Sample sizes to estimate mean values for tassel traits in maize genotypes

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ABSTRACT. Tassel traits are important in maize breeding programs aiming to reduce the size and number of branches and maintain satisfactory pollen production in order to increase grain yield. The objectives of this study were to determine the sample size (number of tassels) required to estimate the mean values for tassel traits in maize genotypes and to verify the variability of sample size among genotypes. Twenty maize genotypes were evaluated in an experiment carried out in a randomized block design with three replicates. Twenty tassels were randomly collected in each plot, for a total of 1200 tassels. In each tassel, the following traits were measured: peduncle dry matter, branching space dry matter, central spike dry matter, tassel dry matter, peduncle length, branching space length, central spike length, tassel length, tassel dry matter to tassel length ratio, number of primary branches, number of secondary branches, and tassel branch number. Measures of central tendency and variability were calculated, analysis of variance and mean comparison tests were performed, normality was

verified, and the sample size was determined. In order to estimate the means with the same precision, the sample size for weight traits was greater than that for length traits. For tassel traits, 11, 20, and 43 tassels are sufficient to estimate the mean with a precision of 40, 30, and 20%, respectively, of the estimated mean at a 95% confidence level. These data show that there is sample size variability among maize genotypes.

Key words: *Zea mays* L.; Sampling; Experimental precision; Calculating study sample size