Sampling Sorghum Plots for Kernel Protein

W. M. Ross, R. Ritter, and J. W. Maranville

ABSTRACT

When yields of sorghum [Sorghum bicolor (L.) Moench] plots are determined from unthreshed head weights, as is common in large breeding programs, grain quality analyses must be based on head sampling. Protein contents of kernel samples composited from mid-panicle branches of five to seven heads per plot were compared with the protein in samples from threshed whole plots in two grain hybrid experiments of 100 and 120 entries each and in one experiment of 20 parental lines to evaluate the accuracy of head sampling.

Protein differences between sampling methods were low (0.5, 0.1, and 0.4%), but statistically significant within the three experiments. Simple correlation coefficients between sampling methods were highly significant (0.65, 0.70, and 0.83) for the three experiments.

The method × entry interaction was significant for protein only in the first hybrid experiment, probably due to sampling problems arising from selfed heads of certain female parents. In all cases, the entries × methods mean squares were relatively low, which suggested that analyses of five to seven head samples using near-infrared reflectance would be satisfactory for screening homogeneous lines and hybrids for grain protein.

Additional index words: Sorghum bicolor (L.) Moench, Near-infrared reflectance, Grain quality, Plant breeding.

Although sorghum [Sorghum bicolor (L.) Moench] grain is one of the world's main carbohydrate sources, its kernel protein also is important in human and animal nutrition. The near-infrared analyzer now enables rapid estimation of protein content in grain (1, 3) so that data can be collected on many lines and hybrids in early stages of breeding and testing rather than only on limited advanced materials.

A subsample of kernels from a threshed whole plot is probably the best basis for chemical analyses, but in practical breeding programs not all experimental line and hybrid materials are threshed even though kernel protein data may still be of interest. Yields, if taken, are often based on head weights by use of a threshing percentage or are calculated by use of a regression analysis. When individual heads are harvested, kernels must be sampled from the plots so that a subsample still reflects the true composition of the genotype.

No sorghum data are known that involve a critical comparison of kernel protein percentages from a few heads and from whole plots. Two experiments (2, 4) suggested five and 10-head samples, respectively, but had no experimental basis for the numbers. Both experiments indicated that seed samples from the middle branches of the head were most representative of the whole head for protein analyses.

MATERIALS AND METHODS

Sorghum was planted on 26 May 1977 at the University of Nebraska Field Laboratory, Mead, on a Sharpsburg silty clay loam soil (Typic Argiudoll) to which 80 kg/ha of N as NH₄NO₃ had been applied. Experiment 1 consisted of 100 F₁ hybrids, Experiment 2 of 120 F₁ hybrids, and Experiment 3 of the 20 parental lines of the hybrids in Experiment 1.

Four replications of...
single-row plots, 7.6 m long with rows 0.76 m apart, were used in each experiment.

In the fall of 1977, 4.5 m of rows with good stands were marked for harvest. Shortly after the first killing frost, samples of panicle branches were pinched from the midsections of five to seven main heads of the approximately 30 total plants per row and composited. The seed branches were then dried in a Udy mill, tempered for moisture, and analyzed for crude protein with a Technicon® Infra-Alyzer Model 2.5A that had been calibrated for grain sorghum. The correlation between Kjeldahl- and Technicon-determined protein for these 25 samples was 0.98.

The data were analyzed as a split-plot design with entries as main plots and methods as subplots. Individual analyses also were made of each method in each experiment to verify the assumed equality of standard errors in the combined analyses of variance. Simple correlations were made between the two methods in each experiment.

RESULTS AND DISCUSSION

In each experiment the ranges, means, and standard errors (S.E.) for kernel protein from each sampling method were similar (Table 1). The means for methods, however, differed significantly in every experiment, although the magnitude of the difference was sometimes as low as 0.1%. These small, but statistically significant differences, were the consequence of many measurements for each method (400, 480, and 80, respectively) and the low S.E.'s associated with the means.

Entries were significantly different for grain protein in each of the three analyses (Table 2) as expected. In Experiment 1 the mean square value for entries was lower than for methods which was unexpected. Ample variability among entries existed for protein in Experiment 1, but sampling problems may have influenced the results with respect to methods. Several female parents of the hybrids in Experiment 1 were experimental lines, and two male steriles apparently shed pollen at the time the crossed seed was produced. Therefore some selfed heads were produced. Other females may have had self-fertility problems to a lesser degree which were undetected. Inclusion of one or more selfed heads in a composite of only five to seven hybrid heads, as in Method 2, could influence the chemical analyses. Method 1 samples would not be influenced as much. The females in Experiment 2 were common inbred lines with excellent male sterility and the lines in Experiment 3 were inbreds where the fertile counterparts or B-lines were used rather than male-sterile A lines. Methods in the latter two experiments had much lower mean square values than in Experiment 1 (Table 2).

Entries X method interactions are of primary importance in experiments like this since selection differentials are applied to a group of genotypes and the best-fraction is saved for further study. Relative, rather than absolute, performance is the main criterion. The interactions were nonsignificant in Experiment 2 and 3 but significant in Experiment 1. The significant interaction might be related to the occurrence of selfed plants in this experiment. The entry X method interaction mean square values in all experiments were relatively low.

Another way to compare sampling methods is by simple correlation. All were significant at the 0.01 probability level and had values of 0.65, 0.70, and 0.83 for the three respective experiments. Ideally these correlations should be higher, but they are sufficient to indicate that Method 2 has plant breeding values, particularly where moderate selection differentials are applied to a large number of genotypes.

The genotypes in the above experiments were hybrids or lines and were quite homogeneous. If genotypes are heterogeneous, as in segregating rows or as in families from populations, then more than five to seven heads will probably need to be sampled. In all cases care should be taken to represent all heads equally in the sample.

REFERENCES