Full Length Research Paper

Determination of genetic distances in spring wheat by cluster analysis in Mazandaran province (North of Iran)

Khavarinejad M. S.

Agricultural and Natural Resources Research Center of Mazandaran, Iran.

Forty-eight genotypes were planted in BIEKOL station field in 2009-2010. This study was carried out in augmented design with three check cultivars in three blocks (a total of 57 genotypes). In order to know uniformity, variance analysis of check genotypes showed that replications were not significant indicating no need for genotypes correction. Mean, standard deviation and coefficient variation for traits were different. The most and the least % CV were related to yield and duration of heading. In cluster analysis, yield components had important roles in cluster distinction. These traits became significant in variance analysis of clusters. In this case, cluster 6 with 8 and cluster 1 with 21 members had the most means in traits.

Key words: Wheat, coefficient of variation, mean, standard deviation, cluster.

INTRODUCTION

Mazandaran Province is a Caspian province in the north of Iran. Located on the southern coast of the Caspian Sea, it is bordered clockwise by the Golestan, Semnan, Tehran, Alborz**,** Qazvin, and Gilan provinces. However, while wheat is grown in over 60,000 ha in this province, its economic value is smaller than that of rice and citrus. Genetic diversity of the wheat landraces must be investigated for use in wheat breeding. More information about the genetic diversity within and relationships among landraces would be invaluable for the conservation and utilization of existing genetic resources. As regards wheat origin, Iran is one of the locations of diversity of common wheat with a long cultivation history. In addition, wheat genetic resources are sent from

CIMMYT to Mazandaran Agricultural Research Center as international nurseries.

Basically, calculation of cluster numbers is based on numbers of principal components; however, 4 clusters were selected on the basis of Squared Euclidean Distance cluster because of the more obtained groups to each other than to those in other groups. Thus it can be used to distinguish genetic similarity or distance in wheat genotypes. Wheat has vast genetic diversity in aspects of quantitative and qualitative traits, environmental adaptability and types of tolerances Poelman (1987). Based on Hair et al. (1995) finding, acceptable genetic distance of within cluster should be less than that between clusters. Principal components analysis (PCA)

Table 1. Pedigree of studied genotypes.

R	Pedigree (Rep 1)
1	*ATTILA/3*BCN*2//BAV92*
2	DARYA (SHA4/CHIL)
3	SW89.3243/PRINIA/4/PRINIA/WEAVER//STAR/3/WEAVER
4	BAV92/5/CNDO/R143//ENTE/MEXI75/3/AE.SQ/4/2*OCI
5	PF74354//LD/ALD/4/2*BR12*2/3/JUP//PAR214*6/FB6631/5/SW89-5124*2/FASAN/6/TILH
6	SHA 7//HAHN"S"*2/PRL"S"/3/VEE/NAC
7	NANJING2149/KAUZ/4/JUP/ALD"S"//KIT"S"/3/VEE"S"/5/SHA 7//HAHN"S"*2/PRL"S"
8	MILAN CM 75118 // KACM 75118/K1/3/TAJAN(DH(
9	BERSEE/3/AZD/VEE"S"//SERI82/ROSH/4/BLOUDAN/3/BB/7C*2//Y50E/KAL*3/CW84
10	PASTOR//NANJING92149/KAUZ/3/PASTOR
11	PASTOR/FINSI
12	N-80-19 (SW89.3064/STAR CMBW91…
13	JUP/ZP//COC/3/PVN/4/TNMU/5/TN
14	MORVARID (MILAN/SHA7(
15	KAUZ//ALTAR 84/AOS/3/MILAN/KAUZ/4/HUITES
16	ATTILA/3*BCN//BAV92/3/TILHI
17	PASTOR/3/VORONA/CNO 79//KAUZ
18	VORONA/ CNO 79//KAUZ/3/MILAN
19	MILAN/S87230//BABAX

	Pedigree (Rep 2)
20	MILAN CM75118/KA CM75118/K 1//TAJAN
21	CAR//KAL/BB/3/NAC/4/VEE/PJN//2*TUI/5/MILAN
22	SHA 7//HAHN"S"*2/PRL"S"/3/ATRAK
23	SIRKKU/FINSI
24	SUNSU/PBW343
25	BL2064//SW89-5124*2/FASAN/3/TILHI
26	DARYA (SHA4/CHIL)
27	OASIS/5*BORL95//SIRKKU/3/CHIBIA
28	BRBT1*2//TUI/CLMS
29	MORVARID (MILAN/SHA7(
30	MILAN/ATTILA//ATTILA-4Y
31	NANJING 82149/KAUZ/3/PFAU/SERI//BOW
32	FRET2/TUKURU//FRET2
33	MILAN/S87230//BABAX
34	SABUF/7/ALTAR 84/AE.SQUARROSA (224)//YACO/6/CROC_1…/
35	N-80-19 (SW89.3064/STAR CMBW91(…
36	SW89.2089/BAKHTAWAR94//SW89.3243
37	CBRD/ARA90
38	BAV92/PRINIA//TAM200/PRL

	Pedigree (Rep 3)
39	WBLL1*2/KKTS
40	BABAX//ATTILA/3*BCN/3/PASTOR
41	CROC_1/AE.SQUARROSA (205)//KAUZ/3/ATTILA
42	MORVARID (MILAN/SHA7(
43	OASIS/SKAUZ//4*BCN/3/2*PASTOR
44	URES/BOW//OPATA/3/ELVIRA/4/SITE/MO/3/VORONA/BAU//BAU
45	LUCO-M//KAUZ/LUCO-M/3/2*PRINIA
46	BABAX/LR42//BABAX*2/3/VIVITSI
47	CAL/NH//H567.71/3/SERI/4/CAL/NH//H567.71/5/2*KAUZ/6/PASTOR

Table 1. Contd.

48	ALDAN/CIANO67//PASTOR
49	DARYA (SHA4/CHIL(
50	CM82A.1294/2*KAUZ//MUNIA/CHTO/3/MILAN
51	N-80-19 (SW89.3064/STAR CMBW91(…
52	HP1761//SW89-5124*2/FASAN
53	WAXWING*2/KIRITATI
54	GONDO//SHA5/WEAVER/3/PASTOR
55	OR 1/GONDO//ESDA/LIRA
56	OASIS/SKAUZ//4*BCN/3/2*PASTOR2
57	WBLL1*2/BRAMBLING

Nos. 2, 12, 14, 26, 29, 35, 42, 49, 51 are control cultivars in blocks.

is a method for complement of cluster analysis (Kantety et al., 1995; Johns et al., 1997; Dubreuil and Charcosset, 1998). According to Hailegiorgis and Mesfin (2011), genetic divergence of 49 bread wheat revealed that nine principal components (PC1 to PC9) accounted for nearly 80% of the total variation, thus these genotypes groups are organized into 9 clusters. Fag et al. (1996) used cluster analysis method on 120 wheat genotypes and obtained different groups based on studied traits. van Beuningen and Busch (1997) evaluated 289 spring wheat cultivars from USA, Canada, and Mexico grown in Minnesota during 1990 and 1991 and evaluated in three environments a total of 35 different cultivars.

However, six cultivars could not be grouped into 17 major clusters; major clusters grouped cultivars of common origin, parentage, and/or era of release. The goal of this study is genetic similarity and distance in spring wheat bread by cluster method.

MATERIALS AND METHODS

This trial was carried out in BIE KOLA (Longitude 53, 13° E and Latitude 36°, 43' and 15° meter sea level) station of Mazandaran Agricultural and Natural Resources Center. The experimental materials consisted of fifty-one varieties/lines of spring wheat (Table 1). The experimental materials consisted of 48 varieties/lines of spring wheat with three check cultivars in three blocks, a total of 57 in 3 blocks with 19 genotypes. The most genotypes were international materials from CYMMIT that we investigate every year. The varieties/lines were planted in augmented design. The field area was $6 \times 5 \times 0.2 = 6$ m². Studied traits including; Date of heading (DHE, Days), Plant height (PLH, cm), Spike length (SPL, cm), Stem length (SL, cm), Stem diameter (SD, mm), flag leaf width (FLW, cm), flag leaf length (FLL), first- inter-node (FDN), second-inter-node (SDN), third inter-node (TDN), forth inter-node (FODN), spikes per m² (SM, No.) Seeds per spike (SS, No.), kernel weight 1,000 (KW, g), yield (yield, gm⁻²), biomass (BIO, g) and harvest index (HI, %). Used methods were:

1) Calculation of yield means, standard deviation and coefficient variation of traits.
2) Analysis of variance to obtain clusters based on traits.
3) Genotypes clustering based on traits.

To ensure uniformity of blocks, simple variance analysis method was used for yield of checks Milan/Sha4, Sw89.3064/STAR, Sha4/Chil by MSTATC program and in order to estimate relationships between traits, which include yield means, standard deviation and coefficient variation of traits and cluster analysis SPSS program was used (Table 5).

RESULTS AND DISCUSSION

In order to determine traits, divergence was carried out in the calculations as shown in Table 2. **CV%** is a parameter which is not related to unit of measured traits and will be effective in comparing the studied traits. **CV%** of the traits varied from 2% for DHE to 38% for Y (Table 2). Obvious differences of **CV%** values among genotypes declared that genotypes had genetic divergence in some traits. Aghaee et al. (2010) reported that DHE had the lowest **CV%,** while yield and weight of seeds per spike has the most **CV%** value. In this case, results showed that coefficient of variation of two traits (PLH) and (DHE) were little, which can be through favorable rainfall. Variation was observed in yield versus yield components. Cluster analysis was used for grouping of genotypes by UPGMA and Euclidean distance method. Table 3 indicated analysis of variance of 6 clusters based on traits. Distribution pattern of all the genotypes into various clusters showed the presence of considerable genetic divergence among the genotypes for most of the studied .traits. Maximum and minimum mean data were observed within cluster 6 and 1 respectively. Thus, selected clusters had high yield, high yield components and high harvest index. In this way, we selected cluster 6, that is, genotypes with the highest yield and yield components in all clusters. Cluster 1 was the lowest group in yield and yield components (Table 4 and Figure 1). Kumar and Lal (2009) used multiple cluster for selecting of genotypes and on the basis of cluster means, he reported cluster 6 has been identified for selecting parents for incorporating grain yield per plant, tillers per plant and plant height; cluster 5 for spike length, grains per spike and early maturity, and cluster 3 for 1,000 grain weight. Selection of plants was argued on the basis of character associations. Chai (2000) reported that results using Euclidean

Table 2. The estimated mean, standard deviation and coefficient of variation (%CV) of quantitative traits for genotypes.

Variables	Mean	Standard deviation	%CV
DHE	119.0	2.42015	2
PLH	93.1228	6.97718	7
SL	82.0000	7.09376	9
SPL	9.9298	0.91651	9
SD	4.5754	0.51592	11
FDN	6.9298	2.05165	30
SDN	12.3509	3.70806	30
TDN	19.2105	3.47946	18
FODN	43.2982	6.11487	14
FLL	22.9439	3.08961	13
FLW	1.8053	.21665	12
SM	355.0877	73.64206	21
SS	52.0351	9.83246	19
KW	32.7807	6.50128	20
Y	490.5017	188.02595	38
BIO	1057.8172	195.85921	19
HI	39.6491	7.61223	19

Duration of heading (DHE), plant height (PLH), stem length (SPL), stem-diameter (SD), first-inter node (FDN), second-inter node (SDN), third inter node (TDN), forth inter node (FODN), flag leaf length (FLL), flag leaf width (FLW), spike No. per m^2 (SM), seeds.per spike (SS), kernel weight 1000 (KW), yield (yield), biomass (BIO) and harvest index (HI).

Table 3. Analysis variance of Cluster for studied genotypes on basis of traits.

Traits	Mean square	df
DHE	7.255	5
PLH	48.409	5
SL	50.195	5
SPL	0.531	5
SD	0.318	5
FDN	0.615	5
SDN	12.887	5
TDN	14.394	5
FODN	18.071	5
FLL	11.740	5
FLW	0.101*	5
SM	41163.43**	5
SS	453.038**	5
KW	247.429**	5
Y	337766.8**	5
BIO	371594.9**	5
HI	223.611**	5

Duration of heading (DHE), plant height (PLH), stem length (SPL), stem-diameter (SD), first-inter node (FDN), second-inter node (SDN), third inter node (TDN), forth inter node (FODN), flag leaf length (FLL), flag leaf width (FLW), spike No. per m^2 (SM), seed per spike (SS), kernel weight 1000 (KW), yield (yield), biomass (BIO) and harvest index (HI).

Table 4. Six obtained clusters with number of members.

No. of clusters	No. of members of clusters
1	21
2	12
3	7
4	4
5	5
6	8
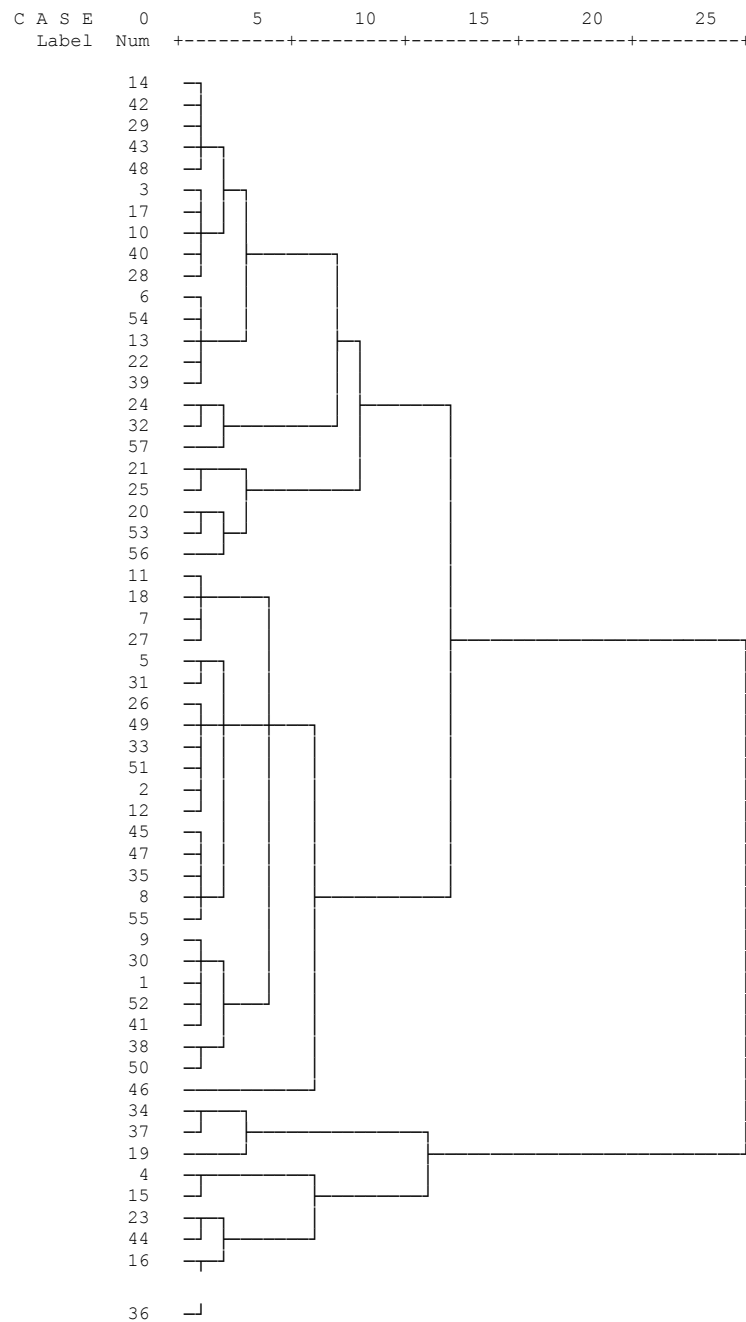
Figure 1. Genotypes grouping in basis of studied.

Table 5. Means of studied traits in six obtained clusters.

Variables	1	2	3	4	5	6
DHE	118.75	118.00	118.25	117.86	118.83	119.95
PLH	96.25	93.6	88.00	91.86	94.75	92.29
SL	85.38	81.4	77.00	80.00	83.50	81.62
SPL	9.54	10.12	9.65	9.93	10.21	9.93
SD	4.30	4.24	4.63	4.76	4.63	4.66
FDN	6.94	6.40	7.50	7.14	6.92	6.88
SDN	12.69	15.10	9.88	12.07	12.17	12.24
TDN	20.06	18.60	16.75	17.21	19.83	19.81
FODN	44.44	41.30	42.88	43.57	45.08	42.31
FLL	24.50	20.80	21.13	23.50	23.21	22.87
FLW	1.84	1.52	1.83	1.87	1.78	1.85
SM	254.63	421.40	500.00	391.86	361.25	334.19
SS	49.13	35.60	57.50	60.00	49.17	55.00
KW	27.21	23.50	40.43	37.63	30.87	35.13
Y	275.7	277.54	922.73	697.57	432.06	505.09
Bio	972.3	695.2	1210.5	1348.4	897.6	1142.3
HI	34.8	28.6	46.8	41.9	40.83	41.38

Duration of heading (DHE), plant height (PLH), stem length (SPL), stem-diameter (SD), first-inter node (FDN), second-inter node (SDN), third inter node (TDN), forth inter node (FODN), flag leaf length (FLL), flag leaf width (FLW), spike No. per m^2 (SM), seeds per spike (SS), kernel weight 1000 (KW), yield (yield), biomass (BIO) and harvest index (HI).

Distance were greater than those using Mahalanobis distance.

REFERENCES

Chai S (2000). Cluster analysis methods appropriate for classification of drought-resistant wheat ecotypes. Ying Yong Sheng Tai Xue Bao, 11(6):833-838. PMid:11767553

Dubreuil P, Charcosset A (1998). Genetic diversity within and among maize populations: A comparison between isozymes and nuclear RFLP loci. Theor. Appl. Genet. 96:577-587. http://dx.doi.org/10.1007/s001220050776

Fag XW, Xiong EH, Zhu W (1996). Cluster analysis of elite wheat germplasm. Jiang Agric. Sci. 4:14-16.

Hailegiorgis T, Mesfin M (2011). Genetic divergence analysis on some bread wheat genotypes grown in Ethiopia. J. Central Eur. Agric. 12:344-352.

Hair JR, Anderson RE, Tatham RL, Black WC (1995). Multivariate data analysis with readings. 4th edition, Prentice-Hall, Englewood Cliffs, NJ. PMCid:PMC2549635

Johns MA, Skrotch PW, Neinhuis J, Hinrichsen P, Bascur G, Munoz-Schick (1997). Gene pool classification of common bean landraces from Chile based on RAPD and morphological data. Crop Sci. 37:605-613. http://dx.doi.org/10.2135/cropsci1997.0011183X003700020049x

Kantety RV, Zeng X, Jeffrey LB, Zehr BE (1995). Assessment of genetic diversity in dent popcorn (*Zea mays* L.) inbred lines using inter-simple sequence repeat (ISSR) amplification. Mol. Breed. 1:365–373. http://dx.doi.org/10.1007/BF01248414

Kumar B, Lal GM (2009). Genetic variability, diversity and association of quantitative traits with grain yield in bread w heat (*Triticum aestivum* L.). Asian J. Agric. Sci. 1(1):4-6

Poelman JM (1987). Breeding Field Crop . Van Nostrand Reinhold. New York. P. 724. http://dx.doi.org/10.1007/978-94-015-7271-2 PMid:3653086

van Beuningen LT, Busch RH (1997). Genetic diversity among North American Spring Wheat Cultivars: III. Cluster Analysis Based on Quantitative Morphological Traits. Alliance of crop, soil. Environ. Sci. Soc. 37:981-988.