	65	ATRI 2445	*T. aestivum* L.	Afghanistan	90	196	ATRI 5585	*T. aestivum* L.	Iran
36	66	ATRI 2448	*T. aestivum* L.	Nepal	91	200	ATRI 5621	*T. aestivum* L.	Iran
37	67	ATRI 2449	*T. aestivum* L.	Afghanistan	92	201	ATRI 5627	*T. aestivum* L.	Iran
38	70	ATRI 2452	*T. aestivum* L.	Nepal	93	202	ATRI 5643	*T. aestivum* L.	Iran
39	74	ATRI 2456	*T. aestivum* L.	Nepal	94	210	ATRI 5721	*T. aestivum* L.	Iran
40	75	ATRI 2458	*T. aestivum* L.	Afghanistan	95	211	ATRI 5727	*T. aestivum* L.	Iran
41	76	ATRI 2484	*T. aestivum* L.	Afghanistan	96	220	ATRI 5855	*T. aestivum* L.	Iran
42	77	ATRI 2494	*T. aestivum* L.	Afghanistan	97	229	ATRI 5938	*T. aestivum* L.	Iran
43	79	ATRI 2536	*T. aestivum* L.	Nepal	98	232-1	ATRI 5947	*T. aestivum* L.	Iran
44	80	ATRI 2541	*T. aestivum* L.	Nepal	99	232-2	ATRI 5947	*T. aestivum* L.	Iran
45	81	ATRI 2547	*T. aestivum* L.	Afghanistan	100	233-1	ATRI 5956	*T. aestivum* L.	Iran
46	83	ATRI 2579	*T. aestivum* L.	Afghanistan	101	233-2	ATRI 5956	*T. aestivum* L.	Iran
47	84	ATRI 2585	*T. aestivum* L.	Afghanistan	102	234-1	ATRI 5961	*T. aestivum* L.	Iran
48	89	ATRI 2607	*T. aestivum* L.	Afghanistan	103	234-2	ATRI 5961	*T. aestivum* L.	Iran
49	91	ATRI 2611	*T. aestivum* L.	Nepal	104	236	ATRI 5975	*T. aestivum* L.	Iran
50	92	ATRI 2613	*T. aestivum* L.	Afghanistan	105	240	ATRI 6005	*T. aestivum* L.	Iran
51	93	ATRI 2614	*T. aestivum* L.	Afghanistan	106	246	ATRI 6084	*T. aestivum* L.	Iran
52	95	ATRI 2626	*T. aestivum* L.	Afghanistan	107	248	ATRI 6112	*T. aestivum* L.	Iran
53	96	ATRI 2632	*T. aestivum* L.	Afghanistan	108	250	ATRI 6135	*T. aestivum* L.	Iran
54	97	ATRI 2635	*T. aestivum* L.	Afghanistan	109	255	ATRI 6274	*T. aestivum* L.	Iran
55	98	ATRI 2636	*T. aestivum* L.	Afghanistan	110	256	ATRI 6322	*T. aestivum* L.	Iran

Supplementary Table 1 (Continued).

Number	Number in gene bank	Accession Number	Scientific Name	Origin	Number	Number in gene bank	Accession Number	Scientific Name	Origin
111	257	ATRI 8156	*T. aestivum* L.	Iraq	166	362	ATRI 16084	*T. aestivum* L.	Iran
112	258	ATRI 8159	*T. aestivum* L.	Iraq	167	363	ATRI 16085	*T. aestivum* L.	Iran
113	259	ATRI 8178	*T. aestivum* L.	Pakistan	168	364	ATRI 16086	*T. aestivum* L.	Iran
114	261	ATRI 8183	*T. aestivum* L.	Pakistan	169	365	ATRI 16087	*T. aestivum* L.	Iraq
115	263	ATRI 8185	*T. aestivum* L.	Iran	170	366	ATRI 17047	*T. aestivum* L.	Turkey
116	268	ATRI 8311	*T. aestivum* L.	India	171	367	ATRI 17039	*T. aestivum* L.	Iran
117	272	ATRI 8315	*T. aestivum* L.	Iran	172	368	ATRI 17047	*T. aestivum* L.	Iran
118	273	ATRI 8316	*T. aestivum* L.	Iran	173	371	ATRI 17191	*T. aestivum* L.	Turkey
119	274	ATRI 8317	*T. aestivum* L.	India	174	372	ATRI 17193	*T. aestivum* L.	Iran
120	275	ATRI 8318	*T. aestivum* L.	Iran	175	373	ATRI 17195	*T. aestivum* L.	Turkey
121	278	ATRI 8349	*T. aestivum* L.	Iraq	176	374	ATRI 17551	*T. aestivum* L.	Iran
122	279	ATRI 8358	*T. aestivum* L.	Iraq	177	375	ATRI 17552	*T. aestivum* L.	Pakistan
123	280	ATRI 8360	*T. aestivum* L.	Iran	178	376	ATRI 17553	*T. aestivum* L.	Pakistan
124	281	ATRI 8366	*T. aestivum* L.	Iraq	179	377	ATRI 17554	*T. aestivum* L.	Tajikistan
125	282	ATRI 8370	*T. aestivum* L.	Iraq	180	379	ATRI 17559	*T. aestivum* L.	Tajikistan
126	283	ATRI 8414	*T. aestivum* L.	India	181	381	ATRI 17561	*T. aestivum* L.	Iran
127	288	ATRI 8419	*T. aestivum* L.	India	182	382	ATRI 17562	*T. aestivum* L.	Tajikistan
128	294	ATRI 9718	*T. aestivum* L.	Iran	183	383	ATRI 17811	*T. aestivum* L.	Turkey
129	295	ATRI 9721	*T. aestivum* L.	India	184	385	ATRI 19186	*T. aestivum* L.	Turkey
130	296	ATRI 9724	*T. aestivum* L.	Pakistan	185	387	ATRI 19218	*T. aestivum* L.	Turkey
131	298	ATRI 9749	*T. aestivum* L.	Iran	186	388	ATRI 19219	*T. aestivum* L.	Iran
132	302	ATRI 9756	*T. aestivum* L.	Iran	187	389	ATRI 19224	*T. aestivum* L.	Turkey
133	304	ATRI 9890	*T. aestivum* L.	Pakistan	188	391	ATRI 19262	*T. aestivum* L.	Pakistan
134	305	ATRI 9897	*T. aestivum* L.	India	189	392	ATRI 19296	*T. aestivum* L.	Turkey
135	308	ATRI 9903	*T. aestivum* L.	Pakistan	190	394	ATRI 22345	*T. aestivum* L.	Turkey
136	311	ATRI 9951	*T. aestivum* L.	Turkey	191	395	ATRI 22976	*T. aestivum* L.	Afghanistan
137	312	ATRI 9956	*T. aestivum* L.	Iran	192	400	ATRI 28703	*T. aestivum* L.	Pakistan
138	313	ATRI 9957	*T. aestivum* L.	Turkey	193	401	ATRI 28704	*T. aestivum* L.	Iran
139	314	ATRI 9961	*T. aestivum* L.	Pakistan	194	403	ATRI 28722	*T. aestivum* L.	Pakistan
140	315	ATRI 9962	*T. aestivum* L.	Iran	195	404	ATRI 28730	*T. aestivum* L.	Iran
141	316	ATRI 9963	*T. aestivum* L.	Iran	196	405	ATRI 28749	*T. aestivum* L.	Pakistan
142	319	ATRI 9969	*T. aestivum* L.	Iran	197	406	ATRI 28818	*T. aestivum* L.	Iran
143	320	ATRI 9970	*T. aestivum* L.	India	198	409	ATRI 29453	*T. aestivum* L.	Turkey
144	324	ATRI 9992	*T. aestivum* L.	Pakistan	199	414	HTRI 6339	*T. aestivum* L.	Iran
145	328	ATRI 10002	*T. aestivum* L.	Pakistan	200	440	HTRI 6515	*T. aestivum* L.	Iran
146	333	ATRI 10293	*T. aestivum* L.	Pakistan	201	452	HTRI 6605	*T. aestivum* L.	Iran
147	334	ATRI 10299	*T. aestivum* L.	India	202	454	HTRI 6614	*T. aestivum* L.	Iran
148	335	ATRI 10304	*T. aestivum* L.	Iran	203	468	HTRI 6689	*T. aestivum* L.	Iran
149	337	ATRI 10429	*T. aestivum* L.	Pakistan	204	475	HTRI 7162	*T. aestivum* L.	Iran
150	339	ATRI 10440	*T. aestivum* L.	Pakistan	205	478	Morvarid	*T. aestivum* L.	Iranian Cultivar
151	343	ATRI 10995	*T. aestivum* L.	India	206	479	Ghods	*T. aestivum* L.	Iranian Cultivar
152	345	ATRI 11530	*T. aestivum* L.	Iraq	207	480	Roshan	*T. aestivum* L.	Iranian Cultivar
153	346	ATRI 11538	*T. aestivum* L.	Iraq	208	481	Kavir	*T. aestivum* L.	Iranian Cultivar
154	347	ATRI 11545	*T. aestivum* L.	Iraq	209	482	Pishtaz	*T. aestivum* L.	Iranian Cultivar
155	348	ATRI 15277	*T. aestivum* L.	Iraq	210	484	Sorkh Tokhm	*T. aestivum* L.	Iranian Cultivar
156	349	ATRI 15280	*T. aestivum* L.	Iraq	211	488	Hirmand	*T. aestivum* L.	Iranian Cultivar
157	350	ATRI 15293	*T. aestivum* L.	Iraq	212	490	Gimaza	*T. aestivum* L.	Iranian Cultivar
158	351	ATRI 15295	*T. aestivum* L.	Iraq	213	518	ATRI 397	*T. aestivum* L.	Iran
159	352	ATRI 15919	*T. aestivum* L.	India	214	519	ATRI 400	*T. aestivum* L.	Iran
160	354	ATRI 16056	*T. aestivum* L.	Iran	215	520	ATRI4939	*T. aestivum* L.	Azerbaijan
161	356	ATRI 16061	*T. aestivum* L.	Iran	216	521	ATRI 5306	*T. aestivum* L.	Azerbaijan
162	357	ATRI 16063	*T. aestivum* L.	Iran	217	522	ATRI 5395	*T. aestivum* L.	Azerbaijan
163	359	ATRI 16076	*T. aestivum* L.	Iraq	218	523	ATRI 7178	*T. aestivum* L.	Azerbaijan
164	360	ATRI 16079	*T. aestivum* L.	Iraq	219	524	ATRI 7204	*T. aestivum* L.	Germany
165	361	ATRI 16081	*T. aestivum* L.	Iran	220	525	ATRI 7244	*T. aestivum* L.	USA

Supplementary Table 1 (Continued).

Number	Number in gene bank	Accession Number	Scientific Name	Origin	Number	Number in gene bank	Accession Number	Scientific Name	Origin
221	527	A TRI9339	*T. aestivum* L.	USA	276	611	ICBW 108723	*T. aestivum* L.	Syria
222	528	ATRI 9687	*T. aestivum* L.	USA	277	614	ICBW 43232	*T. aestivum* L.	Syria
223	529	ATRI 9700	*T. aestivum* L.	USA	278	615	ICBW 43196	*T. aestivum* L.	Syria
224	530	ATRI 9715	*T. aestivum* L.	USA	279	617	ICBW 41556	*T. aestivum* L.	Pakistan
225	531	ATRI 9717	*T. aestivum* L.	Bangladesh	280	619	ICBW 41274	*T. aestivum* L.	Syria
226	532	ATRI 9905	*T. aestivum* L.	Pakistan	281	623-1	ICBW 141055	*T. aestivum* L.	Syria
227	533	ATRI 9917	*T. aestivum* L.	Pakistan	282	623-2	ICBW 141055	*T. aestivum* L.	Syria
228	534	ATRI 10305	*T. aestivum* L.	Pakistan	283	624	ICBW 140872	*T. aestivum* L.	Syria
229	535	ATRI 10311	*T. aestivum* L.	Pakistan	284	625-1	ICBW 138789	*T. aestivum* L.	Syria
230	536	ATRI 11919	*T. aestivum* L.	Pakistan	285	625-2	ICBW 138789	*T. aestivum* L.	Syria
231	537	ATRI 12922	*T. aestivum* L.	Pakistan	286	626-1	ICBW 110707	*T. aestivum* L.	Syria
232	540	ATRI 20541	*Triticum sp.*	Pakistan	287	626-2	ICBW 110707	*T. aestivum* L.	Syria
233	541	ATRI 22282	*T. aestivum L.*	Pakistan	288	627	ICBW 98825	*T. aestivum* L.	Syria
234	542	ATRI 23666	*Triticum sp.*	Unknown	289	628	ICBW 98824	*T. aestivum* L.	Syria
235	543	ATRI 25383	*Triticum sp.*	Tajikistan	290	629	ICBW 95833	*T. aestivum* L.	Syria
236	544	ATRI 27579	*T. aestivum* L.	Tajikistan	291	630	ICBW 42689	*T. aestivum* L.	Syria
237	545	HTRI 6891	*T. aestivum* L.	Turkmenistan	292	631	ICBW 42070	*T. aestivum* L.	Syria
238	555	HTRI 12082	*T. aestivum* L.	Turkmenistan	293	632-1	ICBW 141350	*T. aestivum* L.	Azerbaijan
239	556	HTRI 12741	*T. aestivum* L.	Turkmenistan	294	632-2	ICBW 141350	*T. aestivum* L.	Azerbaijan
240	557	HTRI 15303	*T. aestivum* L.	Turkmenistan	295	633-1	ICBW 140887	*T. aestivum* L.	Azerbaijan
241	560	HTRI 17709	*T. aestivum* L.	Turkmenistan	296	633-2	ICBW 140887	*T. aestivum* L.	Azerbaijan
242	564	01C0200133	*T. aestivum* L.	Czechoslovakia	297	634	ICBW 140437	*T. aestivum* L.	Azerbaijan
243	565	01C0203840	*T. aestivum* L.	Turkmenistan	298	635	ICBW 140436	*T. aestivum* L.	Azerbaijan
244	566	01C0204228	*T. aestivum* L.	Germany	299	636	ICBW 138678	*T. aestivum* L.	Azerbaijan
245	567	01C0204799	*T. aestivum* L.	Turkmenistan	300	637	ICBW 138673	*T. aestivum* L.	Azerbaijan
246	568	01C0204826	*T. aestivum* L.	Turkey	301	638	ICBW 138620	*T. aestivum* L.	Azerbaijan
247	569	01C0204851	*T. aestivum* L.	Czech Republic	302	639	ICBW 138619	*T. aestivum* L.	Azerbaijan
248	570	01C0204897	*T. aestivum* L.	Turkey	303	641	ICBW 138380	*T. aestivum* L.	Azerbaijan
249	571	01C0204936	*T. aestivum* L.	Switzerland	304	652	Arvand	*T. aestivum* L.	Iranian cultivar
250	572	01C0204938	*T. aestivum* L.	Czech republic	305	654	Morvarid	*T. aestivum* L.	Iranian Cultivar
251	573	ICBW 138285	*T. aestivum* L.	Afghanistan	306	657	Bam	*T. aestivum* L.	Iranian Cultivar
252	574	ICBW 127724	*T. aestivum* L.	Turkey	307	659	Sisitan	*T. aestivum* L.	Iranian Cultivar
253	576	ICBW 90192	*T. aestivum* L.	Turkey	308	662	Hirmand	*T. aestivum* L.	Iranian Cultivar
254	578	ICBW 90185	*T. aestivum* L.	Turkey	309	664	Kavir	*T. aestivum* L.	Iranian Cultivar
255	579	ICBW 90161	*T. aestivum* L.	Turkey	310	666	Azar2	*T. aestivum* L.	Iranian Cultivar
256	580	ICBW 89823	*T. aestivum* L.	Afghanistan	311	670	Alboorz	*T. aestivum* L.	Iranian Cultivar
257	583	ICBW 141200	*T. aestivum* L.	Turkey	312	683	Chenab	*T. aestivum* L.	Iranian Cultivar
258	585	ICBW 138690	*T. aestivum* L.	Turkey	313	685	Arta	*T. aestivum* L.	Iranian Cultivar
259	586	ICBW 138668	*T. aestivum* L.	Turkey	314	686-1	Syrvan	*T. aestivum* L.	Iranian Cultivar
260	587	ICBW 138599	*T. aestivum* L.	Turkey	315	686-2	Syrvan	*T. aestivum* L.	Iranian Cultivar
261	588	ICBW 138429	*T. aestivum* L.	Turkey	316	691	Chamran2	*T. aestivum* L.	Iranian Cultivar
262	590	ICBW 138397	*T. aestivum* L.	Turkey	317	696	Gonbad	*T. aestivum* L.	Iranian Cultivar
263	591	ICBW 138363	*T. aestivum* L.	Turkey	318	715-1	Tajan	*T. aestivum* L.	Iranian Cultivar
264	597	ICBW 42741	*T. aestivum* L.	Czech republic	319	715-2	Tajan	*T. aestivum* L.	Iranian Cultivar
265	598	ICBW 42498	*T. aestivum* L.	Japan	320	752	SARC 3	*T. aestivum* L.	Pakistan
266	601	ICBW 42283	*T. aestivum* L.	Japan	321	753	SARC 1	*T. aestivum* L.	Pakistan
267	602	ICBW 144472	*T. aestivum* L.	Iraq	322	754	Arg	*T. aestivum* L.	Iranian Cultivar
268	603	ICBW 141233	*T. aestivum* L.	Iraq	323	755	SARC 4R	*T. aestivum* L.	Pakistan
269	604	ICBW 108814	*T. aestivum* L.	Iraq	324	757	SARC 4W	*T. aestivum* L.	Pakistan
270	605	ICBW 108803	*T. aestivum* L.	Iraq	325	758	SARC 6W	*T. aestivum* L.	Pakistan
271	606	ICBW 108799	*T. aestivum* L.	Iraq	326	769	a line from 628/2	*T. aestivum* L.	Syria
272	607	ICBW 108759	*T. aestivum* L.	Iraq	327	772	a line from 624/2	*T. aestivum* L.	Syria
273	608	ICBW 108753	*T. aestivum* L.	Japan	328	773	a line from 625/2	*T. aestivum* L.	Syria
274	609	ICBW 108748	*T. aestivum* L.	Japan	329	776	a line from 303/2	*T. aestivum* L.	Iraq
275	610	ICBW 108740	*T. aestivum* L.	Syria	330	778	a line from 630/3	*T. aestivum* L.	France

Supplementary Table 1 (Continued).

Number	Number in gene bank	Accession Number	Scientific Name	Origin	Number	Number in gene bank	Accession Number	Scientific Name	Origin
331	779	a line from 633/2	*T. aestivum* L.	Canada	366	907	Shoush	*T. aestivum* L.	Iranian cultivar
332	780	a line from 636/2	*T. aestivum* L.	Egypt	367	908	Shabrang	*T. aestivum* L.	Iranian cultivar
333	782	a line from 639/2	*T. aestivum* L.	Azerbaijan	368	909	Meraj	*T. aestivum* L.	Iranian cultivar
334	783	a line from 640/2	*T. aestivum* L.	Azerbaijan	369	910	Narin	*T. aestivum* L.	Iranian cultivar
335	863	Nodel	*T. aestivum* L.	Mexico	370	1001	Barat	*T. aestivum* L.	Iranian cultivar
336	864	10071	*T. aestivum* L.	Mexico	371	1002	Mehregan	*T. aestivum* L.	Iranian cultivar
337	865	S-90-5	*T. aestivum* L.	Mexico	372	1003	Shoosh	*T. aestivum* L.	Iranian cultivar
338	868	DH-260 U	*T. aestivum* L.	Mexico	373	1004	N-87-20	*T. aestivum* L.	Iranian cultivar
339	880	Heidari	*T. aestivum* L.	Iranian cultivar	374	1005	N-91-17	*T. aestivum* L.	Iranian cultivar
340	881	Mihan	*T. aestivum* L.	Iranian cultivar	375	1006	Baharan	*T. aestivum* L.	Iranian cultivar
341	882	Torabi	*T. aestivum* L.	Iranian cultivar	376	162-1	ATRI 3512	*T. aestivum* L.	India
342	883	Khalil	*T. aestivum* L.	Iranian cultivar	377	162-2	ATRI 3512	*T. aestivum* L.	India
343	884	Sarang	*T. aestivum* L.	Iranian cultivar	378	264-1	ATRI 8306	*T. aestivum* L.	India
344	885	Tirgan	*T. aestivum* L.	Iranian cultivar	379	264-2	ATRI 8306	*T. aestivum* L.	India
345	886	Rakhshan	*T. aestivum* L.	Iranian cultivar	380	277-1	ATRI 8349	*T. aestivum* L.	Iraq
346	887	Talaie	*T. aestivum* L.	Iranian cultivar	381	277-2	ATRI 8349	*T. aestivum* L.	Iraq
347	888	Hana	*T. aestivum* L.	Iranian cultivar	382	303-1	ATRI 9767	*T. aestivum* L.	Pakistan
348	889	Aran	*T. aestivum* L.	Iranian cultivar	383	303-2	ATRI 9767	*T. aestivum* L.	Pakistan
349	890	Setareh	*T. aestivum* L.	Iranian cultivar	384	358-1	ATRI 16073	*T. aestivum* L.	Iraq
350	891	Ofogh	*T. aestivum* L.	Iranian cultivar	385	358-2	ATRI 16073	*T. aestivum* L.	Iraq
351	892	Pishgam	*T. aestivum* L.	Iranian cultivar	386	358-3	ATRI 16073	*T. aestivum* L.	Iraq
352	893	Sirvan	*T. aestivum* L.	Iranian cultivar	387	672-1	Sardari	*T. aestivum* L.	Iranian cultivar
353	894	Pishtaz	*T. aestivum* L.	Iranian cultivar	388	672-2	Sardari	*T. aestivum* L.	Iranian cultivar
354	895	Morvarid	*T. aestivum* L.	Iranian cultivar	389	756-1	SARC 6R	*T. aestivum* L.	Pakistan
355	896	Gonbad	*T. aestivum* L.	Iranian cultivar	390	756-2	SARC 6R	*T. aestivum* L.	Pakistan
356	897	Mehrgan	*T. aestivum* L.	Iranian cultivar	391	781-1	a line from 637/2	*T. aestivum* L.	Azerbaijan
357	898	Behrang	*T. aestivum* L.	Iranian cultivar	392	781-2	a line from 637/2	*T. aestivum* L.	Azerbaijan
358	899	Barzegar	*T. aestivum* L.	Iranian cultivar	393	41T	ATRI 2173	*T. aestivum* L.	Turkey
359	900	Parsi	*T. aestivum* L.	Iranian cultivar	394	62T	ATRI 2441	*T. aestivum* L.	Nepal
360	901	Chamran 2	*T. aestivum* L.	Iranian cultivar	395	71T	ATRI 2453	*T. aestivum* L.	Nepal
361	902	Ehsan	*T. aestivum* L.	Iranian cultivar	396	94T	ATRI 2618	*T. aestivum* L.	Afghanistan
362	903	Kalateh	*T. aestivum* L.	Iranian cultivar	397	116T	ATRI 2809	*T. aestivum* L.	Afghanistan
363	904	Baharan	*T. aestivum* L.	Iranian cultivar	398	120T	ATRI 2818	*T. aestivum* L.	Afghanistan
364	905	Zarrineh	*T. aestivum* L.	Iranian cultivar	399	133T	ATRI 2859	*T. aestivum* L.	Afghanistan
365	906	Barat	*T. aestivum* L.	Iranian cultivar	400	139T	ATRI 2911	*T. aestivum* L.	Afghanistan