Using DArT Markers to Monitor Genetic Diversity throughout Selection in Structured Wheat Populations

Ibrahim El-basyoni[1], Stephen Baenziger[1], Ismail Dweikat[1], Dong Wang[2], Kent Eskridge[2] and Mohamed Saadalla[3].

(1) University of Nebraska-Lincoln, Agronomy and Horticulture Department, Lincoln, NE.

(2) University of Nebraska-Lincoln Statistics Department, Lincoln, NE.

(3) Damanhour University, Crop Science Department, Damanhour, Egypt.

INTRODUCTION

To incorporate and maintain diversity in Nebraska's wheat breeding program, annually we make from 800 to 1000 crosses. In our program, multi-location trails begin in the $F_{3:6}$ generations and evaluated using augmented designs. Furthermore, the earlier generations are grown mainly in eastern Nebraska that may reduce variation necessary for adaptation in western Nebraska. The $F_{3:6}$ nurseries are the preliminary yield trial and the gateway to all advanced breeding trails. Thus having genetic diversity in the $F_{3:6}$ nurseries is critical for selection in later generations (F_7 or later; Baenziger et al. 2011). In this study we used two independent $F_{3:6}$ nurseries (2010 and 2011), but we are presenting data from 2010 nursery only. However the results and conclusion were drawn using both 2010 and 2011 nurseries.

THE MAIN OBJECTIVES

1- Explore the molecular genetic diversity of two $F_{3:6}$ nurseries in which we used to base our selection process.

2- Study the effect of selection on the genetic diversity through out different stages of the selection process to advance elite lines.

ABSTRACT

Assessing the genetic relationship among wheat (*Triticum aestivum L.)* lines in the middle generations of a breeding program has important consequences on conserving the genetic variability for selection in later generations. The objectives of this study were to i) determine the breadth of the genetic base of two $F_{3:6}$ nurseries that we used in our selection process; and ii) to monitor the effect of selection on genetic diversity. The $F_{3:6}$ nurseries were grouped into three main clusters, using DArT marker data. Two approaches were employed to investigate the magnitude of the difference among clusters: first, using statistical tests such as nonparametric multivariate analysis of variance (NPMANOVA) and analysis of similarity (ANSIM); second, comparing the known genetic diversity between the check cultivars with that in the experimental lines. Overall, the results suggested that, in both years, the difference among clusters was significant, and the genetic diversity in the $F_{3:6}$ nurseries exceeded that between the check cultivars. The selection results showed that much of the genetic diversity that we found in the $F_{3:6}$ nurseries was maintained through out the selection process.

MATERIALS AND METHODS

Plant Materials:

Two $F_{3:6}$ nurseries were used (2010, 2011). The first nursery contained 276 lines and two local checks genotyped using 1925 polymorphic DArT markers, while the second nursery contained 278 lines plus the same local checks and genotyped using 2236 polymorphic DArT markers.

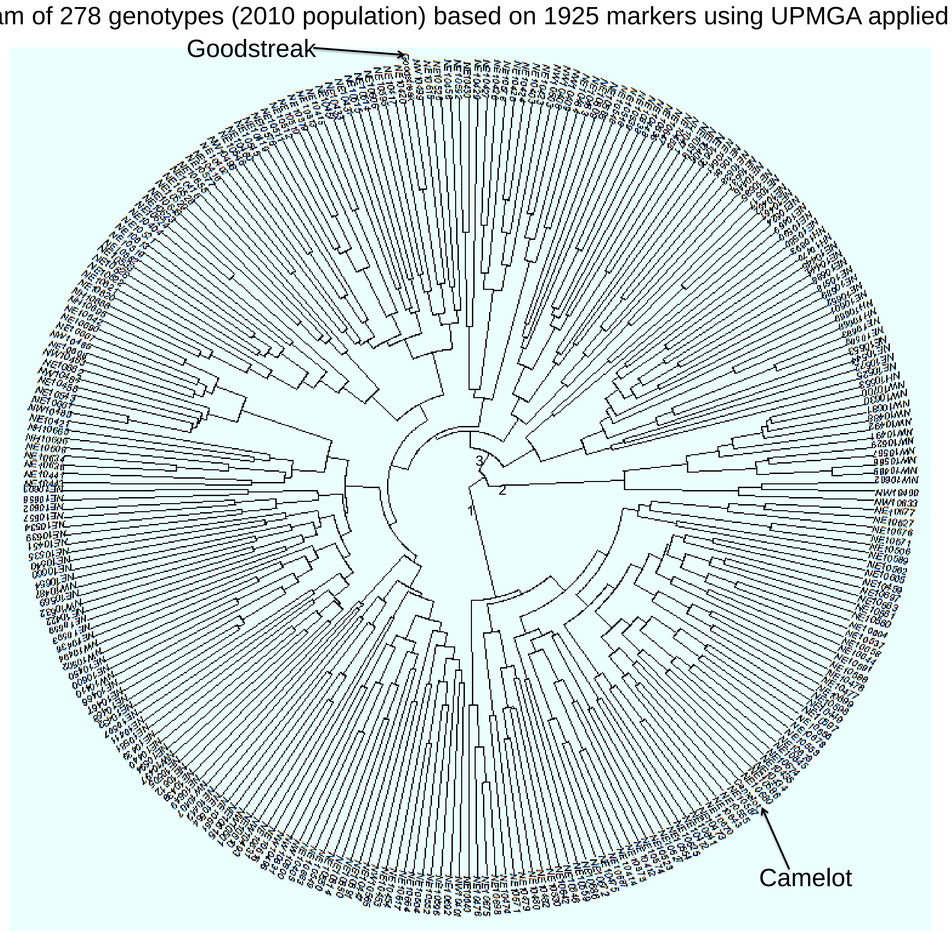
Statistical Analysis:

Jaccard`s similarity coefficients (Jaccard 1908) and the pairwise identity-by-state (IBS) (Knag et al. 2008) were estimated using R/EMMA and R/prabclus. The similarity matrixes then subjected to two different clustering algorithms, UPGMA and neighbor joining (NJ). Multidimensional scaling (MDS) was used as an alternative to hierarchical clustering in that the distance matrix was used to obtain the coordinates. These coordinates were then used to create scatter plots. Nonparametric multivariate analysis of variance (NPMANOVA) and analysis of similarity (ANSIM) were used to compare clusters (Anderson 2001).

Finally, since we used the same check cultivars (Camelot and Goodstreak) in 2010 and 2011, and since the molecular markers, pedigree and phenotypic information indicated that the check cultivars were quite diverse (Baenziger et al. 2004; 2009), these check cultivars used as reference points for the level of the genetic diversity in the nurseries.

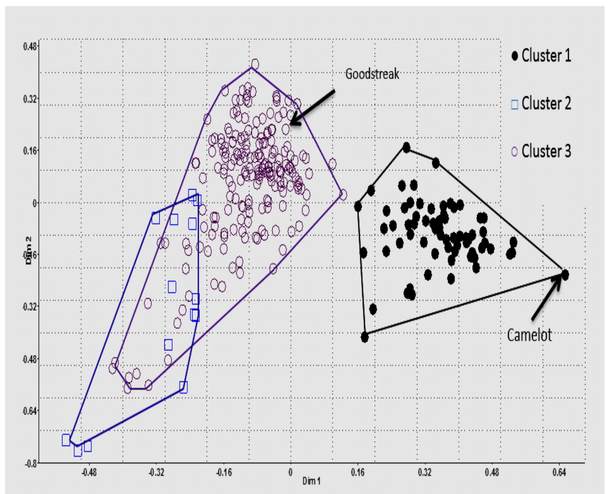
RESULTS

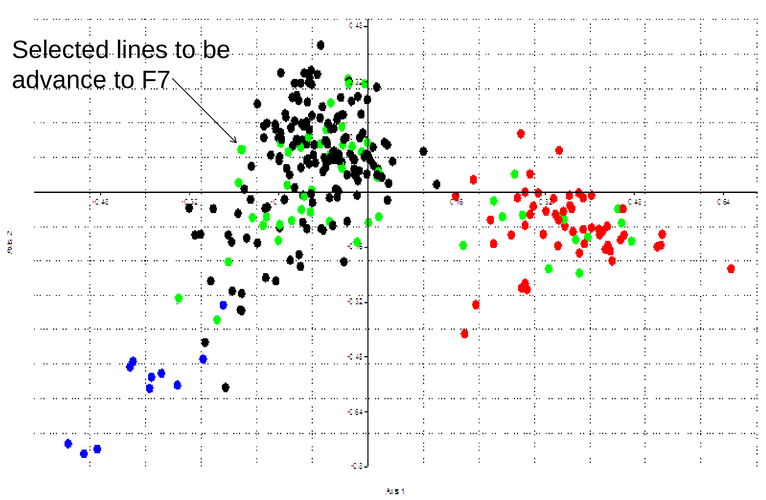
Fig1:Diagram of 278 genotypes (2010 population) based on 1925 markers using UPMGA applied on IBS matrix.



In the 2010 nursery, the 278 lines clustered into three main clusters (Fig1). The check cultivars were located in two different clusters; cluster1 and 3. 158 lines (57%) of the experimental materials had genetic diversity exceeds that between the check cultivars. As for 2011 nursery (data not shown), the 280 lines were clustered into three main clusters. 215 lines (77%) of the experimental materials had genetic diversity exceeds that between the check cultivars.

Fig2: Multidimensional scaling plot constructed using the dissimilarity matrix for 2010 nursery.





Monitoring the effect of selection on the genetic diversity for the 2010 nursery indicated that the selected lines are randomly distributed through the $F_{3:6}$ gene pool and at least two lines from each cluster were advanced to the F_7 nursery (Fig2) and so on for F_8. In 2011 the three main clusters, in F_6, were represented in F_7 with more than two lines. However, as the lines being advanced from F_7 to F_8 no lines were selected from the third cluster.

CONCLUSIONS

In both $F_{3:6}$ nurseries (2010 and 2011), the genetic diversity exceeded that between the check cultivars. The breeder was able to maintain much of the genetic diversity throughout the selection process. However, as the selection intensity increases, as is the case in F_7 and F_8 generation, the probability of losing genetic diversity increases. Thus we recommend applying molecular marker to monitor genetic diversity especially in the late generations; i.e. F_7 and F_8.

REFERENCES

Baenziger, P. S., I. Salah, R. S. Little, D.K. Santra, T.Regassa and M.Wang.2011. Structuring an Efficient Organic Wheat Breeding Program. Sustainability 3(8), 1190-1205; doi:10.3390/su3081190.

Baenziger, P.S., B. Beecher, R.A. Graybosch, A.M.H. Ibrahim, D.D. Baltensperger, L.A. Nelson, Y. Jin, S.N. Wegulo, J.E. Watkins, J.H. Hatchett, M.-S. Chen, and G. Bai. 2009. Registration of 'NE01643' wheat. J. Plant Registrations 2:36-42.

Baenziger, P.S., B. Beecher, R.A. Graybosch, D.D. Baltensperger, L.A. Nelson, J.M. Krall, D.V. McVey, J.E. Watkins, J.H. Hatchett, and M.-S. Chen. 2004. Registration of 'Goodstreak' wheat. Crop Sci. 44:1473-1474.

Jaccard, P. 1908. Nouvelles recherches sur la distribution florale. Bull. Soc. Vaud. Sci. Nat. 44: 223-270.

Kang, H.M., N.A. Zaitlen, C.M. Wade, A .Kirby, D .Heckerman, M.J. Daly, and E.Eskin. 2008. Efficient control of population structure in model organism association mapping. Genetics 178, 1709-23.

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