Studies on Quantitative Morphogenetical Variations and their Relationship among Wheat Varieties (*Triticum aestivum L.*)

Research Article

Sanjay Kumar

Department of Botany, Nagaland University, Lumami 798627, Nagaland, India

*Corresponding author: Sanjay Kumar, Department of Botany, Nagaland University, Lumami 798627, Nagaland, India; E-mail: ksanjay79@gmail.com

Abstract

The morphogenetical characters [number of seeds per inflorescence, seed weight (g), leaf area (cm), shoot length (cm), internode length (cm), root length (cm), shoot biomass fresh weight and dry weight (g-1 FW/DW)] were collected from the three wheat (*Triticum aestivum L.*) varieties (HUW 234, HUW468 and HUW 533) during March 2007-10 every year. The characters were analyzed for each variety separately and merged together and calculated the similarity index for direct or indirect connection of the characters with each other and between the characters by SPSS ver. 16. The result showed that most of the characters were directly associated with each other for growth and development of the crop plant. The distance matrix was estimated using the similarity matrix (Pearson correlation). The distance matrix was utilized to predict the circular tree by UPGMA for the association of characters and relationship of wheat varieties and suggested that wheat varieties could be divided into two different groups. The first group included the HUW 533 and second group included the HUW 234 and HUW 468. The Covariance (Cov), total (HT) and mean (HS) heterozygosity, gene differentiation (GST) and gene flow (Nm) were calculated. The GST and Nm was found to be similar with the values 0.875 and 0.0714 respectively in all the varieties which indicated the varietal origin of the HUW 234, HUW 468 and HUW 533 but the Cov, HT and HS showed partial difference which may be due to environmental effect.

Keywords: Circular tree; Dissimilarity index; Quantitative Traits; Similarity index

Introduction

Wheat (*Triticum aestivum* L.) corresponds to an essential supply of foodstuff and vigor to promptly escalating population of India. It occupies a foremost place in the cropping mold of the nation. The total area under wheat cultivation is 29.8 million hectares with a total production of 86 million tons (estimated 95.91 million tonnes) in India. The National Productivity is about 3 tonnes /ha (3075 Kg/ha) in India [1].

The miscellany in earth, type of weather, height above sea level, landscape and geographical separation factors may be persuaded the enormous range in Indian wheat and their varieties. The different communities and people of an area play an important role in diversification of a crop. The morphological, biochemical and molecular diversification of Indian wheat may be the consequence of genetic load, hybridization, genetic recombination, spontaneous and artificial blend in varied surroundings [2].

The information of variety trials allocate the plant breeders to know the evolutionary associations among the varieties along with germplasm accession to illustrate in a more methodical manner which would be helpful to integrate valuable multiplicity in their breeding plan [3].

The range of varieties has been a ground score in expansion of

inherent property and resulted in amplification of its prospective for grain yield. Wheat varieties may be categorized in diverse clusters depending on their dissimilar function, value and magnitude. The information about the hereditary diversity and genetic relatedness among the varieties along with selected objects is an essential component in plant breeding [4].

The assessment of hereditary assortment in wheat may be on diversity in morphological and agronomic characters or lineage information [5]. Cultivar recognition is valuable for relating a new cultivar, complicated genotype wholesomeness and momentum of sharpness, consistency and steadiness [6]. The digits of techniques are available at present on hand for scrutiny of genetic mixture in a germplasm attainment, breeding lines and to segregate populations. The techniques are based on ancestry, morphological, agronomic production, biochemical and molecular statistics [7]. Molecular pointers are suitable instrument for speedy genetic investigation and permitting to differentiate solitary allele on or after the others. There are several purposeful indicators which have been widened for QTL together with a set of PCR markers which was premeditated to tell apart allelic difference at QTL locus. The fundamental information on genetic systematize of yield and yield apparatus is extremely supportive to a large extent in manipulation of a breeding program [8].

The prospect of our breeding program depends on the ease of use of genetic unevenness to augment yield. The fabrication of wheat production in India has been reduced at some stage in modern years than it was in the past. The yield enhancement in wheat diversity has not been significant in last few years. It may be because of the constricted genetic pedestal exploitation of the germplasm which has been painstaking at the most important grounds. The sustained dis-improvement in efficiency of yield considered a huge threat for the reason that of mounting demand by the silent but on the rise of human being general population.

The understanding of the constitution of the Indian wheat collectively with the bottomless perceptive of the environment and the level of their variation are vital to capably utilize and marmalade the present plant matter and it is essential to learn the prospective of the obtainable wheat varieties in order to devise planned germplasm improvement and expansion curriculum expected for constant wheat production.

The present studies were carried out to have information on the inheritance of yield and its components in wheat varieties (*Triticum aestivum* L. var. HUW 234, HUW 468 and HUW 533) developed at IAS, BHU, Varanasi by Pedigree method as shown below.

$HUW12 \times Sparrow \rightarrow F1 \times HUW12 \rightarrow HUW\ 234$

$CPAN\ 1962 \times TON1 \rightarrow LIRA\ 'S'\ (F1) \times PRL\ 'S' \rightarrow HUW\ 468$

$Unnath - c - 306 \times HUW\ 81 \rightarrow F1 \times K\ 8027 \rightarrow HUW\ 533$

The objective of the present article was to analyze morphogenetic diversity and phylogenetic interrelationship of characters studied in wheat varieties.

Materials and Methods

The experiment was set up in the 1st week of October and the data were collected at the end of March 2007-10 during the harvesting time every year. The average data of yield [number of seeds per inflorescence, seed weight (g)] and quality contributing parameters [leaf area (cm), shoot length (cm), internode length (cm), root length (cm), shoot biomass fresh weight and dry weight (g-1 FW/DW)] often randomly selected plants were recorded. Statistical analyses were done by SPSS ver. 16 and the interrelationship among the traits and varieties (*Triticum aestivum* L. var. HUW 234, HUW 468 and HUW 533) were established using UPGMA method.

Results

The results and calculations on the similarity, dissimilarity, covariance, heterozygosity, gene differentiation, gene flow and circular tree in *Triticum aestivum* varieties based on quantitative traits were presented in Tables 1-11 and Figures 1-5.

Discussion

Triticum aestivum L. var. HUW 234

The similarity matrix (Table 1) in HUW 234 suggested that Leaf area is negatively correlated with root length (-0.655*) at P≤0.05. The internode length is significantly correlated with shoot length (0.930**), seed fresh weight (0.765**), seed dry weight (0.661*) and seeds per inflorescence (0.695*) at (P≤0.05) and (P≤0.01) respectively. Shoot length significantly correlated with Seed dry weight (0.775**) and seeds per inflorescence (0.803**) at P≤0.01. Seed dry weight is significantly correlated with seed per inflorescence (0.985**) at P≤0.01. The positive and highly significant correlation among the traits indicated that the traits are interdependent to each other for their growth and development except the leaf area which is negatively correlated and do not dependent on the root length for its increase or decrease in area.

The distance matrix (Table 2) in HUW 234 suggested that leaf area and shoot length are not correlated with root length with value 1.655 and 1.033 respectively. The seed fresh weight and seed dry weight is not correlated with seed weight with value 1.107 and 1.093 respectively. This may be due to the practical error while conducting the experiment.

The cophenetic correlation coefficient (CP) among the traits studied was found 0.064 (Figure 1). The value indicates that the phenotypic relation among the traits studied were very weak. This may be due to the experimental error while collecting the data on the traits studied.

Triticum aestivum L. var. HUW 468

The similarity matrix (Table 3) in HUW 468 suggested that leaf area is significantly correlated with internode length, shoot length and seed fresh weight with values 0.702*, 0.742* and 0.677* respectively at P≤0.05. It suggested the increase in length of internode and shoot with increase in fresh weight of seeds. The internode length showed highly significant values with shoot length, seed fresh weight, seed dry weight and seeds per inflorescence as 0.916**, 0.877**, 0.802** and 0.853** respectively at P≤0.01. The positive and significant values suggested that internode length is directly associated with the growth of shoot length, increase in seeds fresh and dry weight and increase in number

Table 1: Similarity matrix of quantitative traits in *T. aestivum* var. HUW234.

	LA	IL	SL	SFW	SDW	SPI	SW	RL
LA	1.000	0.292	0.273	0.138	0.123	0.042	0.365	-0.655*
IL		1.000	0.930**	0.765**	0.661*	0.695*	0.304	0.076
SL			1.000	0.574	0.775**	0.803**	0.084	0.019
SFW				1.000	0.284	0.312	0.549	-0.033
SDW					1.000	0.985**	-0.107	0.031
SPI						1.000	-0.093	0.122
SW							1.000	0.064
RL								1.000

Table 2: Dissimilarity matrix of quantitative traits in *T. aestivum* var. HUW234.

	LA	IL	SL	SFW	SDW	SPI	SW	RL
LA	0.000	0.708	0.727	0.862	0.877	0.958	0.635	1.655
IL		0.000	0.070	0.235	0.339	0.305	0.696	0.924
SL			0.000	0.426	0.225	0.197	0.916	0.981
SFW				0.000	0.716	0.688	0.451	1.033
SDW					0.000	0.015	1.107	0.969
SPI						0.000	1.093	0.878
SW							0.000	0.936
RL								0.000

Table 3: Similarity matrix of quantitative traits in *T. aestivum* var. HUW468.

	LA	IL	SL	SFW	SDW	SPI	SW	RL
LA	1.000	0.702*	0.742*	0.677*	0.324	0.432	0.500	-0.133
IL		1.000	0.916**	0.877**	0.802**	0.853**	0.222	-0.481
SL			1.000	0.984**	0.619	0.661*	0.370	-0.407
SFW				1.000	0.627	0.621	0.416	-0.325
SDW					1.000	0.950**	0.150	-0.308
SPI						1.000	-0.005	-0.520
SW							1.000	0.601
RL								1.000

Table 4: Dissimilarity matrix of quantitative traits in *T. aestivum* var. HUW468.

	LA	IL	SL	SFW	SDW	SPI	SW	RL
LA	0.000	0.298	0.258	0.323	0.676	0.568	0.500	1.133
IL		0.000	0.084	0.123	0.198	0.147	0.778	1.481
SL			0.000	0.016	0.381	0.339	0.630	1.407
SFW				0.000	0.373	0.379	0.584	1.325
SDW					0.000	0.050	0.850	1.308
SPI						0.000	1.005	1.520
SW							0.000	0.399
RL								0.00

Table 5: Similarity matrix of quantitative traits in *T. aestivum* var. HUW 533.

	LA	IL	SL	SFW	SDW	SPI	SW	RL
LA	1.000	-0.247	-0.077	0.583	0.470	-0.349	-0.099	-0.101
IL		1.000	0.656*	0.290	-0.185	0.684*	0.314	0.304
SL			1.000	0.437	0.351	0.864**	0.832**	0.203
SFW				1.000	0.596	0.060	0.110	-0.208
SDW					1.000	0.076	0.296	-0.249
SPI						1.000	0.806**	0.117
SW							1.000	-0.235
RL								1.000

Table 6: Dissimilarity matrix of quantitative traits in *T. aestivum* var. HUW 533.

	LA	IL	SL	SFW	SDW	SPI	SW	RL
LA	0	0.000	1.247	1.077	0.417	0.530	1.349	1.099
IL		0	0.000	0.344	0.710	1.185	0.316	0.686
SL			0	0.000	0.563	0.649	0.136	0.168
SFW				0	0.000	0.404	0.940	0.890
SDW					0	0.000	0.924	0.704
SPI						0	0.000	0.194
SW							0	-0.235
RL								0.000

Table 7: Similarity matrix of all grouped quantitative traits in wheat varieties.

	HUW234	HUW468	HUW533
HUW234	1	0.994**	0.991**
HUW468		1	0.989**
HUW533			1

Table 8: Dissimilarity matrix of all grouped quantitative traits in wheat varieties.

	HUW234	HUW468	HUW533
HUW234	0	0.006	0.009
HUW468		0	0.011
HUW533			0

of seeds per inflorescence. The shoot length is highly correlated with seed fresh weight (0.984**) at P≤0.01 and seeds per inflorescence (0.661*) at P≤0.05 which indicated the involvement of shoot length to increase the fresh seed weight and number of seeds per inflorescence. The seed dry weight is highly correlated with seeds per inflorescence (0.950**) at P≤0.01 which suggested the direct involvement of seeds dry weight with number of seeds per inflorescence.

The distance matrix (Table 4) in HUW 468 suggested that leaf area, internode length, shoot length, seeds fresh weight, seeds dry weight and seeds per inflorescence are uncorrelated with root length with value 1.133, 1.481, 1.407, 1.325, 1.308 and 1.520 respectively. This

may be due to the practical error while conducting the experiment.

The cophenetic correlation coefficient (CP) among the traits studied was found 0.436 (Figure 2). The value indicates that the phenotypic relation among the traits studied were good to increase and development of the plant.

Triticum aestivum L. var. HUW 533

The similarity matrix (Table 5) in HUW 533 suggested that internode length showed significant values with shoot length and seeds per inflorescence as 0.656* and 0.684* respectively at P≤0.05. The positive and significant values suggested that internode length is directly associated with the growth of shoot length and increase in number of seeds per inflorescence. The shoot length is highly correlated with seeds per inflorescence (0.864**) and seed weight (0.832**) at P≤0.01 which indicated the involvement of shoot length to increase number of seeds per inflorescence and weight of the seeds. The seeds per inflorescence is correlated with seed weight (0.806**) at P≤0.01 which suggest that as the number of seeds per inflorescence increase the weight of seeds would increase proportionally.

The distance matrix (Table 6) in HUW 533 suggested that leaf area is not correlated with shoot length, seeds fresh weight, seed weight and root length with value 1.247, 1.077, 1.349 and 1.099 respectively. The internode length is uncorrelated with seeds per inflorescence with the value 1.185. This may be due to the practical error while conducting the experiment.

The cophenetic correlation coefficient (CP) among the traits studied was found 0.819 (Figure 3). The value indicates that the phenotypic relation among the traits studied were very good and associated with development of the plant.

The similarity matrix (Table 7) of pooled traits (all the traits combined together) among wheat varieties suggested that all the three varieties were highly correlated with each other on the traits studied and very negligible distances (Table 8) among the wheat varieties were found. Also, CP among the wheat varieties were high with a value of 0.917 which suggested that there may not be morphologically or genetically much differences among the wheat varieties (Figure 4).

The gene differentiation and gene flow was calculated and found no difference with a value of 0.875 and 0.0714 respectively while covariance, total and mean heterozygosity showed some certain variation among the wheat varieties (Table 9).

Correlation of individual characters in T. aestivum L. var. HUW 234 with HUW 468 and HUW 533

The similarity and disdimilarity matrix of individual characters or traits of HUW 234, HUW 468 and HUW 533 were presented (Table
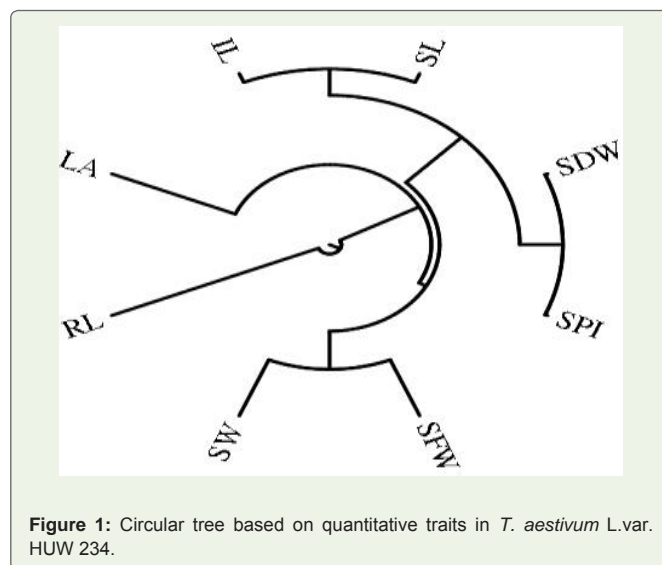

Figure 1: Circular tree based on quantitative traits in *T. aestivum* L.var. HUW 234.
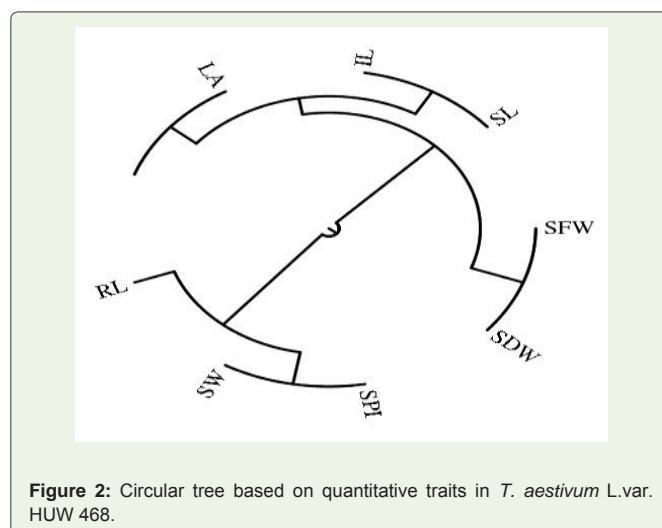
Figure 2: Circular tree based on quantitative traits in *T. aestivum* L.var. HUW 468.
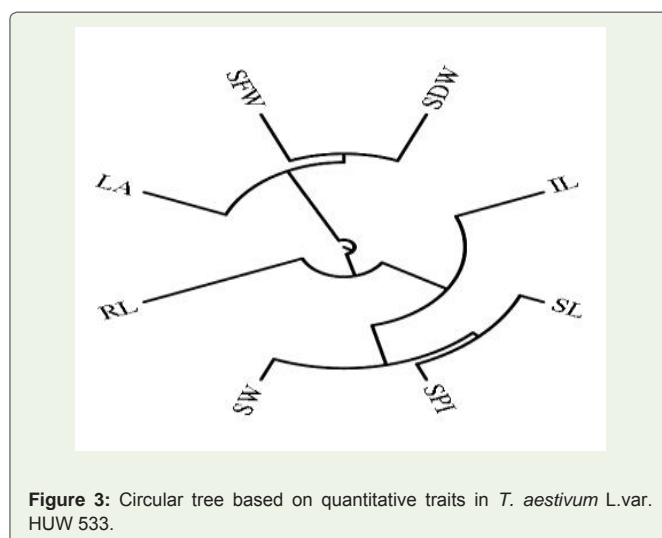
Figure 3: Circular tree based on quantitative traits in *T. aestivum* L.var. HUW 533.

Table 9: Estimated Covariance (Cov), Total Heterozygosity (H_T), Mean Heterozygosity (H_S), Gene Differentiation (G_{ST}) and Gene Flow (N_m) among *T. aestivum* L. varieties.

T. aestivum L. varieties	Cov	H_T	H_S	G_{ST}	N_m
HUW 234	9.18	44.665	5.583	0.875	0.0714
HUW 468	8.32	33.921	4.240	0.875	0.0714
HUW 533	6.06	26.317	3.289	0.875	0.0714

Table 10: Similarity matrix of all quantitative traits in wheat varieties based on Pearson correlation

	H234LA	H234 IL	H234SL	H234SFW	H234SDW	H234SPI	H234SW	H468LA	H468 IL	H468SL	H468SFW	H468SDW	H468SPI	H468SW	H533 LA	H533 IL	H533 SL	H533SFW	H533SDW	H533SPI	H533SW	H234RL	H468RL	H533 RL
H234 LA	1	0.292	0.273	0.138	0.123	0.042	0.365	0.310	0.246	0.136	0.036	0.070	0.332	0.632	0.428	0.046	0.074	-0.149	-0.164	0.154	0.349	-0.655*	-0.661*	0.027
H234 IL		1	0.930**	0.765**	0.661*	0.695*	0.304	0.936**	0.889**	0.839**	0.784**	0.620	0.694*	0.433	-0.129	0.282	0.829**	0.027	0.313	0.849**	0.940**	0.076	-0.238	-0.241
H234 SL			1	0.574	0.775**	0.803**	0.084	0.976**	0.728*	0.812**	0.773**	0.400	0.479	0.532	-0.214	0.559	0.923**	0.118	0.202	0.904**	0.902**	0.019	-0.129	-0.250
H234 SFW				1	0.284	0.312	0.549	0.523	0.966**	0.871**	0.864**	0.852**	0.850**	0.166	-0.085	-0.320	0.412	-0.142	0.524	0.389	0.717*ª	-0.033	-0.480	-0.467
H234 SDW					1	0.985**(	-0.107	0.799**	0.464	0.605	0.524	0.110	0.243	0.504	0.155	0.593	0.837**	0.519	0.446	0.691*	0.545	0.031	-0.229	-0.239
H234 SPI						1	-0.093	0.822**	0.479	0.605	0.543	0.163	0.255	0.605	0.064	0.582	0.864**	0.468	0.398	0.711*	0.562	0.122	-0.136	-0.294
H234 SW							1	0.158	V0.480	0.289	0.261	0.253	0.312	-0.352	0.218	-0.468	-0.084	-0.412	0.271	-0.070	0.222	0.064	-0.546	0.000
H468 LA								1	0.702*	0.742*	0.677*	0.324	0.432	0.500	-0.122	0.581	0.922**	0.135	0.224	0.926**	0.879**	0.103	-0.133	-0.106
H468 IL									1	0.916**	0.877**	0.802**	0.853**	0.222	-0.047	-0.116	-0.581	-0.051	0.518	0.581	0.834**	-0.044	-0.481	-0.379
H468 SL										1	0.984**	0.619	0.661*	0.370	-0.154	0.124	0.697*	0.076	0.553	0.636*	0.821**	-0.060	-0.407	-0.418
H468 SFW											1	0.627	0.621	0.416	-0.278	0.091	0.646*	0.000	0.489	0.583	0.772**	-0.040	-0.325	-0.473
H468 SDW												1	0.950**	0.150	-0.103	-0.450	0.259	-0.125	0.283	0.255	0.583	-0.133	-0.308	-0.600
H468 SPI													1	-0.005	0.115	-0.376	0.327	0.029	0.347	0.319	0.665*	-0.283	-0.520	-0.545
H468 SW														1	-0.483	0.511	0.697*	0.311	0.192	0.587	0.382	0.650*	0.601	-0.164
H533 LA															1	-0.247	-0.077	0.583	0.470	-0.349	0.099	-0.175	-0.592	-0.101
H533 IL																1	0.656*	0.290	-0.185	0.684*	0.314	0.157	0.390	0.304
H533 SL																	1	0.437	0.351	0.864**	0.832**	0.265	0.045	-0.203
H533 SFW																		1	0.596	0.060	0.110	0.213	-0.019	-0.208
H533 SDW																			1	0.076	0.296	0.261	-0.433	-0.249
H533 SPI																				1	0.806**	0.166	0.121	0.117
H533 SW																					1	0.040	-0.194	-0.235
H234 RL																						1	0.622	0.273
H468 RL																							1	0.327
H533 RL																								1

10,11). The leaf area of HUW234 is negatively correlated with root length of HUW 468 at P≤0.05 which suggest that increase in the leaf area decreases the root length. The internode length of HUW 234 is positively correlated with leaf area, internode length, shoot length, seeds fresh weigth at P≤0.01, number of seeds per inflorescence at P ≤0.05 with HUW 468 and shoot length, number of seeds per inflorescence, seed weight with HUW 533 at P≤0.01 which showed that internode length is an important character for overall growth of the plant. The shoot length of HUW 234 has direct effect on the leaf area, shoot length, seed fresh weight at P≤0.01, and internode length at P≤0.05 with HUW 468 and shoot length, number of seeds per inflorescence and seed weight at P≤0.01 of HUW 533 which showed that shoot length is an important character for overall growth of the plant. The seeds fresh weight (HUW234) showed positive correlation with internode length, shoot length, seed fresh weight, seed dry weight, number of seeds per inflorescence at P≤0.01 of HUW468. The seed dry weight (HUW 234) is directly associated with number of seeds per inflorescence (HUW533 at P≤0.05), leaf area HUW 468 at P≤0.01, shoot length HUW 533 at P≤0.01. The number of seeds

per inflorescence (HUW234) may be similar in growth of leaf area (HUW 468 at P≤0.01), shoot length (HUW 533 at P≤0.01) and number of seeds per inflorescence(HUW 533 at P≤0.05). The seed weight (HUW234) showed the correlation with number of seeds per inflorescence (HUW468 at P≤0.05) and seed weight (HUW 533 at P≤0.05).

Correlation of individual characters in T. aestivum L. var. HUW 468 with HUW 533 and HUW 234

The leaf area (HUW468) showed association with shoot length, number of seeds per inflorescence and seed weight of HUW 533 at P≤0.01. The internode length (HUW 468) showed similarity with seed weight (HUW 533 at P≤0.01). The shoot length (HUW 468) is associated with shoot length, number of seeds per inflorescence (HUW 533 at P≤0.05) and seed weight (HUW 533 at P≤0.01). The seed fresh weight (HUW468) showed association with shoot length at P≤0.05 and seed weight at P≤0.01 of HUW533. The number of seeds per inflorescence (HUW 468) showed connection with seed weight of HUW533 at P≤0.05. The seed weight (HUW 468) is in line with shoot

Table 11: Dissimilarity matrix of all quantitative traits in wheat varieties based on Pearson correlation.

	H234LA	H234 IL	H234SL	H234SFW	H234SDW	H234SPI	H234SW	H468LA	H468 IL	H468SL	H468SFW	H468SDW	H468SPI	H468SW	H533 LA	H533 IL	H533 SL	H533SFW	H533SDW	H533SPI	H533SW	H234RL	H468RL	H533 RL
H234 LA	0	0.708	0.727	0.862	0.877	0.958	0.635	0.690	0.754	0.864	0.964	0.930	0.668	1.632	0.572	0.954	0.926	1.149	1.164	0.846	0.651	1.655	1.661	0.973
H234 IL		0	0.070	0.235	0.339	0.305	0.696	0.064	0.111	0.161	0.216	0.380	0.306	0.567	1.129	0.718	0.171	0.973	0.687	0.151	0.060	0.924	1.238	1.241
H234 SL			0	0.426	0.225	0.197	0.916	0.024	0.272	0.188	0.227	0.600	0.521	0.468	1.214	0.441	0.077	0.882	0.798	0.096	0.098	0.981	1.129	1.250
H234 SFW				0	0.716	0.688	0.451	0.477	0.034	0.129	0.136	0.148	0.150	0.834	1.085	1.320	0.588	1.142	0.476	0.611	0.283	1.033	1.480	1.467
H234 SDW					0	0.015	1.107	0.201	0.536	0.395	0.476	0.890	0.757	0.496	0.845	0.407	0.163	0.481	0.554	0.309	0.455	0.969	1.229	1.239
H234 SPI						0	1.093	0.178	0.521	0.395	0.457	0.837	0.745	0.395	0.936	0.418	0.136	0.532	0.602	0.289	0.438	0.878	1.136	1.294
H234 SW							0	0.842	0.520	0.711	0.739	0.747	0.688	1.352	0.782	1.468	1.084	1.412	0.729	1.070	0.778	0.936	1.546	1.000
H468 LA								0	0.298	0.258	0.323	0.676	0.568	0.500	1.122	0.419	0.078	0.865	0.776	0.074	0.121	0.897	1.133	1.106
H468 IL									0	0.084	0.123	0.198	0.147	0.778	1.047	1.116	1.581	1.051	0.482	0.419	0.166	1.044	1.481	1.379
H468 SL										0	0.016	0.381	0.339	0.630	1.154	0.876	0.303	0.924	0.447	0.364	0.179	1.060	1.407	1.418
H468 SFW											0	0.373	0.379	0.584	1.278	0.909	0.354	1.000	0.511	0.417	0.228	1.040	1.325	1.473
H468 SDW												0	0.050	0.850	1.103	1.450	0.741	1.125	0.717	0.745	0.417	1.133	1.308	1.600
H468 SPI													0	1.005	0.885	1.376	0.673	1.029	0.653	0.681	0.355	1.283	1.520	1.545
H468 SW														0	1.483	0.489	0.303	0.689	0.808	0.413	0.618	0.350	0.399	1.164
H533 LA															0	1.247	1.077	0.417	0.530	1.349	1.099	1.175	1.592	1.101
H533 IL																0	0.344	0.710	1.185	0.316	0.686	0.843	0.610	0.696
H533 SL																	0	0.563	0.649	0.136	0.168	0.735	0.955	1.203
H533 SFW																		0	0.404	0.940	0.890	0.787	1.019	1.208
H533 SDW																			0	0.924	0.704	0.739	1.433	1.249
H533 SPI																				0	0.194	0.834	0.879	0.883
H533 SW																					0	0.960	1.194	1.235
H234 RL																						0	0.378	0.727
H468 RL																							0	0.673
H533 RL																								0

length (HUW533 at P≤0.05) and root length (HUW234 at P≤0.05).

Since the characters influencing the growth parameters within and among the varieties, it may be suggested that a small part of genome contains the genes for other variety (as all are the same species) such as HUW 234 contains a part of HUW 468 or HUW 533 and vice versa.

The cophenetic correlation coefficient (CP) among the traits studied was found 0.576 (Figure 5). The value indicates that the overall phenotypic relation among the traits studied were approximately good for growth and development of the plant.

The degree of variation was high for all the traits studied at P≤0.05 and P≤0.01. The results were obtained are in accordance with reports of others [9-15]. Morphological characters possibly will be used for evaluate genetic diversity but are influenced by the atmosphere. The diverse gene action like additive gene action and partial dominance with additive gene action may be involved in crop shoot length, internode length, leaf area, root length, seed weight, grain yield and most of other yield components in wheat [16]. The deviation of characters in crop might be genetic or environmental but the deviation supposed to be heritable since the competence of plant assortment primarily depends on additive genetic variance, management of the environment and the interface between genotype and environment [17]. Therefore, the evaluation of genetic differences may be critical for varietal improvement and genetic reserve protection [18].

The close kinship was observed among the varieties both in morphological and genetic characteristics (Table 7-9). The occurrence of close resemblance among the varieties may be due to the gene exchange among them [19]. Inbreeding and genetic drift may influence the crops vigor by increasing the appearance of recessive lethal alleles and enhance the homozygosity among the undersized population of crops. Genetic drift could be anticipated to decrease
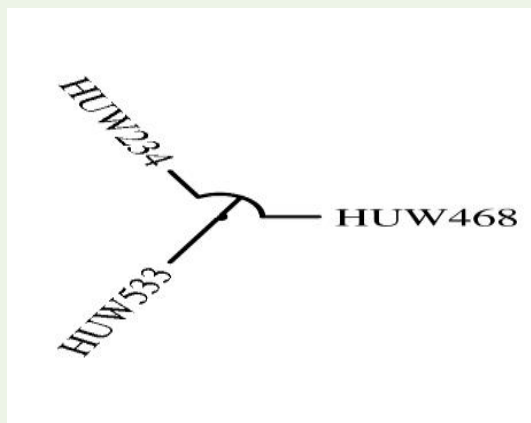
Figure 4: Circular tree based on all combined quantitative traits in T. aestivum L. varieties.
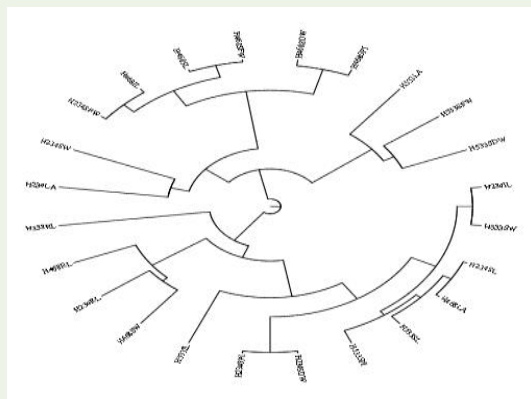

Figure 5: Circular tree based on all separate quantitative traits in T. aestivum L. varieties.

distinction within small population of crops and causes loss of low frequency alleles which ultimately associated with the fitness of the crops.

Therefore, it may be concluded that the genetic factors (inbreeding, genetic drift, demography, species life history, biogeography and gene flow) play a significant role in estimating the modern genetic composition of crop populations with genetic exchange, genetic differentiation, heterozygosity and gene flow among them [20].

References

1. DWR (2014) Wheat scenario-A snippet. Issue 2, Directorate of Wheat Research (DWR), India.

2. El-Mohsen AA, Hegazy SRA, Taha MH (2012) Genotypic and phenotypic interrelationships among yield and yield components in Egyptian bread wheat genotypes. Journal of Plant breeding and Crop Science 4: 9-16.

3. Mekonnon B, Lakew B, Dessalegn T (2015) Morphological diversity and association of traits in ethiopian food barley (*Hordeum vulgare* L.) landraces in relation to regions of origin and altitudes. Journal of Plant Breeding and Crop Sciences 7: 44-54.

4. Zhu Y, Chen H, Fan J, Wang Y, Li Y, et al. (2000) Genetic diversity and disease control in rice. Nature 406: 718-722.

5. Salem KFM, El-Zanaty AM, Esmail RM (2008) Assessing wheat (*Triticum aestivum* L.) genetic diversity using morphological characters and microsattelite markers. World journal of Agricultural Sciences 4: 538-544.

6. Sun H, Lu J, Fan Y, Zhao Y, Kong F, et al. (2008) Quantitative trait loci (QTLs) for quality traits related to protein and starch in wheat. Prog Nat Sci 18: 825-831.

7. Mohammadi SA, Prasanna BM (2003) Analysis of genetic diversity in crop plants salient statistical tools and considerations- Review and interpretation. Crop Science 43: 1235-1248.

8. Talebi R, Fayaz F, Karami E (2012) Morphometric and amplified fragment length polymorphism marker analysis in some landrace wheat (*Triticum aestivum*) genotypes collected from north-west Iran. Environ Exp Biol 10: 49-56.

9. Annicciarico P, Royo C, Bellah F, Moragues M (2009) Relationships among adaptation patterns, morphophysiological traits and molecular markers in durum wheat. Plant Breeding 128: 164-171.

10. Altintas S, Toklu F, Kafkas S, Kilian B, Brandolini A, et al. (2008) Estimating genetic diversity in durum and bread wheat cultivars from Turkey using AFLP and SAMPL markers. Plant Breeding 127: 9-14.

11. Akar T, Yazar S, Donmez E, Avci M, Dusunceli F (2007) Current status of national winter wheat breeding in Turkey. Journal Agric Res 45: 1-8.

12. Mishra R, Baenziger PS, Russell WK, Greybosch RA, Baltensperger DD, et al. (2006) Crossover interactions for grain yield in multienvironmental trials of winter wheat. Crop Sci 46: 1291-1298.

13. Bilgin O, Korkut K Z (2005) Determination of some bread quality and grain yield characters in Bread wheat (*Triticum aestivum* L.). International Journal of Agriculture and Biology 7: 125-128.

14. Fufa H, Baenziger PS, Beecher BS, Greybosch RA, Eskridge KM, et al. (2005) Genetic improvement trends in agronomic performances and end use quality characteristics among hard red winter wheat cultivars in Nebraska. Euphytica 144: 187-198.

15. Karagoz A, Zencirci N (2005) Variation in wheat landraces from different altitudes of three regions of Turkey. Genetic Resources and Crop Evolution 52: 775-785.

16. Savii G, Nedelea G (2012) Estimation of interrelationships among different yield traits in winter wheat. J Horticult For Biotechnol 16: 115-118.

17. Gulnaz S, Khan SH, Shahzad M, Ashfaq M, Sajjad M (2012) Genetic evaluation of spring wheat (*Triticum aestivum* L.) germplasm for yield and seedling vigor traits. Journal Agric Soc Sci 8: 123-128.

18. Singh G, Khan MH, Bhan SK (2008) Genetic divergence in wheat (*Triticum aestivum* L.). New Botanist-Int J Plant Sci Res 35: 81-88.

19. Gaskin JF, Shafroth PB (2005) Hybridization of *Tamarix ramosissima* and *T. chinensis* with *T. aphylla* in the south western USA determined from DNA sequence data. Madrono 52: 1-10.

20. Ijbari H, Sheidai M, Mehrabian AR, Noormohammadi Z, Ghasemzadeh-Baraki S (2014) K-means clustering and STRUCTURE analysis of genetic diversity in *Tamarix* L. accessions. Turk J Bot 38: 1080-1094.