



## Sample size to estimate the standard deviation of the hundred-grain mass in soybean cultivars

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## Abstract

The hundred-grain mass (HGM) is an important genetic descriptor and productive component in soybean cultivars, which can vary between genotypes and within the genotype as a result of environmental factors. The objective was to determine the sample size (n) to estimate the standard deviation (SD) of the HGM in precision levels. An experiment was conducted at the Federal University of Pampa, Itaqui, RS, with eight soybean cultivars and three replications. At harvest, the HGM of 2400 plants (300 per cultivar) was determined. Next, 294 sample sizes (n = 7, 8, 9, ..., 300 plants) were simulated. In each n, 10000 samples were obtained with replacement and, in each sample, the SD for HGM was estimated. The 95% confidence interval (CI95%) was calculated by the difference between the 97.5 and 2.5 percentiles and, based on the mean values of SD and  $CI_{95\%}$ , the CI<sub>95%</sub>/SD×100 ratio was calculated. Variation limits of 30% (highest precision), 40%, 50% and 60% (lower precision) were established. The smallest simulated value that allowed obtaining the ratio within the established limits was considered as n. To estimate the SD of HGM with a variation of 30%, the *n* ranged from 92 to 146 plants, with an average among cultivars of 111 plants. For 40%, the *n* ranged from 53 to 77 plants, with an average of 63 plants. For 50%, the *n* ranged from 34 to 51 plants, with an average of 41 plants, and for 60%, the *n* ranged from 25 to 35 plants, with an average of 28 plants.

Keywords: Glycine max; resampling; experimental precision; simulation.

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