Introduction
There is genetic variation for the quantitative trait of ovariole number in *Drosophila melanogaster*. An ovariole is a series of storage rooms of a fly ovary where the eggs of the fly mature. The mutation rate for ovariole number is under great selection because of its association with fecundity.

Genetic variation in a population is divided into several sources of variation (i.e., additive variance, dominance variance, environmental variance and epistatic variance). We examined two components of genetic variance in new mutations spontaneously accumulated for ovariole number: the additive variance, which is the mean effects of substituting one allele for another; and the dominance variance, which is the difference at a single locus attributed to the relationship of the specific alleles at that locus. Using this information, we can calculate the ratio of additivity to dominance for new mutations, and use this information to understand how genetic variation is maintained for the trait.

Methods
- Two isogenic lines of *D. melanogaster* from Winters, California that accumulated spontaneous mutations for approximately 30 generations were used (Higgins et al. 2009).
- Flies were reared in incubators at 25°C, at a density of ten males and ten females.
- Mutations Accumulation (MA) line males were bred with collected virgin females from a reference wild type line (i.e., making MA either homozygous or heterozygous with the isogenic line Diallel2) to establish the level of dominance of the new mutations for ovariole number according to the midparent model (Shaw et al. 2006).
- Progenies were frozen then dissected under the microscope, using a toothpick-mounted minuten needle. Both ovaries were dissected for ovarioles which were counted in a droplet of Ringer’s solution after being stained in a solution of potassium dichromate.

Results & Conclusion
There is strong overdominance characteristic for the new spontaneous mutations when analyzing the means of both homozygotes and heterozygotes (Fig.1).

The genetic variance components are analyzed through a given scale $k = d/a$, such that values of $k=-1, 0, 1$ imply recessive, additive, and dominant, respectively (Falconer and Mackay 1996). Through the histogram of $k$, one can also see that accumulated mutations both increase or decrease the count of ovariole number (Fig. 2). Additivity, where $k=0$, is not always seen but informs that $d=0$, which make the midparent value equals the heterozygous value.

Mutations of fitness-related traits are usually deleterious and have directional dominance. Intense selection can eliminate the genetic variation by altering allele frequencies within the population (Wayne et al. 1998). In this study, overdominance is potentially the mechanism behind the variation in ovariole number. One can tell that the genetic variation seen for the quantitative trait of ovariole number is due to greater dominance variances relative to additive variances.

![Figure 1. Average of ovariole number for both homozygotes parents (MA homozygotes and Diallel2) and heterozygotes progeny. Ovariole means are arranged in ascending order and Y error bars show standard error for each different line. The heterozygote values to the left of the diallel2 bar show overdominance. The heterozygote values to the right of the diallel2 bar show underdominance.](image)

![Figure 2. Histogram of K: Distribution of dominance variance. Mutational effects values of k for the lines analyzed is at the maximum at 1, where k=1 means complete dominance. A non-symmetrical distribution around k=0 shows that dominance is directional.](image)

Literature Cited