

QUANTITATIVE GENETICS

Purpose:

Provide students with practice in calculating genotypic values, population averages, Breeding Values, and Dominance Deviations for single, pairs and three loci.

Goal:

Determine genotypic values, population averages, Breeding Values, and Dominance Deviations for single, pairs and three loci.

ALA: Estimate breeding values using quantitative genetic models

Consider the population consisting of RILs in the file named "QG_Mod5_ALA5.2_ds.xlsx" Imagine that this population random mates for 10 generations. For the same three loci obtain a sample of 400 individuals. Create a new worksheet (name the worksheet Individuals). Create a column labeled individual and fill it with individuals i1 to i400. Remember the frequency of the alleles will not change but the frequency of the genotypes will change. We expect each marker locus to segregate $p^2:2pq:q^2$. Create these genotypes using a random number generator (RAND), for all individuals. Simulate coded genotypic values of 5 for TT, -5 for CC, and $d=0$ at locus M1, -5 for AA, 5 for GG, and $d=2.5$ at locus M2, and 5 for AA, -5 for GG, and $d=-5$ at locus M3.

1. What will be the average effect of each of the alleles at each of the loci in the random mated population?
2. What is the average effect of an allele substitution at each of the loci in the random mated population?
3. What are the breeding values of the expected genotypes at each of the loci in the random mated population? Hint: There are a total of 27 possible genotypes in this population and each has a unique breeding value.