The influence of autosomal genetic background on the fitness of a mutant sex-linked gene and linked loci in *Drosophila melanogaster*.

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"There is an abundance of evidence that the effects of a mutation depend on its genetic background" (Fay, 2011). This fluctuation in gene expression is due to epigenetic interactions of the mutations with other genes. Epistasis has been observed for lethal and visible mutations in *D. melanogaster*, where mutations acting together have a larger effect on fitness than is expected based on multiplicative interactions (Kitagawa, 1967; Mukai, 1969; Temin *et al.*, 1969; Seager *et al.*, 1982; Whitlock and Bourguet, 2000). Similar epistatic interactions occur for some human diseases (Zhang and Liu, 2007). Yet, others have not observed negative synergistic epistasis (for reviews of this topic see Wolf *et al.*, 2000; Sanjuan and Elena, 2006; Azevedo *et al.*, 2006; Arjan *et al.*, 2007). Hence, the presence and role of negative synergistic epistasis in evolution, where the genetic background can influence fitness, is still unclear.

In this study we will measure the influence of the autosomal genetic background on the fitness of the w^{1118} mutation, and linked genes on the X, in males in comparison to C(1)DX, *y f* / Y females, which have two X chromosomes attached to a single centromere, yellow body color (*y* mutation), and small bristles (*f* mutation) (Lindsley and Zimm, 1992). It is our hypothesis that the genes of the second, third, and fourth chromosomes (the autosomes) from different wild-type stocks will alter the recovery of males with the w^{1118} mutation and other sex-linked genes.

We first replaced the second, third, and fourth chromosomes of the C(1)DX, *y f* stock with autosomes from one of four different wild-type stocks [CS, OBL1&2, Per^{+}(2000) and Per^{+}(2013)] by eight generations of backcrossing C(1)DX, *y f* females with each of the wild-type stocks as follows (using the CS stock as an example with the CS autosomes marked as $+^{c}$ and the C(1)DX, *y f* autosomes marked as +). By the G3 cross, some autosomes in the C(1)DX, *y f* females will be homozygous for the CS autosomes, and by the G8 (eighth generation) females should have all CS autosomes. Also note that the following crosses give matroclinous female offspring that receive their compound-X chromosome from their mothers.

G1 C(1)DX, *y f* / Y ; +/+; +/+; +/+ virgin females × CS / Y ; $+^{c}/+^{c}$; $+^{c}/+^{c}$; $+^{c}/+^{c}$ males

↓

G2 C(1)DX, *y f* / Y ; $+/+^{c}$; $+/+^{c}$; $+/+^{c}$ virgin females × CS / Y ; $+^{c}/+^{c}$; $+^{c}/+^{c}$; $+^{c}/+^{c}$ males

↓

G3 C(1)DX, *y f* / Y;$+^{c}/+^{c}$; $+/+^{c}$; $+/+^{c}$ virgin females × CS / Y ; $+^{c}/+^{c}$; $+^{c}/+^{c}$; $+^{c}/+^{c}$ males

↓

G4 C(1)DX, *y f* / Y ; $+^{c}/+^{c}$; $+^{c}/+^{c}$; $+/+^{c}$ virgin females × CS / Y ; $+^{c}/+^{c}$; $+^{c}/+^{c}$; $+^{c}/+^{c}$ males

↓

↓

G8 C(1)DX, *y f* / Y ; $+^{c}/+^{c}$; $+^{c}/+^{c}$; $+^{c}/+^{c}$ virgin females

Then single G8 C(1)DX, *y f* / Y ; $+^{c}/+^{c}$; $+^{c}/+^{c}$; $+^{c}/+^{c}$ virgin females were mated to single w^{1118} males and progeny scored for w^{1118} males and C(1)DX, *y f* females. The same crosses were performed with the other three wild-type stocks and the ratio of males to total progeny was compared among the four autosomal genetic

backgrounds with the results from the stock control. We predict that there will be significant differences in male to total progeny ratios for the five backgrounds.

Results

A total of 121 crosses were set up, including 24 w^{1118} control crosses (with the w^{1118} autosomal background) (mean = 0.51; variance = 0.17), 25 crosses with the CS autosomal background (mean = 0.59; variance = 0.13), 21 crosses with the OBL1&2 background (mean = 0.63; variance = 0.24), 31 crosses with the Per+(2000) background (mean = 0.58; variance = 0.13), and 20 crosses with the Per+(2013) background (mean = 0.60; variance = 0.13). The results of these crosses are shown in Figure 1. All four of the crosses with new autosomal genetic backgrounds had significantly higher male/total progeny means compared to the w^{1118} control (P values were 0.0005 for the CS autosomal background, 0.0004 for OBL1&2, 0.002 for Per+(2000), and 0.0007 for Per+(2013).

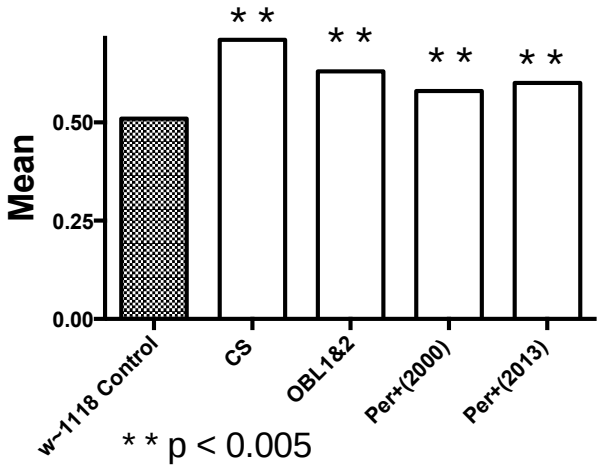

Figure 1. Comparison of the means of male progeny to total progeny in lines with different autosomal genetic backgrounds.

Hence, the effect of the w^{1118} mutant, and its X-linked genes, on viability (male progeny to total progeny) does depend on epistasis with genes on the autosomal genetic background.

A class discussion of the results of this study might include the role of single genes *vs*. multiple-genes in the evolution of adaptive traits. An example of an adaptive trait caused by a single gene is coat color in deer mice (Linnen *et al.*, 2009), whereas an example of a trait associated with selection caused by multiple genes is corn kernel oil content (Laurie *et al.*, 2004).

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Establishment of double mutant strains of *Drosophila melanogaster* (Diptera, Drosophilidae) for teaching purposes.

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