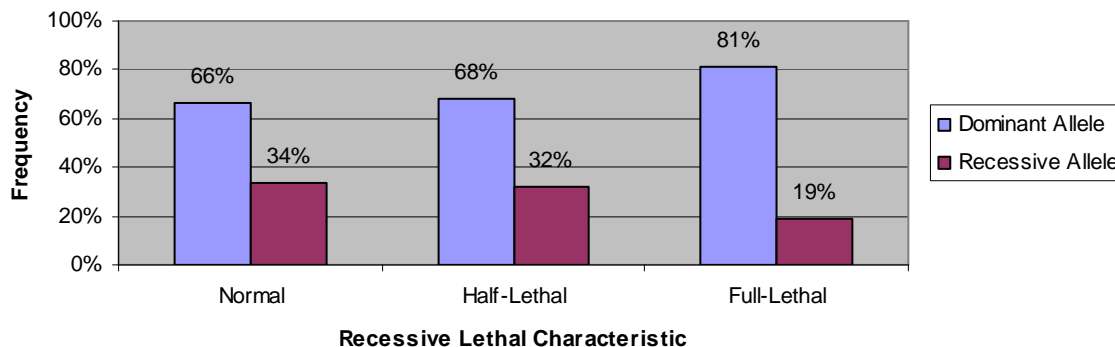


## Observing Gene Frequency Behaviors

**Summary:** My group and I tested whether allele frequencies remain relatively constant from one generation to the next by random mating within a small population. We did this by configuring a system to produce random pairings of a single set of dominant and recessive alleles across three successive generations, making appropriate adjustments to the resulting allele totals between generations based on observed results. For each simulation, our data shows that frequencies do not remain constant and always favored the dominant allele—expectedly so in situations where the recessive allele has a lethal attribute. Our results are supported by the knowledge that estimations of population size can be made from the variance in allele counts (*Waples, 1989*). It is also known that allele frequencies are easily calculated from sample proportions from pedigree analysis (*Boehnke, 1991*).

**Methods & Results:** To obtain our data, my group and I used a simplistic system of red and white colored beans for the D and d alleles, respectively. Fifty beans of each color were put into a brown paper bag and random pairs were pulled out and tallied on a sheet of paper enough times to simulate the allele types of fifty offspring. Frequency values were then calculated based on these readings and adjustments to the bean totals were made to properly simulate another fifty offspring for the next generation. Expected genotype frequencies were also calculated using the Hardy-Weinberg Principle equation ( $p^2 + 2pq + q^2 = 1$ ) and then compared to the observed values.

These procedures were followed for three separate simulations, each of which contained three successive generations. For the first, both homozygous DD and dd were considered to be normal attributes, with neither granting the offspring an undesirable and noncompetitive attribute. However, in the second simulation homozygous dd resulted in death before reproduction 50% of the time, while for the third simulation it always resulted in death before reproduction (100% lethal). After three complete generational cycles for each simulation, the following table of data was produced:



In each case, the dominant allele D was most pronounced. This was expected only in the circumstances where the recessive allele d was determined to produce a lethal attribute. In the first simulation, when this was not a factor, the allele frequency shifted between each generation, initially towards favoring the recessive allele and finally towards the dominant allele. We expect that subsequent generations would result in similar fluctuations, from one back to the other.

Based on these results, allele frequencies can only remain constant when neither one produces a noncompetitive attribute.

### References:

Waples, R.S., 1989. A Generalized Approach for Estimating Effective Population Size from Temporal Changes in Allele Frequency, *Genetics*, 121(2), pp. 379-391.

Boehnke, M., 1991. Allele Frequency Estimation from Data on Relatives, *The American Journal of Human Genetics*, 48(1), pp. 22-25.