
Plant Breeding Decisions Based on Different Amounts of Data: Judicious Use of Replication

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Abstract

In order to allocate fixed resources in a plant breeding program to maximize efficiency, a balance must be achieved between the accuracy of estimation of a trait and the number of estimations conducted. Typically, greater accuracy of estimation is achieved through replicated measurements of a trait or a more refined analysis. However, these options come at the cost of reducing the number of different lines that can be evaluated. Decisions based on different amounts of yield data (number of replicates, locations) were compared. Using three years of data, the comparison of one replicate at two locations to two replicates and two locations was found to retain about 80% of the decisions in common. Under this scenario, twice as many entries can be evaluated using the same plot resources while risking 20% more wrong decisions. A stronger selection intensity that would follow with a larger number of entries may ameliorate some of the 20% questionable decisions. This study of yield estimations in the U of S durum breeding program is used to modify the structure of the program to maximize the likelihood of identifying a superior cultivar.

Introduction

For plant breeding programs to be effective and competitive, resources must be properly allocated to provide the most value per plant breeding dollar spent. A balance must be struck for each trait under consideration between accuracy of estimation, number of estimations to be made, and the value of the lines being considered. A general rule of thumb might be that minimal resources are applied to many lines of unproven potential. As potential is demonstrated, additional testing is used to elucidate it.

This study used data collected from the U of S durum breeding program to look for opportunities to adjust the structure of the program with respect to the measurement of yield. A structural problem within this program was recognized wherein not enough testing of lines at the preliminary yield testing level was occurring. At the same time, additional resources (land, labour, money) to conduct testing of more lines using the current approach are not available. To arrive at a resolution for this problem, the following questions were considered: 1) what is the best way to handle spatial variability that exists between and within testing locations and 2) how well must I measure a trait in order to make appropriate decisions?

Materials and Methods

Ten yield tests each consisting of 25 entries replicated twice and grown at two locations (Saskatoon and Scott, SK) in each of three years were analyzed. Nearest neighbours analysis (NNA)

(Stroup et al. 1994) was used to adjust replicated data at each location. Moving means analysis (MMA) (Townley-Smith and Hurd 1973) was used to adjust the data of the first replicate of each experiment at each location. Both NNA and MMA are methods used to adjust data based on spatial variability in the test area. Analyses of variance were conducted on unadjusted and NNA adjusted yield data using all data or on unadjusted and MMA adjusted data from the first replicates only. Decision outcomes were compared using numeric differences of the entries from Plenty durum in 1997 or AC Avonlea in 1998 and 1999. Comparisons were between unadjusted and adjusted data sets and between using two location two replicate data sets versus two location single replicate data sets. As each test consisted of three check cultivars and 22 entries, a total of 660 (22 entries * 10 tests * 3 years) decisions were considered. All analyses were conducted using Agrobases 98 software.

Results and Discussion

Analyses of Variance

The yield tests used in this study represent the first time that these breeding lines were yield tested. Even so, unadjusted and adjusted yield data typically did not result in a significant F-ratio for entry indicating that variability for yield was not great and could be ascribed to the low level of replication. This is a typical result in plant breeding trials. However, additional replication is not possible as seed is limiting. Location almost always showed significant F-ratios and indicated that the two locations were different from each other. This implies that sampling these different locations was important. Genotype X environment (GxE) interaction effects were not shown to be significant when unadjusted yield data was used but were always significant when nearest neighbours analysis was used to adjust the data. GxE cannot be evaluated when single replicate data is used. Both methods of data adjustment (NNA, MMA) resulted in smaller least significant differences (LSD) between entry means in 1997 and 1998. In 1999, the average LSD among tests was the same for both unadjusted and NNA adjusted data. MMA adjusted data resulted in an average LSD and was slightly larger than that obtained from the unadjusted data.

| | 1997 | | 1998 | | 1999 | |
|---------------------------------|------|------|------|------|------|------|
| | Mean | Stds | Mean | Stds | Mean | Stds |
| Discards (%) | | | | | | |
| 2R/2L | 55 | 24 | 29 | 16 | 70 | 27 |
| 2R Kernen | 47 | 25 | 35 | 23 | 62 | 30 |
| 2R Scott | 67 | 23 | 43 | 31 | 82 | 17 |
| 1R/2L | 49 | 34 | 41 | 24 | 76 | 26 |
| | | | | | | |
| Decision Differences (%) | | | | | | |
| 2R/2L vs 1R/2L | 25 | 9 | 29 | 17 | 17 | 15 |
| 2R Kernen vs 1R/2L | 25 | 12 | 34 | 14 | 24 | 15 |
| 2R Scott vs 1R/2L | 35 | 11 | 37 | 23 | 23 | 23 |
| 2R Kernen vs 2R Scott | 37 | 14 | 49 | 21 | 32 | 20 |

Discard rates and decision differences

In table 1, the discard rate and standard deviation (lines discarded because they were numerically lower than Plenty or AC Avonlea) are shown for each year of the study. Each location that the test was grown is shown as is the combined analysis using the appropriate data adjustment method. Discard rates for the 2 replicate/2 location data sets were similar to the single replicate/2 location data sets in 1997 and 1999. In 1998, the discard rate was higher when the single replicate/two location data set was used.

The percent decision differences shown in Table 1 are derived from adjusted data. In general, the fewest decision differences occurred when entries were evaluated using both locations 2R/2L/ versus 1R/2L. The most decision differences occurred when decisions based on Kernen data were compared with those of Scott. These percent decision differences were significantly higher for all years than those occurring when the 2R/2L versus 1R/2L option was considered. This outcome is expected given the significant GxE interactions that were detected from the analysis of variance.

Table 2. Decision Outcomes

| | |
|-------------------------------------|------------|
| Total possible decisions | 660 |
| Total similar decisions | 505 |
| Total dissimilar decisions | 155 |
| Mistakes based on 1R/2L vs 2R/2L | 118 |
| Decisions within 20 g of check | 37 |
| Proportion correct decisions | 82% |

The decisions for each entry were compared using the various data adjustments and amount of replication used per location. When comparing decisions based on different amounts of data, it is assumed that the values obtained when all data are used will provide the best estimation of yield for an entry. Of the 660 possible decisions (Table 2), 505 were the same when using either one replicate or two replicates and the appropriate spatial variability adjustment method. Of the 155 decisions that differed when the two approaches were compared, 118 differences were attributed to reduced replication. Thirty-seven differences were associated with entries with numeric differences from the check that were less than 20 g using the single replicate data set but were apparently higher yielding according to the complete data set. These would not have been discarded normally and were considered as correct decisions. Therefore, over the three years of the study, the proportion of similar decisions obtained using reduced replication was 82% of when both replicates were used.

The value in being able to retain 82% of similar decisions with ½ the number of replications is that twice the number of yield test entries can be tested without requiring additional plot resources.

References

- Stroup et al. 1994. *Crop Sci* 34:62-66.
Townley-Smith and Hurd. 1973. *Can. J. Plant Sci.* 53:447-450