QUANTITATIVE GENETICS

Title: Estimating heritability from a sample of a testcross population

Purpose:

Reinforce understanding to estimate heritability from a sample of a testcross population

Goal:

Demonstrate ability to estimate, genotypic, non-genetic, additive, variances and heritability.

ALA: How to estimate heritability of a testcross population.

We have a hybrid development project. From the project, we have identified six elite lines, referred to as P1, P2, P3, P4, P5 and P6. From past trials conducted across 100 environments (year x location combinations), we know that the average phenotype for P1xT = 250, P2xT= 260, P3xT=255, P4xT=250, P5xT=220 and P6xT=235. We make three breeding crosses P1xP2, P3xP4 and P5xP6, and derive 100 doubled haploid (DH) lines from each family. These DH lines are evaluated in hybrid combination with a tester. We refer to each set of DH lines as families F1, F2, and F3. The results of the phenotypic evaluations are in "QG_Mod7_ALA 7.2_ds.csv".

1.   What are the relationships among DH's within a family?

2.   Is it possible to determine the additive, dominance, and epistatic sources of phenotypic variability from these data?

3.   Conduct exploratory data analyses on the Phenotype.

4.   In the ANOVA evaluate the contributions of replicates, families, lines, and residual variability to the total phenotypic variability. Remember to provide a linear model with definitions for all parameters and variables.

5.   What is the estimated narrow sense heritability on a testcrossed entry mean basis for each family?

6.   What is the estimated ratio of genotypic variance to phenotypic variance combined across families?