

# Assessing Genetic Diversity of Wheat from Turkey and Great Plains Using Morphological Characters and SSR Markers

Anyamanee Auvuchanon<sup>1</sup>, Stephen Baenziger<sup>1</sup>, Ismail Dweikat<sup>1</sup>, Kent M. Eskridge<sup>2</sup>, Robert Graybosch<sup>1</sup> and Sahin Dere<sup>3</sup> (Deceased)

(1) Agronomy and Horticulture Department, University of Nebraska-Lincoln, Lincoln, NE, (2) Statistics Department, University of Nebraska-Lincoln, Lincoln, NE, (3) Agronomy Department, Faculty of Agriculture, University of Ordu, Ordu, Turkey

## Abstract

'Turkey' wheat is the original hard red winter wheat landrace introduced from Turkey to the Great Plains of North America. Many modern Great Plains wheat cultivars are either derived from Turkey wheat or its related lines. The genetic diversity of wheat cultivars from Turkey and the US Great Plains were studied to investigate how the two gene pools have differentiated over time through breeding. Twenty-two Turkish and twenty-three US Great Plains wheat cultivars were selected for a genetic diversity study using molecular marker (SSR), agronomic, and quality trait data. Field experiments were conducted in three environments in Nebraska. The cultivars and cultivar by environment interactions for all agronomic and quality traits were significant. Most Turkish wheat cultivars were injured by the Nebraska winter and hence, showed lower grain yields. Cluster analysis based on SSR clustered the forty-five wheat cultivars into five groups and the clustering largely followed their country of origin and pedigree. According to this cluster analysis, modern Great Plains wheat cultivars diverged from Turkish wheat cultivars by breeding for adaptation and historic Great Plains wheat cultivars were grouped with the Turkish wheat cultivars. Also, four of the five historic cultivars were clustered in a group with the Turkish wheat cultivars by agronomic traits. The clustering analysis based on wheat quality traits indicated six clusters that often included both US Great Plains and Turkish wheat cultivars. This result may indicate parallel breeding criteria on quality traits in both programs. It is possible to use those Turkish wheat cultivars most closely related to Great Plains wheat cultivars as potential sources of germplasm to add new alleles into the US Great Plains wheat without adding too much exotic genetic diversity.

## Objective

1. To investigate the genetic diversity of some hard red winter wheat cultivars from US Great Plains and from Turkey using SSR markers and morphologic traits
2. To determine agronomic and end-use quality trait variation among cultivars and the cultivar by environment interaction for these traits
3. To compare Turkish wheat cultivars to some historic and modern Great Plains wheat cultivars to see how the two gene pools have diverged over time.

## Materials and Methods

Twenty-two Turkish wheat and twenty-three Great Plains hard red winter wheat cultivars released between 1874 and 2006 were selected for this study. Ninety SSR primer pairs were screened and the NTSYS program version 2.0 was used for UPGMA method (Michener & Sokal 1957) cluster analysis based on Dice similarity coefficient.

Field experiments were conducted in two years at three environments in Nebraska [Lincoln (2006-2007), Mead and North Platte (2007-2008)] using incomplete block design with nine incomplete blocks of five plots each and three replications for Lincoln, North Platte and two replications for Mead.

Nine agronomic traits and four quality traits were analyzed from individual environment using PROC MIXED. Homogeneity of variance was tested using  $F_{max} < 5$ . All homogeneous traits were analyzed in a combined ANOVA.

All agronomic and quality traits were standardized by PROC STANDARD and genetic distances were measured based on Euclidean method using PROC DISTANCE. Cluster analysis was conducted using PROC CLUSTER based on "Average Linkage Cluster Analysis" using SAS 9.1 package procedure (SAS 2002).

## Results and Discussion

Table 1. Analysis of variance for nine agronomic traits and four quality traits from Lincoln 2007, Mead and North Platte 2008

Source of variance	Agronomic traits									Quality traits						
	df	Grain yield (kg/ha)	Number of spikes per m <sup>2</sup>	Grain Volume (kg/ha)	Winter Survival (%)	Flowering (day)	Plant Height (cm)	Kernel number per spike	Kernel weight (g)	Kernel weight per spike (g)	Source of variance	df	Floor Yield (%)	Protein content (%)	Mixing Time (min)	Mixing Tolerance (D-7)
Environment	2	417971510	2969514	7295.11	438.34	8469.49	13693	75.63	4945.83	6.492	Environment	2	2805.56	144.85	0.228	1.795
Block (Env)	69	125421	8692	4.79	33.47	1.23	19.88	14.75	4.57	0.0202	Block (Env)	61	10.026	0.203	0.134	0.351
Cultivar	44	2805282**	71860**	99.60**	1117.47**	16.93**	298.11**	151.82**	52.33**	0.1253**	Cultivar	44	46.96**	1.996**	1.776**	4.219**
C x E	88	472643**	11256**	26.34**	255.89**	2.488**	39.93**	26.25**	15.43**	0.0685**	C x E	88	11.564**	0.602**	0.194**	0.407**
MSE	156	109478	4470	3.77	51.87	0.903	11.58	12.95	4.37	0.0179	MSE	84	7.862	0.14	0.093	0.172
C.V. (%)		8.67	12.72	1.83	7.97	0.63	3.65	11.16	8.89	13.82	C.V. (%)		4.16	3.05	10.92	12.48

\*\* highly significant at 1%; df = degree of freedom

The variances of each trait were homogeneous. The combined analysis of variance showed highly significant differences for cultivars and cultivar x environment interaction for all agronomic and quality traits (Table 1). When multi-environments were tested, the mean squares of G x E interaction were smaller than genotype mean square, hence, the ranking of cultivars was considered to be the similar across environments.

## Results and Discussion (cont.)

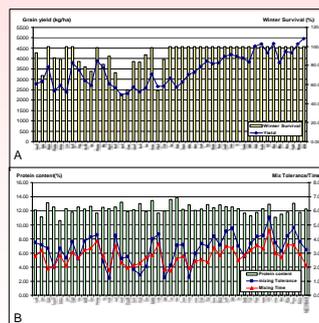


Figure 1. Agronomic and quality of forty-five wheat cultivars (A) Grain yield and winter survival (B) Protein content (%), mixing tolerance (0-7), mixing time (min)

Fifty-four SSR primers (60%) produced polymorphic alleles with PIC average 0.503 (0.126-0.96). Dice similarity coefficient were between 0.348 and 0.849. UPGMA method based on SSR clustered the forty-five wheat cultivars into five groups explained by their pedigrees and country of origin. Clustering analysis based on agronomic and quality traits clustered all wheat cultivars into four and six groups, respectively (Figure 2).

Clustering analysis based on SSR markers and agronomic traits clustered the historic US Great Plain wheat cultivars (Turkey, Cheyenne, and Kharkof) with a group of Turkish wheat cultivars and modern US Great Plains wheat cultivars diverged from historic Great Plains wheat and Turkish wheat cultivars by breeding for adaptation. Quality trait clustering often included both US Great Plains and Turkish wheat cultivars in the groups. However, two Turkish wheat cultivars (Dogu-88 and Lancer) were clustered in Great Plains wheat group by all clustering methods and may be useful parents.

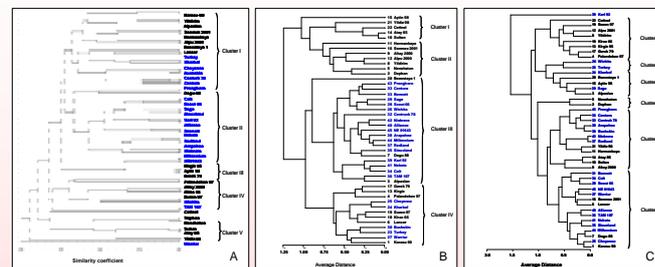


Figure 2. Dendrogram of 45 wheat cultivars based on SSR markers (A), nine agronomic traits (B), and flour quality traits (C) (Black = Turkish wheats; Blue = Great Plains wheats)

## Conclusion

Most Great Plains and Turkish wheat cultivars were clustered into groups that can be explained by their country of origin and line parentage by SSR markers.

Cluster analysis from SSR markers and agronomic traits revealed that modern Great Plains wheat cultivars diverged from most Turkish wheat cultivars through breeding and adaptation. However, a few Turkish wheat cultivars were clustered into Great Plains groups due to germplasm exchange, origin, and possibly breeding history.

Breeding for wheat quality traits had similar trends in both Turkish and Great Plains breeding programs indicating similar selection criteria.

## Acknowledgement

This study was conducted under small grain breeding group, University of Nebraska-Lincoln. We are grateful to Dr. Sahin Dere who provided Turkish wheat seed for this study. Special thanks to Mr. Greg Dorn, Mr. Mitch Montgomery, and Mr. Richard Little for their assistances in the field and greenhouse. Thanks to the Thai Government for providing funding to the senior author for her education.