NOTE

SELECTING PARENTAL MATERIALS FOR HYBRIDIZATION BY MEASURING GENETIC DIVERSITY[1]

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ABSTRACT

Genetic diversity (D^2), among 30 winter wheat cultivars originating from the U.S.A., former U.S.S.R. and European countries, was estimated from yield component data collected at two locations in one year. Yield and yield components were the criteria for estimating D^2. The genotypes were grouped into clusters according to their D^2 values. The method of choosing parents for hybridization and the relationship between geographical distribution and genetic diversity are described.

گزینش والدین جهت دورگه گیری بوسیله اندازه گیری تنوع ژنتیکی

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به ترتیب دانشجوی سابق دکترا (اکنون استادیار بخش زراعت و اصلاح نباتات دانشکده کشاورزی دانشگاه شیراز) و استاد بخش آگرونومی، دانشگاه ایالتی اکلاهوما، استیل واتر، اکلاهوما ۷۴۰۷۸-۰۵۰۷، آمریکا.

چکیده

تنوع ژنتیکی (D^2) در ارقام گندم های پائیزه آمریکایی، کشورهای شوروی سابق و اروپایی که در دو ایستگاه مختلف کشت شده بودند، اندازه گیری گردید. عملکرد دانه و اجزاء آن به عنوان معیارهای تخمین D^2 مورد استفاده قرار گرفتند. ژنوتیپ ها بر حسب ارزش D^2 به گروه های مختلف تقسیم بندی گردیدند. روش گزینش والدین در دورگه گیری و ارتباط بین توزیع جغرافیایی و تنوع ژنتیکی توضیح داده شده اند.

INTRODUCTION

The basic importance of genetic diversity in breeding for high yield has long been recognized. Suneson (9) emphasized the importance of genetic diversity as a potential reservoir of alleles to provide protection against plant diseases and insects. Adaptation was mentioned to be partly due to genetic diversity of populations (1). The magnitude of heterosis in wheat has been reported to be dependent on the degree of genetic diversity between parental stocks (8). This may be used as an indicator of the inherent yielding capacity of a cross.

One of the statistical approaches for measuring genetic diversity is Mahalanobis' generalized distance D^2 (1, 5, 8). The type of component characters that should be taken into account for measurement of divergence should have economic importance under crop improvement programs (7). In a few studies, the relative contribution of different yield components to the total divergence was much greater than yield *per se* (5). The genetic divergence, as measured by the D^2 statistic, is reflected to some extent in the combining ability effect. In *Linum usitatissimum*, the crosses of the most divergent cultivars have shown the largest specific combining ability effects for a majority of characters (4). Populations may be grouped into several clusters depending on their distances measured by mean D^2. Cultivars which are grouped together come under one or more of the following categories: 1) related by pedigree, 2) originating in the same or similar ecological regions, and 3) similar in characters which are known to contribute to genetic divergence (8). The objective of this study was to measure genetic diversity among populations of wheat cultivars originating from different ecological areas as a basis for selecting parental materials for hybridization and, to see if there was a relationship between geographical distribution and genetic diversity.

MATERIALS AND METHODS

Thirty cultivars originating from the U.S.A., former U.S.S.R. and European countries (Tables 1 and 2) were grown at Stillwater and Lahoma Oklahoma, U.S.A. in 1979. A randomized complete block design with four replications per location was utilized. An experimental unit consisted of four 3-meter rows; rows were 30 cm apart. Grain yield, fertile tiller number per square unit area, the mean number of kernels per spike and the mean kernel weight were measured. Four entries were eliminated from Stillwater because of late maturity.

Table 1. Geographical origin, mean yield and yield components for entries grown at Lahoma, OK.

Parent No.	Entry	Origin	Tiller (No./ 900 cm^2)	Seeds per spike	Kernel weight (gm/ 1000 seeds)	Yield (gm/ plot)
7	Turkey	Turkey	70	30	30	418.75
9	Triumph 64	USA (OK)	61	24	37	452.50
8	Scout 66	USA (NB)	66	25	36	475.75
4	Bezostaia 1	USSR	47	34	40	473.75
5	Odesskaya 51	USSR	55	31	41	462.60
6	Priboy	USSR	57	30	45	457.50
1	Osage	USA (OK)	63	31	33	488.75
3	Sturdy	USA (TX)	59	34	32	505.00
2	Tam W-101	USA (TX)	73	23	43	665.00
11	Burgas 2	Bulgaria	54	32	38	571.25
12	Sadovo 1	Bulgaria	48	29	44	498.75
31	NR 72-837	Austria	51	38	29	480.00
13	Vona	USA	67	36	28	636.25
14	Newton	USA (KS)	58	33	35	545.00
15	Payne	USA (OK)	72	30	32	600.25
16	Lovrin 6	Romania	50	27	47	492.50
17	F23-71	Romania	44	46	36	437.50
32	Lovrin 6/T-W-101F6	Rom./USA	62	25	47	473.75
26	TX71A562-6	USA (TX)	60	34	33	608.75
27	TAM W-103	USA (TX)	75	30	30	543.75
33	MS TAM 103/ TXR344-6 F1	USA	67	34	34	576.25
34	TXR-Line 344-6	USA (TX)	63	30	32	501.25
35	Dekalb 589	USA	58	24	39	437.50
36	Pioneer HR940	USA	70	25	36	438.75
37	Hart	USA (MO)	65	25	37	453.75
28	NR 31/74	Austria	62	39	34	472.50
29	NR 173/75	Austria	51	34	39	497.50
38	NR 391/76	Austria	49	40	38	501.25
39	Russian	USSR	57	32	39	441.25
40	OK77827	USA (OK)	62	32	28	415.00

Table 2.   Geographical origin, mean yield and yield components for
entries grown at Stillwater, OK.

Parent No.	Entry	Origin	Tiller (No./ 900 cm^2)	Seeds per spike	Kernel weight (gm/ 1000 seeds)	Yield (gm/ plot)
9	Triumph 64	USA (OK)	50	34	38	618.75
8	Scout 66	USA (NB)	62	33	38	683.75
4	Bezostaia 1	USSR	41	43	41	695.00
5	Odesskaya 51	USSR	49	53	41	708.75
6	Priboy	USSR	44	38	44	720.00
1	Osage	USA (OK)	54	42	34	630.00
3	Sturdy	USA (TX)	50	40	32	591.25
2	Tam W-101	USA (TX)	63	32	41	692.50
11	Burgas 2	Bulgaria	37	43	38	656.25
12	Sadovo 1	Bulgaria	40	38	48	645.00
13	Vona	USA	59	43	31	705.00
14	Newton	USA (KS)	55	45	32	672.50
15	Payne	USA (OK)	55	41	30	567.50
16	Lovrin 6	Romania	46	37	51	735.00
32	Lovrin 6/T-W-101F6	Rom./USA	50	35	45	671.25
26	TX71A562-6	USA (TX)	63	44	32	725.00
27	TAM W-103	USA (TX)	59	41	31	636.25
33	MS TAM 103/ TXR344-6 F1	USA	50	42	35	681.25
34	TXR-Line 344-6	USA (TX)	46	40	33	525.00
35	Dekalb 589	USA	49	40	38	638.75
37	Hart	USA (MO)	59	37	37	736.25
28	NR 31/74	Austria	52	46	36	751.25
29	NR 173/75	Austria	37	45	42	721.25
38	NR 391/76	Austria	40	54	40	786.25
39	Russian	USSR	44	41	42	702.50
40	OK77872	USA (OK)	56	41	26	327.50

Analysis Procedures

Analysis of variance was carried out for yield and yield components at each location separately. The application of the D^2 statistic is to measure the degree of divergence for individual characters, or the pooled effect of several characters. Based on genetic diversity, a crossing program between genotypes may be initiated. The approach is based on the assumption that the potentially best crosses should be between parents showing the maximum genetic divergence. Genetic diversity between two genotypes is measured by:

$$D^2 = (U_1 - U_2)'' \Sigma^{-1} (U_1 - U_2)$$

where U_1 is a vector with three elements, each representing the average of one yield component in a cultivar. U_2 is defined similarly for a second cultivar. Σ is a symetric 3×3 genotypic variance, covariance matrix (3) as follows:

$$\Sigma = \begin{pmatrix} \sigma^2_{Gs} & \sigma_{GsGk} & \sigma_{GsGt} \\ & \sigma^2_{Gk} & \sigma_{GkGt} \\ & & \sigma^2_{Gt} \end{pmatrix}$$

where σ^2_{Gs}, σ^2_{Gk} and σ^2_{Gt} are the genotypic variances for the number of seeds per spike, kernel weight and tiller number, respectively. σ_{GsGk}, σ_{GsGt} and σ_{GkGt} are the genotypic covariances between each pair of components. Since the phenotypic variance (σ^2_P) is composed of genotypic (σ^2_G) and environmental (σ^2_E) components, then $\sigma^2_P = \sigma^2_G + \sigma^2_E$ (2). In estimating the varicance, covariance components the expected entry mean square (M. S.) and mean products (M. P.) were partitioned as follows:

E [entry (M. S.)] = error (M. S.) + 4 entry (M. S.)= $\sigma^2_E + 4\sigma^2_G$

E [entry (M. S.)] = error (M. S.) + 4 entry (M. P.)= $\sigma_{GaGb} + 4\sigma^2_{Ga+Gb}$

where σ_{GaGb} is the covariance of two characters a and b and σ^2_{Ga+Gb} is the joint genotypic variance of characters a and b. Genetic diversity was measured between any two cultivars by D^2, as mentioned above. Cultivars were grouped into a number of clusters, D^2 being treated as the square of

generalized distance according to the method described by Tocher, as cited by Rao (6).

RESULTS AND DISCUSSION

The mean grain yield and its components for different locations are shown in Tables 1 and 2. Before measuring D^2, it was necessary to find out if the cultivars differred significantly among themselves with respect to yield components. The analysis of variance corresponding to each character evaluated at two locations (Table 3) for the four treatments showed significant differences among entries at the 0.01 level of probability.

Table 3. Mean squares for tiller mumber, seeds per spike, kernel weight and yield.

Location	TLR	Seeds/spike	Kernel wt	Yield
Lahoma	537.90**	684.37**	698.34**	16879.16**
Stillwater	497.33**	558.73**	842.50**	32453.24**

** Significant at the 0.01 level of probability.

The value for the genotypic variances and covariances are as follows:

	σ^2_{Gs}	σ^2_{Gk}	σ^2_{Gt}	σ_{GsGk}	σ_{GsGt}	σ_{GkGt}
Stillwater	21.19	34.42	51.81	−6.36	−13.24	−27.24
Lahoma	27.15	28.26	58.44	−9.98	−18.70	−17.57

All of the genotypic covariances are negative, indicating that variations of any two components are in the opposite direction.

There are 435 possible distances between all pairs of the 30 cultivars. Distances were arranged in order of magnitude, and cultivars in each experiment were grouped into a number of clusters. There is no formal rule for defining the clusters because a cluster is not a well defined term (6). The criterion we employed was that any two cultivars belonging to the same cluster should show at least on the average, a smaller D^2 than those belonging to two different clusters. On this basis, thirty cultivars at Lahoma could be grouped into nine clusters as follows:

1. Turkey, Triumph 64, Scout 66, Osage, Sturdy, Newton, TX 71A562-6, TXR-Line 344-6, Dekalb 589, Pioneer HR 940, Hart and Ok 77827.

2. Bezostaia 1, Odesskaya 51, Burgas 2, Sodova 1, NR 173-75 and Russian.

3. Priboy and Lovrin 6/T-w-101 F6.

4. Tam W-101.

5. NR 72-837.

6. Lovrin 6.

7. F 23-71 and NR 391-76.

8. Vona, Payne, Tam W-103 and MS Tam 103/TXR 344-6F1.

9. NR 31-74.

Cluster 1 consisted of twelve cultivars, all originating from the U.S.A., except Turkey which might have been involved as parental stock for developing other members of the group. The pattern of cultivars in different clusters shows that cultivars originating from the U.S.A. were all grouped into two clusters (1 and 8). This is not in agreement with some reports (1) that genetic diversity is not related to geographical distribution. On the other hand, the four cultivars that originated from Austria (NR 72-837, NR 31-74, NR173-75 and NR 391-76) were in four different

clusters (2, 5, 7 and 9), and the four cultivars that originated from the U.S.S.R. (Bezostaia 1, Odesskaya 51, Russian and Priboy) were in two different clusters. It may be interpreted that cultivars in one cluster are related to each other by a combination of factors, including geographical distribution and similarity in characters contributing to genetic diversity.

The intra- and inter-cluster mean D^2 values for Lahoma are shown in Table 4. The largest distance was between cluster 4 and 5. The next

Table 4. Intra-and inter-cluster mean D^2 at Lahoma.

	1	2	3	4	5	6	7	8	9
1	2.451	4.304	9.634	11.484	7.474	7.700	12.138	5.491	9.563
2		1.355	6.152	13.054	7.310	2.516	6.182	8.765	8.650
3			1.212	3.582	22.983	3.822	11.193	8.958	8.047
4				0.000	31.179	11.203	20.867	7.539	10.501
5					0.000	15.030	10.294	13.848	15.203
6						0.000	10.728	13.861	13.731
7							1.248	10.765	4.494
8								1.408	3.090
9									0.000

largest D^2 values were between cluster 3 and 5, 4 and 7. Hybrids developed by crossing members of divergent groups should give promising results. In choosing among the genotypes of a cluster, other practical considerations, such as disease resistance, quality and lodging, should be taken into account.

The generalized distances for each pair of cultivars grown at Stillwater were also arranged in order of magnitude and, all 26 cultivars were grouped into nine clusters as follows:

1. Sturdy, Burgas 2, TXR-line 344-6 and Ok 77827.

2. Bezostaia I, Priboy, Sadova 1, Lovrin 6/T-W-101F6, NR 173-75 and Russian.

3. Triumph 64.

4. Scout 66, Tam W-101 and Hart.

5. TX 71A562-6.

6. Lovrin 6.

7. NR 391-76.

8. Vona, Payne, Tam W-103, Osage, Newton, MS Tam 103/TX R344-6F1 and Dekalb 589.

9. Odesskaya 51 and NR 31-74.

Four cultivars made single-genotype clusters. The three cultivars in cluster 4 and seven cultivars in cluster 8 all originated from the U.S.A. This probably results from the pedigree relationship between the members within each cluster. Cluster I had four cultivars originating from the U.S.A. and Bulgaria. The distribution of cultivars in different clusters shows that geographical diversity may be one of the factors grouping cultivars in the same cluster.

Comparison of cluster composition between Lahoma and Stillwater shows that some of the cultivars were grouped together in both locations. The only cultivar which made a single genotype cluster in both locations was Lovrin 6. Cultivars in cluster 8 at Lahoma were also all in cluster 8 at Stillwater.

The intra- and inter-cluster averages D^2 for Stillwater are shown in Table 5. Clusters 1 and 6 had the largest distance followed by clusters 5

and 8. Crosses between members of diverse clusters should produce promising progenies.

Table 5.   Intra-and inter-cluster mean D^2 at Stillwater.

	1	2	3	4	5	6	7	8	9
1	0.000	6.863	4.587	8.445	4.053	28.626	13.688	24.150	12.904
2		1.913	5.992	6.223	7.340	12.971	3.942	8.312	11.342
3			2.165	9.231	7.574	14.602	6.616	18.241	6.210
4				1.417	16.544	23.322	7.192	8.375	6.661
5					2.600	24.978	15.281	26.845	21.856
6						0.000	2.298	12.160	15.545
7							1.007	4.316	6.313
8								0.000	13.910
9									0.000

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