Purpose:

Students will learn how to estimate epistatic effects based on quantitative genetic models concepts.

Goal:

Assess ability to estimate genotypic values, population averages and calculate breeding values and dominance deviations for single, pairs and multiple loci when physiological epistasis is part of the genetic architecture.

ALA: Estimate Epistasis using Quantitative Genetic Models.

Population 1: Consider the RILs in QG_Mod5_ALA5.2 ds.xlsx. Simulate coded genotypic values of 15 for TT, 10 for CC, and 15 for the heterozygote at locus M1. Simulate GV's of 20 for AA, 30 for GG, and 27.5 for AG at locus M2. Simulate GV's of 25 for AA, 15 for GG, and 25 for AG at locus M3, except when CC exists at M1 and AA or AG exists at M3. CC will suppress the positive values of A_ at M3. So that when CC exists at M1, all phenotypes of the A_ genotypes will be the same as the GG genotype at M3.

Population 2: Imagine that we now allow this population to random mate for 10 generations. The phenotypic values will be governed by the same expression rules as in Population 1. The differences between population 1 and 2 will be due to different frequencies of the genotypes.

1. What are the population means for each population?
2. What will be the average effect the alleles at each of the loci in each population?
3. What is the average effect of allele substitutions at each of the loci in each population?
4. What are the breeding values of the 27 genotypes in each population?