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Heritability for bristle number in *Drosophila melanogaster.*

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For a quantitative trait to respond to human (experimental) selection or to evolve by natural selection it must be at least partially under genetic control, *i.e.*, have heritability. Heritability is defined either as the fraction of the total variation in a trait that is due to variation in genes, or the proportion of phenotypic variance that parents can pass to offspring. Environmental factors can also influence quantitative traits (see a discussion of this topic in Falconer and Mackay, 1996; Frankham, Ballou, and Briscoe, 2002).

Heritability in the narrow sense (h^2) is the fraction of the total variation in a trait that is due to the additive effects of genes. There can also be dominant effects and interactions between genes and the environment. Narrow sense heritability is the best measure of whether a trait will evolve or respond to selection (Allendorf and Luikart, 2007). How can one estimate h^2? One way is to examine the slope of the regression line of trait values between parents and their offspring. For example, in Figure 1 an estimation of h^2 of 0.69 is determined from the slope of the regression between the height of students and their mid-parent values (Woodruff, unpublished). Comparisons where the regression slope is zero would have a h^2 of zero, whereas a slope of one would have a h^2 of one.

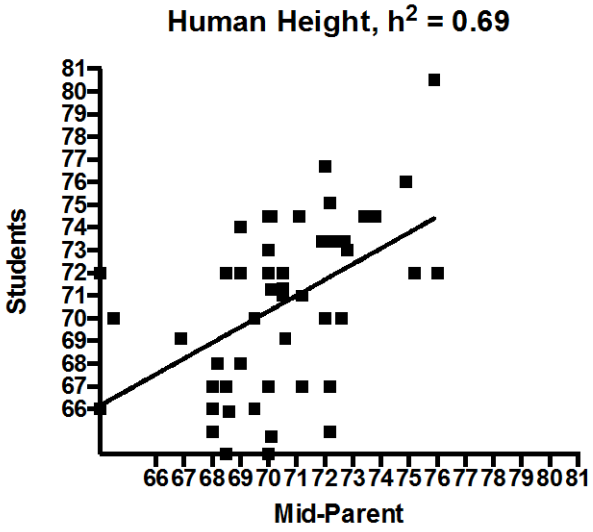

Figure 1. Student height heritability estimate.

In this study, we measured h^2 for sternopleural bristle numbers in *D. melanogaster* by the slope of the regression line of midparent bristle number and the offspring bristle number. Sternopleural bristles are shown in Figure 2 (Woodruff and Thompson, 2005). Estimations of h^2 for sternopleural bristle number in *Drosophila*, which are based on selection experiments and parent offspring regression analysis, ranged from 0.01 to 0.75 (Roff and Mousseau, 1987; Falconer and Mackay, 1996; Woodruff and Thompson, 2005; van Heerwaarden *et al*., 2008).

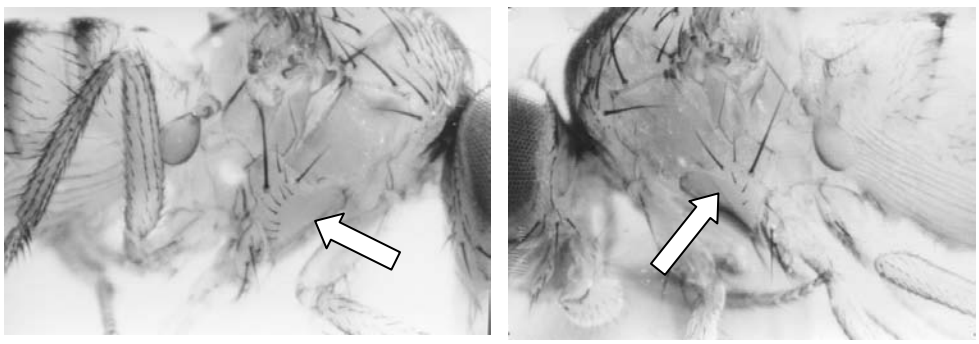

Figure 2. Sternopleural "heart-shaped" section of two *Drosophila* marked with white arrows. Sternopleural bristle numbers are: left, 11; right, 6 (Woodruff and Thompson, 2005).

To measure h^2 for bristle numbers we performed the following crosses (OBL1&2 is a wild-type stock that was established from natural population flies in 2010 (Carr *et al.*, 2010); bristles were counted for both sides; and a total of 55 crosses were scored for sternopleural bristle numbers).

one OBL1&2 virgin female × one OBL1&2 male

↓

one progeny female and one progeny male

Narrow sense heritability was determined by the slope of regression line for female and male progeny *vs* the mid-parent values (Figures 3, 4), using the Prism program.

The mean (± standard error) number of bristles for female (18.22 ± 0.22) and male (17.45 ± 0.23) progeny are significantly different (P = 0.02; Figure 5).

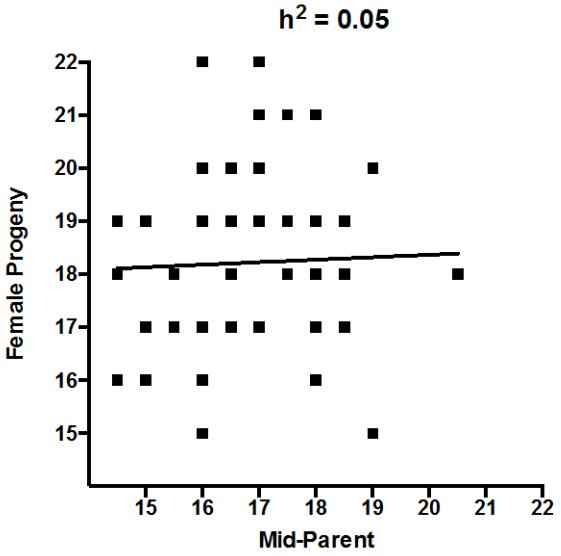

Figure 3. Estimation of narrow sense heritability (h^2) for sternopleural bristle numbers using female progeny.

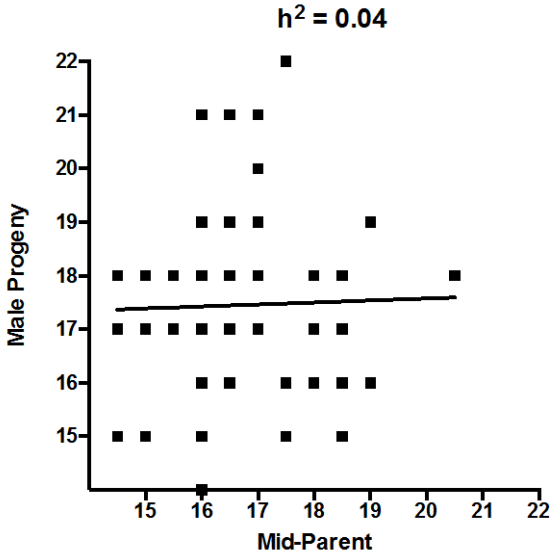

Figure 4. Estimation of narrow sense heritability (h^2) for sternopleural bristle numbers using male progeny.

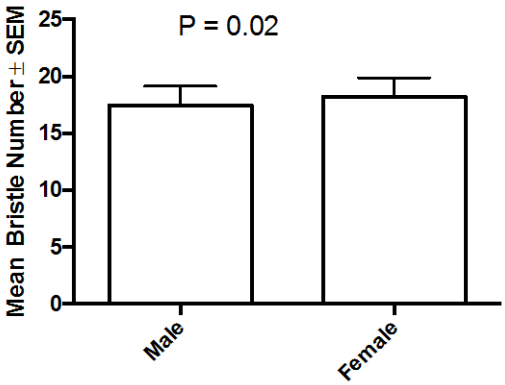

Figure 5. Mean (± standard error) of the sternopleural bristle numbers in males and females (P = 0.02, paired t test).

The observed h^2 values of 0.05 using female progeny and 0.04 using male progeny for sternopleural bristle numbers are at the low end of those reported in the literature (Falconer and Mackay, 1996; van Heerwaarden *et al*., 2008). Woodruff and Thompson (2005), however, reported h^2 values of 0.01 for females and males based on a selection response experiment in lines that were inbred by brother-sister matings for 41 generations and possessed low levels of genetic variation, whereas flies with greater levels of genetic variation had h^2 values of 0.11 for males and 0.15 for female. Since the OBL1&2 wild-type stock used in this study had been maintained in the laboratory for six years before this study (Carr *et al*., 2014), it may contain a reduced amount of genetic variation due to partial inbreeding, resulting in the observed low h^2 values.

A class discussion of the results of this study could include: 1) Ask students to estimate the number of quantitative trait genes controlling bristle number in *D. melanogaster*. It is about eight (Gurganus *et al*., 1999). 2) Ask students to estimate the narrow sense heritability for height in humans by determining the slope of the regression line for their heights *vs*. their mid-parent heights. The height of female parents and students should be multiplied by 1.08, because of the difference in height of men and women.

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Description of a double mutant strain of *Drosophila melanogaster* useful for genetic laboratory courses.

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Many years ago, individuals showing drastically reduced eyes arose in our laboratory *e* (*ebony*) strain (Bridges and Morgan, 1923). We selected those flies presenting both traits and constituted a new double mutant strain *e su* (*e*, ebony; *su*, '*sense ulls*', eyes drastically reduced). Both mutations were linked and located in the chromosome III. We used this strain in linkage analyses with our undergraduate students. We then proceeded to assess which described gene was allelic to our *su* mutation. With a recombination experiment we deduced that *su* was located at 36.7 m.u. from the *e* gene. Consulting the genetic map of chromosome III we hypothesized that *su* could be the *eyg* (*eyegone*) gene (Ives 1940), whose phenotype is also eye reduction. We carried out a pseudodominance study using a deletion that covered the *eyg* region (ED2015, http://flybase.org/), and we observed that the individuals not showing the dominant marker (*Sb*, *Stubble*, Dobzhansky 1930) of the balancer chromosome (TM6C, Chyb and Gompel 2013) presented drastically reduced eyes. Finally, we wanted to confirm that *su* was actually *eyg* carrying out a complementation test crossing both strains. We obtained *eyg* strain from a stock center and the result of complementation test confirmed that *su* was a mutation of *eyg* gene.

This double mutant strain *e su* can be used for different genetic laboratory courses and we can send it upon request.

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