

Purpose:

- Design an experiment that will provide data for determining narrow sense heritability.
- Calculate narrow sense heritability from a MET designed to provide clean estimates of additive genetic variability.

Keywords:

Phenotypic and Genotypic Values, Genetic Variance Components, Genetic Covariance Heritability, additive genetic variance, heritability, entry mean basis

References:

- Captivate: Genetic Covariance and Heritability
- Captivate: Genetic Variance Components
- Bernardo-Sections 4.5, 6.5, 6.6, 6.9, 6.10, 7.8

ALA

Imagine that you are responsible for developing popcorn hybrids. Recently, a new landrace of open pollinated popcorn has been discovered in the highlands of Guatemala. For a fee the Guatemalan government will provide a 1 Kg bag that can be used for evaluation, but not breeding. You would like to quickly determine if this landrace has useful additive genetic variability for your hybrid development program. If it does, then you will negotiate for use of the landrace in breeding.

1. In order to assess the additive genetic variability, describe the genetic materials that you can quickly develop using one of your inbreds as a tester. Assume that you need enough seed to evaluate 60 replicates of each entry; six replicates for each of 10 farm cooperators. [Below is a paragraph describing how I would design the materials. If you can think of a better way to obtain clean estimates of heritability in the narrow sense, let me know].

For this test you decide to plant a sample of 500 kernels and cross those that ‘nick’ (flower at the same time as the tester) with the tester. While it would be easiest to simply detassel the popcorn plants, the need for extensive testing forces you to carry pollen from individual landrace plants to several plants of the tester. Let’s say that you obtain enough seed for the field trials from 103 of the plants that nicked with the tester. You also have two check hybrids.

The data from the field trials can be found in “Genetic Covariance and Heritability ds7.csv”. Samples 104 and 105 represent your current two best hybrids. The remaining sample ids refer to test cross hybrids from individual plants crossed to your tester.

1. Evaluate these data (EDA, AOV etc) and generate a brief report on the data quality.
2. For data that are of high quality, estimate heritability on a plot basis and on an entry mean basis.
3. Which of these estimates provide broad sense or narrow sense estimates of heritability?
4. If you can obtain an estimate of additive genetic variance, place confidence intervals on your estimate. What does this CI tell you about your estimate of heritability?