

ALA Genotypic Values and Population Mean for a Single LocusPurpose:

Provide practice in estimating genotypic values and population average for a single locus.

Goal:

Demonstrate steps to calculate the population average as a function of allele frequencies.

ALA: How to calculate estimates of GV and population average.

A maize field is harvested, and 10,000 kernels were evaluated for carotene with a NIR spectrophotometer. The results are reported on a scale of 25 to 35, where 35 represents most carotene (yellow kernels) and 25 represents no carotene (white kernels). Associated with the carotene scores is A SNP locus where a score of 35 is associated with GG, a score of 25 if it is AA, and a score of 32.5 if it is GA. Code the genotypic values and population mean.

Solution:

Hints: Create a table similar to Table 2 in Chapter 5 as a guide. Here we denote alleles as G and A

	Genotype			
	GG	GA	AA	Total
Number	1257	4576	4167	1000
Phenotypic Value	35	32.5	25	
Coded GV	5	2.5	-5	
Freq. X Coded GV	0.6285	1.1440	-2.0835	-0.3110

Determine the allele frequencies

$$f(G) = p = 0.1257 + (0.4576)/2 = 0.3545$$

$$f(A) = 1 - p = 0.6455$$

Next, determine the mid-homozygous value

$$= (35 + 25)/2 = 30$$

The coded genotypic values are deviations from 30 (5, 2.5, -5).

Next determine the population mean

$$\bar{Y} = mh + a(p - q) + 2pqd$$

QG

Genotypic Values and Population Mean

$$\bar{Y} = 30 + (0.1257 \times 5) + (0.4576 \times 2.5) + (0.4167 \times (-5)) = 29.69$$

when $0 < d < a$ (or $-a$) there is partial dominance

$d = 2.5$. Thus, the locus Y for kernel colour exhibits partial dominance.