GENETIC DIVERGENCE ANALYSIS AMONG 56 BREAD WHEAT GENOTYPES

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ABSTRACT

Genetic diversity analysis could be used to identify those genotypes, which are useful not only for sampling in subsequent studies but also for parental selection in breeding programs. To test these applications in bread wheat (*Triticum aestivum* L.), relationships among 56 wheat genotypes were measured using cluster analysis of earliness components and grain yield characters. Entries were planted in replicated field trails in three sowing dates i.e. 1Oct.,29 Oct. and 26 Nov. Data were obtained for days to heading, days to maturity, grain filling period, grain filling rate and grain yield in 2003/2004 season at Sakha Agric. Res. Station.

The genetic divergence among genotypes on Euclidean distance revealed some sort of dissimilarities between genotypes for earliness, plant height and grain yield characters. Grain filling rate and days to heading were the most important source of variation among genotypes. At 75 Euclidean distances, the 56 genotypes were distributed in three different clusters. At a similarity lower than 50 Euclidean distance, the 56 genotypes were distributed in six different clusters. Moreover, at 25 Euclidean distance, the studied genotypes divided into 13 clusters, while, entry 15 formed a single cell cluster.

Clustering method was effective in detecting the yielding and earlier clusters, which have almost similar genotypes in such attributes. The selected clusters based on clustering pattern at 25 Euclidean distance appeared to be more accurate than those at 50 Euclidean distance.

INTRODUCTION

Genetic relationships among individuals and populations could be measured by similarity of any number of quantitative characters, where characters are agronomic characters of the plant such as duration of growth stage , grain yield, or inflorescence size (Souza and Sorrells 1991). This assumes that the differences between characters of the genotypes reflect the genetic divergence of those genotypes. Genetic relationships among a large number of cultivars could be summarized using cluster analysis to place similar genotypes into phenotypic groups. Genetic relationships among cultivars have been shown to be useful for selection of parents to produce hybrids (Frei *et al.*, 1986and Menshawy *et al.,* 2004), for the prediction of variances for some characters in the F_2 and inbred generations (Cowen and Frey 1987) and for the analysis of cultivars variability (Reddy 2001)

Genetic diversity in breeding populations is important to assure continued genetic improvement. Souza and Sorrells (1991) used cluster analysis of 13 quantitative characters in oat germplasms. They reported that heading date was important as a source of variation and for grouping genotypes. Date of heading of oats concerning genetic similarity, suggested that clusters based on quantitative characters would drive a biased genetic-relationship measure. Clustering by morphology may, however, be valuable for identification of genotypes with similar adaptations for breeding and

agronomic research programs. Shamsuddin (1985) reported that genetic distance between spring wheat parents could predict parental specific combining ability in F_1 progeny.

Furthermore, categorizing the populations into similar groups or clusters is most useful to assure continued genetic improvement (Murphy *et al.*, 1986; *Souza et al.*, 1994 and Van Beuningen and Busch 1997). Menshawy (2000) applied genetic diversity on F_3 families in wheat crosses and reported that clustering method was effective in detecting the earlier and yielding clusters, having families almost similar in such attributes. Consequently, the clustering pattern of F_3 families seems to be a better tool for breeders in selecting and identifying superior families within clusters compared to the other methods.

The objectives of this study were to divide large genotypes of spring wheat into groups that have similar morphology and development. And also to evaluate the relationship between genotypes based on Euclidean distance.

MATERIALS AND METHODS

Fifty-six bread wheat (*Triticum aestivum* L) genotypes were used in this study. Entries used were; (i) check cultivars; (ii) pure lines selected from National Wheat Research Program; and (iii) selected entries from exotic material. Studied entries and their origins are listed in Table 1.

Table 1: Pedigree and origin of the 56 studied wheat genotypes.

Ser#	Cross Name	Origin
1	Bl1133/3/Cmh79a.955*2/Cno 79//Cmh 79a.955/ Bow "S"/4/Plo/Tr810328	Egypt
2	Sakha 12/5/Kvz//Cno 67/Pj 62/3/Yd"S"/ Blo"S"/4/K 134(60)/Vee	Egypt
3	Kauz / Pastor	CIMMYT
4	Croc-1 / Aeg..Squarrosa(205) // Kauz /3/ Sasia	CIMMYT
5	Weebill 1	CIMMYT
6	Isd-75-3-1/M088//Prl/Vee # 6	CIMMYT
7	Chen/ Aeg. Squarrosa (Taus) // Bcn/3/ Vee # 7/….	CIMMYT
8	Tr801504/Sakha 69	Egypt
9	Bow "S" /Kvz"S"//7c/Seeri 82/3/Gem #5/4/Sids #6	Egypt
10	C182-24/C168.3/3/Cno/7c*2//(CC/Tob// Myna"S"Voc"S"/4/ Sakha 8	Egypt
11	Prl"S"/Toni//Attila	Egypt
12	Bl 1496/Sids 8	Egypt
13	Nkt"S"/3/Mai"S"/Pj//Emu"S"/Faly/Sjm// Aldan "S"/4/Gem#3	Egypt
14	Gemmeiza#9//Cs/TH-SC // 3*PVN /3/ Mirlo / Buc	Egypt
15	PF70354/Ald"S"//Vee"S"//Chil/2*Star	Egypt
16	Gem#/Pl//Cmh70a-955*2/Cno 79 /3/ Bow "S"4 Sids#6	Egypt
17	Sakha 93	Egypt
18	Bhrikuti	CIMMYT
19	Choix/Star/3/Hei/3*Cn079//2*Seri	CIMMYT
20	Sw89.5181/Kauz	CIMMYT
21	84.40023/Weaver//Borl95	CIMMYT
22	Milan/Ducula	CIMMYT
23	Galvez/Weaver/3/Vorona/Cn079//Kauz	CIMMYT
24	Giza 168	Egypt
25	Cmh76a977/Seri//Cmh76.977/Cmh79a. 307/3/A041/Emu//Cn079*2/Hel	Egypt

Table 1:Continued

Ser#	Cross Name	Origin
26	Cmh76a977/Seri//Cmh76.977/Cmh79a. 307/3/A041/Emu//Cn079*2/Hel	Egypt
27	Buc//7C/Ald/5/Maya74/On//1160.147/3/Bb/Gll/4/Chat"S"/6/R16040/54Y R//AG/5*YR	Egypt
28	Vee/Pjn/6/Cmh80a.253/4/M2a/Cml//Ald/3/Ald4/5/Bh1146/H567.71 CIMMYT//Bh1146/3/ Cmh78.390	
29	Weaver/4/Nac/Th.Ac//3*Pvn/3/Mirl0/Buc	CIMMYT
30	Choix/Star/3/He1/3* Cvn079 //2*Seri	CIMMYT
31	Choix/Star/3/He1/3* Cvn079 //2*Seri	CIMMYT
32	Kauz/Pastor	CIMMYT
33	Sw89-5181/Kauz	CIMMYT
34	Gemmiza 9	Egypt
35	Tc750451-Zc-100r/H8ra**2f2/ Inia66**B6 / 2f2 /5/ Kvz /4/ Cc / Inia /3/ Cno // Elgau / Son64 /4/ Sakha 10 /6/ Tepoca // Altar84 // Aos /3/ Tepoca	Egypt
36	Tepoca//Altar84/Aos/3/Tepoca/4/ Sids 7	Egypt
37	Sids7/5/Cmh78.390 / Cmh77a.917 / /Cmh 74.390/3/ Cmh79.215 //MRNG/ALDAN	Egypt
38	Sids 7/3/Ning No.8308/Bali "S"// Star"S"	Egypt
39	Kea"S"/Vee#5"S"/3/Ww33/Vee"S"// Bow	Egypt
40	Weebill 1	CIMMYT
41	B1/6/ Koel /3/Cno.67/2*7c// Col/4/ Dove / Buc /5/K 143(60Vee"S").	Egypt
42	Sakha 61	Egypt
43	Bl1133/3/Cmh79a.955*2 / Cno 79 // Cmh79a.955 / Bow"S" /4/ Giza 164 / Sakha 61	Egypt
44	Sakha 12/5/Kvz//Cno 67/Pj 62/3/Yd"S"/Blo"S"/4/K 134(60)/Vee	Egypt
45	Sakha 12/5/Kvz//Cno 67/Pj 62/3/Yd:S:/Blo"S"/4/K 134(60)/Vee	Egypt
46	Cno"S" / Gll /3/ Son 64 / Klre // Bb /4/ Up 301 /5/ Tl // Fn.Th / 2*Nar 59 /6/ (Bb*Cno**Cno*Tota/Jar) 2f5/ 2f2** (In*Tglr** Cno"S" *Pj 62*Jar"S") 2f1 /7/ Bl1133 /3/ Cmh 79a.955* / Cno 79 // Cmh 79a.955 / Bow"S"	Egypt
47	Baw 898	CIMMYT
48	Kan Chan – Obgd	CIMMYT
49	Sids 4	Egypt
50	Nd/Ug9144//Kal/Bb/3/Yaco"S"/4/Vee#"S"/5/K134(60)/4/ Tob/Bman//Bb/3/Cal	Egypt
51	Giza 167/4/F3-71/Trm//Buc/3/Lira	Egypt
52	Giza 167/5/Kauz*3/4/Fg/Ato//Hui /3/Rok	Egypt
53	Giza 164//Chil/2* Star	Egypt
54	Maya"S"/ Mon"S"// Cmh 72 A.428/ Mrc// Jup /3/ Cmh 74a.582/5/*2 Sakha 8*/6/Bani- Swef 2/5/Mri/Buc//Seri	Egypt
55	Giza 164//Ch1l/2* Star	Egypt
56	Bl1133 /3/ Cmh 79a.955*2/ Cno 79 // Cmh 79a.955 / Bow"S"	Egypt

Genotypes were planted in a field trail experiment in three sowing dates i.e. 1 Oct.,29 Oct. and 26 Nov., in a randomized complete blocks design with three replications in 2003/2004 wheat growing season, at Sakha Agriculture Research Station. Each plot consisted of six rows, raw was 2m long and at spaced 20-cm apart. Thus, the size of each plot was 2.4 m^2. The recommended package of culture practices was followed.

Data were recorded for four agronomic characters: days to heading, days to maturity, plant height and grain yield. Two characters were derived from the above measurements (i) grain filling period, that is days from heading to maturity and (ii) grain filling rate, the grain yield (kg/ fadan) divided by grain filling period.

The means of all entries for earliness component traits, plant height and grain yield were subjected to a multivariate analysis. This technique was found to resolve several phenotypic measurements into fewer more interpretable and more easily visualized dimensions (Johnson and Wichern, 1988). Therefore, hierarchical clustering procedure using Ward's minimum variance method, which minimize within cluster sums of squares across all partitions, was applied. The procedure used a method performing a disjoint cluster analysis on the basis of Euclidean distances as described by Anderberg (1973) and developed by Hair *et al.* (1987). In the application of Ward's method, genetic divergence among wheat genotypes and clustering patterns are presented as dendrograms. The dendrogram is constructed on Euclidean distance basis. All these computations are performed using SPSS computer software (1995).

RESULTS AND DISCUSSION

Simple correlation coefficients between traits (6 by 6) were significant for all values except between days to maturity and plant height as seen in Table 2. The high degree of correlation of grain filling rate and days to heading with other characters was supported by contributions of the studied characters toward divergence where, grain filling rate and days to heading were a primary source of variation with the high values (Table 3).

Table 2: Simple correlation coefficients between earliness component and some agronomic characters.

Characters	DM	PH	GY	GFP	GFR
Days to heading (DH)	0.79**	0.44**	0.77**	-0.83**	0.84**
Days to maturity (DM)		0.12	0.58**	-0.32*	0.53**
Plant height (PH)			0.52**	-0.58**	0.57**
Grain yield (GY)				-0.66**	0.95**
Grain filling period (GFP)					-0.82**
Grain filling rate (GFR)					

*, ** Significant at 0.05 and 0.01, probability levels, respectively.

Each trait contributed to the information used to group these genotypes. However, some characters have greater importance as contributor toward divergence than others. The data in Table 3 revealed that the grain filling rate followed by days to heading were the major contributor toward divergence. However, days to maturity and grain yield were the least contributors. Souza and Sorrells (1991) reported that days to heading was a primary source of variation. Meanwhile, Menshawy (2000) stated that

clustering of F_3 families of bread wheat could be attributed mainly to differences in grain yield and days to heading.

Table 3: Contribution of the studied characters toward divergence of the 56 wheat genotypes.

Characters	Variance	% of contribution
Days to heading	76.09	21.20
Days to maturity	26.17	7.29
Plant height	45.07	12.55
Grain yield	14.88	4.14
Grain filling period	31.48	8.77
Grain filling rate	165.29	46.04
Total	358.98	100.00

Genetic Divergence

The genetic divergence can provide visual idea about variabilities presented in wheat genotypes, in additions, to assuring the continued genetic improvement (Martin et al., 1991). The genetic divergences based on Euclidean distances using some earliness and yield characters among fifty six wheat genotypes are graphically illustrated as dendrogram (tree diagram) in Figure 1.

The estimates of Euclidean distances corresponding to the 1540 possible comparisons, taking two genotypes at a time, showed that about 76% of the values were significant, more than the corresponding Chi-square value at 0.05 level. These results indicated that the genotypes are exhibiting a broad spectrum of variabilities. This conclusion might reflect some sort of dissimilarities between these genotypes for the studied characters. The standardized Euclidean distances were ranged from 1.09 to 370 Euclidean distance. The minimum Euclidean distance was observed between the entries 37 and 39, while, the maximum distance was observed between the entries 15 and 45. In this connection, Martynov *et al.*, (1997) studied genetic divergence among 62 cultivars of Czech and Slovak wheat using coefficient of parentage of each one. Also, Qixin *et al.*, (1998) reported that genetic diversity values between Tibetan wheat and common wheat were lower than that between Tibetan wheat and Split wheat.

Clustering Pattern of Entries

Genetic relationships among genotypes could be summarized using cluster analysis to place entries into phenotypic groups. The clustering pattern of 56 genotypes was determined at three grouping levels, (below 75 Euclidean distances), at six- group level (below 50 Euclidean distance) and thirteen group level (below 25 Euclidean distance)

At three group level

It is evident from the dendrogram that, at 75 Euclidean distances all 56 genotypes were not grouped in one cluster but distributed in three different clusters. The clusters A, B and C were composed of 24, 16 and 16

genotypes, respectively as seen in Figure 1. Cluster A is characterized by early heading and maturity, long grain filling period, low grain filling rate and grain yield. Cluster B and C exhibited almost the same grain yield and plant height but different in earliness components. Cluster C grouped 16 Egyptian genotypes, while cluster A and B grouped Egyptian and exotic genotypes. These results reflected the presence of similarity in genetic background of these Egyptian genotypes. Yau *et al.*, (1989) classified some wheat entries of different origin; CIMMYT, ICARDA, and TURKEY; into two major clusters, A and B, in addition to seven lines formed single cell clusters. Cluster A yielded more than cluster B while lines in cluster B were later in heading and maturity than those in cluster A.

Table 4: Cluster means for the contributed characters toward genetic divergence of the 56 bread wheat genotypes at the three groups, six groups and final groups.

Cluster of Number	Genotype	Days to heading (day)	Days to maturity (day)	Plant height (cm)	Grain* yield (Ard./fad.)	Grain filling period (day)	Grain filling rate (kg/Fad./d)
Three group level							
A	24	76.9	152.0	109.5	21.4	65.0	57.6
B	16	85.5	158.2	110.6	25.0	62.7	68.1
C	16	83.8	155.7	110.9	24.1	61.9	67.8
Six group level							
A1	14	86.8	158.1	110.3	25.1	61.2	69.6
A2	10	91.7	159.5	113.8	27.8	57.9	80.7
B1	16	78.6	151.6	113.2	22.6	63.0	62.1
C1	2	63.0	151.3	93.1	12.7	78.3	31.4
C2	6	68.7	145.5	108.8	18.1	66.8	47.9
C3	8	77.1	156.8	104.9	21.1	69.7	52.4
Final group level							
G1	7	86.0	157.3	105.4	25.7	61.4	72.6
G2	2	95.2	162.6	109.3	22.0	57.3	62.1
G3	5	85.7	157.9	117.5	25.9	62.2	69.8
G4	6	89.5	160.4	115.5	28.3	60.9	78.4
G5	4	94.9	158.2	111.3	27.3	53.3	84.2
G6	7	78.4	151.3	114.8	24.0	62.9	65.8
G7	9	78.8	151.8	111.9	21.6	63.1	59.2
G8	2	63.0	151.3	93.1	12.7	78.3	31.4
G9	3	65.8	146.0	101.7	18.0	70.2	45.7
G10	3	71.7	145.0	116.0	18.2	63.3	50.0
G11	3	83.5	161.1	108.1	21.0	67.6	52.5
G12	5	73.3	154.3	103.0	21.1	70.9	52.3
Entry 15		103.1	160.3	120.0	27.2	47.2	90.3

*Ard. and Fad.=Ardp and Faddan respectivly (one Ardp=150kg and one Faddan=4200m^2)

At six group level.

Figure1 illustrated the dendrogram for clustering pattern of wheat genotypes based on Euclidean distance.

F1

F1

The dendrogram made of the contributed quantitative characters presented six variety of grouping of the 56 wheat entries, at similarity lower than 50 Euclidean distance. The six clusters A1, A2, B1, C1, C2 and C3 were composed of 14, 10, 16, 2, 6 and 8 genotypes, respectively. Cluster B1 was the largest, while cluster C1 was the smallest one. Cluster C3 grouped three Egyptian cultivars e. i., Sakha 61, Sakha 93 and Giza 168 and five Egyptian genotypes, this reflected the presence of similarity in the genetic background of these cultivars at this level. Meanwhile, the cultivars Sids 4 and Gemmeiza 9 were clustered with group C2 and group A2, respectively. Reddy (2001) reported that 52 strains of hexaploid trical including two wheat genotypes were grouped into four clusters to determine genetic divergence. Cluster III was the largest group consisting of 36 genotypes followed by cluster IV with eight, cluster II with six and cluster I with two genotypes.

Table 4 illustrated the mean values of the studied characters in each cluster. The data revealed that cluster A2 contained genotypes that possessed the latest heading and maturity, tallest genotypes, shortest grain filling period, highest filling rate and highest grain yield followed by cluster A1.

Meanwhile, cluster C1 had the earliest heading and maturity, shortest height least grain yield and grain filling rate and long grain filling period. Cluster C1 and B1 exhibited similar yield, days to heading but differed in the other characters. However, cluster C2 had the earlier maturity while other characters were intermediate.

Moreover, clustering was unsatisfactory for fitting subgroups A1, A2, B1, C1, C2 and C3. Thus, dichotomous splitting continued down the main branches of the denderogram until thirteen final groups of genotypes from G1 to G13 were obtained. Clusters G1 and G3 grouped 7 and 5 genotypes respectively, these clusters had almost equal mean values for all studied characters except for plant height as presented in Table 4. Cluster G2 included genotypes which had late heading and maturity, tall plant height, moderate grain yield, grain filling period and rate. Clusters G4 and G5 had highest grain yield, high grain filling rate and short grain filling period. Cluster G6 and G7 had almost similar values for earliness and grain filling period but differed in other characters. Cluster G8 had earliest heading and maturity, shortest plant height, lowest grain yield, and grain filling rate and longest grain filling period. Clusters G9 and G10 had almost equal days to maturity and grain yield but differed in other traits. Clusters G11 and G12 were intermediate in all characters. These clusters had equal grain yield and grain filling rate. Meanwhile, entry 15 formed single cell cluster where this entry had the latest heading, tallest height, shortest grain filling period, highest grain filling rate and high grain yield. All genotypes included in the clusters G2 and G8 to G12 were Egyptian entries only. The other clusters comprised Egyptian and Exotic entries. Clusters G4 and G5 contained genotypes which had the highest grain yield and grain filling rate and were moderate for the other characters. The data in Table 4 was used to select genetically diverse and agronomically superior genotypes from the 56 studied genotypes Cluster 4 had highest mean values for grain yield, grain filling rate and short grain filling

period, while it showed moderate mean values for heading and maturity. Therefore, this cluster was count to be the "best" for selecting diverse and agronomically desirable genotypes. In this study, the genotypes which were exceptionally good in respect to one or more characters and at least comparable with respect to the other characters to the beast check were deemed desirable. The desirable genotypes were also selected from other clusters which were widely separated from clusters G5, G6 and G10, and simultaneously had the desirable genotypes for yield and earliness. As these selected divergent genotypes were often exceptionally superior to all remaining genotypes (tested in this study) for one or more traits and concurrently were not poor for any trait.

Therefore, it is proposed that these genotypes may be involved in a multiple crossing program to recover transgressive segregation with high genetic yield potential. Similar approach was also followed by several workers in the past, such as Johnson et al.(1973) and Sharma et al (1998) in wheat and Cox and Frey (1985) in oat.

On the basis of genetic divergence and at 25 Euclidean distances based on the studied characters; the diversity noticed in the genotypes are expected to gave better results as the exhibited greater diversity and high performances. This study also provided that the opportunity to select diverse parents for better recombinants for various characters and utilization of such diverse genotypes of wheat in breeding seems appropriate in achieving better and quicker gains.

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تحليل التباعد الوراثي بين ٥٦ تركيب وراثي من قمح الخبز

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** قسم بحوث التكثيف المحصولى- معهد بحوث المحاصيل الحقلية ـ مركز البحوث الزراعية

تحليل التباعد الوراثي من الممكن أن يستعمل فى تعريف التراكيب الوراثية التي تفيد فى نمـاذج الدراسات اللاحقة واختيار الآباء فى برنامج التربية. لاختبار هذه التطبيقات فى قمح الخبز، قيست العلاقات بين ٥٦ تركيب وراثي من قمح الخبز مستخدما تحليل الـ Cluster لصفات مكونات التبكير ومحصول الحبوب وطول النبات. زرعت التراكيب الوراثية فى تجارب حقلية مكررة فى ثلاث مواعيد هي ١، ٢٩ أكتوبر، ٢٦ نوفمبر موسم ٢٠٠٣/ ٢٠٠٤ بمحطة البحوث الزراعية بسخا، وقيمت لصفات عدد الأيام حتى طرد السنابل، عدد الأيام حتى النضج، وفترة امتلاء الحبوب ، معدل امتلاء الحبوب ومحصول الحبوب. أوضح التباعد الوراثي ما بين التراكيب الوراثية اعتماد على Euclidean distance نوعاً من عدم التشابه بالنسبة للصفات المدروسة. أظهرت النتائج أن صفتى معدل امتلاء الحبوب وعدد الأيام حتى طرد السنابل كانتا أهم مصدرين للتباين بين التراكيب الوراثية . عند مسافة ٧٥ (Euclidean distance) توزعت الـ ٥٦ تركيب وراثي فى ثلاثة Clusters مختلفة. فى حين انه عند ٥٠ (Euclidean distance) توزعت التراكيب الوراثية فى ستة Clusters مختلفة. اما عند ٢٥ (Euclidean distance) توزعت التراكيب الوراثية فى ١٣ Clusters،بالإضافة الى السلالة رقم ١٥والتى كونت مجموعة فردية. إن طريقة الـ Clustering كانت فعالة فى تحديد الـ Clusters ذات المحصول العالى والمبكرة والتى تشتمل علـى التراكيب الوراثية المتشابهة فى هذه الصفات. وتبعاً لذلك فأن طريقة تحليل الـ Clustering استناداً الى

Euclidean distance قد تكون مفيدة ومؤثرة لمربى النبات فى تحديد التراكيب الوراثية المفضـلة والأكثر تفوقاً داخل الـ Clusters وذلك لإستخدامها فى برامج التربية.