

Purposes:

Students should be challenged to move beyond simple calculations with equations. At this point in their preparation, they need to use reasoning to frame the question and subsequently apply appropriate equations. They should also become comfortable with developing a systematic evaluation of data sets from one-to-many families and from one-to-many environments to obtain estimates of variance components that will be used to estimate heritabilities on entry mean bases. Both MoM and REML methods should be used to obtain the estimates of variance components.

Goal:

Demonstrate ability to estimate heritability using field data of testcrossed hybrids derived from DH's.

ALA: Estimates of heritability on a progeny mean basis and a family mean basis

Most breeding programs have family structures created with every new set of crosses and subsequent development of replicable progeny. By assigning families to incomplete blocks, blocks could be confounded with families. On the other hand, mixing progeny from different families could create unfair competition between adjacent plots. Use data file QG_Mod9_ALA9.2_ds.csv

- a. Describe a field plot design that will avoid confounding block and family effects without creating competition between hybrids derived from different families.
- b. What are the relationships among and within DH families before they are crossed to a common tester?
- c. Conduct exploratory data analyses on the phenotypic data. Remember to explicitly state your model and define all of the terms for any ANOVA that you might conduct.
- d. Provide estimates of heritability on a progeny mean basis and a family mean basis using the Method of Moments.
- e. Provide estimates of heritability on a progeny mean basis and a family mean basis using the REML.