QUANTITATIVE   GENETICS

<u>Title</u> Evaluating new potential breeding germplasm

Purpose: How to evaluate new germplasm using heritability estimates

<u>Goals</u>**:**

1. Design crosses to provide estimates of heritability for a new source of genetic variability.

2. Demonstrate ability to calculate and interpret narrow sense heritability from a sample of a testcross population

<u>ALA:</u> Evaluating new potential breeding germplasm by estimating heritability from a sample of a testcross population

Imagine that you are responsible for developing popcorn hybrids. Lately, you have noticed that the yields of new hybrids are about 110 bu/ac (6.9 ton/ha), but do not seem to be increasing as fast as they did for the previous breeder and the company management is beginning to notice. You have estimated the testcross genotypic variance of the current breeding population to be about 9.

A new landrace of open pollinated popcorn has been discovered in the highlands of Guatemala. For a fee, the Department of Interior for Guatemala 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 want to negotiate access to the OP population.

For your evaluation, you decide to plant a sample of 500 kernels and cross those that flower at the same time as one of your elite lines with the elite line used as a tester. You would like to evaluate the hybrids at six sites within each of ten regions. Let's say that you obtain enough seed for the field trials from 103 of the plants that flowered at the same time as the tester. You also have two check hybrids.

The adjusted grain yield data from the field trials can be found in ALA 7.1 ds.csv. Sample id's 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.   How did you obtain enough testcrossed popcorn seed representing each sampled plant for 60 field plots each?

2.   Evaluate the yield data using EDA and generate a brief report on the data quality.
3.   For data that are of high quality, estimate heritability on an entry mean basis.
4.   Does this estimate provide broad sense or narrow sense heritability? Justify your answer.
5.   Place confidence intervals (CI) on the predicted values of the testcross hybrids.
6.   Decide whether you want to negotiate for access to this new source of genetic variability. Justify your decision.